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Northeast Section	July 8–12, 2013	Indianapolis, IN
National Annual Meeting (with ADSA)	July 8–12, 2013	Indianapolis, IN
Southern Section (with SAAS)	February 1–4, 2014	Dallas, TX
Midwestern Section (with ADSA)	March 16–18, 2014	Des Moines, IA

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SYMPOSIA AND ORAL SESSIONS

Teaching/Undergraduate and Graduate Education: Teaching and Learning in the Animal Sciences: New Grounds for the 21st Century

1 How to incorporate high-impact practices in the animal sciences curriculum. N. Cockett*[1] and D. Buchanan[2], [1]*Utah State University, Logan,* [2]*North Dakota State University, Fargo.*

The animal sciences curriculum has remained fairly static in relation to changes in the student population, agricultural practice, scientific advances and the place of agriculture in the greater culture. Changes in the curriculum frequently arise by developing new classes or increasing the number of credits for existing classes while the method of teaching frequently remains as standard lecture or lab format. We propose that teaching must rapidly evolve to include high impact practices that are tailored to the demography of the students and the most effective means of conveying the various types of information that will be important for careers of the future. Practices such as first year seminars, learning communities, undergraduate research, global learning, service or community based learning, industry internships and capstone projects need to be ubiquitous in the curriculum instead of operating as isolated pieces. The presentation will include a review of research about the advantages associated with such practices, some examples of high impact practices already being used in animal science and a challenge to "deconstruct" the curriculum and attempt to rebuild it with content that will be relevant, intellectually stimulating and preparatory for careers that our student will likely have. The curriculum should also focus on the most appropriate practices for each component within the Animal Sciences degree.

Key Words: curriculum, undergraduate

2 Courses and high-impact practices to equip students with knowledge, skills, and experiences for the 21st century: Views of animal sciences faculty. M. A. Wattiaux* and P. Crump, *University of Wisconsin-Madison, Madison.*

Our objective was to identify types of courses and high impact practices (HIPs) that animal sciences faculty associated with important knowledge and skills that students should gain during a 4-yr degree program. Data were from a survey of 49 faculty from 33 institutions who attended a June 2012 national conference. Using a scale of 1 (not at all) to 5 (a great deal), participants scored the importance of 17 items describing knowledge and skills (KS) and 16 items describing courses and experiences (CE), seven of which were HIPs. The Kruskal-Wallis test was used to detect differences among professorial ranks and Spearman correlation was used to explore relationships among survey items. The top 8 KS items (scores ranging from 4.81 to 4.45) were in decreasing rank-order: Gain oral and written communication skills (KS1); Demonstrate an ability to apply, analyze, and evaluate (KS2); Gain interpersonal communication skills (KS3); Problem-solving skills as an individual (KS4); Problem-solving skills in team settings (KS5); In depth knowledge of disciplines in the major (KS6); Leadership development skills (KS7); Gain life-long learners' skills (KS8). The top 8 CE items (scores ranging from 4.78 to 4.20) were in decreasing rank-order: Practicum-based courses or courses with hands-on labs (CE1); Courses that include real-world, project-based activities (CE2); In-country internships (CE3); Capstone courses or projects (CE4); Courses that include collaborative assignments and projects (CE5); Undergraduate research experience (CE6); Using the Internet as a learning tool (CE7); Writing intensive courses (CE8). Full professors scored items KS1, KS2, and CE6 (all $P < 0.02$), and item KS4 ($P < 0.06$) lower compared with assistant or associate professors. Items CE2 and CE5 were correlated ($r > 0.4$ and all $P < 0.01$) with 10 and 12 of the 17 KS items, respectively, whereas PowerPoint lecture-based courses (CE15) were not correlated with any KS items. Among the HIPs, items CE3, CE4, CE6 and CE8 were correlated with 7, 10, 2, and 1 KS items, respectively, illustrating that not all HIPs were perceived as of equal relevance.

Key Words: undergraduate curriculum

3 How to incorporate active learning practices in animal sciences classrooms. D. K. Aaron* and C. A. Tilghman, *University of Kentucky, Lexington.*

Most educators agree students retain more knowledge if they are engaged in active learning. Dale's Cone of Experience (Edgar Dale, Audio-Visual Methods in Teaching, 1969) suggests students remember 70% of what they say and 90% of what they both say and do. Conversely, they remember only 20% of what they hear and 30% of what they see. The former is active involvement, the latter is passive. Traditional classroom lecture achieves active involvement by teachers but often restricts students to passive roles. While this may be comfortable for both, it does not maximize learning. Furthermore, changing demographics of students enrolled in animal sciences courses (more students from urban areas with little to no agricultural experience, greater diversity and an increase in nontraditional students) requires both lecture-based teaching and hands-on experiences. This presentation will discuss ways of engaging students in animal sciences courses, from classrooms to labs. It will begin with class attendance. This may seem obvious, but the first step in achieving active learning is making sure students show up to class. It will progress to note taking, which as old-fashioned as it may seem, is an integral part of the learning process because it keeps students engaged. Ways of asking questions and encouraging students to ask questions, thereby turning lectures into conversations, will also be discussed. Finally, some ideas for engaging students through real or simulated experiences and hands-on activities will be presented. Examples of experiential learning opportunities will include those used in an introductory animal sciences course (feeding trials with chicks and lambs, livestock handling and management situations, a livestock judging "contest") and an upper-level course in animal genetics (problem-solving lab exercises, an interactive genetic simulation program). These student-centered, experiential learning activities pave the way for retained knowledge in the subject matter and encourage students to look beyond the planned curriculum to explore continuous learning.

Key Words: teaching, learning, student engagement

Triennial Growth Symposium: Vitamin D—Establishing the Basics to Dispel the Hype

4 Vitamin D: Bones and beyond. H. Deluca* and L. Plum, *Department of Biochemistry, University of Wisconsin-Madison, Madison.*

We now understand that vitamin D is the starting material of an endocrine system primarily devoted to the regulation of serum calcium, serum phosphorus and bone. Vitamin D is normally produced in skin by a photochemical reaction of 7-dehydrocholesterol. It is subsequently converted in the liver to a circulating form (25-hydroxyvitamin D_3) that is then converted by the kidney to a hormonal form, 1a,25-dihydroxyvitamin D_3. The vitamin D hormone acts through a single nuclear receptor in carrying out these functions. The presence of this receptor in a variety of tissues signals functions beyond bone, calcium and phosphorus. This presentation will provide the basic biology of the endocrine system, the current concepts of the molecular mechanisms by which it functions, and a look at the proven and putative functions of the hormone in the various target tissues.

Key Words: vitamin D, 1,25-dihydroxyvitamin D

5 Basics for establishment of 2011 vitamin D guidelines in humans. C. M. Weaver*, *Purdue University, Department of Foods and Nutrition, West Lafayette, IN.*

The 2011 vitamin D recommendations set by the Food and Nutrition Board of the Institute of Medicine was the first time that estimated average requirements (EAR) and recommended dietary intakes (RDA) were given for vitamin D. Previous versions (i.e., 1997 and earlier) used adequate intakes, which implied less certainty of values. Vitamin D is difficult to set requirements for because it behaves more like a hormone than a nutrient and because diet is not the only source of vitamin D. In fact, more vitamin D comes from cutaneous production than from diet for most people. Thus, one cannot use the common factorial approach of estimating daily losses adjusted by absorption and needs during growth to set intake recommendations. The basis for the 2011 vitamin D recommendations was for bone health. Systematic reviews showed vitamin D status levels associated with calcium absorption, bone mineral density, and risk of osteomalacia or rickets. An integrated model was used to set vitamin D status, measured by serum 25(OH)D levels, at 40 nmol/L for the EAR and 50 nmol/L for the RDA. Vitamin D intakes to achieve these levels became the recommended intakes based on a nonlinear model of the relationship of vitamin D intake and achieved serum 25(OH)D levels. The panel assumed all vitamin D intakes should come from diet in their recommendations because many groups are not exposed to UVB light or are elderly or dark skinned which limits cutaneous production. However, intakes are well below recommended levels. Clinical guidelines for patients at risk for vitamin D deficiency were also established in 2011 by the Endocrine Society, which gave physicians more latitude for vitamin D recommendations.

Key Words: vitamin D, humans, dietary reference intakes

6 Novel roles for FGF23 signaling in vitamin D and phosphate homeostasis. B. Lanske*, *Harvard School of Dental Medicine, Boston, MA.*

FGF23 is primarily produced in osteoblasts and osteocytes where it is secreted into the blood stream to act hormonally on specific target tissues. In the kidney, it has been shown to inhibit phosphate reabsorption and vitamin D synthesis by down-regulating the renal sodium phosphate co-transporters NaPi2a and NaPi2c and suppressing the expression of 1a(OH)ase in the proximal tubules. Mutations in the FGF23 gene itself or in genes regulating its expression and activation have been linked to disease processes including autosomal dominant hypophosphatemic rickets (ADHR), oncogenic osteomalacia (OOM) and X-linked hypophosphatemia (XLH), autosomal recessive hypophosphatemia with hyperphosphaturia (ARHR), confirming the role of FGF23 in regulating phosphate and vitamin D metabolism. A new role for FGF23 was discovered when Klotho, a previously described aging-related gene, was found to be a co-factor for FGF23 signaling. Apart from the kidney Klotho expression has also been detected in the parathyroid gland. More recent experiments have established a role for FGF23 in suppressing PTH transcription and secretion. These findings indicate that FGF23 can indirectly affect calcium homeostasis. Furthermore, the high levels of FGF23 found in patients with chronic kidney failure have been associated with increased risk of mortality and morbidity. FGF-23 has also been found to affect bone mineralization independent of its role in systemic phosphate homeostasis, adding significant new data regarding the physiological properties of FGF-23. Although the underlying mechanisms are still unclear, FGF23 appears to regulate the expression of various matrix mineralization inhibitors such as osteopontin, matrix Gla protein and dentin matrix protein. The novel findings that Klotho might also be expressed in bone cells strengthen the observation that FGF23 has paracrine action on bone. In summary, changes in FGF23 activity and the resulting effects on serum phosphate and calcium homeostasis have severe consequences on bone mineralization and ultimately on survival in mice and men.

Key Words: osteoblast, Klotho, FGF23

7 The rise and fall of clinical cases of vitamin D deficiency in commercial swine operations. D. M. Madson*, *Department of Veterinary Diagnostic and Production Animal Medicine, Iowa State University, Ames.*

Hypovitaminosis D is not a new disease; however, in recent years there has been a resurgence of clinical disease within the US swine population. Clinical signs of re-emergence of this disease were first recognized in early 2010 and included lameness, posterior paresis, broken bones, muscle fasciculation/tremors, and sudden death. Morbidity of 50% and mortality in the range of 20% was common. The initial cases of hypovitaminosis D were connected to a particular feed manufacturer supplying a premix devoid of vitamin D which ultimately led to a national recall within five months of the first cases. This recall slowed the number of diagnostic cases and the attention associated with it motivated swine veterinarians and researchers to further investigate this issue. From 2010-present, the Iowa State University Veterinary Diagnostic Laboratory (ISU VDL) diagnosed over 100 cases. Case investigations typically involved determination of serum calcium, phosphorus, and vitamin D levels, assessment of bone quality, and microscopic evaluation of bones and joints. In many of these investigations the ISU VDL worked in collaboration with Heartland Labs in Ames, Iowa. These investigations generally led to the realization that large populations of pigs across the U.S. were either clinically or subclinically deficient in vitamin D. Clinical and diagnostic evidence continues to indicate that subclinical hypovitaminosis D as measured by serum vitamin D status is still occur-

ring. Four companies have introduced oral products for supplementation of pigs, particular aimed at the weaned pig. Supplementation along with increased monitoring of bulk feed vitamin D samples, which have been shown to degrade with time, have reduced the incidence within the swine population. Speculations about alternative feed ingredients, calcium-phosphorus ratios, and even phytase usage have been made as a potential contributor to this recent rise in hypovitaminosis D in pigs. However, the primal underlying cause for these continued cases has not been elucidated at this time.

Key Words: vitamin D, deficiency, lameness

8 Basis for establishment of the 2012 vitamin D requirements in swine. C. Lauridsen*, *Aarhus University, Department of Animal Science, Tjele, Denmark.*

In swine nutrition, little is known about vitamin requirements for reproductive processes and bone health, especially vitamin D. Supplemental vitamin D is usually added to animal feed as cholecalciferol (vitamin D_3), which is transported to the liver and hydroxylated to 25(OH)D_3, which is released into the circulation. Recently, 25(OH)D_3 has become commercially available (Hy-D, DSM Nutritional Products). A dose-response trial with 4 doses of both vitamin D_3 and 25(OH)D_3 was performed. In Exp.1, 160 gilts from first estrus until d 28 of gestation were fed diets containing 4 concentrations of 1 of 2 vitamin D sources [200, 800, 1,400, or 2,000 IU·kg^{-1} from cholecalciferol or corresponding levels of 5, 20, 35 or 50 μg·kg^{-1} from 25(OH)D_3 (Hy-D)]. Concurrently in Exp. 2, the same 8 dietary treatments were fed to 160 multiparous sows from the first day of mating until weaning. In Exp. 1, gilts were killed at d 28 of gestation, the reproductive organs were obtained and number of ovulations was assessed by counting corpora lutea and implanted embryos. In addition, blood samples were obtained at slaughter for plasma separation, and metacarpal bones dissected from the left foot. In Exp. 2, performance data and blood samples were obtained from the sows and the piglets throughout the experiment, and their vitamin D status was assessed by 25(OH)D_3 plasma concentrations. Although no major differences among dietary vitamin D treatments were detected in performance, reproduction and bone status markers of gilts and sows, the observed lower number of still born piglets and the higher vitamin D concentrations may indicate a dietary level around 1,400 IU vitamin D to be recommendable for reproducing swine. The potency of the dietary Hy-D relative to vitamin D_3 depended on the level tested but above 200 IU, Hy-D was more bioavailable than vitamin D_3, and could as such been considered as an equivalent or even more advantageous source of vitamin D.

Key Words: requirements, 25(OH)D_3, reproduction

9 Analytical methods to measure vitamin D in blood, feed and tissues: Application to diagnosis of vitamin D deficiency and excess in livestock. R. L. Horst*, *Heartland Assays LLC, Ames, IA.*

Contemporary views categorize vitamin D_3 (cholecalciferol) not as a vitamin but as a pro-steroid hormone. The significance of vitamin D_3 as a pro-steroid hormone became clear in 1967 when Deluca's lab isolated a new metabolite of vitamin D_3, 25-hydroxyvitamin D_3 (25OHD) which acted more rapidly than vitamin D_3 and was established as the precursor to the active form of vitamin D_3 namely 1,25-dihrdroxyvitamin D_3 [1,25(OH)$_2$$D_3$]. A further complication for analysis is the presence of vitamin D_2. This form and its precursor, ergosterol, are present in plants and is metabolized to vitamin D_3, thus contributing to the overall vitamin D status in mammals. In addition to skeletal benefits, vitamin D has significant roles in extraskeletal health. Too little or too much vitamin D can lead to poor performance and death. Access to reliable analytical methods is, therefore, imperative for monitoring vitamin D and/or vitamin D metabolite concentrations in a variety of matrices. 25-Hydroxyvitamin D, the major circulating form is widely accepted as the best in vivo indicator of vitamin D status. Many methods are available but work only with human sera and do not work properly with sera from livestock. For example, methods used widely in human medicine rely on dissociative methods for detaching 25OHD from its binding protein (VDBP). These methods do not work properly with serum/plasma from livestock. Radioimmunoassays involving protein denaturation to release 25OHD from VDBP work quite well and have been used extensively during the past few years to assist clinicians in uncovering widespread deficiencies of vitamin D in swine and other species. Tissue concentrations of vitamin D and to a lesser extent 25OHD can also be of some diagnostic value (particularly liver and kidney) but limited information is available associating tissue and diet concentrations. Feed analysis of vitamin D can be erratic and accuracy is dependent upon proper mixing and sampling techniques. Challenges in applying analytical procedures to measuring vitamin D will be discussed.

Key Words: serum 25OHD, radioimmunoassay, vitamin D binding protein

10 Novel roles for vitamin D in animal health and immunity. D. R. Barreda*, *University of Alberta, Department of Agricultural, Food and Nutritional Science, and Department of Biological Sciences, Edmonton, Canada.*

Recent years have seen an increased interest in the extra-skeletal roles of vitamin D_3. Pleiotropic effects on the immune system include those on monocyte, macrophage, neutrophil, B and T lymphocyte, and dendritic cell functions. The impacts to cellular immune mechanisms are relevant for host antimicrobial responses, inflammation, hematopoietic cell turnover and others. This presentation will discuss a recent study that examined the modulation of weanling pig cellular immunity in response to diet supplementation with 25-hydroxyvitamin D_3 [25(OH)D_3]. Analysis of functional traits showed that leukocyte cell numbers ($P < 0.05$) as well as proportions of individual granulocyte ($P < 0.01$) and lymphocyte subpopulations ($P < 0.05$) were significantly and differentially affected. There was also positive modulation of leukocyte survival across blood ($P < 0.01$) and bronchoalveolar ($P < 0.05$) compartments, highlighting the potential contributions to systemic and mucosal antimicrobial responses. This was consistent with a parallel upregulation in phagocytic functional responses in Hy-D supplemented pigs ($P < 0.05$). Importantly, challenges remain as we consider the mechanistic basis of these cellular changes. Recent approaches in cellular analysis provide novel alternatives for analysis, particularly in non-classical animal model systems where reagents such as leukocyte antibody-based markers are not as readily available.

Key Words: vitamin D, cellular immunity, animal health

11 The role of vitamin D in skeletal muscle development and growth. J. D. Starkey*, *Texas Tech University, Lubbock.*

The extra-skeletal functions of vitamin D have gained greater attention in recent years. Emerging evidence that vitamin D and its metabolites are indeed involved in the proper development and growth of skeletal muscle in both mammalian and avian species will be the primary focus of this presentation. Recent work conducted in swine suggests that oral administration of 25-hydroxycholecalciferol (25OHD_3) in place

of a majority of dietary vitamin D_3 improves both maternal and fetal vitamin D status as measured by circulating concentrations of $25OHD_3$. These improvements in vitamin D status resulted in enhancement of fetal skeletal muscle fiber number and alteration of fetal skeletal muscle satellite cell proliferation kinetics. These changes in fetal skeletal muscle developmental characteristics may result in improvements in the postnatal growth potential and ultimate red meat yield of these offspring. The cellular and molecular mechanisms by maternal supplementation and vitamin D status improvement augmented fetal development will require further effort. There is a growing body of commercial field research in which up to a 2% increase in breast meat yield has been observed when $25OHD_3$ is included in broiler chicken diets. As is common in the broiler industry, replacement of the greater part of dietary vitamin D_3 with $25OHD_3$ in caged-raised broilers resulted in a classic satellite cell-mediated muscle hypertrophy response in fast-twitch (pectoralis major) muscle. This conclusion is based on observation of increases in satellite cell density on d 14 and 21, nuclear density on d 28, and muscle fiber cross-sectional area at the conclusion of the study on d 49 in $25OHD_3$-fed birds. A mystery remains as to why a similar response was not observed in slow-twitch (biceps femoris) muscles also examined in the study. These findings shed light on the cellular mechanism behind the intriguing results obtained in field studies. Further investigation into the mechanisms by which vitamin D and its metabolites affect both pre- and postnatal development and growth of skeletal muscle is certainly warranted given the large number of questions that remain unanswered at this time.

Key Words: vitamin D, skeletal muscle, satellite cells

12 Practical applications of vitamin D supplements in swine diets. G. Weber*, *DSM Nutritional Products, Basel, Switzerland.*

Vitamin D_3 is an essential micronutrient, which regulates the absorption of calcium and phosphorus. This homeostatic function of vitamin D_3 is important to provide sufficient minerals for incorporation into the bone matrix and to avoid disorders of various origins. To become active, vitamin D_3 has to be metabolized through two subsequent hydroxylation steps, first to the 25-hydroxyvitamin D_3 (25-OH-D_3) in the liver and second to 1,25-dihydroxyvitamin D_3 (1,25-$(OH)_2$-D_3) in the kidney. The major form of vitamin D_3 in blood plasma of animals is 25-OH-D_3. If absorption of vitamin D_3 is hampered or the metabolic function of the liver is impaired by diseases or stress, the released 25-OH-D_3 may not suffice to secure adequate mineral supply. Feeding high-yielding farm animals with 25-OH-D_3 (Hy-D) could therefore optimize mineral homeostasis and improve productivity. Partial or full replacement of vitamin D_3 by Hy-D in swine feeds resulted in higher concentrations of 25-OH-D_3 in blood and in several tissues. In sows 25-OH-D_3 plasma levels are cyclic, being highest in early gestation and lowest at weaning. In a five-parity study, Hy-D supplementation secured that 25-OH-D_3 plasma concentrations never dropped below the threshold to vitamin D insufficiency. The elevated 25-OH-D_3 levels during lactation resulted also in an increased plasma concentration of the active form 1,25-$(OH)_2$-D_3. Higher 25-OH-D_3 levels in milk were measured as well, which improved the vitamin D_3 status of the suckling piglets. In a growth trial 50 mcg 25-OH-D_3/kg improved performance of growing pigs in comparison to a control group with 2000 IU vitamin D_3/kg. Bone strength and bone mineralization were better with Hy-D both in the post-weaning and in the growing-finishing period. Optimum leg confirmation is of particular importance for the selection of gilts for breeding. When supplementing Hy-D during the full growth cycle, the selection rate of gilts was markedly improved under various production systems. Furthermore, the productivity of sows was ameliorated, related to piglets, born alive and litter weight at weaning. In conclusion, Hy-D is a versatile nutritional supplement, improving swine production at different levels.

Key Words: vitamin D, swine, bone strength

13 Practical application for use of dietary vitamin D to promote structural soundness in swine. M. A. Pérez-Alvarado, D. Braña, and J. A. Cuarón*, *Centro Nacional de investigación Disciplinaria en Fisiología Animal, INIFAP, México.*

Even with safety margins of vitamin D (VD), Ca and P, over 8% of growing pigs may either be culled, or experience reduced growth due to structural unsoundness. Structural unsoundness is also a major cause for removal of breeding sows. Recently, the incidence of ostechondrosis (OC) lesions in sows was not linked to bone mineral concentrations. However, diets that provide excess Ca and P may increase mineral density of subchondral bone, possibly creating a rigidity stress on the cartilage preventing chondroblasts differentiation. A deficiency of VD may induce osteomalacia in adults, but bone mineralization in the offspring may also be affected. These responses may be mediated by P through FGF23. Thus, development of dietary inputs to regulate Ca and P homeostasis are necessary to sustain animal wellbeing. Traditional skeletal and extra-skeletal effects of VD are well accepted but an understanding of the non-classical responses within bone, such as effects on cartilage via cell differentiation may expand the practical applications for a role of VD in structural soundness. Epidemiological studies and empirical trials are needed to titrate VD requirements relative to structural soundness, but these trials are hampered by methods used to assess responses beyond those of bone mineralization. Assuming a greater absorption of 25OHVD than VD, our approach has used an assessment of a soundness scores to evaluate apparent OC in concert with measurements of Ca and P balance, particularly in lactating first litter gilts fed diets with varied VD, Ca and P concentrations. Growth performance and fibula ash validated the method of visual appraisal for structural soundness and gilts fed diets with 25OHVD had a greater number of femur osteoblast cells ($P < 0.02$). During lactation, at lower intakes, Ca and P retention were similar or improved ($P < 0.01$) by 25OHVD. Thus provision of greater dietary levels of VD from 25OHVD is a resource to sustain structural soundness of gilts and to protect efficiency of Ca and P use.

Key Words: structural soundness, 25-OH-D_3, osteochondrosis

T1 Effect of supplementation with dehydrated molasses lick blocks on performance of growing dairy-beef steers grazing pasture. J. B. Aveling[1], M. R. Walton[2], and K. Stelwagen*[3], *[1]Ballance Agri-Nutrients, Tauranga, New Zealand, [2]Kaitaringa Farms Ltd., Waiotira, New Zealand, [3]SciLactis Ltd, Hamilton, New Zealand.*

During late summer and in the fall, pasture quality tends to deteriorate. Molasses lick blocks (MLB) offer a convenient way to supplement grazing cattle. A study was conducted to investigate the effect of dehydrated MLB on the performance of growing Friesian cross (Hereford or Angus) steers kept on pasture. The control group (CON; n=25) and MLB group (n = 26) were randomly assigned to adjacent paddocks of similar botanical and nutritional quality (start of trial, CON vs. MLB pastures: DOMD, 65.9 vs. 70.2%; ME, 10.6 vs. 11.2 MJ/kg DM; end of trial: DOMD, 57.4% vs. 61.7%; ME 9.2 vs. 9.9 MJ/kg DM); pasture coverage and quality were at no time during the trial limiting. MLB-steers had ad libitum access to MLB tubs (Crystalyx Forage Plus: ME 12.0 MJ/kg DM, oil 6%, protein 12%, sugar, 35%, minerals and vitamin A, D, E). At the end of the trial a randomly chosen subset of steers (MLB, n = 6; CON, n=6) were subjected to blood sampling to measure plasma selenium, ferroxidase and vitamin B12 levels. The trial was conducted during late summer and fall (22 Jan to 2 May). MLB-steers consumed on average 102 g/d of MLB during the trial. No differences existed between crosses and data were subsequently pooled, with results shown in the Table. MLB-steers gained significantly more BW and faster than those without, resulting in an approximately 15 kg higher final live weight compared to CON steers. MLB steers had significantly higher selenium and vitamin B12 levels, but ferroxidase activity did not differ between groups (respectively, CON vs. MLB ± pooled SE: 230 vs. 475 ± 51 nmol/L, $P < 0.001$; 84 vs.118 ± 10 pmol/L, $P < 0.01$; 19 vs. 16 ± 3 IU/L, $P < 0.25$). In conclusion, MLB can improve performance in growing steers kept on pasture.

Table 1.

	CON	MLB	Pooled SEM	*P* <
Start BW (kg)	128.9	127.5	3.9	0.722
Final BW (kg)	178.8	192.6	5.0	0.001
Weight gain (kg)	49.9	65.1	2.7	0.001
ADG (g/d)	494	644	27	0.001

Key Words: dairy-beef steer, molasses lick block, pasture

T2 Trace minerals: A new approach in nutritional requirements. L. F. C. Silva*, S. C. Valadares Filho, P. P. Rotta, M. I. Marcondes, F. A. Sales, E. C. Martins, A. T. Tokunaga, and D. F. T. Sathler, *Universidade Federal de Vicosa, Vicosa, Minas Gerais, Brazil.*

An experiment was conducted to estimate the trace minerals requirements: chromium (Cr), cupper (Cu), manganese (Mn), iron (Fe) and zinc (Zn) in Nellore bulls. Thirty-seven Nellore bulls with initial shrunk body weight of 259 ± 24.9 kg were used in a comparative slaughter technique. The bulls were randomly divided into 3 groups: 5 bulls to the reference group, whereas 4 were fed at maintenance level and 28 were fed ad libitum. The bulls fed ad libitum were separated into 4 groups, one of which was slaughtered every 42 days. The reference group was slaughtered at the start of the experiment. All the animals were fed with corn silage and concentrate (55:45). Before each slaughter, the digestibility trial was done during 3 d. In each slaughter, the noncarcass components were weighted and a sample was collected for posterior analysis. After 18 hours of slaughter, the half-left carcass was dissected into muscle, fat and bone fractions and they were weighed. The samples were lyophilized, partially defatted and grounded. Feed, urinary, fecal and body trace mineral concentrations were evaluated by atomic absorption spectrophotometer. The net requirements for gain were calculated by the derivative of the allometric equation between body trace mineral concentrations and the empty body weight (EBW). Evaluation of the net requirements to maintenance was performed the regression between each absorbed trace mineral and its intake. After the sum of net requirements for maintenance and gain was divided by the absorption coefficient, the diet requirements were achieve. Data were analyzed using NLIN procedure of SAS. The net requirements for maintenance of Cr, Cu, Mn, Fe, and Zn were, respectively, 9.18; 90.5; 289.3; 856.1 and 266.3 µg/kg of EBW/day. The absorption coefficients for Cr, Cu, Mn, Fe, Zn were, respectively, 0.68; 0.68; 0.45; 0.27 and 0.41. The net requirements for gain (mg/d) to Cr, Cu, Mn, Fe, and Zn were estimated by following equations: Cr = 14.56 × EBW-0.182; Cu = 75.86 × EBW-0.512; Mn = 3.43 × EBW-0.261; Fe = 424.31 × EBW-0.207; and Zn = 151.73 × EBW-0.045. In this study, as the animal gain weight, the trace mineral requirements increase.

Key Words: comparative slaughter, mineral, Nellore

T3 Intake, duodenal flow, and intestinal digestibility of amino acids from canola meal or corn and wheat distillers grains in growing beef heifers. C. Li[1,2], L. Xu[2,4], S. Ding*[2,3], K. A. Beauchemin[2], and W. Z. Yang[2], *[1]College of Animal Science and Technology, Inner Mongolia University for the Nationalities, Tongliao, Inner Mongolia, China, [2]Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [3]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, [4]College of Food Science and Engineering, Inner Mongolia Agricultural University, Hohhot, Inner Mongolia, China.*

The objective of this study was to evaluate the intake, duodenal flows, and intestinal digestibility of amino acid (AA) from canola meal (CM) or type of dried distillers grains with solubles (DDGS) in growing beef heifers. Five ruminally and duodenally cannulated Angus heifers (BW 386 kg) were assigned to a 5 × 5 Latin square design. The diets consisted of 60% barley silage and 40% barley-based concentrate (DM basis) with differing protein supplements: control (CON; no protein supplement), CM, wheat DDGS (wDDGS), corn DDGS (cDDGS) or fractional corn DDGS (fDDGS). The fDDGS was produced by fractionation dry-grinding process where corn kernels are physically separated into high-fiber bran, germ and endosperm prior to mashing and fermentation of the endosperm. Contents of CP were 12.0, 14.1, 14.2, 14.1 and 14.2% (DM basis), respectively, for CON, CM, wDDGS, cDDGS and fDDGS diets. Intakes (g/d) of AA were lower ($P < 0.05$) for CON (631) than the protein supplemented diets (averaged 895), which were not different. Flows (g/d) of EAA and total AA to the duodenum were greatest ($P < 0.05$), respectively, for heifers fed wDDGS (521 and 1168) or fDDGS (534 and 1172), medium for CM (484 and 1069) or cDDGS (475 and 1059), and lowest for CON (385 and 846). The profiles of individual EAA (% of total AA) in duodenal flows were generally not different among treatments except for Lys (DDGS vs. CON and CM; 7.5 vs. 8.2%), Leu (corn DDGS vs. other diets; 9.2 vs. 8.1%), and Met (fDDGS vs. other diets; 1.2 vs. 1.6%). Digestibility of AA in the intestine (% of duodenal flow) generally did not differ (70 to 73% for EAA and 71 to

74% for total AA) except for Leu, Val, and Ala of which the digestibility was greater ($P < 0.05$) for fDDGS than for CON. These results indicate that wDDGS and fDDGS supplemented diets delivered greater amount of AA at the small intestine compared to CM and cDDGS when the diets were formulated to be isonitrogen. Corn and wheat DDGS can be used to replace CM to meet the protein requirements of growing cattle fed diets based on barley grain.

Key Words: beef heifer, duodenal flow of AA, protein supplement

T4 Effects of cottonseed meal and dried distillers grains supplementation on rice straw utilization by Brahman steers. J. C. McCann*, J. E. Sawyer, and T. A. Wickersham, *Texas A&M University, College Station.*

Seven ruminally cannulated Brahman steers were used in a 7 × 4 incomplete block design to determine the effects of cottonseed meal (CSM; 43.9% CP, 82.9% degradable protein) or dried distiller's grain (DDG; 27.5% CP, 43.6% degradable protein) supplementation on rice straw utilization. Treatments consisted of a control (no supplement) and three levels (60, 120, and 180 mg N/kg BW) of either CSM or DDG. Periods were 14 d with 9 d for adaptation and 5 d for data collection. Steers had ad libitum access to rice straw (4.7% CP, 68% NDF) and were fed supplements at 0630 daily. Increased supplementation resulted in a linear increase ($P \leq 0.06$) in forage OM intake from 13.5 g/kg BW (control) to 16.1 and 15.5 g/kg BW for 180 mg N/ kg BW of CSM and DDG respectively, with no difference between sources ($P = 0.84$). Total digestible OM intake was increased by supplementation (linear, $P < 0.01$) from 8.0 g/kg BW (control) to 11.7 and 12.9 g/kg BW for 180 mg N/ kg BW of CSM and DDG respectively. A greater response was observed for DDG ($P = 0.05$) due to greater provision of supplement (g DM/d) to achieve isonitrogenous treatment levels. Total tract OM digestion was linearly increased ($P < 0.01$) by CSM and DDG supplementation. Although CSM and DDG improved NDF digestibility (linear, $P \leq 0.06$) from 49.6% (control) to 53.7% and 54.9% at 180 mg N/kg BW respectively, estimated forage NDF digestibility was not significantly increased ($P > 0.10$). Ruminal ammonia concentrations peaked 4 h after supplementation with the greatest concentration (4.0 m*M*) observed for 180 mg N/kg BW of CSM and the lowest concentration observed in the control (0.8 m*M*). Provision of CSM resulted in a linear increase ($P < 0.01$) in ruminal ammonia in contrast to the quadratic response ($P = 0.02$) observed with DDG supplementation. Total VFA production followed a similar trend with a linear increase for CSM and DDG supplementation, respectively ($P = 0.09$, $P = 0.01$). Protein supplements containing high and low levels of degradable intake protein were effective at improving intake and utilization of rice straw.

Key Words: forage, protein, supplement

T5 Impact of chromium supplementation on lactating beef cows. M. J. Faulkner*[1], P. M. Walker[1], A. L. Wagner[2], R. E. Hall[2], and R. L. Atkinson[3], *[1]Illinois State University, Normal, [2]Cooperative Research Farms, Richmond, VA, [3]Southern Illinois University, Carbondale.*

The trace mineral, chromium (Cr), is required for digestion of carbohydrates, lipids and proteins. Recognized as the active component of the glucose tolerance factor, Cr aids in insulin signaling. When glucose metabolism is increased by production or other stressors, Cr deficiencies can occur. Because glucose metabolism is altered during gestation and lactation, Cr supplementation may be beneficial. Improved pregnancy rates and reduced postpartum BW have been demonstrated when beef cows were supplemented with Cr. The objective of this study was to determine if providing supplemental Cr to lactating beef cows improves calf weaning weights and cow conception rates. Angus × Simmental crossbred cows (n=119) were limit-fed one of two dietary treatments beginning at the birth of the first calf through calf weaning (n = 190 d). Cows were blocked by parity (first parity n = 32, second parity n = 26 and multiparous n = 61) and stratified within parity by BW subject to variation in BCS to 16 pens. Each block was equally represented within treatment. Cows were fed a base diet of corn silage and modified wet distiller's grains with solubles to provide 14.0% CP. Control cows were not fed supplemental Cr (T1) and treatment cows were fed supplemental Cr propionate [4 mg/(cow-d); T2]. All data, excluding reproduction, were analyzed using PROC MIXED of SAS, P=0.05 and the experimental unit = pen. The model statement included TREATMENT and the RANDOM statement included pen within treatment. Pregnancy rates were analyzed using the PROC FREQ procedure with the χ^2 option. No differences ($P > 0.05$) between treatments were observed for calf weaning weight or cow conception rates; mean weaning weight was 290 and 292 kg, and mean cow conception rates were 90 and 87%, for T1 and T2, respectively. No differences ($P > 0.05$) between treatments were observed for mean cow BW change (−76 and −80 kg), mean BCS change (−0.2 and −0.2), mean birth weight (40.7 and 41.1 kg) and mean daily milk production (6.20 and 5.97 kg), for T1 and T2, respectively. Based on the results of this single study, there appears to be no added benefit for supplementing lactating beef cows in optimum BCS with chromium propionate.

Key Words: chromium, lactating beef cow

T6 Effects of two experimental direct-fed microbial products on performance and carcass characteristics of finishing beef cattle. E. M. Domby*[1], U. Y. Anele[1], K. K. Gautam[1], C. H. Ponce[1], J. S. Schutz[1], M. Garner[2], and M. L. Galyean[1], *[1]Texas Tech University, Lubbock, [2]MicroBios Inc., Ithaca, NY.*

Despite reported increases in ruminal pH and nutrient digestion, responses in feedlot performance with direct-fed microbial (DFM) products in small-pen research studies have generally been equivocal. Our objective was to evaluate performance and carcass characteristics of finishing beef cattle fed 2 experimental DFM products. One hundred forty-four single-source steers (average initial BW = 311 ± 2.6 kg) were used in a randomized complete block design experiment. Steam-flaked corn was the basal grain, and treatment diets contained 25% (DM basis) wet corn gluten feed. The 3 treatments (12 pens/treatment) were (1) no DFM; (2) a *Lactobacillus acidophilus*-based DFM fed at a dose of 1×10^7 cfu/(steer·d) during the entire feeding period; and (3) the *L. acidophilus*-based DFM at 1×10^7 cfu/(steer·d) during the first 30 d, followed by a *Propionibacterium freudenreichii*-based DFM fed at a dose of 1×10^8 cfu/(steer·d) for the remainder of the feeding period. Although the DFM treatments numerically increased performance during the first 140 d of the feeding period, no differences ($P \geq 0.11$) for pen-based ADG, DMI, and G:F (averages of 1.52 kg, 8.49 kg/d, and 0.179, respectively) were detected for the overall (average = 187 d) feeding period. Carcass characteristics (HCW, dressing percent, 12th rib fat thickness, longissimus muscle area, calculated yield grade, and marbling score) did not differ ($P \geq 0.36$) among treatments, nor was the distribution of quality grades affected ($P = 0.950$) by treatments. Under the conditions of this study, results suggest neither positive nor negative effects on performance and carcass traits of beef steers associated with feeding the 2 DFM products evaluated.

Key Words: beef cattle, *Lactobacillus acidophilus*, *Propionibacterium freudenreichii*

T7 Influence of organic chromium and tannins extract supplementation on performance of bull calves during the first 50 days in the feedlot. A. Montoya[1], J. J. Bermudez[2], and R. Barajas*[1], *[1]Facultad de Medicina Veterinaria y Zootecnia, Universidad Autonoma de Sinaloa, Culiacan, Sinaloa, Mexico, [2]Ganaderia Integral Vizur, S.A. de C.V., Culiacan, Sinaloa, Mexico.*

Six hundred and seven bull calves (240.9 ± 1.01 kg) were utilized in an experiment to evaluate the influence of organic chromium and tannins extract supplementation on feedlot performance of bull calves during the first 50 d in the feedlot. Calves were individually weighed, and blocked by initial weight. Groups of 48 to 54 the calves were placed in 12 dirt floor pen (15 × 45 m). Pens within a block were randomly assigned to one of four treatments: (1) Basal diet with 87% concentrate (13.7% CP, 2.02 Mcal NE_m/kg DM), formulated with steam-flaked corn and soybean meal (Control); (2) Control supplemented with 0.49 mg Cr/kg DM (CR); (3) Control supplemented with 0.37% (DM basis) tannins extract (TE); and (4) Control supplemented with 0.49 mg Cr/kg DM and 0.37% (DM basis) tannins extract (CRTE). Organic chromium was provided as chromium methionine (MiCroPlex, Zinpro Corporation) and tannins extract was supplied as condensed hydrolysable tannins extract blend (ByPro, Silvateam). Results were analyzed by ANOVA for a randomized complete block design with a 2 × 2 factorial arrangement of treatments, using pen as the experimental unit. Chromium supplementation increased ($P = 0.04$) final weight in 3% (319.86 vs. 310.55 kg), enhanced ($P = 0.05$) ADG 12.3% (1.57 vs. 1.40 kg), and improved ($P = 0.05$) feed/gain ratio 11.4% (4.085 vs. 4.613). Dry matter intake was not affected by treatments ($P = 0.10$). The TE and CRTE treatments had no effect on any of measured variables ($P = 0.18$). As a main factor, TE increased DMI ($P = 0.05$). There was not observed CR × TE interaction for any variables. Supplementation of chromium methionine 0.49 mg Cr/kg DM, is effective for improved performance of bull calves during their first 50 d in the feedlot. Adding TE to diets containing supplemental chromium did not show any additional performance response.

Key Words: bull calves, chromium, feedlot performance

T8 Influence of tannins extract supplementation on feedlot performance and plasma urea nitrogen of nonimplanted growing heifers. B. J. Cervantes[1], A. Camacho[2], J. A. Vazquez[3], M. A. Espino[2], T. J. Heras[2], L. R. Flores[2], J. J. Lomeli[2], and R. Barajas*[2], *[1]Ganadera Los Migueles, S.A. de C.V., Culiacan, Sinaloa, Mexico, [2]Facultad de Medicina Veterinaria y Zootecnia, Universidad Autonoma de Sinaloa, Culiacan, Sinaloa, Mexico, [3]CUALTOS, Universidad de Guadalajara, Tepatitlan, Jalisco, Mexico.*

Forty nonimplanted Brahman heifers (195.8 ± 0.66 kg) were utilized in an 84-d experiment to evaluate the influence of tannins extract supplementation on feedlot performance and plasma urea nitrogen of nonimplanted growing heifers. Heifer were weighed individually, and in groups of five placed in dirt floor pens (6 × 12 m). In accord with initial weight, heifers were grouped in four weight-blocks. Within a block, pens were randomly assigned to one of two treatments: (1) Feeding a 56% roughage diet (15% CP, 1.37 Mcal NEm/kg DM) formulated with corn straw, corn silage without grain, ground sorghum grain and peanut meal (Control); or (2) Similar to control supplemented with 0.28% (DM basis) of tannins extract (TE). In pens assigned to Tannins treatment, daily were offered 87.7 g of tannin extract premix ByPro (Silvateam) premix that contains 72% of a condensed and hydrolysable tannins blend. TE was top-dresed on the diet in the feed bunk. Daily dose was equivalent to 14.54 g TE for each heifer inside the pen. Heifers were weighed on d 1 and d 84. On d 28 and 56, blood samples were taken from jugular vein. Experiment was analyzed by ANOVA for a randomized complete block design. TE improved 2.5% ($P = 0.03$) the final weight (279.2 vs. 272.3 kg), increased 8.88% ($P < 0.01$) ADG (0.993 vs. 0.912 kg/d), and 3.37% ($P < 0.01$) the dry matter intake (6.375 vs. 6.167 kg). TE supplementation enhanced ($P < 0.01$) the gain/feed ratio in 5.4% (0.156 vs. 0.148 kg/kg), and improved 3% ($P < 0.01$) observed/expected NEm and NEg ratio, with values of 1.01 vs. 0.98 for TE and Control heifers, respectively. In d 28, TE have no effect ($P = 0.57$) on plasma urea nitrogen concentration (PUN); however in d 56 TE supplementation diminished 16% PUN value ($P = 0.02$) with mean values of 14.00 and 11.75 mg/dL for TE and Control treatments, respectively. It is concluded; that tannins extract supplementation reduces N wastage measured as PUN and improve feedlot performance of nonimplanted growing heifers

Key Words: feedlot performance, heifer, tannin

T9 Influence of tannins extract and organic chromium supplementation on carcass characteristics of finishing bulls. A. Montoya[1], M. A. Espino[1], B. J. Cervantes[2,1], M. Verdugo[1], and R. Barajas*[1], *[1]Facultad de Medicina Veterinaria y Zootecnia, Universidad Autonoma de Sinaloa, Culiacan, Sinaloa, Mexico, [2]Ganadera Los Migueles, S.A. de C.V., Culiacan, Sinaloa, Mexico.*

Eight hundred and fifty bulls (338.8 ± 3.55 kg) were involved in a 92-d experiment to evaluate the influence of tannins extract and organic chromium supplementation on carcass characteristics of finishing bulls. Bulls were individually weighed and blocked by initial weight. Groups of 51 to 56 bulls were placed in 16 dirt floor pen (15 × 45 m). Pens within a block were randomly assigned to one of four treatments: (1) Finishing diet with 88% of concentrate (14% CP, 1.98 Mcal NEm/kg DM), (Control); (2) Control supplemented with 0.24 mg of Cr/kg DM (CR); (3) Control supplemented with 0.3% (DM basis) of tannins extract (TE); and (4) Control supplemented with 0.24 mg of Cr/kg DM and 0.3% (DM basis) of tannins extract (CRTE). CR was provided as chromium methionine (MiCroPlex, Zinpro Corporation). TE was supplied as condensed hydrolysable tannins extract blend (ByPro, Silvateam). Bulls were harvested after finishing period and hot carcass weight obtained. After 24 h of chilling, carcass characteristics were measured. Results were analyzed by ANOVA for a randomized complete block design with a 2 × 2 factorial arrangement of treatments. TE supplementation increased 2% ($P = 0.05$) hot carcass weight compared with Control (299.8 vs. 293.8 kg). TE augmented ($P = 0.02$) KPH-fat (2.66 vs. 2.30%). Hot carcass weight and KPH-fat of bulls in CR and CRTE treatments exhibits intermediate values and were not different ($P > 0.10$) of Control and TE. Back fat thickness, marbling score, and LM area were not affected by treatments ($P > 0.10$). An interaction CR × TE was observed in KPH-fat ($P = 0.02$). In muscle colorimetric measurements, L values were not affected by treatments ($P > 0.10$). Intensity of color measured as "a" and "b" were increased ($P = 0.01$) by TE supplementation. Interactions CR × TE were detected for "a" and "b" values. It is concluded that supplementation of 0.3% of tannins extract improves hot carcass weight and muscle color intensity, but additional organic chromium supplementation to finishing bulls consuming tannins extract did not produces any additional benefices.

Key Words: bulls, carcass, tannins

T10 Influence of tannins extract and organic chromium supplementation on feedlot performance. A. Montoya*[1], J. J. Bermudez[2], and R. Barajas[1], *[1]Facultad de Medicina Veterinaria y Zootecnia, Universidad Autonoma de Sinaloa, Culiacan, Sinaloa, Mexico, [2]Ganaderia Integral Vizur, S.A. de C.V., Culiacan, Sinaloa, Mexico.*

Eight hundred and fifty bulls (338.8 ± 3.6 kg) were utilized in a 92 d experiment to evaluate the influence of tannins extract and organic chromium supplementation on feedlot performance. Bulls were individually weighted and blocked by initial weight. Groups of 51 to 56 bulls were placed in 16 dirt floor pen (15 × 45 m). Pens within a block were randomly assigned to one of four treatments: 1) Finishing diet with 88% of concentrate (14% CP, 1.98 Mcal NEm/kg DM), formulated with steam-flaked wheat and soybean meal (Control); 2) Control supplemented with 0.24 mg of Cr/kg DM (CR); 3) Control supplemented with 0.3% (DM basis) of tannins extract (TE); and 4) Control supplemented with 0.24 mg of Cr/kg DM and 0.3% (DM basis) of tannins extract (CRTE). Chromium was provided as chromium methionine (MiCroPlex, Zinpro Corporation) and TE was supplied as condensed hydrolysable tannins extract blend (ByPro, Silvateam). Results were analyzed by ANOVA for a randomized complete block design with a 2 × 2 factorial arrangement of treatments. At the end of experiment, bulls in TE were 2.8% heavier ($P = 0.05$), and gained 8.4% more weight ($P = 0.02$) than those in the Control group. Final weight and ADG of bulls in CR and CRTE treatments exhibits intermediate values and were not different ($P > 0.10$) of Control and TE. An interaction CR × TE was observed for ADG ($P = 0.04$). Bulls supplemented with Cr and TE gained less than those fed Cr or TE separately (1.36, 1.41, 1.47 and 1.40 kg/d for Control, CR, TE, and CRTE treatments, respectively). TE supplementation increased HCW by 2% ($P = 0.05$) compared with Control (299.8 vs. 293.8 kg). As a main factor, bulls fed TE ate 3% more DM ($P = 0.05$) than animals that no received tannins (7.8 vs. 8.0 kg/day). Feed/gain ratio was not affected by treatments ($P > 0.10$). It is concluded that supplementation of 0.3% of tannins extract could improves weight gain and carcass weight, but organic chromium supplementation to bulls consuming tannins extract did not produces any additional benefices.

Key Words: bull, feedlot, tannin

T11 Interaction of tannin extract and zilpaterol hydrochloride supplementation on feedlot performance of bulls. R. Barajas*[1], B. J. Cervantes[2], M. A. Espino[1], A. Camacho[1], M. Verdugo[1], L. R. Flores[1], and J. A. Romo[1], *[1]Facultad de Medicina Veterinaria y Zootecnia, Universidad Autonoma de Sinaloa, Culiacan, Sinaloa, Mexico, [2]Ganadera Los Migueles, S.A. de C.V., Culiacan, Sinaloa, Mexico.*

Eighty bulls (341.7 ± 10.1 kg) were utilized in a 108 d experiment to evaluate the interaction of tannin extract and zilpaterol hydrochloride supplementation on feedlot performance of bulls. Bulls were individually weighed and blocked by weight. Groups of five bulls were placed in16 dirt-floor pens (6 × 12 m). Pens within a block were randomly assigned to treatments follows: (1) Finishing diet (14% CP, 1.83 Mcal NE_m/kg) formulated with ground sorghum grain (Control); (2) Control added with zilpaterol hydrochloride (ZH); (3) Control supplemented with 0.3% (DM basis) of tannin extract (TE); and (4) Control added with ZH and TE (ZHTE). Both, ZH and TE treatments were top-dress on the diet in the feed bunk. Zilpaterol hydrochloride was supplied daily as 1.63 g of Zilmax (Merck Animal Health)/bull (which equate to 0.15 mg ZH/kg BW). Zilmax contains 4.8% zilpaterol hydrochloride. Zilmax was withdrawn three days prior harvest. TE was provided feeding daily 35.5 g of condensed hydrolysable tannin blend (ByPro, Silvateam). The experiment was analyzed by ANOVA for a completely randomized design with 2 × 2 factorial arrangement of treatments. Orthogonal contrasts were used to compare ZHTE vs. each one of remainder treatments. TE supplementation increased ($P < 0.05$) final weight, ADG, and hot carcass weight. ZH decreased ($P < 0.05$) DMI as percentage of BW, improved feed/gain ratio, hot carcass weight, and carcass dressing. An interaction ($P < 0.05$) TE × ZH was observed in DMI mean values were 2.8, 2.5, 2.7 and 2.73% of BW for Control, ZH, TE, and ZHTE treatments, respectively. Contrasts indicated that carcass of bulls in ZHTE extract treatment were heavier ($P < 0.05$) than remainder treatments, with means of 324.6, 330.5, 329.8 and 345.4 kg for Control, ZH, TE, and ZHTE treatments, respectively. Results suggest that coupled supplementation of Zilmax and tannin extract contributes to increases in weight gain, final weight, and heavier carcass in finishing bulls.

Key Words: finishing-bulls, tannins, zilpaterol

T12 Influence of zinc methionine and zilpaterol hydrochloride supplementation on feedlot performance and carcass characteristics of yearling-finishing bulls. M. Verdugo[1], B. J. Cervantes[2], M. A. Espino[1], J. A. Romo[1], and R. Barajas*[1], *[1]Facultad de Medicina Veterinaria y Zootecnia, Universidad Autonoma de Sinaloa, Culiacan, Sinaloa, Mexico, [2]Ganadera Los Migueles, S.A. de C.V., Culiacan, Sinaloa, Mexico.*

Eighty yearling-bulls (488.8 ± 4.17 kg) were utilized in a 32-d experiment to evaluate the influence of zinc methionine and zilpaterol hydrochloride supplementation on feedlot performance and carcass characteristics of yearling-bulls fed a finishing diet. Cattle were individually weighed, and groups of 5 were placed in 16 pens (6 × 12 m). Pens were randomly assigned to one of four treatments: (1) Basal diet (CTRL); (2) CTRL plus zilpaterol hydrochloride (ZH); (3) CTRL plus 40 mg Zn/kg DM (ZN); or (4) CTRL plus zilpaterol hydrochloride and zinc-methionine (40 mg Zn/kg DM; ZHZN). The basal diet (14% CP; 1.86 Mcal of NE_m/kg and 60 mg Zn/kg of DM) was supplemented with 57 mg of Zn/kg using zinc sulfate. Both, ZH and ZN were top-dress on the diet in the feed bunk. The ZH was supplied daily as 1.63 g of Zilmax (Merck Animal Health)/bull (which equate to 0.15 mg ZH/kg BW). Zilmax was withdrawn 3 d prior to harvest. The ZN was daily supplemented as 4.6 g Zinpro (Zinpro Corporation)/per bull. The ZINPRO product contains 10% Zn as zinc-methionine complex. The experiment was analyzed by co-variance as a completely randomized design with 2 × 2 factorial arrangement of treatments. Initial weight was the associate co-variable. Feeding ZH increased ($P < 0.05$) final weight (1.9%) and ADG (29.9%), improved ($P < 0.05$) feed/gain ratio 31%, and augmented ($P < 0.01$) hot carcass weight 14.3 kg, and dressing percentage by 1.4%. The ZN has no effect on the measured variables ($P > 0.20$). A tendency ($P = 0.11$) was observed for ZH × ZN interaction on carcass weight, with mean values of 328, 337, 323, and 342 kg for CTRL, ZH, ZN and ZHZN, respectively. A ZH × ZN interaction ($P < 0.05$) was detected for dressing percentage with mean values of 62.8, 63.2, 61.5 and 64.0 for CTRL, ZH, ZN and ZHZN, respectively. Treatments had no effect on carcass characteristics ($P > 0.20$). Results suggest that the ZN supplementation to diets that contains ZH could contribute to increased dressing percentage and heavier hot carcass weight of yearling finishing bulls.

Key Words: yearling bull, zilpaterol hydrochloride, zinc

T13 Effect of direct-fed microbials on ruminal fermentation and lactate utilization in steers consuming a high concentrate diet. N. M. Kenney*, S. M. Wingard, E. S. Vanzant, D. L. Harmon, and K. R. McLeod, *University of Kentucky, Lexington.*

Direct-fed microbials (DFM) have been shown to alter ruminal fermentation and may modulate fermentation during transition to high concentrate diets. To test this hypothesis, 12 ruminally cannulated Angus steers (385 ± 35 kg) were used in split-plot design with the whole plot consisting of control or DFM, and the sub-plot consisting of week of

dietary adaptation. The DFM was a mixed bacterial culture, primarily *Lactobacillus acidophilus* and *Enterococcus faecium*, fed at 1 billion cfu/d. A 90:10 concentrate to forage, corn-based diet was fed twice daily and top-dressed with DFM or lactose carrier. Rumen fluid was sampled on d 14 and 28 at 0, 3, 6, 9 and 12 h post-feeding. Steers were ruminally pulse dosed with a 2 L solution of neutralized DL lactate (0.56 *M*) and CrEDTA 3 h post-feeding on d 15 and 29. Ruminal samples were collected at 10- and 20-min intervals for the first and second hour post-dosing. Total VFA concentration and molar proportions of butyrate were unaffected by DFM ($P \geq 0.19$) or week ($P \geq 0.24$). Molar proportions of acetate exhibited a DFM by hour interaction ($P = 0.04$); however, on average, molar proportion of acetate was 4.4% greater for DFM. Conversely, DFM did not affect propionate ($P = 0.39$). On average, molar proportions of propionate and acetate increased ($P = 0.07$) and decreased ($P = 0.07$), respectively, across weeks. Mean daily ruminal pH was similar for control on d 14 (6.04) and 28 (6.09), whereas mean pH increased from d 14 (6.05) to d 28 (6.35) for DFM (DFM × week; $P = 0.08$). Minimum pH remained unchanged for control over time but increased from d 14 (5.70) to d 28 (6.16) for DFM (DFM × week; $P = 0.10$). Maximum pH decreased from d 14 to 28 in control but increased over time with DFM from 6.31 to 6.53 (DFM × week; $P = 0.05$). Total and L-lactate utilization were unaffected by DFM ($P \geq 0.33$) or week ($P \geq 0.50$). These data indicate that DFM may be beneficial during dietary adaptation, as evidenced by shifts in ruminal VFA profile and pH; however, DFM did not appear to influence ruminal lactate utilization.

Key Words: direct-fed microbial, pH, lactate

T14 Influence of feeding chelated chromium and enzymatically hydrolyzed yeast on growth performance, dietary energetics, and carcass characteristics in feedlot cattle. B. Sánchez-Mendoza*[1], A. Montelongo[1], A. Plascencia[1], R. Ware[2], and R. Zinn[3], *[1]UABC, Mexicali, BC, Mexico, [2]Varied Industries Corporation, Mason City, IA, [3]University of California, Davis.*

Forty crossbred steers (245 ± 0.95 kg) were used in a 222-d feeding trial to assess the effects of a chelated chromium enriched extract of enzymatically hydrolyzed yeast cell wall (EHY) on growth performance, dietary energetics and carcass characteristics. Treatments consisted of a steam-flaked corn-based finishing diet supplemented with 0 or 500 ppb of chelated chromium (Cr) enriched EHY (TruMax, Vi-COR, Mason City, IA). Steers were blocked by weight and randomly assigned to 8 pens (5 steers/pen, 4 pens/treatment). Pens were 43 m^2, with 22 m^2 of shade, automatic waterers, and 2.4-m fence-line feed bunks. Supplemental Cr intake average 4.3 mg/d. During the initial 112-d period, Cr supplementation increased ADG (6.8%, $P = 0.03$) and tended to increase (5.9%, $P = 0.07$) DM intake. However, Cr supplementation did not affect overall (222-d feeding period) growth performance. Nevertheless, Cr supplementation increased LM area (6.8%, $P < 0.01$) and tended to increase retail yield (1.6%, $P = 0.07$), and decrease carcass fat thickness (10%, $P = 0.09$). Results indicate that Cr supplementation has a modulating effect on carcass quality, and may enhance DMI and corresponding ADG of feedlot cattle.

Key Words: chromium chelate, finishing, steer

T15 Influence of feeding yeast cell wall extract on growth performance of feedlot cattle during periods of elevated ambient temperature. M. Montano*[1], A. Plascencia[1], N. Torrentera[1], R. Ware[2], and R. Zinn[3], *[1]UABC, Mexicali, BC, Mexico, [2]Varied Industries Corporation, Mason City, IA, [3]University of California, Davis.*

Eighty crossbred steers (235 ± 0.59 kg) were used in a 229-d feeding trial to assess the effects of an enzymatically hydrolyzed yeast cell wall (EHY) on growth performance and carcass characteristics. Treatments consisted of a steam-flaked corn-based finishing diet supplemented with 0, 1, 2, or 3 g/hd/d of EHY (Celmanax, Vi-COR, Mason City, IA). Steers were blocked by weight and randomly assigned to 16 pens (5 steers/pen). Pens were 78 m^2, with 27 m^2 of shade, automatic waterers, and 4.3-m fence-line feed bunks. There were no effects on growth performance during the initial 84-d period. However, from d 84 to harvest, EHY supplementation increased ADG (10.7%, $P = 0.08$) and gain efficiency (8.6%, $P = 0.09$). From 139-d to harvest, when 24-h temperature humidity index averaged 80, EHY increased DMI (4.8%, $P = 0.03$). Supplementation with EHY had a quadratic effect ($P = 0.02$) on KPH. Otherwise, there were no treatment effects on carcass composition. Enhancements in DMI and ADG during periods of high ambient temperature indicate a potential role of EHY in association with heat stress.

Key Words: cattle, performance, yeast

T16 Effect of level and source of supplemental tannin on growth-performance of Holstein steers during the late finishing phase. C. Rivera*[1], A. Plascencia[1], N. Torrentera[1], and R. Zinn[2], *[1]UABC, Mexicali, BC, Mexico, [2]University of California, Davis.*

Two trials were conducted to evaluate the effects of tannin source and level on feedlot cattle performance during the late finishing phase, when metabolizable protein intake is not limiting requirements for growth. In Trial 1, 96 calf-fed Holstein steers (476 ± 6 kg) were used in a randomized complete block design experiment (4 pens/ treatment) to evaluate level of tannin supplementation. Treatments consisted of a steam-flaked corn-based finishing diet supplemented with 0, 0.2, 0.4, and 0.6% condensed tannin. Across the 84-d feeding period, tannin supplementation increased ADG (1.37, 1.42, 1.48, and 1.50 ± 0.04 kg/d, respectively; $P = 0.05$), gain efficiency (0.122, 0.128, 0.128, and 0.129 ± 0.002, respectively; $P = 0.04$) and observed/expected diet NEm (0.92, 0.95, 0.94 and 0.95 ± 0.01, respectively; $P = 0.06$). In Trial 2, 96 calf-fed Holstein steers (392 ± 4 kg) were used in a randomized complete block design experiment (4 pens/ treatment) to compare the influence of tannin source (condensed vs. hydrolysable) on cattle performance during the late finishing phase. Dietary treatments consisted of a steam-flaked corn-based finishing diet supplemented with 0% supplemental tannin, 0.6% condensed tannin, 0.6% hydrolysable tannin, and a mixture of 0.3% condensed and 0.3% hydrolysable tannin (DM basis). Across the 84-d feeding period, tannin supplementation tended to increase ADG (1.53, 1.64, 1.61, and 1.65 ± 0.06 kg/d, respectively; $P = 0.08$) and DMI (10.0, 10.3, 10.2, and 10.7 ± 0.15 kg/d, respectively; $P = 0.06$). There were no treatment effects on gain efficiency (0.152, 0.159, 0.157, 0.155 ± 0.005, respectively; $P = 0.42$), and observed/expected diet NEm (0.97, 0.99, 0.99 and 0.97 ± 0.02, respectively; $P = 0.38$). It is concluded tannin supplementation may enhance feedlot cattle growth performance during the late finishing phase independently of effects on ruminal metabolism protein (metabolizable protein supply from the basal unsupplemented diet already in excess of requirements for growth).

Key Words: cattle, performance, tannin

T17 Influence of supplemental urea withdrawal during the late finishing phase on growth performance and digestive function in feedlot cattle. D. May*[1], J. Calderon[1], M. Montano[1], A. Plascencia[1], and R. Zinn[2], *[1]UABC, Mexicali, BC, Mexico, [2]University of California, Davis.*

Two trials were conducted to evaluate the influence of supplemental urea withdrawal on characteristics of digestion (Trial 1) and growth performance during the late finishing phase (trial 2). In Trial 1, 6 Holstein steers (160 kg) with cannulas in the rumen and proximal duodenum were used in a replicated 3 × 3 Latin square experiment. Treatments consisted of a steam-flaked based finishing diet, where dietary urea supplementation was adjusted to provide 100, 80 and 60% of expected urea fermentation potential. Daily DMI was restricted to 2.5% of BW. Decreasing supplemental urea decreased (linear effect) ruminal digestion of OM ($P = 0.04$) and NDF ($P = 0.05$), and nonammonia N flow to the small intestine ($P = 0.04$), and tended to decrease ($P = 0.06$) ruminal microbial protein synthesis. There were no treatment effects on total tract digestion of OM, NDF and starch digestion. Decreasing supplemental urea tended to decrease (linear effect) total tract digestion of OM ($P = 0.06$) and NDF ($P = 0.06$), and decreased (linear effect) total tract digestion of N ($P = 0.04$), and DE ($P = 0.05$). Ruminal and total tract starch digestion were unaffected by treatments. There were no treatments effects on ruminal pH. However, decreasing urea supplementation decreased (linear effect, $P = 0.007$) ruminal ammonia N, and increased (linear effect, $P = 0.04$) ruminal acetate:propionate molar ratio and estimated methane production. In Trial 2, 90 crossbred steers (468 kg), were used in a 40 d feeding trial (5 steers/pen, 6 pens/ treatment) to evaluate treatment effects on final-phase growth performance. Decreasing urea supplementation did not affect DMI, but decreased (linear effect, $P < 0.01$) ADG, gain efficiency, and dietary NE ($P = 0.03$). There were no treatment effects on carcass characteristics. In addition to effects on net protein flow to the small intestine, depriving cattle of otherwise ruminally degradable N during the late finishing phase may negatively impact site and extent of digestion of OM digestion and NE value of the diet, as well as ADG.

Key Words: cattle, performance, urea

T18 Evaluation of maternal trace mineral source on cow/calf performance and the subsequent feedlot performance of beef calves. R. L. Stewart Jr.*[1], T. J. Wistuba[2], G. I. Zanton[2], and A. L. Jones[3], *[1]The University of Georgia, Athens, [2]Novus International, St. Charles, MO, [3]The University of Georgia, Tifton.*

A 2-yr study was conducted to assess the effect of trace mineral source (15 ppm Cu, 30 ppm Zn, and 40 ppm Mn; based on a 4-oz mineral intake) on performance of cows and calves and the subsequent feedlot performance and carcass characteristics of beef calves. Each year, the 216 cow herd (BW = 623 ± 21 kg) at the University of Georgia Northwest Georgia Research and Education center was blocked by age (senior cows, junior cows, and first calf heifers) and randomly assigned to receive trace minerals from an inorganic (INORG) or chelated (CHEL; Mintrex, Novus International Inc.) (n=6). A methionine supplement was added to the inorganic source to balance the 2-hydroxy-4-methylthio butanoic acid provided by the Mintrex. Minerals were offered as a component of a free choice mineral, and were offered starting 30 d prior to calving of yr-1 and continuing through weaning of yr-2. Calves were maintained with the dam through weaning. After weaning in yr-1, steers were grouped by treatment and backgrounded for 45 d prior to shipping to a finishing facility. All steers were commingled and fed a common finishing diet for 107 or 142 d, based on estimated final back fat thickness of 1.27 cm. Cow BW at weaning (598 and 610 kg, respectively) and BW change from prepartum to weaning (−20.3 and −9.3) kg, respectively) did not differ ($P \geq 0.15$) between INORG and CHEL treatments. Calf birth weight (34.3 and 34.4 kg, respectively) and adjusted 205-d weaning weight (242 and 249 kg, respectively) did not differ ($P \geq 0.25$) between INORG and CHEL treatments. However, kg of calf weaned per cow exposed to breeding was greater ($P < 0.01$) for CHEL compared to INORG (240 and 228 kg, respectively). During the finishing period, average daily gain was similar ($P = 0.75$) between INORG and CHEL (1.18 and 1.20 kg, respectively). Carcass characteristics were similar between treatments ($P \geq 0.40$), however CHEL tended ($P = 0.07$) to yield more carcasses grading low choice or higher (87.5 and 79.3%, respectively). These data indicate chelated minerals can improve calf production per cow and subsequently improve carcass quality of beef calves.

Key Words: beef, chelated, trace mineral

T19 Influence of abomasal infusion of phenylalanine on characteristics of digestion of a steam-flaked wheat-based finishing diet fed to Holstein steers. A. A. Vite[1], A. G. Alvarez*[1], A. P. Marquez[1], M. F. Montano[1], N. G. Torrentera[1], and R. Zinn[2], *[1]UABC, Mexicali, BC, Mexico, [2]University of California, Davis.*

Four Holstein steers with cannulas in the rumen, abomasum, and proximal duodenum, were used in a 4 × 4 Latin square design experiment to evaluate the influence of abomasal infusion of phenyalanine (PHE, 0, 5, 10 or 15 g/hd/d) on feed intake and digestive function. Steers were allowed ad libitum access to a steam-flaked wheat-based diet (DM basis; 72% steam-flaked wheat, 12% sudangrass hay, 9% sugarcane molasses, 3% yellow grease, 1.9% limestone, 1.3% urea, and 0.5% minerals and vitamins). Chromic oxide was added (0.3% as DM basis) as internal digesta marker. There were no treatment effects ($P > 0.10$) ruminal OM digestion or ruminal microbial efficiency (microbial N/kg OM fermented). However, PHE infusion increased rumen pH (linear component, $P = 0.07$), and ruminal NDF digestion (linear component, $P = 0.09$). There were no treatment effects ($P > 0.10$) on total tract OM and N digestion. However, PHE infusion increased (linear component, $P = 0.03$) total tract NDF digestion (largely attributable to the increased ruminal NDF digestion). Changes in ruminal NDF digestion due to PHE infusion were associated with increased ($P = 0.06$; linear component) rate of ruminal NDF digestion (KdNDF) and decreased rate of ruminal NDF passage (KpNDF). This latter effect may evidence a role for PHE in regulation ruminal emptying and passage of chyme to the small intestine.

Key Words: cattle, digestion, phenylalanine

T20 Effects of postruminal amino acid supply on dietary protein flow from the rumen in forage based diet using a continuous culture system. M. M. Masiero*, J. H. Porter, M. S. Kerley, and W. J. Sexten, *University of Missouri, Columbia.*

Three diets with increasing ruminal undegraded AA, 80% (LO), 100% (MD) and 120% (HI) of the requirements for a 200 kg steer, were fed (50g/d) to continuous culture fermenters (FER) to characterize RUP supplementation (porcine blood meal and Aminoplus) in forage-based diet. We hypothesized increasing diet RUP concentration would increase RUP flow from the rumen without influencing microbial fermentation. Diets were randomly distributed over FER (n = 24), acclimated for 4 d, and sampled over 3 d. FER content was monitored at 0h and 4 h post feeding for pH and analyzed for VFA (m*M*) and ammonia concentration (AM) (m*M*/dL). The pH was greater ($P = 0.005$ and 0.0008) for HI, 6.46 and 6.42, compared to MD, 6.34 and 6.27, and LO, 6.32 and 6.24, for 0 and 4 h, respectively. AM increased as RUP increased (LO 3.18; MD 5.30; HI 8.79) at 0 h, however at 4 h, AM was greater ($P < 0.0001$) for HI (10.58) compared to MD (6.10) and LO (4.26). Acetic, propionic, valeric, total VFA and acetic:propionic did not differ ($P = 0.44$) at 0 and

4 h. Butyric did not differ ($P = 0.37$) at 0 h. At 4 h butyric was greater ($P = 0.036$) for LO (16.9) compared to HI (15.4), however MD (16.5) did not differ between treatments. Isobutyric was greater ($P < 0.0001$) for HI (1.5) compare to MD (1.2) and LO (1.1) at 0 h. At 4 h, isobutyric increased as RUP increased (LO 1.2; MD 1.4; HI 1.6; $P < 0.0001$). Isovaleric was greater ($P < 0.0001$) for HI, 2.9 and 3.0, compared to MD, 2.5 and 2.6, and LO, 2.2 and 2.4, for 0 and 4 h, respectively. OM, NDF and ADF digestibility, microbial efficiency and g of bacterial N/d did not differ ($P = 0.4$). Protein digestibility (%) was greater ($P = 0.042$) for LO (47.2) and HI (46.0) compared to MD (38.3). At the lower RUP inclusion levels RUP was recovered in effluent flow however at greater RUP inclusion levels 34% of added RUP was recovered in effluent flow. In conclusion, RUP supplementation in forage-based diets increased RUP flow from the rumen without influencing microbial fermentation. Reduced RUP for HI compared to MD may be due to microbial adaptation to greater RUP levels.

Key Words: digestibility, fermentation, RUP

T21 Phosphorus excretion in beef steers as affected by increasing levels of corn gluten feed supplementation. D. D. Harmon*[1], E. A. Riley[1], A. L. Zezeski[1], J. K. Smith[1], H. L. M. Tucker[2], S. J. Neil[1], B. D. Dalton[1], and M. A. McCann[1], *[1]Virginia Polytechnic Institute and State University, Department of Animal and Poultry Sciences, Blacksburg, [2]Virginia Polytechnic Institute and State University, Department of Dairy Science, Blacksburg.*

Overfeeding of phosphorus (P) is a contributing factor to P levels in the Chesapeake Bay. The objective of this study was to determine the impact of increasing levels of corn gluten feed as a supplemental organic source of P. Eight Hereford steers (427 ± 79 kg) were randomly assigned to one of four dietary treatments in a 4 × 4 replicated Latin square design. Steers were fed a basal diet of chopped grass hay (0.13% P) and 0, 0.5, 1.0 or 1.5 kg/d of dried corn gluten feed pellets. All steers were supplemented with 0.91 kg/d beet pulp, 0.45 kg/d rumen-inert fat supplement and 18 g/d trace mineral salt. Urea was added to the respective diets at levels of 95.34, 72.64, 49.94, and 31.78 g/d to ensure equal dietary protein across treatments. Steers were housed individually and fitted with total fecal collection bags. Steers were adjusted to each diet for 9 d followed by a 5-d collection period. Following the final collection of each period, a 10 ml jugular blood sample was collected and analyzed to determine serum inorganic P. Feed and fecal samples were dried, ground, subsampled and analyzed for inorganic and total P. Dietary P increased ($P < 0.05$) as level of corn gluten feed increased: 10.14, 14.19, 18.26 and 22.30 g/d. Dry matter digestibility increased linearly ($P < 0.05$) as dietary P increased: 51.15, 52.25, 52.72 and 54.10%. Total P excretion increased linearly ($P < 0.05$) with increasing dietary P content: 9.42, 10.76, 15.51, 16.40 g/d. Inorganic P excretion increased linearly ($P < 0.05$) with increasing dietary P content: 4.26, 6.17, 8.68 and 10.25 g/d. Total P excretion was highly correlated ($P < 0.05$; $r = 0.81$) with inorganic P excretion. Serum inorganic P increased linearly ($P < 0.05$) with increasing dietary P content: 5.61, 5.87, 6.64 and 6.80 mg/dL. Fecal P increased as dietary P increased in steers fed varying dietary levels of P from organic sources. Prevention of overfeeding of P on beef cattle operations is a strategic, managerial practice that can reduce P levels.

Key Words: beef cattle, byproduct feedstuffs, phosphorus

T22 Effect of Bovamine on lactation performance by dairy cows. L. F. Ferraretto* and R. D. Shaver, *University of Wisconsin-Madison, Madison.*

The objective of this study was to evaluate the effect of direct-fed microbial (Bovamine) addition to a TMR on lactation performance by mid-lactation dairy cows. One hundred and twelve Holstein cows (28 primiparous and 84 multiparous; 139 ± 47 DIM at trial initiation) were stratified by parity and DIM and randomly assigned to 14 pens of 8 cows each. Pens were then randomly assigned to 1 of 2 treatments in a continuous-lactation trial consisting of a 2-wk covariate adjustment period with cows fed the basal TMR followed by a 10-wk treatment period with cows fed their assigned treatment diets. The two treatments were: basal TMR plus either 1 g/cow/d Bovamine (BOV, 1×10^9 cfu/g *Lactobacillus acidophilus* NP51 and 2×10^9 cfu/g *Propionibacterium freudenreichii* NP24) or placebo (CON). Data were analyzed as a completely-randomized design with the data from the preliminary period as a covariate using PROC MIXED in SAS. The model included treatment, week and treatment × week interaction as Fixed effects, and pen within treatment as a Random effect. Milk yield was similar ($P > 0.10$) between treatments and averaged 44.9 kg/d. There was a trend ($P < 0.08$) for DMI to be decreased by 0.4 kg/d per cow for BOV overall, and DMI was lower ($P < 0.05$) for BOV than CON during wk 2, 3, 6, 9 and 10 ($P < 0.001$ for week × treatment). However, measures of feed conversion (milk or component-corrected milk yields per unit DMI) were unaffected ($P > 0.10$) by treatment. Milk fat, protein and urea nitrogen concentrations were unaffected ($P > 0.10$) by treatment and averaged 3.75%, 3.11% and 15.2 mg/dL, respectively. Likewise, body weight change and condition score were unaffected ($P > 0.10$) by treatment. Under the conditions of this study, with mid-lactation cows fed a 54% forage TMR (DM basis), there was no improvement in lactation performance from the inclusion of Bovamine in the diet.

Key Words: direct-fed microbial, dairy cow, milk production

T23 Use of plasma lysine to assess postruminal amino acid bioavailability in rumen bypass lysine from Megamine-L. E. Evans*[1], N. Clark[2], and E. Block[3], *[1]Essi Evans Technical Advisory Services Inc., Bowmansville, ON, Canada, [2]Atlantic Dairy and Forage Institute, Fredericton Junction, NB, Canada, [3]Arm & Hammer Animal Nutrition, Princeton, NJ.*

An experiment was conducted to assess the use of plasma Lys to determine post-ruminal absorption. Rumen cannulated, post-peak production cows were housed in stanchion stalls. Cows had ad libitum access to a TMR that met their Lys needs based on CPM Dairy. Four treatments were evaluated in a Latin square design with periods of 14 d. Control was 50g of abomasally infused Lys (63.4g of Lys HCl) and was compared to 37.5, 50 and 62.5 g of abomasally Lys from cows receiving a single rumen dose of Megamine-L (Church & Dwight Co., Inc.). Actual amounts of Megamine-L were calculated to deliver the desired abomasal Lys based on predetermination of soluble protein at 28.6%, a degradation rate of 2.02%/hr, an assumed escape of 50% of the Lys, and 16% free Lys the product. One day prior to application (d 13 of each period) of the test article, blood was drawn via jugular catheter at 0800, 1200, 1600, 2400 and 0400 h to determine baseline plasma Lys levels. At 0800 h on the day of the experiment (d 14 of each period) the Megamine-L treatments were administered as a single dose through a rumen cannula. The control Lys infusion consisted of 63.4g of Lys-HCl (50 g of Lys) dissolved in 3 L of water and was administered over a 2-h period. Blood was drawn at 0745, 1200, 1600, 2400 and 0400 h. Lysine availability was calculated from the area under the curve (AUC). AUC for the control treatment was assumed to represent a digestibility of 98%. Lys bioavailability from Megamine-L increased ($P < 0.05$) with the amount of Lys supplied (57.7, 67.2 and 70.2% calculated absorption

at 37.5, 50.0 and 62.5 g of abomasal Lys). Previously reported trials (digestibility-metabolism trial design) estimated metabolizable Lys in Megamine-L at 46% which is lower than the results in this trial design. Use of plasma Lys to assess Lys status is not accurate, and likely varies with gut and hepatic uptake and utilization. It is likely that compounds exiting the rumen more gradually in normal feeding situations would be disadvantaged relative to the single bolus doses of Lys administered in this trial.

Key Words: metabolizable lysine, rumen bypass lysine, dairy cows

T24 Lactational performance and ruminal fermentation profiles of dairy cows fed different corn silage hybrids ensilaged without or with microbial inoculant. M. N. McDonald[1], M. S. Holt[1], A. J. Young[1], J.-S. Eun*[1], and K. E. Nestor[2], *[1]Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan, [2]Mycogen Seeds, Indianapolis, IN.*

A lactation study was conducted to examine the effects of a silage inoculant (SI) applied onto conventional (CCS) or brown midrib corn silage (BMRCS) in lactation diets on lactational performance and ruminal fermentation of dairy cows. Forty multiparous Holstein cows were used starting at 20-58 DIM in a completely randomized design with a 2 × 2 factorial arrangement of treatments. Cows were randomly assigned to 1 of 4 diets: CCS TMR without SI, CCS TMR with SI (CCS+SI), BMRCS without SI, and BMRCS with SI (BMRCS+SI). The experiment lasted a total of 10 wk (2 wk of adaptation and 8 wk of data and sample collection). The SI (Agmaster XV, DuPont, Waukesha, WI) was applied at 1.25×10^5 cfu/g of corn crop to the CCS+SI and the BMRCS+SI. Cows fed BMRCS increased DMI compared to those fed CCS (27.9 vs. 25.6 kg/d; $P = 0.05$), but SI did not affect DMI. Milk yield averaged 45.8 kg/d across treatments, and it was not affected by dietary treatments. In contrast, milk fat concentration and yield increased ($P < 0.05$) due to feeding BMRCS, leading to an increase in ECM yield by feeding BMRCS (47.5 vs. 43.2 kg/d; $P = 0.03$). Dietary treatments did not influence concentrations of milk protein and MUN. Digestibility of DM was similar among treatments, whereas feeding BMRCS increased ($P = 0.05$) digestibilities of NDF and ADF. Ruminal pH averaged 6.29 across treatments and did not differ. Concentration of VFA was not affected by dietary treatments. While feeding BMRCS increased ($P = 0.05$) molar proportion of acetate, it decreased ($P = 0.05$) molar proportion of propionate, resulting in an increase in acetate-to-propionate ratio ($P = 0.05$). Applying SI did not influence VFA profiles. Ammonia-N concentration was similar in response to dietary treatments. The SI tested in this study did not affect lactational performance and ruminal fermentation. However, cows fed BMRCS increased yields of milk fat and ECM due to increased fiber digestion and ruminal acetate production.

Key Words: brown midrib corn silage, silage inoculant, lactating dairy cows

T25 Efficacy of various adsorbents to reduce aflatoxin M_1 levels in milk of lactation cows fed aflatoxin B_1. M. Savari[1], M. Dehghan-Banadaky*[1], K. Rezayazdi[1], and M. Javan-Nikkhah[2], *[1]Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran, Karaj, Tehran, Iran, [2]Plant Protection Department, University College of Agriculture and Natural Resources, University of Tehran, Karaj, Tehran, Iran.*

The aim of this study was to comparison of various adsorbents including Bentonite, Zeolite, Mycosorb (Alltech) and Biotox (Biochem) on their ability to reduce aflatoxin in milk of Holstein cows. Thirty-five Holstein cows divided into 5 groups (with average 37.3 kg/day milk yield and 114 DIM). Experimental groups were included these treatments: (1) Aflatoxin B_1 (300 µg aflatoxin B_1 dissolved in water) + 40 g Bentonite; (2) Aflatoxin B1 + 20 g Zeolite; (3) Aflatoxin B_1 + 20 g Mycosorb; (4) Aflatoxin B_1 + 20 g Biotox; and (5) aflatoxin B_1 without adsorbent. Milk sampling was performed 4 days (1 day before of treatment and 3 days after that). Data were analyzed using the mixed procedure of the SAS in a completely randomized design with 7 replications. The results of this study showed that milk production was not affected by treatments. In case of milk fat percentage on the second day after treatment, the difference between treatments was significant ($P < 0.05$). As follows the second treatment and the control treatment showed the highest (3.8%) and lowest (3%) percentage of milk fat. On the third day after treatment, respectively treatment 1 and treatment 3 showed the highest (4%) and the lowest (3.2%) percentage of milk fat ($P < 0.05$). In case of the percentage of protein and lactose in milk at the second day after treatment, the second treatment had the highest value ($P < 0.01$). After analysis of the data from ELISA test of AFM1 in milk was determined that most of aflatoxin contamination was observed on the day of treatment and it was related to the control treatment (400.49 ppt) and the lowest contamination in the same day belonged to the first group of cows means consuming 40 g of bentonite (253.89 ppt). According to the results of this experiment the excretion aflatoxin in milk immediately after consumption of toxin by animal in the first milking time was the maximum amount and this amount decreases gradually in the next milking. The sort ascending of efficiency absorption of toxin by absorbent was as follows: Mycosorb, Zeolite, Biotox, and Bentonite.

Key Words: aflatoxin B_1, aflatoxin M_1, mineral and organic adsorbents

T26 Effect of yeast probiotic (*Saccharomyces cerevisiae)* in milk or starter on growth performance, fecal score and rumen parameters of dairy calves. M. Hoseinabadi, M. Dehghan-Banadaky*, and A. Zali, *Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran, Karaj, Tehran, Iran.*

The objective of this study was to determine how yeast probiotic in milk or starter affects growth performance, fecal score and rumen parameters of dairy calves. Thirty Holstein female calves (14 ± 1 d old) divided to 3 groups, using a completely randomized design with 51-d periods. The treatments included: (1) 2 g yeast probiotic in milk (PM); (2) 2 g yeast probiotic in starter (top dress, PS); (3) control, without probiotic (CON). Animal were individually housed and had free access to water and starter concentrate (21.6% CP and 80% TDN). All calves were offered 6 L/d of milk replacer (22% CP, 19% EE) from birth, which was incrementally reduced after 6 wk to enable weaning by the end of wk 8. The study finished at 65 days old. Fecal scores (fecal scoring: fluidity, 1 = normal, 2 = soft, 3 = runny, 4 = watery) and starter intake were evaluated daily. Calves were weighted at 28, 42, 56, 65 days of age. At 65 d of age, ruminal fluid samples were collected using an oro-ruminal probe and a suction pump for pH and N-NH_3 determination. The results exhibited that experimental diets had not affected body weight changes, average daily gain, and feed efficiency ($P > 0.05$), but dry matter intake was significantly lower in treatment 2 than treatment 3 ($P < 0.01$). pH, N-NH_3 concentration of rumen fluid and blood parameters was not affectd by treatments ($P > 0.05$). Fecal score and health in treatments 1 and 2 were significantly lower than control. Generally using yeast probiotic in milk appeared to be an acceptable alternative than yeast probiotic in starter.

Table 1. Effect of yeast probiotic in milk or starter of Holstein calves

Item	PM	PS	CON	*P*-value	SEM
DMI, g/d	1145[ab]	998[b]	1219[a]	0.006	79.3
ADG, kg/d	0.67	0.65	0.67	NS	0.07
ADG/DMI	0.41	0.44	0.39	NS	0.044
BW, kg	64.7	63.0	64.7	NS	1.27
pH	7.20	6.73	7.10	NS	0.225
$N\text{-}NH_3$, mg/dL	8.25	10.84	7.53	NS	1.937
Fecal score	1.28[b]	1.37[b]	1.51[a]	0.01	0.06

[a,b]In the same row, means with different letter has significant difference ($P < 0.5$).

Key Words: milk, starter, yeast probiotic

T27 Effects of rare earth-chitosan chelate on blood biochemical parameters in lactating dairy cows. R. X. Hu[1,2], J. Q. Wang*[1], D. P. Bu[1], J. B. Cheng[1], F. D. Li[2], H. Y. Zhao[1], S. H. Dong[1], and C. Y. Ren[1,2], *[1]State Key Lab of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agriculture Sciences, Beijing, China, [2]College of Animal Science and Technology, Gansu Agricultural University, Lanzhou, Gansu, China.*

This study examined the effects of different proportion of rare earth-chitosan chelate on blood biochemical parameters in lactating Chinese Holstein dairy cows. Forty-eight lactating cows (days in milk = 130 ± 5; average milk yield = 33.2 ± 5.1 kg/d) were blocked based on days in milk, milk production, and parity and were randomly assigned to 1 of 4 treatments. Dietary treatments were 4 adding levels of RECC (rare earth-chitosan chelate):0 (control), 0.15%, 0.75%, and 1.5%, respectively. The experiment lasted 9 wk including the first week for adaptation. Blood was collected in evacuated tubes via caudal venipuncture at 0, 2, 4, 6, 8 week and placed on ice immediately following collection. In the present study the mean corpuscular hemoglobin and mean corpuscular volume were significantly ($P < 0.05$) affected of the entire hematological indices measured in the 0.15% RECC group vs. control and other groups. Feeding 0.75% or 1.5% RECC resulted in lower white blood cell count and hemoglobin vs. 0.15% RECC group ($P < 0.01$). 0.15% RECC-added in animals thrombocytocrit and platelet were higher than control and 0.75% group ($P < 0.05$). No significant difference in the serum hematocrit, intermediate cell, amylase, alkaline phosphatase and blood urea nitrogen were detected among groups ($P > 0.23$). In general the red blood cell, lymphocyte and neutrophilic granulocyte were consistently enhanced in cows with 0.15% RECC supplemented vs. control, and while the different counts did not follow a particular trend ($P > 0.06$). However, greater intake of RECC (0.75% or 1.5%) decreased red blood cell, lymphocyte and neutrophilic granulocyte vs. control ($P > 0.06$). This suggested that greater intake of RECC have a possible adverse effect of dairy cows, and further confirmed that the tolerable level of RECC adding in dairy cow diet could be 0.75% or 1.5%.

Key Words: rare earth-chitosan chelate, dairy cow, blood biochemical parameter

T28 Effects of rare earth-chitosan chelate on performance and milk composition in dairy cows. R. X. Hu[1,2], J. Q. Wang*[1], D. P. Bu[1], J. B. Cheng[1], F. D. Li[2], H. Y. Zhao[1], S. H. Dong[1], and C. Y. Ren[1,2], *[1]State Key Lab of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agriculture Sciences, Beijing, China, [2]College of Animal Science and Technology, Gansu Agricultural University, Lanzhou, Gansu, China.*

Rare earth-chitosan chelate could improve animal performance supplemented low amount, while increased high level may have a inhibition of production. This study examined the effects of different proportion of rare earth-chitosan chelate on performance and milk content in lactating Chinese Holstein dairy cows. Forty-eight lactating cows (days in milk = 130 ± 5; average milk yield = 33.2 ± 5.1 kg/d) were blocked based on days in milk yield, lactation day, and parity and were randomly assigned to one of 4 treatments. Four dietary treatments were adding levels of RECC (rare earth-chitosan chelate): 0 (control), 0.15%, 0.75% and 1.5% of concentrate feed, respectively. The experimental period was 8 weeks. DMI (dry matter intake), milk yield were recorded daily, and milk composition (fat, protein, and lactose) were analyzed weekly. Data were analyzed by mixed or GLM procedure of SAS software. Feeding 0.15% RECC resulted in greater DMI and milk yield vs. Control and other groups ($P < 0.01$), but greater intake of RECC decreased DMI and milk yield ($P < 0.01$).Milk protein rate was significantly decreased to 3.07% and 2.97% in 0.15% or 1.5% RECC groups vs. control (3.2%) and 0.75% RECC group (3.18%; $P < 0.01$). Compared with control, milk fat was lower while 0.15% or 1.5% of RECC were supplemented, but there was no difference between control and 0.75% RECC-added animals ($P = 0.078$). Adding 1.5% RECC significantly lower total milk solid vs. control and 0.75% RECC group ($P = 0.017$), and the reduction depended on intake of RECC. In addition, feeding RECC have no significant effect on lactose, milk urea nitrogen and milk SCC ($P > 0.31$). It was concluded that add 0.15% RECC could increase milk yield and milk content in dairy cows, but greater intake of RECC (1.5%) have a negative effect of production.

Key Words: rare earth-chitosan chelate, dairy cow, performance and milk composition

T29 Effect of dietary N-carbamoyl glutamate on milk production and nitrogen utilization in high yielding dairy cows. B. Chacher[1,2], W. Zhu*[1,2], J. A. Ye[1,2], D. M. Wang[1,2], and J. X. Liu[1,2], *[1]Institute of Dairy Science, College of Animal Sciences, [2]MoE Key Laboratory of Molecular Animal Nutrition, Zhejiang University, Hangzhou, China.*

High-yielding cows fed diet rich in protein impaired the ureagenesis and decreased feed intake and milk production. Arginine (Arg) played a key role in urea cycle regulation. Due to the high rumen degradation, feeding rumen-protected Arg seemed to be uneconomical. Alternatively, N-carbomyl glutamate (NCG) was of relatively lower rumen degradation rate and known as a potential Arg raiser, but the effect of NCG in dairy cows has not been determined. Thus, the objective of the current study was to determine the effect of NCG on milk production and nitrogen utilization in high yielding dairy cows. Sixty multiparous cows [DIM = 78 (SD 17.3), milk yield = 41.9 (SD 7.90) kg/d] were blocked based on milk yield and DIM, and randomly allocated to receive each of 4 dietary treatments supplemented with 0 (control), 10, 20 or 30 g/d NCG, respectively, for 7 weeks. Milk yield was recorded weekly. Dry matter intake, milk composition, plasma variables and urea N content (plasma, urine and milk) were determined every other week. Data were analyzed using the MIXED procedure of SAS. A statistically significant difference was defined at $P < 0.05$, and trends were declared at $0.05 \leq P \leq 0.10$. Dry matter intake did not change by NCG supplementation of NCG. Compared to the control, cows fed 20 g/d NCG tended to have higher milk yield and milk protein yield (40.01 and 1.12 kg/d vs. 38.09 and 1.04 kg/d). Contents of milk protein and lactose linearly increased ($P < 0.01$) with the supplementing NCG. Cow fed 20 or 30 g/d NCG

enhanced ($P < 0.01$) plasma nitric oxide and decreased ammonia N compared with the control. Plasma Arg concentration increased ($P < 0.01$) by 3.5 and 8.5% in cows fed 20 or 30 g/d NCG, respectively. Supplementation of 20 g/d NCG linearly decreased ($P < 0.01$) the urea N in milk, plasma and urine, while the N utilization (0.283 vs. 0.263) tended to be improved. In summary, supplementation of 20 g/d NCG may alter the plasma metabolite and milk contents, and hence improve lactation performance of high yielding dairy cows.

Key Words: N-carbamoyl glutamate, lactation performance, nitrogen utilization

T30 Predicting prolamin and ruminal starch digestibility in corn silage and high moisture corn using near infrared spectroscopy. K. Foerder* and J. Horst, *Agri-King Inc., Fulton, IL.*

Prolamin levels in corn have been shown to be negatively correlated to starch digestibility in dairy cows. Current analysis methods for prolamin and ruminal in vitro starch digestibility (IVSD) are costly and time consuming. Therefore, it would benefit producers to have a rapid, economic method to more effectively predict prolamin and IVSD of available feedstuffs. The objective was to determine if the use of near infrared spectroscopy (NIRS) could effectively predict prolamin and/or IVSD in corn silage (CS) or high moisture corn (HMC). Samples of CS and HMC were selected to represent regions across the United States and a variety of hybrids. Samples ranged from fresh, unfermented to well fermented and included a wide range of moisture levels. The samples were selected by spectra using WINISI software. A modified turbidimetric zein method developed by Larson and Hoffman (2008) was used to determine the prolamin concentration of each sample. The coefficient of variation (CV) in the prolamin assay is 6.5% using a ground shell corn standard across multiple assays and the results were used to create NIRS calibrations using a 5000 Foss Instrument. The wet chemistry results correlated to the NIRS calibration resulting in an R^2 of 0.91 for CS and 0.78 for HMC. The IVSD was determined on the same set of samples using a standardized 7-h in vitro method with rumen fluid from continuous cultures. The CV across multiple assays for the IVSD assay was 1.89% using a corn silage standard. The NIR spectra were collected and used to determine if NIRS could also predict IVSD. The resultant IVSD calibration resulted in an R^2 of 0.80 for CS and 0.82 for HMC. The development of NIRS calibrations for prolamin and IVSD in both CS and HMC would allow for rapid and economical predictions of starch utilization and better usage of feedstuffs by dairy producers.

Key Words: prolamin, starch digestibility, near infrared spectroscopy

T31 Mineral containing dehydrated molasses lick blocks precalving provide a viable alternative for addressing mineral imbalances during calving in pasture-based New Zealand dairy cows. M. H. Oliver*[1,2], S. Rossenrode[1], and J. B. Aveling[3], *[1]UniServices Ltd., University of Auckland, Auckland, New Zealand, [2]Liggins Institute, University of Auckland, Auckland, New Zealand, [3]Ballance Agri-Nutrients, Tauranga, Bay of Plenty, Tauranga, New Zealand.*

Milk fever and associated conditions occurring in NZ dairy cows around calving are often prevented by dusting pasture or supplementary feed with MgO and also by adding minerals (Mg, Co, Se, Cu, Zn, I) to drinking water up to 2 months before calving. An integrated approach to precalving supplementation using mineral containing dehydrated molasses-based lick blocks (Dry Cow) was evaluated in a trial beside traditional mineral supplementation in a typical NZ Friesian herd with a previous history of milk fever. Cows were recruited in their second or later pregnancy and randomly assigned to traditional mineral supplementation (TM, n = 290) or Dry Cow blocks (DC, n = 207). TM cows had MgO dusted on feed at a rate of 50 g/cow/day and minerals added to water. Dry Cow was provided at a minimum of one 22.5 kg block/20 cows, intake was estimated at 230 g/cow/day. Swedes and silage were fed precalving. Cows entered calving areas 1 week before calving; TM had a mineral additive added to feed at 120 g/cow/day, while DC had continued access to Dry Cow and both treatment groups had minerals added to their shared water supply. Thirty cows per group were blood sampled at the start of the trial before mineral provision, again 6 weeks later and then within 2 weeks following calving. Incidence of milk fever in all cows was low (2.6%) while mastitis (6.2%), retained placenta (8.1%) and assisted calving (8.9%) were moderate. Incident occurrence was not different between treatment groups. Body condition score was slightly higher in DC than TM before the trial (4.6± 0.1/6 vs. 4.8 ± 0.1/6, $P < 0.05$), but was identical following calving (4.5 ± 0.1/6). Serum Mg and B_{12} were not different at any stage while Ca was higher in DC after supplementation and calving ($P < 0.05$). Serum Se and Zn were higher after 6 weeks of supplementation in DC ($P < 0.001$) but not different after calving. In conclusion, mineral containing dehydrated molasses lick blocks offer a convenient method to supply minerals to pregnant cows on pasture, yielding comparable results to traditional methods in common use in NZ.

Key Words: mineral, calving, hypomagnesemia

T33 Milk and milk quality evaluated on a commercial Holstein dairy following an OmniGen-AF dry cow and early lactation feeding strategy. A. E. Holland*[1], J. D. Chapman[1], and L. O. Ely[2], *[1]Prince Agri Products Inc., Quincy, IL, [2]University of Georgia, Athens.*

The goal of this study was to evaluate milk production in multiparous Holstein cows fed OmniGen-AF (OG) during the dry period and into 30 d in milk (DIM). An 8,000 cow dairy farm consisting of 2-4,000 cow side-by-side mirror image units, identified as U1 and U2 were used. Each unit maintained separate dry and lactating herds and both fed the same dry and milk cow diets delivered as TMR. Cows were milked 2x and housed in open free-stall barns. To assess the effect of OG feeding (56 g/h/d) to dry and fresh cows on milk production, 4-90 d periods (P1 to P4) were used. In P1, both U1 and U2 cows received the control diet (no OG). In P2, U2 cows were fed OG and U1 were controls. In P3, both units were fed the control diet, and in P4, U1 cows were fed OG and U2 were controls. Cow groups within period by unit were balanced on parity, previous 305ME, total milk and predicted calving date using Dairycomp305 resulting in 2,337 enrolled cows. Other inclusion criteria were d in the dry period (>45 d) and 3 consecutive test-day milk weights. PROC GLM (SAS) was used to test for differences in first-test (FT), week 4 (W4) and peak (PK) milks and first test log score (LS). In P1, no differences were detected between U1 and U2 for FT (37 kg, 38.3 kg), W4 (39.7 kg, 40.4 kg) and PK (44.2 kg, 44.5 kg) milks. Similar results were observed at U1 and U2 in P3 (FT: 37.2 kg, 37.9 kg, W4: 39.2 kg, 40.6 kg, PK: 42.8 kg, 43.4 kg). In P2, OG was fed to U2 cows and milk yields differed from U1 for FT (37.2 kg, 32.7 kg, $P < 0.001$), W4 (41.5 kg, 38.2 kg, $P < 0.001$), and PK (47.0 kg, 44.6 kg, $P < 0.01$) milks. A similar trend was observed when units fed OG were reversed in P4. Milk yields for cows at U1 were different from U2 cows for FT (36.2 kg, 33.5 kg, $P < 0.01$), W4 (39.6 kg, 37.1 kg, $P < 0.001$), and PK (45.7 kg, 42.8 kg, $P < 0.01$) milks. No differences in LS were observed between U1 and U2 in P1-3; however, differences were detected ($P < 0.01$) in P4 (U1: 4.17, U2: 3.44). In this study the feeding of OmniGen-AF to multiparous Holstein cows during the dry period and into 30 DIM enhanced early lactation.

Key Words: cow, milk, OmniGen-AF

T34 Interaction between forage source and monensin on the formation of biohydrogenation intermediates in continuous cultures. Y. Sun*[1], T. C. Jenkins[2], and A. L. Lock[1], [1]*Michigan State University, East Lansing,* [2]*Clemson University, Clemson, SC.*

A dual-flow continuous fermenter study with a 2 × 2 factorial arrangement of treatments examined the interaction between forage source and monensin on the formation of biohydrogenation intermediates (BHI). Cultures (4 per treatment) were fed diets (50:50 forage:concentrate ratio) for 10 d with the last 3 d for sample collection for fatty acid analysis and samples taken on d 10 at 0, 2, and 4 h after the morning feeding for VFA determination. Treatments were two forage sources: 100% corn silage (100CS) vs. a 1:1 ratio of corn silage and alfalfa haylage (50CS) in combination with two levels of monensin (0 and the equivalent to 350 mg/cow/d). Corn oil was included in all treatments at 2% dietary DM. Data were analyzed as a randomized complete block design. The 100CS diet had higher ($P < 0.05$) propionate and lower ($P < 0.05$) acetate concentrations and acetate/propionate at all sampling times. Monensin did not affect VFA concentrations at the 0 or 2 h sampling times; at 4 h after feeding monensin decreased ($P < 0.05$) acetate/propionate from 1.76 to 1.51. Compared to 50CS, the 100CS diet had a higher ($P < 0.05$) extent of biohydrogenation (BH) for oleic acid (30.6 vs. 44.1%) but lower ($P < 0.05$) BH of linolenic acid (48.7 vs. 34.9%); treatments did not affect extent of linoleic BH. Monensin did not affect extent of BH of oleic, linoleic, or linolenic acid. The 100CS diet had lower ($P < 0.05$) total fatty acid output from cultures than the 50CS diet. Total *trans* 18:1 production was higher ($P < 0.05$) for 100CS than for 50CS (383 vs. 195 mg/d), accounted for mostly by an increase ($P < 0.05$) in the daily production of *trans*-10 18:1 (326 vs. 130 mg/d). There were no differences between the two forage sources on daily production of *trans*-10, *cis*-12 18:2. Monensin had no effect on the formation of BHI. In conclusion, monensin supplementation to continuous cultures caused an expected drop in acetate/propionate but did not increase the production of BHI. Corn silage as the only forage source increased the formation of BHI, particularly *trans*-10 18:1 that is normally associated with increased risk of milk fat depression.

Key Words: continuous culture, fatty acid, monensin

T35 Lysine loss during aerobic exposure of a corn silage based ration with mechanical extracted soybean meal with gums and various rumen-protected lysine products. D. A. Sapienza*[1] and C. A. Macgregor Jr.[2], [1]*Sapienza Analytica LLC, Slater, IA,* [2]*Grain States Soya Inc., West Point, N.*

Lysine loss was evaluated during in vitro aerobic exposure of a ration mixed with either nothing (B, ration blank), mechanical extracted soybean meal (MES) with gums (MESG) (P1), MESG with rumen-protected lysine (RPL) (MESGL) first production run (P2), MESGL second production run (P3), RPL (P4), or MESGL third production run (P5). MESGL was manufactured by inserting RPL into soy gums and drying the gums onto MES. RPL comprised lysine monohydrochloride embedded in a rumen-inert fat matrix. Two ration moisture (M) levels were evaluated: 48% M (L) (as fed 45% corn silage, 55% grain mix) and 58% M (H) (as fed 40% corn silage, 42% grain mix and 18% added water). Free lysine was quantified in water extracts taken from treatments at 0, 6, 18 and 24 hours. Eight replicates were taken for each treatment at each exposure time and lysine reported as microgram lysine per gram of water. Quadratic (orthogonal) polynomials were fitted to characterize the lysine concentration time trends separately for data acquired at L and H. Time trends for MESG runs with (P2, P3, P5) or without (P1) RPL where best characterized as linear trends. Trends for P2, P3, and P5 were not significantly different (F = 0.29 on 6 and 11 df, $P = 0.92$ at 48% M; F = 0.05 on 3 and 11 df, $P > 0.99$ at 58% M). The trend for P1 showed a significantly lower mean concentration at 48% M ($t = -2.52$ on 11 df, $P = 0.03$). Overall linear trends for P2, P3 and P5 were not significantly different from P1 ($P = 0.25$ at L; $P = 0.81$ at H). The concentration time trend for RPL alone (P4) was clearly significantly different from the MESG runs with a highly significant ($P < 1e\text{-}10$) quadratic coefficient, much higher average slope and higher mean concentration (or intercept). The overall linear trend of lysine release from RPL, when RPL was inserted into gums under the conditions of this study, was not different from the linear trend of lysine release from native lysine in MES and was different from the linear trend of lysine release from RPL when it was not in gums.

Key Words: rumen-protected lysine, mechanical extracted soybean meal, soy gum

T36 Consequences of supplementing lactating Holstein cows with an exogenous amylase on milk performance and rumen fermentation. A. Bach*[1,2], E. Azem[3], W. Steinberg[3], and V. Glitsø[4], [1]*ICREA, Institut de Recerca i Estudis Avançats, Barcelona, Spain,* [2]*Department of Ruminant Production, IRTA, Caldes de Montbui, Spain,* [3]*DSM Nutritional Products, Basel, Switzerland,* [4]*Novozymes, Bagsvaerd, Denmark.*

Improving feed efficiency and digestion may increase the economic profitability of dairy herds and minimize the environmental impact of milk production. To evaluate the effects of supplementing cows with an exogenous amylase, 240 lactating Holstein cows (BW = 653 ± 80 kg, DIM = 225 ± 112 kg, and milk yield = 39.2 ± 8.5 kg/d) distributed in 3 pens consuming exactly the same TMR (15.1% CP, 31.4% NDF, 1.69 Mcal of NEl/kg on DM basis) participated in a truncated Latin square experiment with three 29-d periods and 2 treatments: unsupplemented (CTR) and supplemented with 300 Kilo Novo Units of Ronozyme RumiStar CT per kg of TMR dry matter (RS). Within each pen, there were 5 rumen-cannulated cows that were used to determine ruminal degradation kinetics of corn and corn silage. Feed consumption, BW, and milk yield were recorded daily. In addition, during the second period, 2 rumen-cannulated cows from each treatment were used to place in situ bags containing: corn or corn silage to determine DM, NDF, and starch rumen degradation kinetics. The experimental unit for intake and performance data was pen. Data were analyzed using a mixed effects model. Overall, milk production was not affected by treatment. However, there was a significant interaction ($P < 0.001$) between treatment, parity, and stage of lactation. Cows on RS produced more milk ($P < 0.05$) than CTR cows in early stages of lactation (DIM < 150 d), and this increase was more pronounced ($P < 0.05$) in multiparous (42.5 vs. 41.0±1.47 kg/d, respectively) than in primiparous cows (35.1 vs. 34.0 ± 1.52 kg/d, respectively). Primiparous cows on RS gained more BW (16 ± 2.1 kg per period) than CTR cows (12.1 ± 2.1 kg per period), and multiparous cows on RS also recovered more BW than CTR cows after 150 DIM (13.5 vs. 9 ± 1.9 kg per period after 150 DIM, respectively). There was a tendency ($P = 0.07$) for the rate of DM and starch degradation for corn, and NDF for corn silage to increase with RS supplementation. These results suggest that RS supplementation may have increased nutrient availability to cows.

Key Words: digestibility, enzyme, yield

T37 Apparent synthesis of riboflavin and niacin in rumen of lactating dairy cows fed alfalfa or orchardgrass silages. D. S. Castagnino*[1,3], K. L. Kammes[2], M. S. Allen[2], R. Gervais[3], P. Y. Chouinard[3], D. E. Santschi[4], and C. L. Girard[1], [1]*Agriculture and Agri-Food*

Canada, Sherbrooke, Quebec, Canada, [2]Department of Animal Science, Michigan State University, East Lansing, [3]Departement de Sciences Animales, Universite Laval, Quebec, Quebec, Canada, [4]Valacta, Dairy Production Centre of Expertise in Quebec and the Atlantic regions, Ste-Anne-de-Bellevue, Quebec, Canada.

Effects of forage family (legume vs. grass) on apparent ruminal synthesis and post-ruminal supply of riboflavin and niacin were evaluated using 13 ruminally and duodenally cannulated lactating Holstein cows. The experiment was a crossover design with two 18-d treatment periods following a preliminary period during which all cows were fed a diet intermediate in composition between the treatment diets. Treatment diets were formulated to contain 25% forage NDF, 30% total NDF and contained as sole forage, alfalfa (AL, 42.3% NDF) or orchardgrass (OG, 58.2% NDF) silages. Intakes of riboflavin and niacin were greater ($P <$ 0.05) for AL than OG (riboflavin: 1179 vs. 372 ± 32 mg/d; niacin: 1253 vs. 1106 ± 61 mg/d). Alfalfa tended to increase the duodenal flow of riboflavin compared with OG ($P = 0.07$; 1131 vs. 902 ± 85 mg/d) but the duodenal flow of niacin was not affected by treatment ($P > 0.61$; 1993 vs. 1879 ± 154 mg/d for AL and OG respectively). Alfalfa decreased apparent ruminal synthesis of riboflavin compared with OG ($P < 0.01$; −47 vs. 530 ± 79 mg/d) but the apparent ruminal synthesis of niacin was not affected by treatment ($P = 0.87$; 739 vs. 773 ± 144 mg/d for AL and OG respectively). Riboflavin intake was correlated positively with its duodenal flow ($r = 0.44$, $P = 0.02$) but negatively with apparent ruminal synthesis of the vitamin ($r = -0.71$, $P < 0.01$). On the other hand, apparent ruminal synthesis of niacin was correlated positively with its duodenal flow ($r = 0.95$, $P < 0.01$). Forage family affected the apparent ruminal synthesis of riboflavin but had limited effects on the amounts of riboflavin and niacin reaching the sites of absorption.

Key Words: dairy cow, riboflavin, niacin

T38 The effect of a feed additive on the feeding value of a silage-based TMR exposed to air. M. Windle* and L. Kung Jr., *University of Delaware, Newark.*

The objective of this study was to evaluate the effect of feeding a fresh or aerobically spoiling silage-based TMR with or without Omnigen WYC (OWYC, Prince Agri Products Inc., Quincy, IL) on intake and rumen fermentation parameters in heifers. Four Holstein heifers with ruminal cannula were fed 1 of 4 treatments, in a 4 × 4 Latin square design utilizing 14-d periods. The four specific treatments were (A) fresh TMR fed for d 1 to 14, (B) fresh TMR fed for d 1 to 7, spoiled TMR for d 8 to 14, (C) fresh TMR for d 1 to 7, spoiled TMR plus OWYC for d 8 to 14, or (D) fresh TMR plus OWYC for d 1 to 7, spoiled TMR plus OWYC for d 8 to 14. Freshly mixed TMR was prepared daily and fed immediately for all treatments during the first 7 d of each period. To prepare aerobically spoiled feed for the second 7 d of each period, fresh TMR was allowed to spoil for several (2 to 5) d prior to feeding. The TMR exposed to air had a greater pH ($P < 0.01$), more yeasts ($P <$ 0.01), and lower concentrations of lactic acid ($P < 0.01$), acetic acid (P < 0.01), and ethanol ($P < 0.01$) than fresh TMR, and had temperatures 5 to 30°C above ambient (20-22°C) temperatures, indicating that it was spoiling. Feeding spoiled TMR alone during d 8 to 14 resulted in a lower DM intake (treatment B) when compared to feeding fresh TMR alone (treatment A) ($P < 0.05$). Heifers fed OWYC (treatments C and D) had DM intakes that were numerically but not statistically greater than heifers fed treatment B. Heifers consuming spoiled TMR (treatments B, C, D on d 8 to 14 of each period) had more yeasts in their rumen fluid than heifers fed fresh TMR (treatment A) ($P < 0.05$). There was a trend ($P = 0.14$) for heifers that were fed spoiled TMR and who received OWYC for the entire 14 d of each period (treatment D) to have a greater average rumen pH and maximum rumen pH than cows fed fresh TMR (treatment A). There were no differences among treatments in ruminal VFA. Relative to cows fed the fresh TMR, digestion of DM was not affected by feeding spoiled TMR. Feeding a spoiled TMR to heifers reduced intake and supplementing spoiled TMR with OWYC tended to moderate this effect.

Key Words: aerobic stability, spoilage, yeast

T39 Effects of treatment with propylene glycol in fat transition cows. V. Bjerre-Harpøth*, A. C. Storm, T. Larsen, and M. Larsen, *Department of Animal Science, Aarhus University, Foulum, Tjele, Denmark.*

The aim was to investigate the capability of propylene glycol supplementation to impact on the metabolic adaption to lactation in fat transition cows with the object to reduce the risk of fatty liver and ketosis. The experiment was a completely randomized design. Ten ruminal cannulated and intercostal artery catheterized fat Holstein cows (body condition score 2 wk prepartum: mean ± SD = 3.8 ± 0.3) were at parturition randomly assigned to a ruminal pulse dose of 500 g propylene glycol (PGG) or of 500 g water (CON) once a day (at morning feeding) for 4 wk postpartum (pp). All cows were fed the same diet. Milk samples were taken at every milking, 3/d. Two sets of blood samples were collected; weekly blood samples were taken from the tail vein, whereas daily blood sample was collected from the artery ±7 days from parturition. Data were analyzed using PROC MIXED in SAS with treatment (trt), day/week, and the interaction as fixed effects. Cow was considered as random effect, and day/week within cow as repeated measurement. Dry matter intake, body condition score and milk yield were not affected by propylene glycol ($P > 0.38$). The PGG resulted in decreased milk fat concentration ($P = 0.04$). The trt × day interaction revealed higher concentration of milk lactose ($P < 0.01$) and lower concentration of milk protein ($P < 0.01$) with PGG. In d 13-28 pp, the concentration of milk BHBA with PGG was below the concentration with CON (interaction: P = 0.05). In the first 4 wk pp, there was a smaller decline in body weights with PGG (interaction: $P = 0.02$). The PGG displayed highest plasma concentration of glucose during 1 to 7 d pp (P= 0.05) and in the entire 4 wk of allocation ($P < 0.01$). In d 1 to 7 pp, the plasma concentration of non-esterified fatty acids was decreased with PGG compared to CON (P=0.03). The trt × week/day interactions revealed lower concentration of BHBA in plasma with PGG in d 1 to 7 pp ($P = 0.05$) and in the entire allocation period ($P = 0.01$). In conclusion, allocation of propylene glycol to fat transition cows depicted amendments in body weights, metabolism and milk composition suggesting decreased fat mobilization in the fatty cows pp, and thereby implying a reduced risk of fatty liver and ketosis.

Key Words: propylene glycol, transition cow

Ruminant Nutrition: Feeding, Ruminal Fermentation, and Efficiency of Production I

T40 Effects of restricted versus conventional dietary adaptation over periods of 6 and 9 days on rumen papillae of feedlot Nellore cattle. A. Perdigão[1,3], M. D. B. Arrigoni[1], D. D. Millen*[2], C. L. Martins[1], R. S. Barducci[1], M. T. Cesar[1], D. D. Estevam[2], T. V. B. Carrara[2], D. V. F. Vicari[2], and R. F. Pessin[1], *[1]São Paulo State University (UNESP), Botucatu, São Paulo, Brazil, [2]São Paulo State University (UNESP), Dracena, São Paulo, Brazil, [3]Supported by FAPESP, São Paulo, São Paulo, Brazil.*

This study was designed to determine effects of restricting DMI of the final finishing diet (REST) as a means of dietary adaptation compared with diets increasing in concentrate (STEP) over periods of 6-d and 9-d on morphological parameters of rumen papillae of feedlot cattle. The experiment was designed as a completely randomized block with a 2 × 2 factorial arrangement with repeated measures over time, replicated 6 times (5 bullocks/pen), in which 120 22-mo-old yearling Nellore bulls (352.03 ± 19.61 kg) were fed in 24 pens for 84-d according to the treatments: STEP for 6-d, STEP for 9-d, REST for 6-d, and REST for 9-d. The STEP program consisted of ad libitum feeding of two adaptation diets over periods of 6-d or 9-d with concentrate level increasing from 61% to 85% of diet DM. After adaptation one animal per pen (n = 24) was slaughtered for rumen papillae evaluations. The remaining 96 animals were harvested after 84-d on feeding. At harvest, rumenitis incidence (RUM) was determined, on the entire washed rumen, using a scale of 0 (no lesions noted) to 10 (severe ulcerative RUM). Likewise, a 1-cm^2 fragment of each rumen was collected from cranial sac. Manually, the number of papillae per cm^2 of rumen wall (NOP) was determined and 12 papillae were randomly collected from each fragment; scanned, and mean papillae area (MPA) was measured by software for image analysis. The rumen wall absorptive surface area (RASA) in cm^2 was calculated as follows: 1 + (NOP × MPA) – (NOP × 0.002). No significant (P > 0.10) main effects or interactions were observed for NOP and RASA. A significant (P = 0.03) interaction between protocol and days was observed, in which animals adapted for 9-d in STEP protocol and for 6-d in REST protocol had lesser RUM. Moreover, a significant (P = 0.04) interaction between days and harvesting dates was observed, in which animals adapted for 9-d at the end of adaption period had smaller MPA (0.35 cm^2) than animals adapted for: (1) 9-d after finishing (0.48 cm^2), (2) 6-d after adaptation (0.51 cm^2), and (3) 6-d after finishing (0.52 cm^2). For adaptation during 6-d and 9-d, a REST and STEP protocols, respectively, should be used.

Key Words: rumenitis, Zebu

T41 Effects of restricted versus conventional dietary adaptation over periods of 9 or 14 days on total tract digestibility of NDF and TDN of feedlot Nellore cattle. D. H. M. Watanabe[2], A. L. N. Rigueiro[2], R. S. Barducci[1], C. L. Martins[1], M. D. B. Arrigoni[1], M. C. S. Pereira[2], J. Silva[2], T. V. B. Carrara[1], F. Perna Junior[3], M. C. S. Franzói[1], and D. D. Millen*[2], *[1]São Paulo State University (UNESP), Botucatu, São Paulo, Brazil, [2]São Paulo State University (UNESP), Dracena, São Paulo, Brazil, [3]University of São Paulo (USP), Pirassununga, São Paulo, Brazil.*

This study, conducted at the São Paulo State University feedlot, Botucatu Campus, Brazil, had the objective to evaluate step up (STEP) and restriction (REST) protocols to high concentrate diets over periods of 9 or 14 days on total tract digestibility of NDF and TDN of Nellore cattle finished in feedlot. The experiment was designed as a completely randomized block with 2 × 2 factorial arrangement, replicated 6 times (5 bullocks/pen), in which 120 22-mo-old yearling Nellore bulls (361.3±30.2 kg) were fed in 24 pens for 84 days according to the treatments: STEP for 9 days and 14 days, REST for 9 days and 14 days. Measures over time were taken on days 5, 10, 15, and 20 of experimental period. The STEP program consisted of ad libitum feeding of 3 adaptation diets over periods of 9 or 14 days with concentrate level increasing from 55% to 85% of diet DM. The REST program consisted of restricted intake of the final diet (85% concentrate) with programmed increases in feed offered until yearling bulls reached ad libitum access over periods of 9 or 14 days. Fecal samples were collected just before morning (0800) and afternoon (1500) meals, and a composite sample per pen in each day was made. For the NDF and TDN digestibility, it was observed (P < 0.05) interaction between protocols, length of protocols and days. Yearling bulls adapted for 14 days had greater NDF digestibility on the first day of the finishing period (day 15: STEP in 14 days = 70.44%, REST in 14 days = 61.54%) than those adapted for 9 days (day 10: STEP in 9 days = 58.28%, REST in 9 days = 35.04%); however no differences (P > 0.10) between treatments were observed on day 15. Likewise, yearling bulls adapted for 14 days had greater TDN digestibility on the first day of the finishing period (day 15: STEP in 14 days = 78.81%, REST in 14 days = 81.38%) than those adapted for 9 days (day 10: STEP in 9 days = 69.66%, REST in 9 days = 72.33%); however, no differences (P > 0.10) between treatments were observed on day 15. Thus, according to the present data, yearling Nellore bulls should be adapted in 14 days, regardless of the protocol.

Key Words: adaptation, NDF, TDN

T42 Potential proteolytic bacteria adherent to soybean meal in the rumen revealed by PCR-DGGE. D. Jin[2], J. Q. Wang*[1,2], D. P. Bu[2], and S. G. Zhao[2], *[1]Agronomy College of Heilongjiang August First Land Reclamation University, Da qing, Heilongjiang, China, [2]Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Rumen bacteria metabolize dietary protein to provide enough N for animal health and production. Soybean meal is widely used as protein source in ruminant feeds and protein degradation by the adherent bacteria is the first essential step for rumen N metabolism. In order to get the information of bacteria involved in protein degradation, denaturing gradient gel electrophoresis (DGGE) was used to reveal the potential proteolytic bacteria adherent to soybean meal in the rumen of Holstein dairy cows. Three healthy Chinese Holstein dairy cows fitted with rumen cannula and similar body weight were selected (n = 3). Soybean meals were placed into nylon bags and then incubated in the rumen for 0, 12, 24, 48 h. Rumen degradability of DM was estimated, and N concentration was determined by Kjeldahl N apparatus. Bacteria adherent to soybean meal were eluted with phosphate buffer saline. Patterns of bacterial composition were compared by DGGE profiling and some special bands from different incubation time were selected and sequenced. Results showed that DM was degraded at 55.5, 70.1, and 96.3%, whereas CP was degraded at 36.9, 58.4, and 95.7%, respectively, after incubation for 12, 24, and 48 h. The DGGE profiles showed the number and intensity of bands from varying samples were different, and the dendrogram of the PCR-DGGE fingerprint showed that they were

assigned to different clusters by different incubation time. The amounts and types of special strains increased significantly after incubating for 12 h and these may be closely related to protein degradation. Shannon-Wiener index of different time differed ($P < 0.01$). Sequencing results derived from 16S rDNA analysis for the DGGE bands showed that most of them belonged to *Prevotella* sp. and uncultured bacteria. The results showed that more proteolytic bacteria were from uncultured bacteria. In future, metagenomic analysis should be applied to these uncultured bacteria for key proteolytic enzyme exploration.

Key Words: PCR-DGGE, rumen bacteria, soybean meal

T43 Effect of changing ratios of corn silage and alfalfa on ruminal fiber digestion in high producing lactating cows. F. Lopes*, D. E. Cook, and D. K. Combs, *Department of Dairy Science, University of Wisconsin, Madison.*

The aim of this study was to compare ruminal fiber digestion and passage of alfalfa and corn silage in lactating cows. Alfalfa silage and corn silage with similar NDF content (33.2%) and in vitro 48-h NDF digestibilities of 44.2 and 38.4% respectively, were used. Eight rumen-cannulated dairy cows (110 ± 5 d in milk) were utilized in a 4 × 4 Latin square design with 21 d period to test 4 rations of corn silage:alfalfa silage; 100:0 (A), 66:33 (B), 0:100 (C) or 33:66 (D). Total mixed rations contained approximately 55% of DMI as forage, with 28.8, 29.1, 32.9 and 29.7% of NDF for ration A, B, C and D, respectively. Intake and milk production were measured during d 14 to 21. Ruminal contents were evacuated manually 4h after and 2 h before feeding on d 20 and 21 to evaluate rumen nutrient pool sizes and turnover. Ruminal contents were analyzed for OM, NDF and iNDF content. Data were analyzed with MIXED-SAS with fixed effect of square, diet, period, and cow within square was the random effect. Milk production was 39.2, 37.6, 36.9 and 37.7 kg/d for A, B, C, and D, respectively, with significantly ($P < 0.05$) higher yield for ration A. Dry matter and NDF intake were lower ($P < 0.05$) for diet D than other treatments. Indigestible NDF intake was greater for diets C and D than diets A and B (Table 1). Ruminal digesta volume did not differ by treatment; but ruminal mass was greater for diets with more corn silage compared to alfalfa silage. Rumen pools and turnover of NDF and iNDF were affected by different rations of corn:alfalfa silage. Fiber turnover rates increased as more alfalfa was included in the diets.

Table 1.

	CS:ALF				
Item	A (100:0)	B (66:33)	C (0:100)	D (33:66)	SEM
DMI, kg/d	28.62[a]	28.39[a]	25.24[b]	28.39[a]	1.13
NDF, kg/d	8.11[ab]	7.82[ab]	7.33[b]	8.50[a]	0.37
Indigestible NDF intake, kg/d	2.09[b]	2.26[b]	2.49[a]	2.47[a]	0.10
Digesta mass, kg	80.56[a]	80.55[a]	74.17[b]	76.75[ab]	2.51
Ruminal pool, kg					
DM	11.07[a]	11.39[a]	10.00[b]	10.29[ab]	0.45
NDF	5.87[a]	5.72[a]	4.75[b]	5.38[ab]	0.25
iNDF	3.20	3.30	3.18	3.26	0.19
Ruminal turnover rate, %/h					
DM	11.11[ab]	9.25[b]	10.85[ab]	12.67[a]	0.73
NDF	5.81[ab]	5.24[b]	6.69[a]	7.08[a]	0.38
iNDF	3.17[ab]	2.69[b]	2.97[ab]	3.46[a]	0.27

[ab]$P < 0.05$.

Key Words: corn silage, fiber digestion, turnover

T44 Dry matter intake and nutrient intake of crossbred cattle ¾ Zebu x ¼ Holstein fed different levels of calcium and phosphorus in the diet. L. F. Prados*, S. C. Valadares Filho, S. A. Santos, D. Zanetti, A. N. Nunes, L. D. S. Mariz, F. C. Rodrigues, P. M. Amaral, A. S. F. Veiga, E. Detmann, and F. A. S. Silva, *Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil.*

This study aimed to evaluate the intake of dry matter and nutrient intake of crossbred bulls. A total of 36 ¾ Zebu × ¼ Holstein crossbred bulls with an initial weight of 214 ± 4 kg and a mean age of 11 ± 0.2 mo were used in the study. The animals were fed ad libitum and distributed in a completely randomized design with a 3 × 3 factorial arrangement for treatments, with 3 levels of calcium and phosphorus and 3 periods of feedlot (56, 112 or 168 d). The 3 levels of calcium and phosphorus were: low = 0.18 and 0.22%, medium = 0.30 and 0.24%, normal = 0.42 and 0.26%, respectively for calcium and phosphorus on a dry matter basis. The diets were isonitrogenous (12.6%) and consisted of corn silage and concentrate (60:40). The amount of feed supply was recorded daily, and samples were collected from corn silage and orts of each animal. Samples of feed and orts were measured for dry matter (DM), mineral matter (MM), crude protein (CP), neutral detergent fiber (NDF), ether extract (EE), calcium (Ca) and phosphorus (P). Intake of DM was not affected ($P > 0.05$) by the level of Ca and P in the diet. Intake of DM, CP, EE, organic matter (OM) and non-fiber carbohydrates, when expressed as kg/d, were higher ($P < 0.05$) for animals in feedlot for longer periods. Intake of DM as a function of body weight (BW) decreased ($P < 0.05$) in animals confined for longer periods. This decrease in the ratio of intake of DM to BW can be explained by the reduction in maintenance requirements because of a decrease in organ tissue as a proportion of overall BW. Differences were observed ($P < 0.05$) in Ca intake with increasing levels of Ca in the diet and for different feedlot periods. There were no significant differences in P intake ($P > 0.05$) by the level of Ca and P in the diet. We observed higher intake of Ca and P ($P < 0.05$) for animals in feedlot for longer periods this can be explained by a higher intake of DM of these animals. It was concluded that reductions in the levels of Ca and P in cattle diets did not change DMI and nutrient intake of animals, and the periods of feedlot influenced DMI.

Key Words: calcium, nutrient intake, phosphorus

T45 Relationship of residual feed intake with heart rate and heat production in Nellore steers. A. S. Chaves*[1], M. L. Nascimento[1], R. R. Tullio[2], M. M. Alencar[2], A. N. Rosa[3], and D. P. D. Lanna[1], *[1]University of Sao Paulo/ESALQ, Piracicaba, SP, Brazil, [2]Embrapa Cattle Southeast, Sao Carlos, SP, Brazil, [3]Embrapa Beef Cattle, Campo Grande, MS, Brazil.*

The objective of this work was to examine the relationship between RFI, heart rate (HR) and heat production (HP) of Nellore steers. The animals (n = 39) were individually fed twice daily with 5% of orts, for 84 days. BW was measured at 14-d intervals. HR was recorded during a 4 day period with measurements at 60 seconds intervals. HR and O_2 consumption (VO_2) were collected at the same time during 15 minutes using a face mask open-circuit respiratory system (Exhalyzer). These measurements were used to calibrate the volume of O_2 per heart beat. O_2Pulse (O_2P) was calculated as the VO_2 per beat. Daily HP (kcal/kg$^{0.75}$) was calculated multiplying O_2P by the average HR obtained during the 4 days, assuming 4.89 kcal/L de O_2. Daily gain (DG) was estimated by slope of the individual regression between BW and days on feed. RFI was obtained using mixed models in which metabolic BW and DG were included to predict the feed

intake. The animals were classified as low, medium and high RFI (mean ± 0.5 SD), and then high and low RFI classes were compared using Proc GLIMMIX (SAS). During oxygen calibration, HR was similar to the daily average measurement when the animals were in the stalls, 101 ± 6.2 and 102 ± 2.7 bpm, respectively. This suggests animals were not stressed and O_2P values probably are not biased. Furthermore, HR was 19.4% lower ($P = 0.019$), and the average daily HR tended to be lower for efficient animals ($P = 0.092$). O_2P did not differ between classes ($P > 0.05$), but there was a trend ($P = 0.0956$) toward higher VO_2 in efficient animals. These results suggest that efficient animals, have a slower heartbeat rate, and maybe able to pump a greater amount of oxygen per heart beat. No significant relationships were observed between RFI and HP in efficient and inefficient animals ($P > 0.05$).

Key Words: energy expenditure, feed efficiency

T46 Does the processing method affect cell wall and dry matter degradability of wheat grain. H. Karkhaneh*, K. Rezayazdi, M. Dehghan-Banadaki, and A. Zali, *University of Tehran, Tehran, Iran.*

Four Holstein cattle with rumen fistula were used according to a Latin square design with 4 treatments and 4 periods of 21 days and 4 cows. Treatments include ground wheat (control), dry rolled wheat, steam flaked wheat and wheat processed with formaldehyde 0/4 percent. Cell wall and dry matter degradability of processed wheat were measured at 2, 4, 8, 12, 24 and 48 hours according to the method of Vanzant et al. (1998). Effective degradability of dry matter of different treatments in passage rate r = 0.05, respectively, 87/62, 87/95, 76/50 and 80/62 percent were significantly different ($P < 0.05$). Also effective degradability of cell walls of wheat grain processed with different methods in passage rate r = 0.05, respectively, 64/30, 68/25, 52/85 and 53/97% of which were also significant differences between them. So it can be concluded that treating with formaldehyde and steam rolling can cause a significant reduction in dry matter and cell wall degradability of wheat.

Key Words: processed wheat grain, dry matter degradability, cell wall degradability

T47 The effect of three different dietary starch concentration on some reproductive parameters in lactating dairy cows. G. Y. Mecitoglu[1], E. Karakaya[1], I. Cetin[2], C. Kara[2], A. Orman[3], H. Gencoglu*[2], A. Keskin[1], A. Gumen[1], and I. Turkmen[2], *[1]Department of Obstetrics and Gynecology, Faculty of Veterinary Medicine University of Uludag, Bursa, Turkey, [2]Department of Animal Nutrition and Nutritional Diseases, Faculty of Veterinary Medicine. University of Uludag, Bursa, Turkey, [3]Department of Zootechnics, Faculty of Veterinary Medicine University of Uludag, Bursa, Turkey.*

The aim of this study was to determine the effect of three different dietary starch concentrations on first postpartum (PP) and following induced estrous ovulation times, follicular and luteal size in dairy cows. Primiparous dairy cows (n = 22) were randomly assigned to 1 of the 3 treatment groups at PP 6 d. Cows were fed with low (LS, 16.2% starch, n = 8), medium (MS, 19.8% starch, n = 6) or high-starch (HS, 24.1% starch, n = 8) diets as TMR (DM basis). To determine the time of PP first ovulation, all cows were scanned three times a week until PP 50 d. In order to detect ovulation time after estrus, cows were synchronized. Cows received GnRH and intravaginal progesterone device (CIDR) at PP 60 d and 7 d later CIDR was removed and $PGF_{2\alpha}$ was administered. Cows were scanned 8 h apart as from 48 h after $PGF_{2\alpha}$ administration to determination of ovulation. Furthermore, cows were also scanned 7 d after ovulation to detect luteal size. Data were analyzed according mixed models procedure. Times of PP first ovulations were did not differ among the groups (19.9 ± 5.04 d in LS, 26.3 ± 5.81 d MS and 24.3 ± 4.84 d HS). The size of ovulatory follicle before PP first ovulation was lower ($P = 0.05$) in LS (13.31 ± 1.10) than in HS (14.83 ± 0.51) but did not differ from MS group (14.62 ± 1.91). In addition ovulation time after induced estrous tended to be shorter ($P = 0.09$) in MS group (75.33 ± 13.68h) than in HS (100.33 ± 4.88 h) and LS (100.17 ± 12.96 h) groups. Ovulatory follicle size tended to be lower ($P = 0.08$) in LS (14.70 ± 0.62 mm) than MS (16.67 ± 1.20 mm) and HS (16.25 ± 0.42 mm). Luteal size measured 7 d after ovulation was lower ($P = 0.04$) in LS group (21.92 ± 1.12 mm) than MS (27.67 ± 1.88 mm) and HS (26.33 ± 1.34 mm) groups. Thus, although the ovulation times in both first PP and following induced estrous did not differ among the groups, follicular size in synchronized estrous and luteal size were lower in LS than MS and HS groups.

Key Words: cow, reproductive parameter, starch

T48 Use of simple static models to estimate in vitro methane production. A. Woldeghebriel*, A. Duncan, and M. Worku, *North Carolina A&T State University, Greensboro.*

A two-stage static model developed for ruminant animals was used to determine the amount of carbon dioxide (CO_2) and methane (CH_4) produced in the study. Concentration of CO_2 calculated in the first-stage was then used to determine concentration of CH_4 in the second-phase. Molar concentration of the three VFAs (acetate, propionate and butyrate) used in the model was determined by GC. Feed grab samples from a TMR was oven-dried, coarsely pulverized in a regular kitchen blender for one minute, and separated into three particle-sizes (PS; 0.85, 1.00 and 1.40 mm). The experimental design was a 3 × 4 factorial (3 PS and 4 feed additives at 1:4 feed ratios). The treatments used were: (1) feed only, as control (CON); (2) CON+ nitrate; (3) CON + fumarate; (4) CON + a 50/50 nitrate-fumarate mix. A 4-g sample from each particle-size for each treatment was weighed in triplicates and transferred into a pre-labeled 500 ml flask. Each flask received 400 mL of rumen fluid-buffer mixture according to the Tilley and Terry procedures and CH_4 gas in the over-head space of each flask was directly measured using the G2301Picarro Gas Analyzer (Picarro, CA). While the VFA data obtained from the study was used in the model to estimate CO_2 and CH_4 production, the direct measurements of CH_4 by the Picarro Gas Analyzer were used for comparison using the t-test statistics at 5% probability. Results obtained show that the model underestimated ($P < 0.05$) the amount of CH_4 produced for all PS and feed additive by as much as 15%. However, CH_4 gas concentration data obtained from the model seem to closely follow the same patterns as the direct measurements of the gas by the Picarro Gas Analyzer. It seems therefore the model can appropriately be used to estimate production of methane using VFA data.

Key Words: methane, nitrate, model

T49 Development of equations to estimate microbial contamination in ruminal incubation residues of tropical forage using ^{15}N as a marker. P. A. S. Machado, S. A. Santos, S. C. V. Filho, E. Detmann, L. F. Prados, P. M. Amaral*, L. F. C. Silva, A. C. B. Menezes, F. A. C. Villadiego, and P. P. Rotta, *Universidade Federal de Vicosa, Vicosa, MG, Brazil.*

The objective was to use ^{15}N to label microbial cells to allow development of equations for estimating the contamination in ruminal incubation residues of tropical forage. A total of 24 forages were divided into 3 groups, and each group was incubated in a different steer per period, in a 3 × 3 Latin square design. Ruminal bacteria were labeled with ^{15}N by continuous infusion 60 h before the first incubation and continued until

the end of incubation period. The digesta was collected for the isolation of bacteria before the first infusion of ^{15}N and after the infusion of ^{15}N. Three collections were made on each day, being the first before feeding and two at an interval of 4 h. To determine the contaminated fractions of CP degradation, the restricted model was compared with the full model using the model identity test. Values of the corrected fraction "A" (ACPC) were estimated from its values without correction (ACPWC) by the equation: ACPC= 1.99286 + 0.98256 × ACPWC. The corrected fraction "B" was estimated from its value without correction (WC) and from CP, NDF, neutral detergent insoluble protein (NDIP), and indigestible NDF (iNDF) using the equation BCPC = −17.2181 – 0.0344 × BCPWC + 0.65433 × CP + 1.03787 × NDF + 2.66010 × NDIP – 0.85979 × iNDF, where BCPC = the potentially degradable B fraction of CP corrected for microbial contamination and BCPWC = the fraction WC. The corrected "kd" (kdCPC) was estimated using the equation kdCPC = 0.04667 + 0.35139 × kdCPWC + 0.0020 × CP – 0.00055839 × NDF – 0.00336 × NDIP + 0.00075089 × iNDF, where kdCPWC = the rate of degradation without correction. The equation obtained to estimate the contamination (C) using CP of the feeds was: %C = 79.21 × (1-e-0.0555 × t) × e-0.0874 × CP, where: t = incubation time. It was concluded that A and B fractions and kd of CP would be biased by microbial CP contamination, thus these corrected values could replace the use of microbial markers. The contamination and the corrected apparent degradability of CP could be obtained from values of CP and time of incubation for each feed, which could reduce cost involved when using ^{15}N.

Key Words: degradability, protein fraction

T50 Influence of offering hay free-choice concurrently with total mixed ration on residual feed intake rank differences of beef bulls. E. El-Haroun[1,3], M. Abo-Ismail*[3], H. Salim[2], G. Vander Voort[3], M. McMorris[1], and S. Miller[3], *[1]Beef Improvement Opportunities, Guelph, Ontario, Canada, [2]Department of Animal and Poultry Science, Cairo University, Giza, Egypt, [3]Centre for Genetic Improvement of Livestock, Department of Animal and Poultry Science, University of Guelph, Guelph, Ontario, Canada.*

Individual feed intake data has been collected on growing bulls on a moderate energy pelleted diet, while the bulls had free access to chopped hay as a roughage source, where the hay was not recorded. The objectives of this study were to offer bulls hay free choice in addition to a moderate energy total mixed ration (TMR) and determine if measurement of the hay influenced the bulls ranking for residual feed intake (RFI). The study collected feed intake and BW data from 102 crossbred bulls on a post-weaning growth test over a 2-yr period where individual feed intake was measured using the Insentec Roughage Intake Control (RIC) system. The RFI was calculated using different models, which included ADG, mid-metabolic BW, marbling and backfat. The principal RFI determination in this study RFI_{Koch} was calculated as the residuals from the regression of total DMI (DMI_{hay}+ DMI_{TMR}) on BW and ADG. The RFI_{hay} and RFI_{TMR} were calculated as the residual from the regression of DMI_{hay} and DMI_{TMR}, respectively on BW and ADG. The RFI_{Koch} had the lowest coefficient of determination (R^2; 0.75), and highest, less desirable, Bayesian information criterion (BIC; 286.4). The RFI_{TMR} had the highest R^2 (0.87) and the best BIC (230.1) among the other models, while, RFI_{hay} had a moderate R^2 (0.77) and BIC (283.6). The RFI including carcass traits had the same R^2 (0.76) and BIC (285.6 and 283.6) for marbling and backfat, respectively. The rank correlations among the RFI calculated from different models were obtained. The RFI_{Koch} was highly correlated with RFI_{hay} 0.97%, indicating that the 2 RFI were similar and the relative re-rankings of the bulls were similar regardless of the model used. The rank correlation between RFI_{Koch} and RFI_{TMR} was 74%, thus, the 2 RFI were somewhat different and bulls ranked differently when hay intake was accounted for RFI_{Koch}, compared to when hay intake was not included RFI_{TMR}. These results suggest that when measuring feed intake in young growing bulls, it is important to measure all sources of energy consumption, including hay that has been overlooked in previous studies and test designs.

Key Words: beef, reranking, residual feed intake

T51 Model for estimating enteric methane emissions from black goat. Y. Na*, W. Jeong, O. Yi, S. Hwang, and S Lee, *Department of Animal Science and Technology, Konkuk University, Seoul, Republic of Korea.*

The objective was to develop mathematical models for estimating enteric CH_4 emissions from black goats. Methane production and digestibility of diets were measured using respiration-metabolism chamber with different feeding conditions: different concentrate to roughage ratio (40:60, 50:50, and 60:40), oil sources (soybean oil, coconut oil and palm oil) and roughage sources (timothy, rice straw, corn silage, alfalfa pellet and tall fescue). One hundred and thirty-five observations from these experiments were used for the estimation of model parameters. Dry matter intake, OM intake (OMI), CP intake (CPI), NDF intake (NDFI), digested DMI (DDMI), digested OMI (DOMI), digested CPI (DCPI) and digested NDF intake (DNDFI) were considered for the development of models. Cook's distance tests were performed to identify outliers and SAS PROC REG was used for the calculation of single and multiple simple linear regressions. Root mean square prediction error (RMSPE) and R^2 were used as a measure of prediction accuracy. For the simple linear regression, an equation using OMI as an independent variable most accurately predicted CH_4 emission: CH_4, L/d = 0.1092 + 0.0414 × OMI, g/d (RMSPE = 5.49, R^2 = 0.44) among equations using nutritional intake as an independent variable. An equation using DOMI as an independent variable was the most accurate: CH_4, L/d = 4.5051 + 0.0410 × DOMI, g/d (RMSPE = 5.11, R^2 = 0.52) among equations using digested nutritional intake as an independent variable. For the multiple linear regression, an equation using nutritional intake as independent variables CH_4, L/d = 1.1605 + 0.0078 × DMI, g/d + 0.0250 × OMI, g/d + 0.0167 × CPI, g/d + 0.0037 × NDFI, g/d resulted in the lowest RMSPE value (5.55) and the highest R^2 value (0.45). And an equation using digested nutritional intake as independent variables, CH_4, L/d = 9.2184 – 0.0081 × DDMI, g/d + 0.0133 × DOMI, g/d + 0.0057 × DCPI, g/d + 0.0227 × DNDFI, g/d resulted in the lowest RMSPE value (5.01) and the highest R^2 value (0.55). Therefore, digested nutritional intake (DDMI, DOMI, DCPI, and DNDFI) is better independent variables than nutritional intake (DMI, OMI, CPI, and OMI) for the prediction of CH_4 emissions.

Key Words: black goat, methane, modeling

T52 Effects of forage sources on the gene expression related to milk protein synthesis in the mammary gland of lactating Holstein cows. X. Zhang[1], C. Ao*[1], M. Gao[2], E. Khas[1], H. Zhang[1], L. Song[1], and R. Du[2], *[1]Inner Mongolia Agricultural University, Hohhot, Inner Mongolia, China, [2]Inner Mongolia Academy of Agricultural & Animal Husbandry Sciences, Hohhot, Inner Mongolia, China.*

The objective of this study was to determine the effects of forage sources on gene expression related to milk protein synthesis in the mammary gland of lactating cows. Twenty multiparous Holstein cows (BW = 566 ± 19.6 kg, DIM = 95 ± 24 d) were assigned to a single factor block design with 30 d period. Cows were fed diets with different forage. Diets (on DM base) were: (1) corn straw (35%) and 65% of concentrate (CS; CP: 17.14%, NDF: 41.58% and NEL: 1.58 Mcal/kg); (2) hay (4%), corn silage (27%) and alfalfa (23%) with additional 46% of concentrate (MF; CP: 17.45%, NDF:

38.33% and NEL: 1.6 Mcal/kg),.Nutrient level in the two diets were similar. Mammary gland tissue (500 mg/animal) biopsies were randomly performed for half numbers of cows in each group after milking on the last day of experiment. Statistical analysis was performed using the PROC MIXED procedure of SAS 9.0. We hypothesized that forage sources will affect gene expressions in three aspects : (1) milk protein synthesis (CSN1S1 CSN3); (2) hormone receptors in the cytomembrane of mammary epithelial cells (PRLR GHR1A); and (3) the cell signal regulators involved in milk protein synthesis (mTOR JAK2 STAT5); Results showed that the level of CSN1S1 CSN3 PRLR GHR1A and mTOR mRNA were significantly increased ($P < 0.05$) by the MF treatment, but the mRNA expression of JAK2 and STAT5 were not significantly affected by treatment ($P > 0.05$). In conclusion, forage quality affects the efficiency of milk protein synthesis in lactating Holstein cows. High quality forage can promote PRLR GHR1A and mTOR genes expression, resulting in increased milk protein synthesis.

Key Words: mammary gland, protein synthesis, gene expression

T53 Relationship of flight speed, rectal temperature and infrared thermography of eye with feed efficiency of Nellore beef cattle. A. M. Mobiglia[1], F. R. Camilo[1], V. R. M. Couto[1], E. G. Moraes[2], H. F. Oliveira[1], L. F. N. Souza[2], J. T. Neves Neto[1], T. S. Almeida[1], J. C. Pimenta[1], and J. J. R. Fernandes*[1,2], *[1]Escola de Veterinaria e Zootecnia da UFG, Goiânia, Goiás, Brazil, [2]Nelore Qualitas, Goiânia, Goiás, Brazil.*

The objective of this study was to correlate flight speed (FS), rectal temperature (RT) and eye temperature (ET), measured by infrared thermography, with residual feed intake (RFI), feed efficiency (FE), and feed conversion (FC) of Nellore beef cattle. The bulls (n = 120, 393.04 ± 47.3kg of BW), with an average of 20 mo of age, were housed outdoors in individual pens and weighted at beginning and end of trial. All the animals were fed sorghum silage (27%), sugarcane bagasse (10%) and concentrate (63%). Animals were classified as follows: high RFI (SD >0.42 - less efficient; n = 32), medium RFI (SD ± 0.42; n = 52), and low RFI (SD <0.42 - more efficient; n = 36). We evaluated eye temperature using an infrared portable camera (FLIR I7 of Flir Systems Inc.). In all photographs, we considered a specific shape (circle) in order to keep a constant sub-area (eye surface), and the average was computed. We measured RT and ET simultaneously with a digital thermometer. We measured FS by infrared sensors placed in exit of the crush. The data were analyzed by Pearson using statistical software R (2010). Mean ET and RT were 35.63 ± 1.60°C and 38.39 ± 0.61°C, respectively, ranging between 39.30°C and 31.50°C for ET, and 40.30°C and 37.20°C for RT. In addition, the values of FS were 2.78 ± 1.53m/s (BFS, beginning of feedlot), 1.75 ± 0.6 m/s (EFS, end of feedlot) and −1.02 ± 1.68 m/s (DFS, difference between BFS and EFS). The data of correlation are showed in Table 1 (*$P < 0.05$). Therefore, the RT, ET, and FS did not correlate with feed efficiency. However, the ET showed medium correlation with RT of Nellore beef cattle.

Table 1. Correlation among variables.

	RFI	FE	FC	BFS	EFS	DFS	RT	ET
RFI	—							
FE	−0.38*	—						
FC	0.36*	−0.88*	—					
BFS	−0.11	−0.13	0.06	—				
EFS	0.04	0.11	−0.09	−0.52	—			
DFS	0.12	0.16	−0.09	−0.93*	0.41*	—		
RT	0.06	−0.09	0.11	0.15	0.18*	−0.07	—	
ET	0.01	0.04	−0.04	0.17	0.08	−0.12	0.53*	—

Key Words: efficiency, feedlot, temperature

T54 Bone morphometry and densitometry of goats of different genders subjected to feed restriction. N. C. D. Silva*[1], K. T. Resende[1], M. H. M. R. Fernandes[1], H. C. Bonfá[2], D. C. Soares[1], R. F. Leite[1], F. O. M. Figueiredo[1], M. M. Freire[3], B. R. S. M. Oliveira[4], and I. A. M. A. Teixeira[1], *[1]Unesp Univ Estadual Paulista, Jaboticabal, São Paulo, Brazil, [2]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil, [3]Universidade Federal de Alagoas, Maceió, Alagoas, Brazil, [4]Unesp Univ Estadual Paulista, Araçatuba, São Paulo, Brazil.*

The objective of this study was to evaluate the effect of gender and feed restriction on bone morphometry and bone mineral densitometry (BMD) of 54 Saanen goat kids (18 intact males, 18 castrated males and 18 females) with initial BW of 15 kg. The animals of the same gender were randomly distributed into 6 groups (blocks) of 3 animals subjected to different levels of feed restriction (ad libitum or 0%, 25% and 50% of feed restriction). Then in total there were 18 blocks. A whole group was slaughtered when the kid subjected to 0% of feed restriction reached 30 kg BW. After slaughter and evisceration, the carcasses were weighed and femur of the right leg of each animal was removed for subsequent analyses. Morphometric evaluations were accomplished by measuring femur weight, total length (TL), perimeter proximal epiphysis (PEP) and distal (PED), perimeter of diaphysis (PD), breadth of diaphysis-laterolateral position (LDLL) and craniocaudal position (LDCC). The evaluation of BMD was performed by image generated by X-rays of femur using Lunar DPX equipment. Data were analyzed as a randomized complete block design with a 3 × 3 factorial arrangement, using mixed model of SAS. Gender did not affect TL, PD, LDLL and LDCC, but, femur weight, PEP and PED were lower ($P < 0.05$) in females (100.9 ± 2.6g, 11.8 ± 0.1cm and 15.2 ± 0.2cm, respectively) than intact males (109.4 ± 4.0g, 11.5 ± 0.1cm and 15.9 ± 0.2cm, respectively) and castrated males (116.7 ± 2.3g, 12.4 ± 0.1 cm and 16.1 ± 0.2cm, respectively). Regarding feed restriction level, animals subjected to 50% feed restriction showed lower values ($P < 0.05$) of all morphometric variables compared to the kids subjected to 0% and 25% feed restriction. Bone mineral densitometry was higher ($P < 0.05$) for females fed ad libitum (0.644 ± 0.04 g/cm^2) compared to intact males and castrated fed ad libitum. We concluded that bone morphometry was influenced by gender and feed restriction. Bone mineral densitometry and bone morphometry can be important tools for understanding bone mineral metabolism in goats.

Key Words: bone metabolism, density, nutrition

T55 The National Animal Nutrition Program (NANP): Modeling Subcommittee goals and progress. M. D. Hanigan*[1], C. R. Angel[2], C. F. M. de Lange[3], E. Kebreab[4], J. P. McNamara[5], L. O. Tedeschi[6], N. L. Trottier[7], and M. J. VandeHaar[7], *[1]Virginia Tech, Blacksburg, [2]University of Maryland, College Park, [3]University of Guelph, Guelph, ON, Canada, [4]University of California, Davis, [5]Washington State University, Pullman, [6]Texas A&M, College Station, [7]Michigan State University, East Lansing.*

The NANP is a research-support activity established as National Research Support Project 9 (NRSP-9; http://www.ca.uky.edu/nrsp-9/index.htm). The NRSP are funded from Hatch funds administered by the U.S. Department of Agriculture and drawn from federal allocations prior to formula distribution to experiment stations. The objective of the NANP Modeling subcommittee is to facilitate the use of predictive technologies, tools, and platforms, and to support the efforts of the National Research Council (NRC). The goals are to provide maintenance of the nutrient requirement models and software between NRC releases, to collect user feedback, to provide guidelines and tools for scientists and instructors using modeling to address nutrition problems, and to facilitate knowledge development and dissemination. Two calculation errors in the 2001 Dairy NRC model

were corrected and the installation program was recompiled to support 64-bit Windows installations. We also created an installation program to allow the 2000 Beef NRC to be operated on modern Windows based computers. Both are available on the website. We are working to develop a review of techniques used to evaluate models, an article listing guidelines for reporting dietary information in publications, and an article describing a software platform that could be used across NRC species requirement models. We are also developing a database to store observational data collected by the NRC committees which can be downloaded and used for model development. Future work includes development of a web based mechanism to provide access to the model source code for use by the animal nutrition research community, collection of feedback from model users to help identify software problems and prediction problems, summarization of evaluations of the current NRC models, and an assessment of supply and requirement model subcomponents that could be used across species. These changes will facilitate the use of NRC models in diet formulation, update NRC models more rapidly as new information becomes available and at lower cost, and improve efficiency of feed use and sustainability in animal agriculture.

Key Words: NRC, nutrient requirements, nutrition model

T56 Effects of stage of gestation and diet on maternal fat deposition. P. P. Rotta*[1], S. C. Valadares Filho[1], T. R. Santos[1], L. F. Costa e Silva[1], M. I. Marcondes[1], B. C. Carvalho[2], A. A. G. Lobo[1], J. V. F. Souza[1], M. A. S. Novaes[1], M. F. L Ferreira[1], and J. S. A. A. Santos[1], *[1]Universidade Federal de Vicosa, Vicosa, Brazil, [2]Empresa Brasileira de Pesquisa Agropecuaria, Brazil.*

The objectives were to evaluate the maternal nutrient intake and stage of gestation on mesentery, kidney, pelvic and heart (KPH) fat and fat thickness growth rate in Holstein × Gyr cows. Sixty-two multiparous cows were inseminated with the same Gyr semen and in the d 30 the gestation was confirmed in 44 cows. Six cows non-pregnant were previously slaughtered as reference group. The 44 pregnant cows were randomly distributed in four time of gestation: 140, 200, 240 and 270 days. Thus, 11 cows were slaughtered in each time. These eleven cows were randomly allocated in two different diets: maintenance level (n = 6; 1.1% of body weight) and ad libitum (n = 5). The cows that achieved the time of gestation were slaughtered and necropsied. The mesentery was removed of the viscera and weighted. The KPH fat was removed and weighted. The fat thickness was measured using an electronic caliper rule 18 h after the slaughter. The values are given in function of final body weight. Data were analyzed using MIXED procedure of SAS. Data of non-pregnant cows were used considering as initial time. The growth rate of mesentery for cows fed ad libitum was exponential and the estimated equation was: $y = 2.7808 + 3.9181 \times [1 - \exp(-0.00726 \times \text{days})]$. However, the growth rate of mesentery for cows fed at maintenance level was linear and the estimated equation was: $y = 2.8351 + (0.00484 \times \text{days})$. In the same way, the KPH fat was exponential to cows fed ad libitum: $y = 1.0812 + 6.5984 \times [1 - \exp(-0.00172 \times \text{days})]$ while the estimated equation to cows fed at maintenance level was linear: $y = 1.1236 + (0.002572 \times \text{days})$. The fat thickness was also exponential to cows fed ad libitum: $y = 0.8033 + 0.0111 \times [\exp(0.0186 \times \text{days})]$ in comparison to cows fed at maintenance level, which estimated equation was linear: $y = 0.757 + (0.002986 \times \text{days})$. Thus, cows fed ad libitum present exponential growth rate of fat deposition, while cows fed at maintenance level present linear growth rate. This can be explained by the high dry matter intake observed to this group and the higher average daily gain. In this way, the excess of energy and protein are being deposited as fat.

Key Words: fat thickness, KPH fat, mesentery

T57 Effects of different diets on the gene expression of enzymes related to fatty acid synthesis in the mammary gland of lactating dairy cows. H. Zhang, C. Ao*, L. Song, E. Khas, and X. Zhang, *Department of Animal Science of Inner Mongolia Agricultural University, Huhhot, Inner Mongolia, China.*

The objectives of this study were to determine the effects of three different diets on the genes expression of key enzymes involved in fatty acid synthesis in the mammary gland of dairy cows. Thirty multiparous Holstein cows (BW = 566 ± 19.6 kg, DIM = 95 ± 24d) were assigned to a single factor block design with 30 d period. Animals were fed diets with different roughage and same concentrate profiles, the concentrate-roughage ratio in the treatments were different. Diets (on DM base) were: (1) hay (4%), corn silage (27%) and alfalfa (23%) with additional 46% of concentrate (MF; CP: 17.45%, NDF: 38.33% and NEL: 1.6 Mcal/kg); (2) corn straw (35%) and 65% of concentrate (CSA; CP: 17.14%, NDF: 41.58% and NEL: 1.58Mcal/kg); (3) corn straw (54%) and 46% of concentrate (CSB; CP: 13.80%, NDF: 55.59% and NEL: 1.36 Mcal/kg). Mammary gland tissue (500 mg/animal) biopsies were randomly performed for half numbers of cows in each group after milking on the last day of experiment. Gene expressions for key enzymes involved in fatty acids synthesis were determined by RT-PCR. Statistical analysis was performed using the PROC MIXED procedure of SAS 9.0. Results showed that mRNA abundance for ACACA and FASN which involve in de novo fatty acid synthesis was higher ($P < 0.05$) in MF compared to CSA and CSB. Gene expression for fatty acid desaturase SCD was significantly increased ($P < 0.01$) by MF treatment and gene expression for fatty acid uptake and intracellular trafficking enzymes LPL, ACSL1 and CD36 were increased ($P < 0.05$) also by MF. However, no effects were observed for milk fat synthesis regulator genes PPARA, PPARG, SREBF1 ($P > 0.05$). No effects on the gene expressions for all above enzymes and regulators between CSA and CSB were found. The data indicated that diet with high quality roughage and the same concentrate-roughage can increase the gene expression of enzymes related to fatty acid synthesis and desaturation, but with the same roughage and different concentrate-roughage ratio had no effect on milk fat synthesis key genes in the mammary gland of dairy cows.

Key Words: dairy cow, mammary gland, fatty acid synthesis

T58 Effects of stage of gestation and diet on dairy cow placentomes. P. P. Rotta*[1], S. C. Valadares Filho[1], T. R. Santos[1], L. F. Costa e Silva[1], M. I. Marcondes[1], M. M. Campos[2], F. A. S. Silva[1], J. R. Oliveira[1], A. C. B. Menezes[1], E. C. Martins[1], and F. A. C. Villadiego[1], *[1]Universidade Federal de Vicosa, Vicosa, Brazil, [2]Empresa Brasileira de Pesquisa Agropecuaria, Brazil.*

The objectives were to evaluate the maternal nutrient intake and stage of gestation on caruncular, cotyledon and placentoma growth and number rate in Holstein × Gyr cows. Sixty-two multiparous cows were inseminated with the same Gyr semen and in the d 30 the gestation was confirmed in 44 cows. Six cows non-pregnant were previously slaughtered as reference group. The 44 pregnant cows were randomly distributed in four time of gestation: 140, 200, 240 and 270 days. Thus, 11 cows were slaughtered in each time. These eleven cows were randomly allocated in two different diets: maintenance level (n = 6; 1.1% of body weight) and ad libitum (n = 5). The cows that achieved the time of gestation were slaughtered and necropsied. The gravid uterus was removed and the uterus was separated from placenta. In the uterus, all carunculars were removed, counted and weighted. In the placenta, all cotyledons were removed, counted and weighted. Except for placentomas number, that consider 140 days of pregnancy at minimum, the

other equations consider the time 0 to time of pregnancy. Data were analyzed using MIXED procedure of SAS. Data of non-pregnant cows were used considering as initial time. For all parameters evaluated, the growth rate observed was exponential, except to placentomas number, which was linear. The weight of caruncular was similar ($P > 0.05$) between diets and the estimated equation was: y = −0.5018 + 0.3992 × exp(0.008658 × days). However, the higher ($P = 0.0007$) value to cotyledons weight was observed to cows fed at maintenance level: y = −0.0698 + 0.07697 × exp(0.01249 × days) in comparison to cows fed ad libitum: y = −0.0698 + 0.07697 × exp(0.01115 × days). Placentomas weight were higher ($P = 0.0144$) to cows fed at maintenance level: y = −0.568 + 0.4597 × exp(0.009739 × days) in comparison to cows fed ad libitum: y −0.568 + 0.4597 ×exp(0.009303 × days). The number of placentomas was linear and higher ($P < 0.0001$) to cows fed at maintenance level. The estimated equation to maintenance was: y = −53.8325 + (1.219 × days) and to cows fed ad libitum: y = −53.8325 + (0.9717 × days).

Key Words: caruncular, cotyledon

T59 Rumen epithelial adaptation during the transition period is associated with structural changes and transcriptomic signatures. M. A. Steele*[1], O. AlZahal[1], C. Zettler[1], J. C. Matthews[2], and B. W. McBride[1], *[1]University of Guelph, Guelph, Ontario, Canada, [2]University of Kentucky, Lexington.*

The structural and functional adaptations of the rumen epithelium during the transition period are largely undescribed. To characterize the adaptations of the rumen epithelium during transition, multiparous dairy cattle (n = 12) fed a low energy dry cow diet (1.45 Mcal/kg NE_L) were transitioned abruptly to a high-energy lactating cow diet (1.60 Mcal/kg NE_L) immediately after parturition. Dry matter intake and ruminal pH were monitored at -3 wk, +1 wk, and +6 wk relative to calving. To uncover changes in the ruminal epithelial structure and function, rumen papillae were biopsied at -3 wk, +1 wk, and +6 wk relative to calving. Histomorphometrics of rumen epithelial structure was examined under a light microscope and mRNA profiling was performed using Affymetrix GeneChip. Data pre-processing was conducted using Robust Multichip Average method and detection of significant genes was conducted using ANOVA. Dry matter intake was 13.1 ± 0.84 kg/d at -3 wk and 12.8 ± 0.84 kg/d at +1 wk, and increased ($P < 0.05$) to 21.0 ± 0.84 kg/d at +6 wk. Ruminal pH was reduced ($P < 0.05$) during the onset of lactation from 6.38 ± 0.07 at -3 wk to 5.81 ± 0.07 and 5.85 ± 0.07 at +1 and +6 wk, respectively. Microscopic examination of rumen papillae revealed an increase in epithelial sloughing during early lactation as sloughing scores increased ($P < 0.05$) from 1.7 ± 0.2 at -3 wk to 4.1 ± 0.3 and 3.4 ± 0.2 at +1 and + 6 wk, respectively. A total of 1,144 and 535 differentially expressed genes (False discovery rate of 0.01, $P < 0.01$) were uncovered from -3 wk to +1 wk and +6 wk relative to parturition, respectively. Analysis of microarray results using Ingenuity Pathway Analysis revealed that metabolic and transport genes were regulated during early lactation, including mitochondrial dysfunction being the top pathway identified ($P < 0.01$) between -3 wk and +1 wk and +6 wk. These results suggest that the structure and function of the rumen epithelium is altered during early lactation and is associated with the differential expression of genes involved with metabolic functions.

Key Words: transition cow, rumen, epithelium

T60 Effects of stage of gestation and diet on maternal and fetal growth in dairy cows. P. P. Rotta*[1], S. C. Valadares Filho[1], T. R. Santos[1], L. F. Costa e Silva[1], M. I. Marcondes[1], F. S. Machado[2], L. H. R. Silva[1], B. C. Silva[1], F. A. C. Villadiego[1], M. V. Pacheco[1], D. E. C. Marquez[1], and R. H. M. Ortega[1], *[1]Universidade Federal de Vicosa, Vicosa, Brazil, [2]Empresa Brasileira de Pesquisa Agropecuaria, Brazil.*

The objectives were to evaluate the maternal nutrient intake and stage of gestation on gravid uterus, uterus, fetus and placenta growth rate in Holstein × Gyr cows. Sixty-two multiparous cows were inseminated with the same Gyr semen and in the d 30 the gestation was confirmed in 44 cows. Six cows non-pregnant were previously slaughtered as reference group. The 44 pregnant cows were randomly distributed in four time of gestation: 140, 200, 240 and 270 days. Thus, 11 cows were slaughtered in each time. These eleven cows were randomly allocated in two different diets: maintenance level (n = 6; 1.1% of body weight) and ad libitum (n = 5). The diet was based on corn silage and concentrate at 93:7. The cows that achieved the time of gestation were slaughtered and necropsied. The gravid uterus was removed and weighted. After the opening of gravid uterus, uterus, placenta and fetus were removed and weighted separately. Data were analyzed using MIXED procedure of SAS. Data of non-pregnant cows were used considering as initial time. For all parameters evaluated, the growth rates observed were exponential. The gravid uterus presented a similar ($P > 0.05$) growth rate to cows fed ad libitum or at maintenance. The estimate equation was: y = −1.104 + 1.7406 × exp(0.0132 × days). In the same way, the growth rate of uterus was similar ($P > 0.05$) between diets. The estimated equation was: y = −0.591 + 0.9817 × exp(0.008836 × days). The growth rate of fetus was similar ($P > 0.05$) between diets and the equation was: y = −1.2426 + 0.4939 × exp(0.01589 × days). However, the growth rate of placenta was higher ($P = 0.0125$) to cows fed at maintenance level: y = −0.1324 + 0.1665 × exp(0.0118 × days) in comparison to ad libitum: y = −0.1324 + 0.1665 × exp(0.01144 × days). Placenta is the organ most related to gestation and its growth rate is positively affected by maintenance level. This suggests that the organism tried to develop mechanisms to be more efficient in nutrient transfer to cows fed at maintenance level. In conclusion, the effect of stage of gestation is exponential and cows fed at maintenance level present higher growth rate to placenta.

Key Words: fetus, gravid uterus, placenta

T61 Determination of particle size distribution and physically effective fiber in total mixed ration from 14 dairy farms in the Comarca Lagunera, Mexico. P. A. Robles Trillo*[1], E. Vazquez-Martínez[1], F. G. Veliz-Deras[1], C. A. Meza-Herrera[2], and P. Cano-Ríos[1], *[1]Universidad Autonoma Agraria Antonio Narro, Torreon, Coahuila, Mexico, [2]Unidad Universitaria de Zonas Aridas. Universidad Autonoma de Chapingo., Bermejillo, Durango, Mexico.*

In order to determine the particle size distribution (PSD) and physical effectiveness factor (PEF) in totally mixed ration (TMR) in dairy cattle farms, a cross-sectional study was conducted in 14 stables from the Comarca Lagunera, Mexico (25°N, 103°W). Farms were randomly selected and visited in summer in order to collect two freshly served samples of TMR; both the PSD and PEF were determined by the Penn State Particle Separator technique. The amount of PSD and PEF differed among farms ($P < 0.05$). In nine farms and using a 19 mm-sieve (S) PSD ranged from 4.85 to 8.86%, the remainder ranged from 12 to 23%. Above a S-8 mm the PSD ranged among 32 to 54%, although seven stables had lesser than 40%. Regarding PSD using S 1.18 mm, the variation between farms was 16% (30 to 46%). When analyzing the plastic bottom pan, four farms had less than 10% of food collected while the rest ranged from 12-19%. The PEF 8 mm showed great variation, ranging from 38 to 61%, although eight stables were above 50%. Finally, with the PEF1.18 mm, the range was 81 to 93% for all the stables. In

conclusion, both the PSD and PEF showed differences between farms; moreover the PSD and PEF were in line with some research reports, which can cause variations in DMI, milk production and composition.

Key Words: dairy, feeding, fiber

T62 Relation between ultrasound and carcass measurements in Girolando steers fed spineless cactus. R. A. S. Pessoa*[1], J. R. C. Silva[1], A. S. C. Veras[1], M. A. Ferreira[1], I. Ferraz[2], and P. C. Vasconcelos[1], *[1]Universidade Federal Rural de Pernambuco, Recife, Pernambuco, Brazil, [2]Instituto Agrono de Pernambuco, Recife, Pernambuco, Brazil.*

The objective of this study was to evaluate the correlations between the measurements obtained by ultrasound and from the carcass of the ribeye and back fat thickness in Girolando steers (5/8 Holstein-Zebu). Eighteen animals, no castrated, with average initial body weight of 320 kg and 24 mo of age were used, kept in feedlot system and assigned to a randomized block design, established in accordance with the weight of animals, being 3 treatments and 4 blocks. The experimental period lasted 84 d divided into 3 periods of 28 d. The treatments were 3 urea levels (0.0, 1.5 and 3.0%) in substitution of cottonseed meal (23.0, 11.5 and 0.0%) in diets based on spineless cactus with approximately 12.0% of crude protein and 65.0% of total digestible nutrients. The control diet was composed of 60.0% of spineless cactus, 15.0% of sorghum silage, 0.0% of urea:ammonium sulfate mixture (9:1), 23.0% of cottonseed meal and 2.0% of mineral mixture, in dry matter basis. The animals were slaughtered at 84 d of feedlot. The measurements taken by ultrasound when the steers reached the slaughter point and from the carcass after the slaughter were ribeye and back fat thickness. The fat thickness was evaluated using a paquimeter and the ribeye was evaluated by using a quadrant grade ruler. The data were submitted to ANOVA and correlation of Pearson using the SAS. The replacement of cottonseed meal by urea did not alter the ribeye and back fat thickness ($P > 0.05$) (average of 58.25 and 2.65, respectively). The correlations measured by ultrasound and from the carcass were 0.72 for ribeye and 0.60 for back fat thickness. The characteristics of the measurements taken by ultrasound correlated well with measurements at the time of slaughter in Girolando steers. FACEPE process number: 2008/0979.

Key Words: nitrogen, *Opuntia ficus indica,* ribeye

T63 Effects of grain source and alfalfa hay particle size on feed sorting, feeding behavior, and chewing activity in mid-lactation Holstein dairy cows. S. M. Nasrollahi[1], G. R. Ghorbani[1], M. Khorvash[1], W. Z. Yang[2], and Z. He*[2], *[1]Isfahan University of Technology, Department of Animal Sciences, Isfahan University of Technology, Isfahan, Iran, [2]Lethbridge, Agriculture and Agri-Food Canada, Research Centre, Lethbridge, AB, Canada.*

This study investigated the effects of grain source and alfalfa hay (AH) particle length on feed sorting, feeding behavior, and chewing activity of lactating dairy cows. Eight Holstein dairy cows (175 ± 21 DIM) were used in a replicated 4 × 4 Latin square design with four 21-d periods. The experiment was a 2 × 2 factorial arrangement of treatments with 2 grain sources (barley grain alone or equal blend of barley and corn grains) combined with 2 particle lengths of alfalfa hay (short = 15 mm and long = 30 mm). Diets were fed ad libitum as TMR with a concentrate to forage ratio of 60:40. The TMR and orts were sampled at 0, 1.5, 3, 6, and 24 h post morning feeding for determining particle size distribution. Data were analyzed using Mixed Procedures of SAS with linear models consisting of fixed period, grain source, hay particle size, and grain source × hay particle size effects, plus cow and residuals random effects. Interactions between grain source and AH particle length on feed particle distributions, sorting index, chewing activity, and milk production were minimal ($P > 0.05$). Partially replacing barley grain with corn in the diet generally did not change diurnal distributions of particles retained on the sieves of Penn State Particle Separator ($P > 0.05$) but reduced the proportion of particles on 1.18-sieve and increased that of particles on pan ($P < 0.05$). Grain source did not affect feed sorting index and chewing activity ($P > 0.05$). However, feeding long AH increased intakes of long particles (i.e., 19- and 8-mm), prolonged eating time, and lowered eating rate ($P < 0.05$). Interestingly, cows fed with long AH ate more coarse particle during critical-early time after feeding (i.e., 1.5 h after feeding), which increased eating time and decreased eating rate in the similar moment ($P < 0.05$). The increased eating time as well as decreased eating rate with marginally increasing AH particle length would be beneficial to improve ruminal pH and milk composition because of any undesirable effect on feed sorting.

Key Words: alfalfa hay particle length, dairy cow, feeding behavior

T64 Effect of level and source of supplemental protein on rate of ruminal methane production and methanogen concentration in *Bos taurus* and *Bos indicus* steers fed low-quality forage. N. L. Bell*[1], R. C. Anderson[2], S. L. Murray[1], J. C. McCann[1], K. K. Weldon[1], A. D. G. Wright[3], J. E. Sawyer[1], and T. A. Wickersham[1], *[1]Texas A&M University, College Station, [2]USDA/ARS Southern Plains Agricultural Research Center, College Station, TX, [3]University of Vermont, Burlington.*

The adaptive response of ruminal methanogen populations to substrate availability is not well defined. In this study, 10 ruminally cannulated steers (5 each: *Bos taurus*, Bt, 303 ± 10 kg initial BW and *Bos indicus,* Bi, 323 ± 28 kg initial BW) were used to quantify differences in source and level of protein on rate of ruminal methane (CH_4) production and methanogen concentration. Breeds were assigned to separate 5 × 5 Latin squares and fed low-quality forage (4.5% CP). Treatments were arranged as a 2 × 2 factorial plus a control (no supplement): the first factor was level of protein, 60 or 120 mg N/kg BW daily; and the second was source, DIP (degradable intake protein; 72% DIP) or UIP (undegradable intake protein; 72% UIP). Rumen fluid collected immediately after feeding and 4 h later was processed according to standard laboratory protocols. There was a main effect of time after feeding ($P < 0.01$) for both Bt and Bi steers with CH_4 production being lower at 4 h after feeding versus 0 h (1.75 ± 0.45 and 2.32 ± 0.95 μmol CH_4/mL per h; respectively). There was a protein source by level interaction for Bt ($P = 0.03$) and Bi ($P = 0.07$) steers. In both cases, steers fed 60 or 120 mg N/kg BW UIP had lower levels of in vitro CH_4-producing activity (1.93 ± 0.74 and 1.90 ± 0.91 μmol CH_4/mL per h for Bt and Bi, respectively) than steers fed 60 or 120 mg N/kg BW DIP (2.25 ± 0.88 and 2.20 ± 0.74 μmol CH_4/mL per h for Bt and Bi, respectively). Contrary to our hypothesis, main effects of breed, treatment, or time, and the interactions were not observed ($P > 0.35$) for methanogen concentrations measured by most probable number (MPN) or quantitative PCR. Methanogen concentrations averaged 6.52 ± 1.13 and 7.08 ± 0.86 $\log_{10}$/mL rumen fluid when measured by MPN and PCR methods, respectively. These results suggest that while methanogen concentrations remained unchanged, the population may favor slow growing methanogens expressing high substrate affinity during periods of limiting reductant and favor more rapid growing species with lower substrate affinity when reductant is abundant.

Key Words: protein supplementation, methane

T65 Whole cottonseed can replace barley straw in TMR fed beef heifers at finishing period. S. P. Iraira[1], J. L. Ruíz de la Torre[1], M. Rodríguez-Prado[1], M. Pérez[2], X. Manteca[1], S. Calsamiglia*[1], and A. Ferret[1], *[1]SNiBA, Universitat Autònoma Barcelona, Bellaterra, Spain, [2]Unitat de Qualitat i Carn-IRTA, Girona, Spain.*

To study the effect of whole cottonseed (WCS) on performance and meat quality, and to compare the results with those provided by the use of barley straw (BS) offered either separately or mixed with the concentrate, 27 Simmental heifers (initial BW 265.1 ± 20.4 kg) were assigned to three treatments in a randomized complete block design. Treatments consisted of (1) concentrate and BS, both offered as free-choice in separate feedbunks (CH-BS), (2) concentrate and BS offered as total mixed ration (TMR) with a concentrate to BS ratio of 92 to 8 (TMR-BS), and (3) TMR in which 16% of WCS (DM basis) was used as an alternative fiber source (TMR-WCS). All diets were offered ad libitum and formulated according to NRC (2000) to be isoenergetic (3.0 Mcal ME/kg DM), and isonitrogenous (14% on DM). Animals were allotted to roofed pens with 3 animals per pen, and 3 pens per treatment. Intake, ADG and G:F ratio were registered. Dressing percentage was calculated from hot carcass weight and the BW recorded before transfer to the abbatoir. The Longissimus thoracis (LT) muscle was excised from the 6th rib, and was used for measurements of meat quality. Intake of DM, ADG, and G:F ratio were no different among diets, being on average 8.1 ± 0.34 kg/d, 1.4 ± 0.08 kg/d, and 0.18 ± 0.01, respectively. The concentrate to BS ratio in heifers fed CH-BS was 96 to 4. Intake of CP was greater ($P = 0.013$) in TMR-WCS than in CH-BS and TMR-BS, and NDF intake was greater ($P = 0.05$) in TMR-BS than in TMR-WCS. There were no differences in the carcass characteristics and meat quality among diets, but there were differences in the percentage of some fatty acids. The percentage of C17:0 ($P = 0.005$), and C18:1 *trans*-10, *trans*-11, *trans*-12 ($P = 0.012$) was greater in heifers fed TMR-WCS than heifers fed BS diets, but lesser in the case of C18:1 *cis*-9 ($P = 0.002$). The n-6:n-3 ratio was greater in TMR-WCS than in the other two diets ($P = 0.001$). In summary, these results suggest that WCS can replace BS in finishing beef heifers without affecting DM intake, ADG, G:F ratio, carcass characteristics, and meat quality, although it can cause some changes in the fatty acid profile of the LT muscle.

Key Words: beef cattle, whole cottonseed

T66 Effects of basal diet and degradable intake protein level on the growth response to slow release urea in beef steers. V. B. Holder*[1], J. S. Jennings[2], K. M. McLeod[1], J. M. Tricarico[3], and D. L. Harmon[1], *[1]University of Kentucky, Lexington, [2]Alltech Inc., Brookings, SD, [3]Innovation Center for the U.S. Dairy, Rosemont, IL.*

This experiment was conducted to determine the effects of basal diet, DIP level and urea source on the growth and efficiency of beef cattle. The experiment utilized 240 Angus crossbred steers (BW: 287 ± 1.4 kg) over a 70-d growth period. Steers were blocked by weight and, within block, randomly assigned to treatment. Each treatment combination had 6 replicate pens with 5 head per pen. Treatments were arranged as a 2 × 2 × 2 factorial structure with two concentrate levels (70% vs. 40%), two DIP levels (90% vs. 120% of requirements) and two sources of DIP (urea vs. slow release urea, OptigenII, Alltech Inc.). The basal diet was achieved by the addition of either wheat straw and corn stalks (40% concentrate) or high moisture shelled corn (70% concentrate) to a corn silage-based diet. Feed was offered once per day throughout the experiment and bunks were managed for ad libitum intake. The 70% concentrate diet increased DMI (9.38 vs. 7.76 kg/d, $P < 0.0001$), ADG (1.77 vs. 1.21 kg/d, $P < 0.0001$) and feed efficiency (189.1 vs. 156.4 g/kg, $P < 0.0001$). Similarly, the 120% DIP diets increased DMI (8.82 vs. 8.31 kg/d, $P < 0.0001$), ADG (1.61 vs. 1.38 kg/d, $P < 0.0001$) and feed efficiency (181.2 vs. 164.2 g/kg, $P < 0.0001$). There was an interaction between basal diet and DIP source where slow release urea increased ADG (1.80 vs. 1.75 kg/d, $P = 0.04$) and tended to improve feed efficiency (192.2 vs. 185.9 g/kg, $P = 0.07$) of 70% concentrate diets but tended to decrease these variables in 40% concentrate diets (ADG: 1.18 vs. 1.25 kg/d; efficiency: 154.6 vs. 158.2 g/kg). If provided when DIP is limiting, providing DIP as slow release urea instead of urea may increase performance and feed efficiency of animals on higher concentrate diets but not for the low quality high forage diets used in this experiment.

Key Words: N efficiency, N pollution

T67 In situ disappearance in lactating beef cows of dried distillers grains subjected to different levels of heat damage. K. P. Coffey*, A. N. Young, E. B. Kegley, D. Philipp, P. Hornsby, and J. Hollenback, *University of Arkansas Division of Agriculture, Fayetteville.*

Distillers dried grains (DDG) may be subjected to varied levels of heat damage during processing and transport. Our objective was to determine in situ DM disappearance of conventional (CDDG) or a lower-fat DDG (LFDDG) subjected to varied levels of heat damage. Both CDDG and LFDDG were mixed 80:20 with water, placed in Al pans, covered with foil, and heated for either 3 or 5.5 h at 150C. Contents from the center of each pan were retained separately from the exterior 2 cm of each pan. The exterior 2 cm from the 5.5-h heating was charred excessively and retained to represent excessive heat damage (5.5CHR). Ruminally cannulated beef cows (n=4; 533±14.0 kg BW) were offered bermudagrass hay with either no supplement or 0.45% of BW from either CDDG, LFDDG, or heated LFDDG (3 h at 150°C) in a 4 × 4 Latin square experiment. Nylon bags containing unheated CDDG and LFDDG, those heated for 3 or 5.5 h, and those from 5.5CHR were incubated in the rumen for multiple times up to 108 h. Dry matter remaining was fit to a non-linear model, resulting in estimations of immediately-soluble (A) and potentially degradable (B) fractions, along with disappearance rate (k_d). Cow diet did not affect ($P > 0.29$) in situ parameters. Fraction B was greater ($P < 0.05$), and k_d was less ($P < 0.05$) from CDDG vs. LFDDG. Fraction B was greater ($P < 0.05$) from 5.5CHR and DDG heated for 5.5 h, and k_d was slowest ($P < 0.05$) from 5.5CHR followed by DDG heated for 5.5 h. Neither measure differed ($P > 0.05$) between unheated DDG and DDG heated for 3 h. Linear relationships were strongest ($R^2 > 0.77$) between acid-detergent insoluble N (ADIN, % of total N) and fraction A within DDG type. Linear and quadratic relationships between ADIN and other kinetic parameters were observed ($P < 0.05$), but those relationships were lower ($R^2 \leq 0.41$) than for fraction A, and were even less ($R^2 = 0.06$ to 0.32) when analyzed across types of DDG. Therefore, moderate heat damage had little impact on ruminal DM kinetic measurements, and use of ADIN analyses to assess ruminal DM disappearance characteristics should be viewed with caution, even within DDG processing method.

Key Words: distillers dried grain, in situ disappearance, heat damage

T68 Raw soybeans in a whole corn diet for feedlot heifers. A. J. Pordomingo, N. A. Juan, G. Volpi Lagreca*, and R. Beierbach, *National Institute Agricultural Research (INTA), Anguil, La Pampa, Argentina.*

Small-scale beef producers often use raw soybeans as protein source. Ruminants have the ability to denature in the rumen the antitrypsin factors present in soybeans, but levels are not conclusive and require further elucidation. Ninety-six 285-kg Angus heifers were distributed in 24 feeding pens. Pens were allocated to 8 diets, a factorial combination of processing (raw or roasted) and 4 levels (0, 10, 16 and 22%) of soybeans. Diets were whole corn based and included 5% alfalfa hay, a mineral premix and monensin. Soybean were ground before feeding. Sunflower meal and urea were used to adjust the crude protein content to 14%. Animals were fed in excess to voluntary intake (DMI) over a 90 d period. Processing by level interactions were detected ($P < 0.05$) for final weight, ADG and intake. Increased roasted soybean concentration in the diet tended to improve ADG and final weight (linear trend; P = 0.06) No treatment effects were detected ($P > 0.05$) in DMI for roasted soybeans. A similar response was observed for raw soybeans up to the 16% level in the diet. Treatments with 10 or 16% raw or roasted soybean resulted in similar ($P > 0.627$) ADG, final live weight and intake. On the contrary, the diet with 22% raw soybean resulted in the lowest ADG and feed intake ($P < 0.001$) compared with the other treatments, which elicited the lowest final live weight. This treatment had also the poorest feed efficiency ($P < 0.034$). Increased performance with increasing soybean content could be attributed to the increased oil content of the diet and the quality of protein of soybeans versus sunflower meal. The lower ADG for the 22% raw soybeans vs. the other treatments could be at least in part explained by the presence of antitrypsin factors in the soybeans.

Key Words: antitrypsin factors, feedlot heifers, raw soybeans

T69 Effect of supplemental protein amount and degradability on intake and digestion in *Bos indicus* and *Bos taurus* steers fed rice straw. K. K. Weldon*, J. C. McCann, J. E. Sawyer, and T. A. Wickersham, *Texas A&M University, College Station.*

We evaluated effects of amount and degradability of supplemental protein on utilization of low-quality forage in 5 Angus steers (*Bos taurus*, Bt, BW = 303 ± 10 kg) and 5 Brahman steers (*Bos indicus*, Bi, BW = 323 ± 28 kg). Steers fitted with ruminal and duodenal cannulas were used in concurrent 5 × 5 Latin squares. Treatments were arranged as a 2 × 2 factorial plus a control (CON; no supplementation). Isonitrogenous (27% CP) supplements were formulated to provide different proportions of ruminally degradable protein (DIP; L = 28% DIP or H = 72% DIP). Each type of supplement was fed to deliver 60 or 120 mg of N/kg BW. Steers had ad libitum access to rice straw (4.4% CP, 72.8% NDF). Experimental periods were 15 d; 9 d adaptation and 6 d sample collection. Forage OM intake (FOMI) was greater for Bt than Bi ($P = 0.05$). Supplementation increased FOMI in both Bt and Bi ($P < 0.05$); Bi FOMI was increased from 13.5 g/(kg BW·d) to 14.8 g/(kg BW·d) and Bt from 16.5 g/(kg BW·d) (CON) to 17.6 g/(kg BW·d). Neither protein source, amount, nor their interaction affected FOMI within Bi or Bt ($P > 0.20$). OM digestibility (OMD) was greater in Bi than Bt ($P < 0.01$). Supplementation did not affect OMD in Bt ($P = 0.53$; 54.4% vs. 53.6% for CON vs. supplement), but increased OMD for Bi ($P = 0.02$) from 53.4% (CON) to 57.0% (supplemented). There were no source, amount, or source × amount effects ($P > 0.37$) within Bi or Bt for OMD. Total digestible OM intake (TDOMI) was similar between breeds ($P = 0.12$), and increased ($P < 0.01$) with supplementation. A 14% increase in TDOMI was observed from CON for Bt ($P = 0.04$); TDOMI increased 29% from CON for Bi ($P = 0.05$). There were no source, amount, or source × amount effects ($P > 0.22$) within either breed for TDOMI. While Bt had significantly higher FOMI, an increase in OMD for Bi with supplementation resulted in similar overall TDOMI between breeds.

Key Words: digestion, intake, straw

T70 Effect of degradability and level of protein supplementation on ruminal fermentation in *Bos indicus* and *Bos taurus* steers fed rice straw. K. K. Weldon*, J. C. McCann, J. E. Sawyer, and T. A. Wickersham, *Texas A&M University, College Station.*

We evaluated the effects of amount and degradability of supplemental protein on ruminal fermentation of different breeds of cattle fed low quality forage. Five Angus steers (*Bos taurus,* Bt) and 5 Brahman steers (*Bos indicus*, Bi) with ruminal cannulas were used in concurrent 5 × 5 Latin squares. Treatments were arranged as a 2 × 2 factorial plus a control (CON; no supplementation). Isonitrogenous (27% CP) supplements were formulated to provide different proportions of ruminally degradable protein (DIP; L = 28% DIP or H = 72% DIP). Each type of supplement was fed to deliver 60 or 120 mg of N/kg BW. Steers had ad libitum access to rice straw (4.4% CP, 72.8% NDF). Experimental

periods were 15 d; 9 d adaptation, and 6 d sample collection. Total digestible OM intake (TDOMI) was similar between breeds ($P = 0.12$), and increased ($P < 0.01$) with supplementation. Ruminal ammonia (NH_3-N) concentrations increased with supplementation ($P < 0.01$) versus CON in both breeds. *Bos indicus* steers had greater NH_3-N concentrations than Bt ($P < 0.01$). Supplement amount × source affected NH_3-N in Bt and Bi ($P < 0.01$). In Bt, increasing from 60-L to 120-L had minimal effect; increasing from 60-H to 120-H increased NH_3-N 58%. In Bi, increasing from 60 to 120 increased NH_3-N by 45% for L, but only 26% for H. Plasma urea nitrogen (PUN) was greater for Bi than Bt ($P < 0.01$) for all treatments and at both 0 and 4 h after feeding. Supplementation tended ($P = 0.06$) to increase PUN versus CON in Bt, but not Bi ($P = 0.82$). Increased amount of supplement tended to increase PUN in Bi ($P = 0.08$), while both increased supplement amount and proportion of DIP increased PUN in Bt ($P < 0.01$). *Bos taurus* steers had numerically ($P = 0.19$) greater total volatile fatty acids (VFA) across treatments than Bi steers. Increased amount of supplementation to Bt increased total VFA ($P < 0.01$) from 74.1 m*M* (60) to 76.3 m*M* (120), but did not change VFA in Bi ($P = 0.32$). Overall, Bi had higher ruminal and plasma nitrogen concentration than Bt; these concentrations increased as amount and DIP proportion of supplements increased in both breeds.

Key Words: forage, ruminal, fermentation

T71 Effect of amount and degradability of protein supplements on nitrogen metabolism in *Bos indicus* and *Bos taurus* steers fed rice straw. K. K. Weldon*, J. C. McCann, J. E. Sawyer, and T. A. Wickersham, *Texas A&M University, College Station.*

We evaluated effects of amount and degradability of supplemental protein on nitrogen metabolism in 5 Angus steers (*Bos taurus*, Bt, BW = 303 ± 10 kg) and 5 Brahman steers (*Bos indicus*, Bi, BW = 323 ± 28 kg). Steers fitted with ruminal and duodenal cannulas were used in concurrent 5 × 5 Latin squares. Treatments were arranged as a 2 × 2 factorial plus a control (CON; no supplementation). Isonitrogenous (27% CP) supplements were formulated to provide different proportions of ruminally degradable protein (DIP; L = 28% DIP or H = 72% DIP). Each type of supplement was fed to deliver 60 or 120 mg of N/kg BW. Steers had ad libitum access to rice straw (4.4% CP, 72.8% NDF). Experimental periods were 15 d; 9 d adaptation, and 6 d sample collection. Total nitrogen (N) intake was greater for Bt than for Bi steers ($P = 0.06$). As expected, supplementation increased total N intake vs. CON ($P < 0.01$), and higher amounts of supplemental N increased total N intake within both breeds ($P < 0.01$). Higher DIP supplements increased total N intake for Bt ($P < 0.01$); no effect of supplemental N source was observed in Bi ($P = 0.19$). Fecal N was higher in Bt than Bi ($P < 0.01$). Supplementation increased ($P < 0.01$) fecal N vs. CON for both breeds. Increased amount of N supplementation elevated fecal N in Bi ($P = 0.02$), but not Bt ($P = 0.13$). Urinary N tended to be higher for Bi than Bt ($P = 0.10$). Supplementation increased ($P < 0.05$) urinary N for both breeds. Increasing N amount increased urinary N excretion in Bi ($P = 0.02$), and Bt ($P = 0.06$). Retained N was greater for Bt over Bi ($P = 0.07$). In both breeds, N retention increased with supplementation vs. CON ($P < 0.01$). More N supplement increased N retained ($P < 0.01$). Increased supplementation raised N excreted and N retained for both breeds; fecal N was greater in Bt, while urinary N was greater in Bi. Total N intake tended to be greater in Bt, while total excretion was similar for Bt and Bi, resulting in greater amount of N retained by Bt.

Key Words: forage, nitrogen, balance

T72 Effect of different substitute levels of ground corn by coarsely ground wheat on ruminal fermentation, milk yield and composition in dairy cows. Y. Guo*, Y. Zou, X. Xu, Z. Yang, S. Li, and Z. Cao, *State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing, China.*

Eight multiparous Holstein cows (569 ± 47 kg of BW; 84 ± 17 DIM) were used to evaluate the effects of different levels of coarsely ground wheat (CGW, 3-mm screen, geometric mean particle sizes: 1,139 μm) as replacements for ground corn (GC, 3.5-mm screen, geometric mean particle sizes: 666 μm) in diets on ruminal fermentation, milk yield and composition in dairy cows. The cows were settled in a replicated 4 × 4 Latin square design with 3-wk treatment periods; four cows in one of the replicates were fitted with rumen cannulas. The four diets contained 0, 9.6, 19.2, and 28.8% CGW and 27.9, 19.2, 9.6, and 0% GC (DM basis), respectively. The cows were fed a TMR, with a 47:53 forage to concentrate ratio, where forage was 27% corn silage, 14% alfalfa hay, and 6% Chinese wild rye. The cows were fed and milked twice daily. Substituting CGW for GC had no effect on daily mean ruminal pH, but tended to reduce minimum ruminal pH and increase pH range when the cows were fed the 28.8% CGW diets. Increasing the dietary concentration of CGW resulted in a linear increase in ruminal propionate and ruminal NH_3-N concentration, while ruminal acetate: propionate tended to decrease in cows fed the 28.8% CGW diets. Daily DM intake averaged 19.7kg and tended to increase quadratically. Milk production was not affected by diets; however, percentage and yield of milk fat, 3.5%FCM, and ECM decreased linearly, and milk urea nitrogen increased linearly, when the level of CGW was increased. Dietary treatments had no effect on feed efficiency (milk/DMI), while 3.5%FCM/DMI decreased linearly with increasing levels of CGW. The data indicate that CGW is a suitable substitute for GC in diets of dairy cows and that it may be included up to a level of 19.2% of dry matter without adverse effects on ruminal fermentation, feed intake, milk yield and composition, if the cows are fed fiber-sufficient diets and the levels are adjusted gradually. However, high inclusion levels of CGW, such as in the case of 28.8% CGW diets, could increase the risk of subacute ruminal acidosis, and milk-fat depression.

Key Words: wheat, dairy cow, rumen fermentation

T73 Effects of feeding a corn straw or mixed forage diet to lactating cows on rumen fermentation parameters using a wireless data logger. C. F. Qin[1,2], D. P. Bu[1], J. Q. Wang*[1], P. Sun[1], P. H. Zhang[2], X. W. Zhao[1], J. N. Li[1], and P. Zhang[1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Hunan Provincial Key Laboratory for Genetic Improvement of Domestic Animal, College of Animal Science and Technology, Hunan Agricultural University, Changsha, Hunan, China.*

The objectives of this study were to evaluate the effects of feeding two different diets on ruminal pH, temperature and oxidation reduction potential (ORP) and their rhythms for 24 h through real-time monitoring. Eight primiparous lactating Holstein cows fitted with rumen cannula were blocked by milk yield and body weight and then randomly assigned to high forage diet (HF; forage:concentrate = 60:40) with Chinese wildrye, alfalfa hay and corn silage as the forage source or low forage diet (LF, forage:concentrate = 40:60) with corn straw as the forage source. Ruminal pH, temperature and ORP were real-time monitored by a wireless data logger during a trial period of 14 d. Data were analyzed using the PROC MIXED procedure of SAS. Cows fed LF diet had higher ruminal pH compared to those fed HF diet (6.32 and 6.12; $P < 0.01$),

whereas temperature (38.57 and 38.86 °C; $P < 0.01$) and ORP (−384.25 and −361.88 mV; $P < 0.01$) were lower in LF group. The pH values were higher in LF group compared to those fed HF diet at the minutes when morning (6.33 and 6.17; $P < 0.05$) and evening (6.57 and 6.42; $P < 0.05$) ingestion began and at the minutes when night rumination (6.22 and 6.02; $P < 0.01$) proceeded and when morning (6.30 and 5.99; $P < 0.01$) and evening (6.29 and 6.02; $P < 0.01$) ingestion finished. Cows fed LF diet had less minutes for ruminal pH < 6.0 (161.55 and 449.74 min/d; $P < 0.05$) and pH < 5.8 (79.45 and 230.50 min/d; $P < 0.05$) compared to those fed HF diet, and ruminal pH < 5.6 (31.86 and 79.53 min/d; $P = 0.07$) tended to be less in LF group. However, minutes for pH < 5.2 were not affected by diets. Ruminal pH and ORP rose to their peaks when feeding began but reduced to the minimums when feeding finished. Ruminal temperature reduced to minimum after feeding at noon. The results indicated that rumen fermentation parameters were affected by forage-to-concentrate ratio in the diets, and the wireless data logger system can accurately and precisely measure rumen fermentation parameters.

Key Words: forage pattern, wireless data logger, rumen fermentation parameter

T74 Effect of feeding a corn straw or mixed forage diet on mixed-rumen bacterial fatty acid profiles in lactating cows. C. F. Qin[1,2], J. Q. Wang[1], D. P. Bu*[1], P. Sun[1], P. H. Zhang[2], M. Yi[1], S. K. Jiang[1], and J. N. Li[1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Hunan Provincial Key Laboratory for Genetic Improvement of Domestic Animal, College of Animal Science and Technology, Hunan Agricultural University, Changsha, Hunan, China.*

Rumen microbial matter is a vital source of nutrients for the host animal and it may be affected by diet systems. Our objective was to determine the effect of different forage sources on fatty acid (FA) composition of mixed-rumen bacteria. Twelve primiparous, lactating and ruminally fistulated Holstein cows were used in this study. Cows were randomly assigned to high forage diet (MF, forage:concentrate = 60:40) with Chinese wildrye, alfalfa hay and corn silage as the forage source or low forage diet (CS, forage : concentrate = 40 : 60) with corn straw as the forage source. This study lasted for 9 weeks with 2-week of preliminary period and 7-week of trial period. Rumen samples were collected 4 times daily in the last 3 excessive days to insure each sample was obtained with 2-hour intervals inter. All samples were composited for each cow and kept at -20°C for further analysis. Data were analyzed using the PROC MIXED procedure of SAS 9.1. Compositions of C14:1 (5.53 and 6.09%), C15:0 (3.01 and 3.38%), *trans*-9 C18:1 (0.23 and 0.26%), *trans*-11 C18:1 (1.42 and 1.50%), *cis*-9, *cis*-12 C18:2 (2.66 and 2.85%), *cis*-9, *tran*-11 CLA (1.33 and 1.18%), *trans*-10, *cis*-12 C18:2 (0.33 and 0.37%), C20:0 (0.32 and 0.31%), mono unsaturated FA (11.93 and 11.80%), poly unsaturated FA (4.75 and 4.75%), saturated FA (83.32 and 83.44%) and unsaturated FA (16.68 and16.57%) were not affected by forage sources ($P > 0.05$). Proportions of C18:0 (49.17 and 42.92%; $P < 0.05$), *cis*-9 C18:1 (4.50 and 3.66%; $P < 0.01$), > C16:0 (61.61 and 55.02%; $P < 0.01$) and long chain FA (16.68 and16.57%; $P < 0.01$) were increased in cows fed with CS. Percentages of C16:0 (25.23 and 30.28%; $P < 0.01$), C18:3 (0.20 and 0.36%; $P < 0.01$) and medium chain FA (33.22 and 44.84%; $P < 0.01$) were lower in CS group. The CS diet tended to have a negative effect on proportion of C12:0 (0.80 and 0.99%; $P = 0.09$), C14:0 (3.33 and 3.97%; $P = 0.08$) and C22:0 (0.26 and 0.39%; $P = 0.09$). In conclusion, different forage patterns influenced mixed-rumen bacterial FA synthesis and caused the alteration of rumen microbial FA profiles in cows.

Key Words: forage source, lactating cow, mixed-rumen bacterial fatty acid

T75 Effect of fed a corn straw or mixed forage diet on fatty acid extraction in mammary gland of lactation dairy cows. H. Y. Chen[1,2], D. P. Bu*[1], F. D. Li[2], X. M. Nan[1], X. W. Zhao[2], and H. Hu[1], *[1]Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Gansu Agricultural University, Lanzhou, Gansu, China.*

Changing the fatty acids (FA) profile of plasma might affect FA metabolism in the mammary gland of dairy cows. This study was conducted to evaluate the effect of feed type on the FA profile of plasma, blood parameters and fatty acids extraction in mammary gland of dairy cows in lactation. Twenty lactating Holstein cows (BW = 558 ± 40 kg, DIM at the beginning of the experiment = 83 ± 10 d, n = 10) were randomly assigned to high forage diet (MF, forage : concentrate = 60 : 40) with Chinese wildrye, alfalfa hay and corn silage as the forage source or low forage diet (CS, forage : concentrate = 40 : 60) with corn straw as the forage source. The experiment lasted for 49 d with a 14 d adaptation period for cows to adjust to the treatment diets. On the 48 d and 49 d of the experiment, blood samples were taken from the coccygeal artery (representing mammary arterial supply) and milk vein at 3 hr after morning feeding. Extraction (%) of each FA was assessed via arterial-rectificative venous concentration (AC-RVC) differences. Data were analyzed using the MIXED models of SAS, with treatment as fixed effect. The results showed that MF increased the contents of C14 (0.71 and 0.69, $P < 0.05$), C16:1 (0.72 and 0.55, $P < 0.05$) and PUFA (68.88 and 67.81, $P < 0.05$) in the blood, while the content of c9c12C18:2 in MF was lower than the CS (59.29 and 60.85, $P < 0.01$), A nonsignificant increase of other FA was observed in our trial. Compared to the CS, MF did not affect most of the fatty acids extraction in mammary gland ($P > 0.05$), except C18:3 (24.26 and 42.10, $P < 0.05$). The MF increased content of NEFA in plasma (0.92 and 0.85, $P < 0.05$) and tended to increase the content of TC and LDL. These results indicated that different diet can changed the plasma fatty acid profile, which can cause the fatty acid extraction rate to change. Moreover, the results suggest that when FA taken up from arterial plasma by mammary gland tissues, there is a relationship between them. Changing the type of diet affects FA metabolism in the mammary gland of dairy cows.

Key Words: blood parameter, fatty acid extraction rate, feed type

T76 Effect of replacing timothy silage with alfalfa silage in dairy cow diets on enteric methane production. F. Hassanat*[1], R. Gervais[2], P. Y. Chouinard[2], H. Petit[1], D. Massé[1], and C. Benchaar[1], *[1]Agriculture and Agri-Food Canada, Dairy and Swine Research and Development Centre, Sherbrooke, QC, Canada, [2]Département des Sciences Animales, Université Laval, Québec, QC, Canada.*

The objective of this study was to determine the impact of replacing timothy silage with alfalfa silage (AS) in dairy cow diets on enteric CH_4 emissions. Nine lactating, multiparous Holstein cows (DIM = 92 ± 19; BW = 696 ± 71 kg; milk yield 46.2 ± 4.3 kg) used in a replicated 3×3 Latin square (32-d periods, 14-d adaptation) were fed (ad libitum) a TMR (60:40, forage:concentrate ratio) with the forage portion being either timothy silage (0% AS), alfalfa silage (100% AS) or a 50:50 mixture (50% AS). Diets were formulated to contain 16.5% CP and 1.64 Mcal/kg NE_L. Production of CH_4 was determined (3 consecutive days) using respiration chambers. Digestibility and milk performance were determined over 6 consecutive days. Linear and quadratic contrasts (MIXED Procedure; SAS) were used to determine the effects of increasing AS proportions on response variables. Significance was declared at $P \leq 0.05$ and tendencies at $0.05 \leq P \leq 0.10$. Dry matter (DM) intake (22.5, 23.7, and 24.6 kg/d for 0, 50 and 100% AS, respectively) increased linearly while DM digestibility did

not change as the proportion of AS increased in the diet. Yields of milk, fat-corrected milk (FCM) and energy-corrected milk (ECM) were not affected by increasing dietary AS proportions. Daily CH_4 emission tended ($P = 0.10$) to increase with increasing proportions of AS in the diet (476, 483 and 491 g/d for 0, 50 and 100% AS, respectively). Methane production adjusted for DM (average 19.8 g/kg) or gross energy intake (average 5.83%) was not affected by increasing AS inclusion in the diet. When expressed on FCM or ECM yield bases, CH_4 production increased linearly ($P = 0.03$) with increasing AS proportions in the diet. In conclusion, under the experimental conditions of this study, CH_4 energy losses (% gross energy intake) were not affected by replacing timothy silage with alfalfa silage in dairy cow diets.

Key Words: alfalfa silage, timothy silage, methane

T77 The optimal ratio of canola meal and dried distillers grain proteins in high producing Holstein cow diets. N. Swanepoel*[1,2], P. H. Robinson[1], and L. J. Erasmus[2], [1]*Department of Animal Science, University of California, Davis,* [2]*Department of Animal and Wildlife Sciences, University of Pretoria, Pretoria, South Africa.*

Limited data is available on dairy cow performance when feeding canola meal (CM) and distillers dried grains with solubles (DDGS) as main supplemental crude protein (CP) sources. Our objective was to determine the optimal ratio of CM to DDGS CP in a contemporary California dairy ration by feeding combinations of CM and high protein (low oil) DDG (HPDDG) to high producing dairy cows. The design used 4 pens of 320 high-producing cows/pen in a 4 × 4 Latin square crossover with 28-d periods. Treatments varied in the amount of CM and HPDDG added on a dry matter (DM) basis: (1) 0 CM, 200 g/kg HPDDG, (2) 65 CM, 135 g/kg HPDDG, (3) 135 CM, 65 g/kg HPDDG, (4) 200 CM, 0 g/kg HPDDG. DM intake was not affected (avg: 24.4 kg/d) by the CM/HPDDG ratio. Milk (44.9, 47.4, 47.9, 47.4 kg/d for 0, 65, 135, 200 g/kg CM respectively; $P < 0.01$) and true protein yield (avg: 1.37 kg/d) increased quadratically with the higher CM/HPDDG ratio, peaking at 135 g/kg CM. Milk fat yield (avg: 1.61 kg/d) and true protein (TP) % (avg: 2.93) responded quadratically ($P < 0.01$), peaking at ~120 g/kg CM. Milk fat % (avg: 3.44) had a linear decrease ($P < 0.01$) with lowest values at 200 g/kg CM. Body condition score (BCS) change responded quadratically (0.001, 0.034, 0.08, 0.029 units/28 d for 0, 65, 135, 200 g/kg CM respectively; $P < 0.01$), with highest BCS gain at ~120 g/kg CM. Results suggest the optimum level was 120 to 135 g/kg of supplemental protein from CM. The urine purine derivative to creatinine index increased linearly ($P < 0.01$) with higher CM level, suggesting microbial protein production (MCP) was limited at 0 g/kg CM and progressively stimulated by higher feeding levels of CM. Plasma amino acid (AA) levels suggest a reduction in lysine from dietary protein, with the decreased MCP production, resulted in substantial reduction in lysine available to support milk production, limiting performance in higher HPDDG rations. The only essential plasma AA to linearly decrease ($P < 0.01$) with higher CM were Phe, Leu and Met. The additional quadratic response ($P < 0.01$) of Met and Phe at the 200 g/kg CM treatment suggests that Phe and/or Met limited production in the highest CM ration.

Key Words: urine purines, amino acids

T78 Intake, milk yield, and blood acid-base balance of cows in response to marine algae meal. N. M. Lopes[1], R. A. N. Pereira[2], and M. N. Pereira*[1], [1]*Universidade Federal de Lavras, Lavras, MG, Brazil,* [2]*Empresa de Pesquisa Agropecuaria de Minas Gerais, Lavras, MG, Brazil.*

The skeleton of the marine algae *Lithothamnium calcareum*, a source of calcium carbonate, has been fed to dairy cows as an alkalizer, despite the lack of strong evidence for its effectiveness and for the mode of action. This experiment evaluated the performance, diet digestibility, and venous acid-base balance of cows supplemented with algae meal (Algarea, Brazil) or sodium bicarbonate. Twenty Holsteins (248 DIM) received treatments in 4 × 4, 21-d period, Latin squares. Treatments were: Control (C), 1% of DM of algae meal (A), 0.5% algae meal+0.5% sodium bicarbonate (AB), or 1% sodium bicarbonate (B). Diets had (% of DM): 52.7 corn silage, 2.2 Tifton hay, 21.7 soybean meal, and 20 high moisture corn. On days 19 to 21, acidosis was induced by abrupt replacement of 12.4% DM units of corn silage by high moisture corn. Jugular vein gasometry was performed 9.5h post-feeding on day 19. Pre-planned contrasts were: C vs. A, A vs. B, and AB vs. (A+B). Total tract digestibility, determined by total collection of feces, was not affected by treatments ($P > 0.64$). Milk yield was (kg/d): 21.5 for C, 20.6 for A, 21.5 for AB, and 22.3 for B, and DMI was 18.1, 17.5, 18.0, and 18.8, respectively. There was a trend for decreased DMI when algae meal was added to the control diet ($P = 0.06$), and a linear decrease in DMI ($P < 0.01$) and milk yield ($P = 0.10$) when it replaced bicarbonate. During acidosis induction, the response across treatments in DMI and milk yield followed that same pattern. Satiety, measured as the duration of the first meal, was shortest in C, while the proportion of daily DMI between 7AM and 12AM was smallest in A. Across treatments, the response in satiety paralleled the response in blood gasometry. Treatment A had the strongest measures of blood hypoxia, although a similar, but weaker response, was also elicited by bicarbonate. The net Ca^{++} and Na^{++} absorption apparently induced hypoventilation for the maintenance of blood pH at 7.41. Algae meal was a potent manipulator of acid-base balance, but at 1% of diet DM it did not improve performance or digestibility of cows in late lactation.

Key Words: blood acid-base balance, algae meal, *Lithothamnium calcareum*

T80 Starch digestion variation between in vitro and in situ digestion techniques. C. R. Heuer*[1,2], J. P. Goeser[1], and R. D. Shaver[2], [1]*Rock River Laboratory Inc., Watertown, WI,* [2]*University of Wisconsin, Madison, Madison.*

Starch digestion (starchd) of grains and forages is important to dairy cattle nutritionists. By being able to accurately predict the starchd they are able to maximize milk production and milk fat. Our objective was to determine if different starchd techniques, rumen in vitro (IV) and in situ (IS), generate comparable results and are repeatable across weeks. Corn silage (n = 2), snaplage (n = 2), TMR (n = 2), high moisture corn (n = 2), and dry corn (n = 2) were dried and ground (4 mm). For the IV technique samples were weighed (0.5 g) into 125-mL flask, rumen fluid was collected from 2 lactating dairy cows and went through a standardization procedure. Samples were analyzed in triplicate for 3 and 7 h time points. IS samples were weighed (6 g per bag) in triplicate to be placed in 3 lactating dairy cows consuming a commercial diet for 3 and 7h. Residue bags were rinsed until effluent was clear. Bags were dried and weighed to determine the dry matter digestion. Residue samples were composited and ground to 1mm. Starch content was then determined by the use of an YSI 2700 to determine glucose (g/L). Starch was calculated as 100 × [(volume/weight) × (glucose) × (0.9)/1000]. Starchd was calculated as 100 × [($Starch_{0h}$ − $Starch_{residue}$) / ($Starch_{0h}$)]. Each of these techniques was evaluated 2 weeks to assess repeatability. We analyzed the data set using SAS 9.3 and linear models. Both starchd and technique modeled as response variables, with fixed effects of week and hour in both

and technique in the starchd model and ID as a random effect in both. When comparing techniques, IS was used as the response variable. Means were compared by Tukey's test. IV results yielded greater estimates than IS results (69.2% vs. 56.4%, $P < 0.04$). When comparing the variation IV samples averaged a numerically higher standard deviation than IS samples (7.80 vs. 2.01). The IV results tended to be related to IS results ($P < 0.07$). Results suggest that the IV technique of determining starchd causes elevated digestion levels compared to IS starchd. The tendency in relationship between techniques suggest IV may be an acceptable predictor of IS starchd.

Key Words: starch digestion

T81 Geometric mean diameter fails to reflect diversity in size of particles in processed maize grain. L. J. Nuzback, W. J. Seglar, M. Laubach, T. Hageman, and F. N. Owens*, *DuPont Pioneer, Johnston, IA.*

For feeding livestock, most maize grain is processed to reduce particle size and increase the surface area exposed for digestion. This in turn increases rate of ruminal digestion and total tract digestion of maize starch by lactating cows. Geometric mean diameter (GMD) of feed particles is appraised through measuring the mass retained on stacked sieves of different pore sizes. For forages, 5 sieves are used but for cereal grains a stack of 14 screens commonly are used and samples typically are dried prior to screening. We tested whether fewer screens might be used and the impacts of drying and processing method on GMD. Using dry processed and high moisture maize grain (12 and 7 samples) gathered from various Midwest dairies, GMD by the 14 screen system was determined at a commercial lab. These same samples were appraised through a simpler 4 screen system (Tyler 4, 8, 16 and 30 sieves). With the 4 screen system, GMD was determined with samples that differed in moisture content. For dry (rolled or hammer milled) maize grain samples, GMD was determined as received (85 to 88% DM). For high moisture rolled maize (HMC; 70 to 77% DM), GMD was determined either as received or after being air dried at least 48 hours or being oven dried at 50 C for 24 hours. Correlations of GMD determined at a commercial lab with GMD determined with 4 screens for the 5 sets of samples were high, being 0.99 (dry maize), 0.91 (as received HMC), 0.97 (air dried HMC), and 0.99 (oven dried HMC) with RMSE being 95, 137, 220, and 102 microns, respectively. For field use, GMD determined with the shorter stack system appears suitable. Although the GMD for the rolled and hammer milled dry grain samples did not differ, the standard error of the GMD was greater for hammer milled samples reflecting a wider distribution in particle sizes. GMD values alone fail to reflect this particle size diversity, a factor of interest nutritionally because very small particles may induce acidosis while larger particles likely are digested less extensively.

Key Words: grain, particle size, processing

T82 Performance and digestion of dairy cows in response to exogenous amylase. A. S. R. Andreazzi[2], N. N. Morais Junior[1], R. F. Lima[1], A. C. S. Melo[1], R. B. Reis[2], R. A. N. Pereira[3], and M. N. Pereira*[1], *[1]Universidade Federal de Lavras, Lavras, MG, Brazil, [2]Universidade Federal de Minas Gerais, Belo Horizonte, MG, Brazil, [3]Empresa de Pesquisa Agropecuária de Minas Gerais, Lavras, MG, Brazil.*

Exogenous amylase supplementation of dairy diets may increase the nutritive value of corn, especially when floury endosperm hybrids are not available. Twenty-eight Holsteins (171 ± 80 DIM at day 1) were paired blocked and assigned to a treatment for 70 days, after a two-week standardization period. Treatments were: Control or Amylase (Ronozyme RumiStar, DSM Nutritional Products). The enzyme was mixed to ground corn and added to a mixer to achieve 0.5g of enzyme per kg of TMR DM (300 KNU/kg of DM). Cows were individually fed in tie stalls. The diet contained (% of DM): 32.1% starch, 39.4% corn silage, 11.2% re-hydrated and ensiled mature corn, and 11.7% finely ground mature corn. Corn hybrids were semi-dent or flint type. Milk yield and DMI were recorded daily, milk solids weekly, and BW and BCS at 14-day intervals. On week 10, total tract digestibility and allantoin excretion were determined by total collection of feces and urine, PUN was measured at 0, 1, 2, 3, 6, 9, 12, and 18h post-feeding, and rumen pH and plasma glucose at 12h post-feeding. Eating and rumination pattern was visually evaluated for a 24h period. Data was analyzed with Mixed of SAS as a covariate adjusted randomized block design with repeated measures over time, except when data was obtained once along the experiment. Amylase increased milk yield (33.0 vs. 32.3kg/d, $P = 0.02$) and reduced DMI (19.7 vs. 20.7kg/d, $P < 0.01$), increasing feed efficiency ($P < 0.01$). Body weight and condition score did not differ ($P > 0.44$). Milk lactose production was increased by Amylase ($P = 0.01$) and there was a trend for increased plasma glucose content ($P = 0.07$). Amylase decreased PUN (13.6 vs. 14.7, $P = 0.05$), and induced numerical increase in the relative rumen microbial yield and reduced the duration of the first daily meal and rumen pH, all suggestive of increased ruminal OM fermentation. Total tract digestibility of DM, OM, NDF, and starch were not responsive to the enzyme ($P > 0.41$). Exogenous amylase supplementation increased feed efficiency of dairy cows. The decrease in PUN suggests that the enzyme increased ruminal starch degradation, without affecting total tract nutrient digestibility.

Key Words: amylase, starch, corn

T83 Effects of single or pulse dose of sugar on in vitro DMd and NDFd digestibility of corn silage. D. N. Lobão da Silva*[1], R. S. Younker[2], and N. B. Litherland[1], *[1]University of Minnesota, Saint Paul, [2]Milk Specialties, Eden Prairie, MN.*

DaisyII incubator, (Ankom Technology, Fairport, NY) rotating jar-in vitro system is an inexpensive technique to measure feedstuff digestibility and has potential to serve as a screening tool to evaluate ruminant feeds and feed additives; however, in vitro systems may better mimic natural feeding conditions through pulse dosing of test compounds. The objectives of this study were to evaluate the usage of rotating jar system using one or three pulse doses, and determine the effects of supplementing in vitro rumen culture with commercially available sugar supplement, on 30 h %IVDMd and %IVNDFd of corn silage (CS) with 38.0% NDF, 8.1%CP and 31.6% starch. In the first experiment, 1.3 g of RUMIN8 (R) per 400ml of rumen fluid using a single dose (R1) or three pulses doses (R3) and no sugar supplementation (C1) were evaluated. In the second experiment, 2.1g of 6 types of sugars (R), lactose (L), sucrose (S), molasses (M), whey permeate (W) and corn syrup solids (CSS) were evaluated. Amounts of 1.3g and 2.1g of sugar were calculated to represent in vivo diet inclusions of 0.7% and 1.0% of diet DM /cow/day. In both experiments, replicate samples were placed in Dacron bags and incubated in two Daisy II incubators. Data was analyzed using the MIXED procedure of SAS as completely randomized design. In the first experiment, IVDMD was similar ($P = 0.37$) among treatments and averaged 78.6, 79.5 and 77.76 ± 0.8% and IVNFDd was similar ($P = 0.45$) 39.4, 42.3, and 37.6 ± 2.7% for C1, R1, and R3, respectively. In the first experiment, results suggest that increased dosing frequency of Rumin8 did not increase %IVDMd or %IVNFDd of CS compared to C1. In the second experiment, L and S improved IVDMd ($P < 0.01$) by 4

and 3.5%, respectively compared with C, R, M, W and CSS (75.1, 75.0, 74.8, 76.8, 75.0 ± 0.7%). Also, L and S increased ($P < 0.01$) IVNDFd by 12.7 and 10.8% respectively compared with C, R, M, W and CSS (32.5, 32.1, 31.4, 34.3, 31.4 ± 2.0%). In vitro incubations of CS with sugar supplementation suggested that L and S greatly improve digestibility of DM and NFD compared with C, R, M, W and CSS.

Key Words: fiber digestibility, sugar, corn silage

T84 Feeding of a sugar alcohol during summer months to Holstein cows during transition phase to support subsequent lactation performance. J. A. Davidson*, C. M. Klein, and B. L. Miller, *Purina Animal Nutrition Center, Gray Summit, MO.*

The objective was to determine if a sugar alcohol (Rally) improves milk and component yield of transition cows during the summer months. Holstein cows (44 multiparous and 18 primiparous) were blocked by calving date (June 22 to Sept 4, 2010 and June 20 to Aug 28, 2011) and randomly assigned to dietary treatments of control (C) or sugar alcohol (R) from d -28 to 30 relative to parturition. Individual cows were fed with Calan doors once a day, ad libitum, and diets were formulated to be iso-nitrogenous and iso-caloric. On d 30 postpartum, all cows were fed the same diet. Within the free-stall housing, cows were provided with thermostat-controlled fan cooling only. During the treatment period of d -28 to 30 d, cows experienced environmental temperature humidity index readings greater than 68 for 91.1% of the time. During the prepartum, dry matter intake (DMI) and body weight (BW) were not different. From 0 to 30 DIM, milk yield was greater for R fed cows compared with C (32.5 vs 30.2 kg/d, SE = 0.78, $P < 0.05$). Cows fed R had greater DMI of 1.26 kg relative to C fed (SE = 0.39, $P < 0.05$). Cows fed R had lower milk fat (%) during the first 30 d postpartum than C fed cows with the greatest difference occurring during the first week postpartum ($P < 0.01$). However, component yields were not significantly different. Multiparous cows had greater improvement in milk yield compared with primiparous cows. For 0 to 21 DIM, multiparous cows fed R had lower plasma non-esterified fatty acid concentrations than C fed cows (0.79 vs. 0.93 meq/L, SE = 0.05, $P = 0.07$). Additionally, plasma β-hydroxybutyrate concentrations were also lower (7.6 vs 10.5 mg/dL, SE = 0.61, $P < 0.01$). From d 0 to 60 postpartum, multiparous cows fed R during transition phase produced an additional 2.9 kg/d of milk and consumed an additional 1.6 kg/d of DMI compared with C. When feeding R, cows had lower circulating metabolites and milk fat (%) immediately postpartum may be indicative of changes of metabolism by peripheral tissues. Feeding R during warm seasons improved transition cow milk yield and DMI which may lead to better performance for the entire lactation during the cooler seasons.

Key Words: Rally, cows, lactation

T85 Relationships between circulating plasma amino acid concentrations and milk protein production in lactating dairy cows. R. A. Patton*[1], H. Lapierre[2], and C. Parys[3], *[1]Nittany Dairy Nutrition Inc., Mifflinburg, PA, [2]Dairy and Swine Research and Development Centre, Agriculture and Agri-Food Canada, Sherbrooke, Quebec, Canada, [3]Evonik Industries AG, Hanau, Germany.*

Better understanding of the relation between amino acid (AA) supply and milk protein output may increase protein efficiency. Direct measurements of the digestive AA flow require invasive, expensive experiments. Plasma AA concentrations ([AA]) might be used as surrogates to investigate relationships between AA supply, requirement and milk protein output. A database was developed after a literature search to identify studies in lactating dairy cows reporting circulating plasma [AA], production data, and adequately described rations. A total of 105 studies representing 420 diets were used. Using the AminoCow ration program, duodenal AA flow and metabolizable protein (MP) were estimated. Relationships were evaluated using multi-factorial regression (JMP 10 version of SAS) including study as a random factor. Plasma [Arg] was greater for first parity compared with greater parities. Plasma [AA] was most significantly related to predicted duodenal AA flow: Arg, Ile, Lys, Thr, and Val were related quadratically whereas His, Met and Phe were related linearly to their respective duodenal flow. Highest correlation between duodenal and plasma [AA] was for Arg ($R^2 = 0.90$) and the lowest was for Met ($R^2 = 0.69$). Associations of [AA] with milk protein % (MlkP%) or milk protein yield (MlkPY) were similar whether AA were expressed as plasma [AA], AA duodenal flow (duo: g/d or % of MP).

MlkP% (mean: 3.15%)

= 2.77 + (0.083 × Metduo, %MP) + (0.032 × Lysduo, %MP); RMSE = 0.136; $R^2 = 0.81$

= 3.3437 + (0.0036 × Metduo, g/d) – (0.0028 × Thrduo, g/d); RMSE = 0.139; $R^2 = 0.81$

= 3.17 + (0.0016 × [Lys], μ*M*) – (0.0028 × [Phe], μ*M*); RMSE = 0.140; $R^2 = 0.81$

MlkPY (mean = 0.908 kg/d)

= 0.942 – (0.071 × Thrduo, %MP) + (0.050 × Hisduo, %MP) + (0.029 × Argduo, %MP) + (0.015 × Lysduo, %MP); RMSE = 0.050; $R^2 = 0.94$

= 0.5270 + (0.0018 × Thrduo, g/d) + (0.0007 × Lysduo, g/d); RMSE = 0.050; $R^2 = 0.95$

= 0.8072 + (0.00081 × [Lys], μ*M*) + (0.00016 × [Val], μ*M*); RMSE = 0.050; $R^2 = 0.94$.

Relationships were stronger for MlkPY than for MlkP%. These preliminary results suggest that circulating [AA] could be useful in adequately modeling AA requirements.

Key Words: amino acid, concentration, milk protein yield

T86 Hepatic gene expression and post-ruminal protein supply in lactating dairy cattle. H. Tucker*[1], M. Hanigan[2], and S. Donkin[1], *[1]Purdue University, West Lafayette, IN, [2]Virginia Polytechnic Institute and State University, Blacksburg.*

Metabolizable protein supply limits milk production in dairy cows. Amino acid (AA) availability to extrahepatic tissues, including mammary tissue, is a combined function of the quantity of metabolizable protein supplied and hepatic AA catabolism. The latter is determined by nutrient supply and physiological status. This experiment evaluated the effect of post-ruminal protein infusion on key genes for ureagenesis and amino acid catabolism. Six multiparous early-lactation Holstein cows were utilized in a replicated cross-over design. Cows were fed a TMR (14.5% CP) and given postruminal infusion of either 0 or 600 g/d of milk protein isolate. Periods were 21 d in length consisting of a 14-d washout phase followed by 7 d of protein infusion. On the last day of each infusion, liver samples were collected for mRNA analysis and explant culture, milk samples were collected for mRNA analysis and blood samples were collected for plasma metabolite analysis. Postruminal infusion of protein increased ($P < 0.05$) milk yield by 10.5%, milk fat yield by 12.5%, milk protein yield by 20%, milk lactose yield by 11%, and total solids by 15.5%. Postruminal infusion of protein increased ($P < 0.05$) milk urea N by 23.5%, blood urea N by 18.6%, and abundance

of ornithine transcarbamoylase mRNA by 52.8%. Postruminal infusion of protein did not alter ($P > 0.1$) abundance of argininosuccinate synthase, aminoadipate semialdehyde synthase, cysteine sulfinic acid decarboxylase, cystathionase, and associated milk protein synthesis mRNA. Postruminal protein infusion increased ($P < 0.05$) metabolism of L-[U ^{14}C] Lys to CO_2 by 127% (0.14 vs. 0.063 ± 0.05 nmol substrate converted to CO_2 · mg tissue^{-1} · h^{-1}) while metabolism of L-[U ^{14}C] Ala to CO_2 tended ($P < 0.1$) to be greater (0.52 vs. 0.37 ± 0.06 nmol product · mg tissue^{-1} · h^{-1}) compared with control. These data indicate increased ureagenesis matched by up-regulation of non-essential AA catabolism and a disproportional increase in Lys oxidation in response to increased postruminal protein infusion in lactating dairy cows.

Key Words: protein, gene expression, postruminal protein infusion

T87 Kelp meal (*Ascophyllum nodosum*) did not improve milk yield but increased milk iodine in early lactation organic Jersey cows during the winter season. N. T. Antaya*, A. F. Brito, N. L. Whitehouse, N. E. Guindon, and S. Werner, *University of New Hampshire, Durham.*

Kelp meal (KM) made from dry and ground *Ascophyllum nodosum*, a brown algae, is often fed as a mineral supplement on northeastern organic dairy farms. Sixteen (4 primiparous and 12 multiparous) organic Jersey cows with initial BW of 444 kg (SD ± 46) and DIM of 49 (SD ± 30), were blocked by DIM and parity and randomly assigned to 4 replicated 4 × 4 Latin squares to investigate the effects of incremental dietary levels of KM (0, 57, 113 or 170 g, as fed) on milk yield and composition. Periods lasted 21 d with 14 d for diet adaptation and 7 d for data and samples collection. Data were analyzed using the MIXED procedure of SAS with linear and quadratic contrasts. Cows were fed a TMR containing: (DM basis) 64% alfalfa/grass baleage and 36% of a cornmeal/barley/soybean meal-based concentrate. TMR averaged: 16% CP, 49% NDF, and 34% ADF. To ensure complete consumption, KM was mixed with 227 g concentrate and fed after the a.m. milking, cows on the control treatment (0 g KM) received concentrate only. Feeding incremental levels of KM to early-lactation cows did not affect milk yield, DMI, or concentrations and yields of milk components. However, concentration of milk iodine increased lineally in response to incremental levels of KM, possibly explained by high content of iodine (820 mg/kg DM basis) in this brown algae supplement. Kelp meal did not improve animal performance or milk composition but increased milk iodine to levels that may be of concern to human health, particularly children. Results also suggest that KM may not be a cost effective supplement for organic dairy farms.

Table 1. Effects of kelp meal on milk yield and composition.

	Kelp meal					*P*-value	
	0 g	57 g	113 g	170 g	SED	Linear	Quadratic
Milk yield, kg/d	16.3	16.2	16.4	15.8	0.37	0.27	0.24
DMI, kg/d	17.5	17.6	17.7	17.1	0.36	0.27	0.16
Milk fat, %	5.10	5.10	5.24	5.09	0.10	0.74	0.28
Milk fat, kg/d	0.84	0.85	0.88	0.86	0.04	0.35	0.55
Milk protein, %	3.68	3.70	3.64	3.63	0.06	0.27	0.79
Milk protein, kg/d	0.61	0.62	0.61	0.62	0.02	0.86	0.95
MUN, mg/dL	12.1	11.4	11.6	11.6	0.31	0.18	0.12
Milk iodine, µg/L	178	602	1,015	1,370	81.7	<0.0001	0.55

Key Words: iodine, kelp meal, milk yield

T88 Influence of maize kernel maturity on chemical characteristics, prolamin content, and in vitro starch digestion. . W. J. Seglar*, M. Pauli, A. Patterson, L. Nuzback, and F. N. Owens, *DuPont Pioneer, Johnston, IA.*

As an indicator of starch digestion, commercial laboratories measure in vitro starch disappearance of ground grain incubated for 7 hours (7HSD). As kernels mature, this index has been reported to decrease while prolamin content has been suggested to increase. Both presumably are correlated with kernel density. In trials in 2011 and 2012, we examined the relationships between kernel maturity (half-milk line, near black layer, and at full maturity) and density by gas pycnometer, chemical composition, and 7HSD using grain from 5 (2011) or 6 (2012) commercial Pioneer hybrids grown at 79K/hectare at each of two locations (central and southern Wisconsin). 7HSD and chemical composition were determined at a commercial laboratory. Differences among hybrids and years were detected ($P < 0.01$) for all chemical measurements except for NDF and ash; year by hybrid interactions were detected for 7HSD, prolamin, and starch. With kernel maturation, kernel weight increased stepwise (by 32 and 10% in 2011; 19 and 1% in 2012) while 7HSD percentages decreased slightly in 2011 (73% vs. 75%; $P < 0.05$) but increased slightly in 2012 (70% vs. 65%; $P < 0.05$). At the growing location with higher N fertility, protein and prolamin content of kernels were greater ($P < 0.05$). Within individual years, specific gravity was correlated with prolamin in 2011 (r = 0.63; $P < 0.01$) but not in 2012 (r = −0.15); 7HSD was poorly correlated with prolamin (r = −0.11 in 2011; r = −0.03 in 2012) across all samples but these two factors were correlated more strongly within kernel maturity groups (r = −0.3 to −0.51). The factor related most closely related ($P < 0.01$) to prolamin content was crude protein content of grain (r = 0.91 in 2011; r = 0.55 in 2012). For the hybrids, locations, and kernel maturities tested, kernel maturation failed to increase prolamin content or the prolamin:starch ratio. Neither reliably predicted 7HSD indicating that factors beyond hybrid and maturity were altering these measurements.

Key Words: prolamin, starch digestion, maize

T89 Range in starch content and digestibility of common starch sources in US and Japan and their effect on in vitro microbial biomass production when incorporated into total mixed rations. K. W. Cotanch*[1], H. M. Dann[1], J. W. Darrah[1], R. J. Grant[1], Y. Koba[2], and K. Hirano[2], *[1]William H. Miner Agricultural Research Institute, Chazy, NY, [2]ZEN-NOH National Federation of Agricultural Cooperatives, Tokyo, Japan.*

New methods have been developed to assess fermentability of starch sources including enzymatic digestion at 7 h (Cumberland Valley Analytical Services, Hagerstown, MD) and in vitro measurement of ruminal microbial biomass production (MBP; Fermentrics, Dairyland Labs, Arcadia, WI). The objective of this project was to evaluate the range in starch content, starch digestibility (starch-D), and MBP when common starch sources fed in the US and Japan are incorporated into total mixed rations (TMR). Descriptive statistics were applied to the database to evaluate mean values and ranges. Samples of grains were obtained from across the US, Canada, and Japan (rice only) that included: fine/medium corn (n = 20), flaked corn (n = 12), barley (n = 13), wheat (n = 12), and rice (n = 9). The mean and range of starch content (% of DM) plus 7-h enzymatic starch-D (% of starch) were determined (table). Rations based on corn silage (24.6% corn silage and 30.3% haycrop silage, DM basis), haycrop silage (49.7% haycrop silage), and dry hay (19% alfalfa hay, 16% timothy hay, and 7.6% oat hay) were formulated to contain similar starch content using

each starch source. For corn silage and hay-based TMR, ground rice grain resulted in highest MBP (182 and 188 mg/g, respectively, with range across diets of 137-182 and 130-188 mg/g) whereas for haycrop silage-based TMR fine ground corn resulted in the greatest MBP (141 mg/g with range across diets of 121-141 mg/g). These in vitro measures indicate that starch sources influence fermentation differently depending on the forage base. Existing feed databases used in ration formulation models may be updated with these starch digestibility and in vitro MBP values.

Table 1.

	Starch, % of DM		Starch-D, % of starch		MBP,
Grain	Mean	Range	Mean	Range	mg/g
Fine/medium corn	73.2	71.4 – 75.8	51.3	44.9 – 56.4	186
Flaked corn	74.5	72.2 – 77.3	52.7	40.3 – 63.0	266
Ground barley	59.7	55.3 – 63.9	57.4	46.2 – 62.4	248
Whole rice	79.7	77.3 – 82.2	16.8	13.5 – 18.0	332
Ground wheat	67.7	66.4 – 69.8	59.7	55.4 – 62.5	238

Key Words: digestibility, forage, starch source

T90 Kelp meal (*Ascophyllum nodosum*) did not improve milk yield or mitigate heat stress but increased milk iodine in mid lactation organic Jersey cows during the grazing season. N. T. Antaya*[1], A. F. Brito[1], K. J. Soder[2], N. L. Whitehouse[1], N. E. Guindon[1], A. D. B. Pereira[1], and C. C. Muir[1], *[1]University of New Hampshire, Durham, [2]USDA-ARS, Pasture Systems and Watershed Management Research Unit, University Park, PA.*

Kelp meal (KM) made from dry and ground *Ascophyllum nodosum*, a brown algae, is often used as a mineral supplement on northeastern organic dairy farms. Twenty (12 primiparous and 8 multiparous) organic Jersey cows with an initial BW of 410 kg (SD ± 39) and DIM of 135 (SD ± 52) were blocked by milk yield and parity. Cows were randomly assigned to treatments (0 or 113 g KM as fed) to examine the effects of KM supplementation on milk yield, milk components, plasma metabolites, and indicators of heat stress. The study lasted from June to October 2012 with 4, 28- d periods with the last 7 d used for data and sample collection. Data were analyzed using the MIXED procedure of SAS with repeated measures over time. Cows had access to mixed mostly cool-season grass pasture for 16 h daily, which was managed using rotational strip grazing. Cows were supplemented a TMR made (DM basis) of 51% grass-legume baleage, 47% concentrate, and 2% liquid molasses fed via Calan doors. Kelp meal had no impact on milk yield, components or heat stress indicators. However, concentration of milk iodine was 77% higher in KM fed cows than those fed no KM, which is explained by the high concentration of iodine (i.e., 820 mg/kg DM basis) found in brown algae. No KM effects were seen for plasma cortisol, NEFA, and thyroxine (T_4); a trend for lower plasma triiodothyronine (T_3) was found in KM cows, likely as a result of higher iodine intake. Kelp meal did not improve milk yield or mitigate heat stress but increased milk iodine, which may be of concern to human health, particularly children.

Table 1. Effects of kelp meal on milk yield, plasma metabolites, and heat stress indicators

	Kelp meal			
	0 g	113 g	SED	*P*-value
Milk yield, kg/d	12.4	13.0	0.90	0.56
Milk fat, kg/d	0.54	0.57	0.04	0.47
Milk protein, kg/d	0.44	0.45	0.03	0.59
MUN, mg/dL	11.6	12.1	0.58	0.40
Milk iodine, µg/L	138	592	66.1	<0.001
Plasma cortisol, ng/mL	95.7	111	16.6	0.36
Plasma NEFA, µg/dL	129	111	12.7	0.18
Plasma T_3, ng/mL	0.89	0.81	0.03	0.09
Plasma T_4, ng/mL	41.9	39.7	1.86	0.25
Rectal temperature, °C	38.2	38.3	0.07	0.24
Respiration rate, /min	44.5	44.3	1.79	0.92

Key Words: iodine, kelp meal, pasture

T91 Effects of partial replacement of corn grain with alkaline pretreated corn stover on production of lactating dairy cows. D. E. Cook*[1], M. J. Cecava[2], P. H. Doane[2], M. B. Hall[3], and D. K. Combs[1], *[1]University of Wisconsin-Madison, Madison, [2]ADM Research, Decatur, IL, [3]USDA-ARS, US Dairy Forage Research Center, Madison, WI.*

The fiber digestibility of corn crop residues can be improved by pretreatment with calcium oxide (CaO). The objective of this study was to evaluate how intake and milk production was affected when corn grain was replaced with CaO-treated corn stover. Corn stover was pretreated with CaO (50 g CaO kg^{-1} stover DM in 500 g H_2O kg^{-1} stover DM) at ambient conditions. Sixty-three Holstein dairy cows (101 ± 29 DIM, 39.2 ± 2.4 kg milk d^{-1}) were fed diets containing treated corn stover at 0, 40, 80, 120 g stover DM kg^{-1} TMR. The design of the study was a randomized complete block utilizing a 14-d covariate period, followed by a 6 wk experimental period. Cows were blocked by DIM and parity. Body weight change was not affected by treatment. DMI decreased linearly ($P < 0.01$) with each level of stover inclusion, (Table 1). Milk production as well as fat and protein production ($P < 0.01$ for all) also declined linearly with increasing levels of stover inclusion. Energy-corrected milk (ECM) decreased linearly ($P < 0.01$) from 47.6 kg d^{-1} to 40.7 kg d^{-1}. Stover inclusion had no effect ($P > 0.6$) on feed conversion rate as measured by ECM divided by DMI (1.766 ± 0.14). Overall, in high producing dairy cows, replacement of corn grain with treated stover caused a decline in DMI and milk yield.

Table 1.

	Stover inclusion (g stover DM kg^{-1} TMR DM)				
	0 (n = 16)	40 (n = 16)	80 (n = 16)	120 (n = 15)	SEM
DMI (kg d^{-1})	26.7	25.8	24.3	23.5	0.2
Milk (kg d^{-1})	42.2	40.8	39.4	36.9	0.4
Fat (kg d^{-1})	1.79	1.71	1.60	1.51	0.04
Protein (kg d^{-1})	1.32	1.24	1.17	1.11	0.02

Key Words: calcium oxide, stover, treated stover

T92 Effects of dietary starch content and NDF source on intake and milk production by dairy cows. S. M. Fredin*, L. F. Ferraretto, M. S. Akins, and R. D. Shaver, *University of Wisconsin, Madison, WI.*

An experiment was conducted to evaluate the effects of dietary starch concentration and source of NDF on intake, ruminal fermentation, and milk yield, composition and component yields. Eight ruminally-cannulated multiparous Holstein cows (193 ± 11 d in milk at trial initiation) were randomly assigned to treatments in a replicated 4 × 4 Latin square design with 21-d periods. Treatment TMR were high corn grain (HCG; 38% corn silage, 19% dry ground corn and 4% soy hulls), high soy hulls (HSH; 38% corn silage, 11% dry ground corn, 13% soy hulls), high corn silage (HCS; 50% corn silage, 6% dry ground corn, and 4% soy hulls) and low corn silage (LCS; 29% corn silage, 15% corn, and 19% soy hulls). The HCG, HSH, HCS, and LCS diets contained 29, 23, 24, and 22% starch, 27, 32, 30, and 32% NDF, and 21, 21, 25, and 17% forage NDF, respectively. During each period milk samples were obtained from a.m. and p.m. milkings on d 16 and 17 and rumen fluid four times daily at 2-h intervals on d 18-20 such that the samples represented a 24-h feeding cycle. Data were analyzed using the MIXED procedure of SAS. Mean DMI (24.9 kg/d) and milk yield (36.0 kg/d) were unaffected by treatment. Cows fed LCS had reduced milk fat percentage (3.54%; $P = 0.02$) compared with HSH and HCS (3.85 and 4.00%, respectively). Mean milk fat yield (1.33 kg/d), milk protein percentage (3.29%), and protein yield (1.16 kg/d) were unaffected by treatment. Milk urea nitrogen concentration was greater for HCS (19.8 mg/dL; $P = 0.0001$) compared with the other treatments (mean = 16.1 mg/dL). Rumen ammonia concentration was lower for HCG and LCS (9.6 and 8.0 mg/dL; $P = 0.001$) compared with HCS (12.1 mg/dL). Rumen pH was greater for cows fed HCS (6.25; $P = 0.007$) compared with cows fed LCS (6.04). Feeding a diet with corn silage NDF partially replaced by soy hulls NDF reduced milk fat percentage and rumen pH.

Key Words: dairy cow, NDF, starch

T93 Metabolic profile and onset of puberty of growing dairy heifers fed increased dietary fat from dried distillers grains. J. L. Anderson*[1], K. F. Kalscheur[1], J. A. Clapper[1], G. A. Perry[1], D. H. Keisler[2], A. D. Garcia[1], and D.J. Schingoethe[1], *[1]South Dakota State University, Brookings, [2]University of Missouri, Columbia.*

The objective of this trial was to determine if feeding increased dietary fat from dried distillers grains with solubles (DDGS) to growing dairy heifers affects metabolic profiles and onset of puberty. Thirty-three Holstein heifers (133 ± 18 d old) were fed one of three diets in a 24-wk randomized complete block design. Diets were: 1) control (C) that contained 15.9% (DM basis) ground corn and 17.9% soybean products, 2) low-fat (LFDG) that contained 21.9% reduced-fat DDGS and 11.9% ground corn, and 3) high-fat (HFDG) with 33.8% traditional DDGS. All diets contained 39.8% grass hay, 24.8% corn silage, and 1.5% vitamins and minerals. Although, diets were isonitrogenous and isocaloric, HFDG was formulated to contain 4.8% fat versus 2.8% in C and LFDG. Every 4 wk, jugular blood samples were collected for metabolites and metabolic hormones analysis. When heifers weighed between 200 and 300 kg of body weight (BW), coccygeal vein blood samples were taken two times per wk for progesterone analysis to estimate puberty. Plasma NEFA was similar among treatments ($P = 0.63$) and over time ($P = 0.67$). Plasma BHBA, insulin, IGF-1 and leptin were similar ($P > 0.10$) among treatments, but increased ($P < 0.05$) over time. Serum glucose tended ($P = 0.06$) to be less in heifers fed HFDG compared to C. Plasma urea nitrogen (PUN) was less ($P = 0.03$) in LFDG-fed heifers compared to other treatments and increased ($P < 0.01$) over time in all. Plasma total cholesterol was greater ($P < 0.01$) in heifers fed HFDG compared to other diets. Because cholesterol increased markedly in heifers fed HFDG, but remained more stable in the LFDG and C fed heifers, there were effects of time ($P < 0.01$) and treatment × time ($P = 0.02$). Based on progesterone analysis, 81.8% of heifers fed HFDG were pubertal at < 300 kg of BW compared to 36.4 and 27.3% in C and LFDG, respectively ($P = 0.03$). These findings provide evidence that dietary fat from DDGS can be used in replacement of starch from corn in diet of growing dairy heifers and maintain energy status. Feeding increased fat from DDGS may decrease the body weight at puberty.

Key Words: dairy heifer, distillers grains, metabolic profile

T94 Lactation performance of cows fed soybean meal or canola meal supplements. F. E. Contreras-Govea*[1], S. Bertics[1], G. A. Broderick[2], A. Faciola[3], and L. E. Armentano[1], *[1]University of Wisconsin-Madison, Department of Dairy Science, Madison, [2]US Dairy Forage Research Center, Madison, WI, [3]University of Nevada, Department of Agriculture, Nutrition, and Veterinary Sciences, Reno.*

Performance of mid lactation-Holstein cows fed diets with 17.3% CP based on soybean meal (SBM) or canola meal (CM) was determined. Sixty four cows were housed in a free stall barn equipped with 32 Insentec electronic feeding gates (RIC systems; Insentec BV, Marknesse, the Netherlands). Each gate allows access by one or more selected cows and record individual daily DMI. The SBM diet was assigned randomly to 16 gates, and 32 cows (16 multiparous and 16 primiparous) were assigned randomly to these 16 gates. The additional 32 cows were assigned to the other 16 gates and fed CM. Cows within a diet had access to all 16 gates with that diet, and cow was considered the experimental unit. For 21 d, all cows received a common diet and covariate measurements were obtained. Cows were then fed their treatment diet for the next 63 d. Treatment diets (dry matter basis) were 25.7% alfalfa haylage, 31.6% corn silage, corn grain (24.0% for CM diet, 27.2% for SBM diet), and either 16.5% CM or 13.3% SBM. Cows were milked twice daily and yields were recorded for 84 d. Cow were weighed weekly. Milk composition was determined for two consecutive milkings weekly. Covariately adjusted data were analyzed as a complete randomized block design with cow within treatment and parity as the subject for weekly repeated measurements. Cows fed CM had greater intake (28.4 vs. 23.6 kg DM/d), and yield of milk (39.0 vs. 36.2 kg/d), milk fat (1.44 vs. 1.36 kg/d), milk protein (1.24 vs. 1.15 kg/d), and milk lactose (1.93 vs. 1.78 kg/d), but observed feed efficiency was lower for cows fed CM (1.38 vs. 1.55 kg milk yield/kg intake; all $P < 0.05$). Body weight increased across weeks ($P < 0.05$), but diet by week interaction was not significant ($P = 0.678$) and condition score observations did not reveal an obvious energy balance difference due to diet. The predicted undiscounted TDN for the CM and SBM diets were 71% and 73%, and energy allowable 3.5% fat corrected milk was 47.2 and 39.4 kg/d for CM and SBM. The measured intake differences are larger than expected even considering the greater milk yield and lower predicted energy density of the CM diet.

Key Words: canola, protein, soybean

T95 Utilization of byproducts from human food production as feedstuffs for dairy cattle and relationship to greenhouse gas emissions and environmental efficiency. K. L. Russomanno, T. F. Christoph, R. J. Higgs, and M. E. Van Amburgh*, *Cornell University, Ithaca, NY.*

The objective of this study was to use survey data collected from nutritionists representing significant regions of dairy production to evaluate the methane (CH_4) and carbon dioxide (CO_2) production per unit of dietary byproducts fed. The data included a complete set of diet ingredients, including chemical analysis of individual ingredients and a complete diet summary. In addition, values for group average body weight (BW), dry matter intake (DMI), milk yield (kg), and milk fat and protein concentrations were provided. Ninety-one diets from seventy different farms representing ten different states were compiled, and included a range of different byproducts (e.g., soy hulls, distillers grains, almond hulls), forages, protein feeds, and minerals. The average byproduct concentration in the diets was 31.3% DM with a range of 12.7% and 56.7%, DM. Data were evaluated in the Cornell Net Carbohydrate and Protein System v6.1 (CNCPS; Tylutki et al., 2008, Van Amburgh et al., 2010). Equations for enteric CH_4 and CO_2 emissions were incorporated into the CNCPS from Mills et al., (2003) and Casper and Mertens, (2010), respectively. Total emission of CO_2 per cow was positively related to total milk yield ($R^2 = 0.69$). However, CO_2 emissions per kg of milk yield (kg CO_2/kg milk) resulted in a negative relationship, ($R^2 = 0.81$). The average CO_2 emission per unit of milk yield was 0.353 kg CO_2/kg milk, with minimum and maximum values of 0.283 kg and 0.423 kg, respectively. The mean prediction of CO_2 (kg) per kg of byproducts was 0.05 and the correlation between CO_2 emission and inclusion of byproduct as a proportion of the total DMI was high ($R^2 = 0.81$). CH_4 emissions per kg DMI ranged from 0.021 kg to 0.027 kg with a mean of 0.024 kg CH_4/kg milk. Total CH_4 emissions were positively correlated with milk yield (slope = 0.004; $R^2 = 0.68$) but CH_4 kg/kg milk was negatively correlated (slope = −0.26; $R^2 = 0.88$) similarly to CO_2. Use of byproducts in diets for dairy cattle reduces the environmental impact of human food production and enhances the efficiency of the dairy industry.

Key Words: byproduct, dairy, greenhouse gas

T96 The effects of different ratio of metabolizable protein to metabolizable energy on dry matter intake, average daily gain, and nutrient digestibility in Holstein heifers. H. R. Motalebei, M. Dehghan-Banadaky*, K. Rezayazdi, and H. Kohram, *Department of Animal Science, University of Tehran, Karaj, Tehran, Iran.*

The purpose of this study was to investigate the effects of different ratio of metabolizable protein (MP) to metabolizable energy (ME) on dry matter intake (DMI), average daily gain (ADG), feed efficiency and nutrient digestibility in Holstein heifers. In present experiment 24 Holstein heifers with a mean age of 7 months and the average weight of 217 kg were used. Heifers were randomly assigned to 3 rations: 1) ration which includes 10% metabolizable protein less than NRC (2001) (−10% NRC) 2) control ration which metabolizable protein based on NRC (2001) (NRC). 3) Ration with includes 10% metabolizable protein more than NRC (2001) (+10% NRC). Rice hull and soybean meal used for adjusting diets. Metabolizable energy in all rations was based on NRC requirements. DMI, ADG and feed efficiency were measured once every 14 days and digestibility once every 28 days. The nutrients digestibility was affected by rations ($P < 0.05$) and the nutrients digestibility were higher in ration 1 than rations 2 and 3, but no significant differences were observed in DMI, ADG and feed efficiency between rations. The results showed that by increasing the ratio of protein to energy metabolizable, nutrients digestibility decreased.

Table 1. Effects of different ratio of metabolizable protein to metabolizable energy on DMI, ADG, feed efficiency, and nutrient digestibility

	MP/ME (g/Mcal)				
Item	−10% NRC (31.14)	NRC (34.57)	+10%NRC (38)	*P*-value	SEM
DMI (kg)	6.18	6.20	6.19	NS	0.017
ADG (g)	827	842	817	NS	0.027
Feed efficiency	7.98	8.31	8.22	NS	0.31
Digestibility %					
Dry matter	67.79[a]	64.41[b]	60.31[c]	0.01	1.761
Crude protein	67.74[a]	63.25[b]	60.60[c]	0.007	1.592
Organic matter	69.39[a]	66.10[b]	61.41[c]	0.01	1.865

Key Words: heifer, digestibility, metabolizable protein

Undergraduate Student Competition: ADSA-SAD Undergraduate Poster Competition: Original Research

T98 Feeding 5-hydroxy-L-tryptophan (5-HTP) to transition rats increases serum serotonin (5-HT) and calcium and down-regulates mRNA expression of calcium transporters in the gut. C. Cronick*, J. Laporta, S. Weaver, and L. L. Hernandez, *University of Wisconsin, Madison.*

The absorption of calcium (Ca^{2+}) and role of serotonin (5-HT) in the gut are independently well-understood processes. Less clear is the effect of 5-HT on the absorption of Ca^{2+} by the gut during the transition from pregnancy to lactation. In order to better understand 5-HT's effect on Ca^{2+} dynamics in the gut during lactation we fed female rats two different diets: a control diet (CON, n = 15) and a diet supplemented with 5-hydroxytryptophan (5-HTP, 0.2% of total diet, n = 15), the immediate precursor for 5-HT synthesis, from d13 of pregnancy through d9 of lactation. We collected serum on d1 and 9 of lactation to measure circulating 5-HT and Ca^{2+} concentrations, and also measured Ca^{2+} concentration in the milk. Rats were euthanized on d9 of lactation and gut samples were collected. mRNA expression of tryptophan hydroxylase 1 (TPH1), 5-HT reuptake transporter (SERT), plasma membrane Ca^{2+} ATPase 1 (PMCA1), Na^{+}-Ca^{2+} exchanger 1 (NCX1), transient receptor potential cation channel, subfamily V, member 6 (TRPV6), voltage-dependent Ca^{2+} channel ($Ca_v1.3$), and Ca^{2+} binding protein calbindin-D_{9K} (CalbD9k) were measured by real-time RT-PCR. Serum 5-HT was elevated on d 1 (4.7± 0.39 ng/mL vs. 1.83 ± 0.26) and d9 (8.3 ± 0.7 vs. 3.4 ± 0.25 ng/mL) of lactation in the 5-HTP compared to CON dams. On d 1 of lactation 5-HTP dams had increased serum Ca^{2+} concentrations compared to CON ($P = 0.0085$), while no significant changes in milk Ca^{2+} were observed. On d9 of lactation 5-HTP dams had similar serum Ca^{2+} concentrations to the CON dams, but demonstrated increased milk Ca^{2+} concentrations ($P = 0.032$). Gut mRNA expression of SERT and TPH1 was decreased in 5-HTP dams compared to CON ($P < 0.041$). Gut mRNA expression of all Ca^{2+} transporters evaluated were decreased in 5-HTP dams compared to CON ($P < 0.05$). It is probable that during lactation the gut decreases 5-HT synthesis and reuptake as well as expression of Ca^{2+} transporters, because the mammary gland is increasing production of 5-HT and transport of Ca^{2+} into the milk to provide adequate nutrition to the neonate.

Key Words: serotonin, gut, calcium

T99 Mammary clock regulation and function. E. Erickson*, J. Crodian, M. Schutz, T. Casey, and K. Plaut, *Purdue University, West Lafayette, IN.*

Most physiological processes, including lactation, are controlled by the circadian system, which coordinates growth, development, and metabolism to optimal times of day through generation of circadian rhythms. Approximately 10% of genes expressed show circadian rhythms that are generated by interactions of molecular clock genes (e.g., *Clock*, *Bmal1*, *Per1*). BMAL1-CLOCK heterodimers function as a transcription factor that binds E-box sequences in promoters of clock controlled genes. Little is known about how mammary clock is regulated or what genes it controls. We hypothesize mammary clock is regulated by lactogenic hormones and it regulates genes important to mammary development and milk synthesis. Our objectives were to (1) Determine effects of lactogenic hormones on circadian rhythms of molecular clock genes *Bmal1* and *Per1* in mouse mammary epithelial cells, HC-11; and (2) knock down CLOCK to measure effects on *Per1* and cell cycle gene, cyclin D1 (*Ccnd1*) expression. HC-11 cells were grown to confluence, treated for 2h with RPMI media + 10% calf serum ± lactogens (5 µg/mL insulin, 2 µg/mL prolactin, 40 ng/mL dexamethasone), after which RNA was collected every 4 h for 48 h to capture circadian gene expression. Q-PCR analysis showed lactogens induced 24-h rhythms of *Bmal1* and *Per1* expression and a 2.5-fold increase in *Bmal1* rhythm amplitude (i.e. peak-trough); 2-way ANOVA revealed significant time and treatment effects ($P < 0.05$). For the second objective, HC-11 cells were transfected with shRNA plasmids with insert mouse *Clock* sequence I [AAACCCACATTCCTTAGTAAT] or II [ATCAAACCCTGGATTGAATTT]; a negative control was transfected with plasmid insert sequence: ggaatctcattcgatgcatac. Eighteen clonal cell lines were created through dilution and lines with sequence I or II insert were selected based on greatest *Clock* knockdown. Cells were synchronized by RPMI + 10% calf serum media change and RNA was isolated 4 h later. Q-PCR analysis revealed the 40% knock down of Clock by sequence I and the 42% knock down by II was associated with 70% and 35% knock down of Per1 and a 2.3-fold or 1.8-fold induction of *Ccnd1,* respectively. Data suggest lactogens regulate mammary clock, and mammary clock may regulate *Ccnd1*.

Key Words: lactation, mammary, circadian

T100 Potential for compost bedded pack barns in sustainable organic dairy farming systems. H. A. Mussell*[1], J. L. Taraba[2], and J. M. Bewley[1], *[1]University of Kentucky, Department of Food and Animal Sciences, Lexington, [2]University of Kentucky, Agricultural Engineering, Lexington.*

When managed properly, compost bedded pack barns (CBP) are an excellent housing alternative for dairy cows. Although most CPB barns have been constructed for conventional dairies, these barns fit within the spirit of organic dairy farming by relying on a natural process (composting) to produce a comfortable environment for lactating dairy animals that maximizes cow comfort and longevity and minimizes mastitis and other health problems. These barns provide more freedom for cows to move around or lie down as compared to stall based dairy facilities. The composting process increases the bedding temperature to control disease-causing microorganisms and decreases the bedding moisture by increasing the drying rate. Additionally, CBP barns serve as an area for manure storage and reduce the volume and frequency for manure application to fields. The objective of this study was to examine cow and pack performance metrics within three Kentucky organic dairy farms housing cows in CBP barns. Temperatures (0.1, 0.2, and 0.3 m below pack surface) and bedding samples were collected three times from nine different locations within each barn. Samples were collected at each farm for moisture content and nutrient analysis. Forty cows per farm were scored for hygiene and locomotion at each visit. Mean pack temperature at 0.30 below the pack surface was 27.79 °C ± 12.03. These temperatures were lower than the recommended range of 43 to 65°C. Two of the three farms were not consistently tilling their packs, which may have contributed to the lower temperatures observed during these visits. Mean moisture was 57 ± 7%, within the recommended range of 50 to 60%. Mean C:N ratio was 32:1, higher than the ideal range of 25:1 to 30:1. Mean locomotion and hygiene scores were 1.54 ± 0.28 and 1.72 ± 0.55, respectively, demonstrating that cows managed in organic

dairy compost bedded pack barns can be sound and clean. Compost bedded pack dairy barns could meet the farmer, land and cow needs of organic dairy operations.

Key Words: compost bedded pack barns, cow comfort, organic

T101 Effects of microbial fermentation products on milk production in dairy cows during heat stress. R. M. Wagner*[1], S. I. Kehoe[1], and D. DuBourdieu[2], *[1]University of Wisconsin-River Falls, River Falls, [2]R&D Lifesciences, Menomonie, WI.*

Heat stress is a problem that reduces milk production for dairy producers. The objective of this research was to determine the production benefits of feeding a combination microbial product containing fermentation products from *Bacillus subtilis*, *Trichoderma viride*, and *Aspergillus oryzae* (Lactomace; R & D Lifesciences, LLC, Menomonie, WI) during a summer heat wave. Two pens of lactating dairy cattle were matched in DIM and assigned to either a Control treatment with no microbial product (C) or a Microbial treatment (M) fed 5 gm/hd/day for the first 30 days and 10 gm/hd/d for the second 30 days. Daily milk yield and DMI and calculated 3.5% fat-corrected milk (FCM) and FCM:DMI ratio were recorded. Milk fat and protein % were collected from bulk tank samples after the first 30 d and 60 d. During data collection, heat index (HI) rose to an average of 32°C thereby causing significant heat stress. Data were analyzed using a paired TTest. During periods of high HI, from 29°C to 45°C, least squares means of FCM were significantly higher for the M group compared with C (42.41 ± 1.71 kg and 38.45 ± 1.71 kg, respectively). During this heat time frame, milk yield from C cows was reduced by 15% and M cows by 5% although least squares means were significantly higher for the C group (41.54 ± 1.85 kg and 39.25 ± 1.58 kg for C and M, respectively). The M group had significantly higher FCM:DMI ratios (0.78 ± 0.05 and 0.67 ± 0.05 kg FCM/kg DMI for M and C, respectively). Dry matter intake was not different between treatments (24.60 ± 1.62 kg and 25.26 ± 4.56 kg for M and C, respectively). During the high HI time frame, milk fat % increased in the M treatment compared with a decrease in C cows (+0.56% compared with −0.46% for M and C, respectively). Results of this study conducted on a commercial dairy farm in WI during summer months indicate that FCM is significantly increased with an increased FCM efficiency. These results indicate that supplementation of these fermentation byproducts may improve digestion and utilization of feedstuffs in the diet thus abating the effects of heat stress and supporting production.

Key Words: microbial product, heat stress, milk fat

Graduate Student Competition: ADSA Dairy Foods Division Poster Competition

T102 Effect of micellar casein concentrate fortification on the acidification, physical and rheological properties of nonfat Greek-style yogurt. D. D. Bong* and C. I. Moraru, *Department of Food Science, Cornell University, Ithaca, NY.*

The rising popularity of Greek-style yogurt (GSY) in recent years was one of the most remarkable changes in food production and sales in recent history. One factor that may limit growth of GSY is the production of large quantities of acid whey during the centrifugation step. The objective of this work was to develop and optimize an alternate make process for GSY, in which the desired level of protein is reached by fortification with micellar casein concentrate (MCC) instead of whey removal. The acidification, physical and rheological properties of GSY made by these two methods were evaluated and compared. MCC preparations with 2 levels of serum proteins (SP) (65% SP reduced and 95% SP reduced) obtained from milk by microfiltration were used as sources of protein. GSY with 9.80% protein made from unfortified skim milk using straining at 4°C was the control. Skim milk fortified with 65% and 95% SP reduced MCC to 9.80% protein was used in the alternate process. All samples were inoculated with GSY culture and fermented until pH 4.5.The experiment was repeated three times. Acidification was significantly faster ($P < 0.05$) for MCC fortified GSY than the control. Physical, rheological and acidification properties of MCC fortified GSY were determined after 24 hours storage at 4°C. Water holding capacity of MCC fortified GSY was significantly lower ($P < 0.05$) than the control, due to higher casein-to-whey protein ratio. Dynamic rheological analysis showed a weak frequency dependency of G′ for all samples, with G′ > G″ over the range of frequency tested, indicating that a weak gel network was formed in all samples. Differences ($P < 0.05$) in the magnitude of viscoelastic parameters between the two types of GSY were found, with G′ control > G″ fortified, which indicates a different magnitude of protein interactions in the two types of GSY. The apparent viscosity of all samples decreased as a function of increasing shear rate, indicating shear-thinning behavior, which fitted well the power law model. This study provides a basis for potential adoption of an alternate make process for GSY by the yogurt industry.

Key Words: Greek yogurt, micellar casein, rheology

T103 The effect of feed solids concentration and inlet temperature on the flavor of spray-dried whey protein concentrate. C. W. Park*[1], E. Bastian[2], B. E. Farkas[1], and M. A. Drake[1], *[1]North Carolina State University, Raleigh, [2]Glanbia Nutritionals Inc., Twin Falls, ID.*

Off flavors in whey protein negatively influence consumer acceptance of whey ingredient applications. Previous research has demonstrated that unit operations in whey protein manufacture, such as liquid storage and bleaching, promote off-flavor production in dried whey protein. The objective of this study was to determine the effects of feed solids concentration in liquid retentate and spray drier inlet temperature on the flavor of the resulting whey protein concentrate (WPC). Cheddar cheese whey was manufactured, fat-separated, pasteurized, bleached (250 ppm hydrogen peroxide), and ultrafiltered (UF) to obtain WPC80 retentate that was 25% solids (wt/wt). The liquid retentate was then diluted with deionized water to one of the following solids concentrations: 25%, 18%, or 10%. Each of the treatments was then spray dried at one of the following temperatures: 180°C, 200°C, or 220°C. Experiments were replicated three times. Dried WPC80 were evaluated by sensory and instrumental analyses. Particle size and surface free fat were also analyzed. Both main effects (solids concentration and inlet temperature) and interactions between solids concentration and inlet temperature were investigated. A decrease in feed solids concentration resulted in increased surface free fat, intensities of overall aroma, cabbage and cardboard flavors and increased concentrations of pentanal, hexanal, heptanal, decanal, (E)2-decenal, DMTS, DMDS, and 2,4-decadienal ($P < 0.05$). A decrease in inlet temperature also resulted in increased surface free fat, cardboard flavor and increased concentrations of pentanal, (Z)4-heptenal, nonanal, decanal, 2,4-nonadienal, 2,4-decadienal, and 2- and 3-methyl butanal ($P < 0.05$). Mean particle size was higher for powders from increased feed solids concentration and increased inlet temperature ($P < 0.05$). These results demonstrate that an increase in feed solids concentration in the liquid retentate and inlet temperature within the parameters tested decreases off-flavor intensity in the resulting WPC80 powder.

Key Words: WPC80, flavor, processing step

T104 Enzyme hydrolysis of lactose in milk and dairy co-products. X. E. Li* and M. A. Drake, *North Carolina State University, Raleigh.*

Interest in dietary sugar reduction has led to a search for natural alternatives to sweeten dairy beverages such as chocolate milk. We recently demonstrated that parents were interested in sugar reduction in chocolate milk for their children but that desirable flavor and natural sources of sweet taste reduction were desired. The naturally existing milk sugar lactose has a lower relative sweetness compared to its monosaccharide constituents glucose and galactose. As such, lactose hydrolysis of milk or a dried dairy ingredient may be a natural and label friendly method to reduce added sugar in chocolate milk. The objective of this study was to evaluate and compare enzymatic hydrolysis of lactose from different dairy matrices with different lactase sources. Four commercial lactase enzymes were evaluated. Lactose hydrolysis of whole raw and pasteurized milk, skim pasteurized milk, fresh liquid whey and milk permeates, five rehydrated commercial spray dried whey permeates [5 and 10% (w/w) solids], and two different commercial rehydrated lactose sources [5 and 10% (w/w) lactose in phosphate buffer] were compared at 4°C. Following 12 or 24 h, an aliquot of solution was removed and subjected to 100°C for 5 min to inactivate lactase. Hydrolysis was determined by measurement of lactose in control and treated solutions by high performance liquid chromatography (HPLC). Experiments were conducted in duplicate. Lactose was efficiently hydrolyzed in skim and whole milk, liquid permeates, and lactose solutions by three lactases in 24h (>95%), however the degree of hydrolysis varied in different rehydrated spray dried whey permeates (4 to 90%) and also varied by lactase source ($P < 0.05$). These results provide a better understanding of lactose hydrolysis in milk and dairy co-products which could be applied to naturally enhance the sweetness of dairy beverages such as chocolate milk.

Key Words: lactose hydrolysis, permeate, milk

T105 Impact of gravity separation of raw milk on shelf-life of pasteurized fluid milk. S. L. Beckman* and D. M. Barbano, *Cornell University, Ithaca, NY.*

The objective of this research was to use gravity separation (GS) of raw milk to increase the microbiological shelf-life of pasteurized 2% fat milks. Raw whole milk (experiment 1), and cold (6°C) centrifugally separated (CS) raw skim (experiment 2) milk were GS (4°C, 22 h) to remove bacteria and spores prior to production of standardized 2% fat pasteurized (72 and 80°C, 25 s), homogenized milks. A standard plate count (SPC) was conducted on raw milks (d = 0), and on pasteurized milks initially and every 7 d during 70 d storage at 6°C, with a shelf-life limit of 20,000 cfu/mL. Mesophilic spores were enumerated on raw and initial pasteurized milks. Each experiment was replicated 3 times with different lots of milk. In CS raw skim milk (experiment 2), bacteria ($P < 0.05$), spores ($P < 0.05$), and fat ($P < 0.05$) GS into the top 4% (wt/wt) layer of a column of milk. When used on raw CS skim milk, GS reduced SPC and spores by 0.8 and 0.6 log cfu/mL, respectively. Both GS of raw whole milk (experiment 1) and raw CS skim milk (experiment 2) improved the shelf-life of high-temperature short-time pasteurized milks. Lower SPC ($P < 0.05$) and spores ($P < 0.05$) in GS milks prior to pasteurization created fluid milks that had microbial shelf-lives extending beyond 70 d of storage at 6°C (experiment 1 and 2). The extended shelf-life of pasteurized GS milks compared to CS (conventionally processed) milks can be attributed to the partitioning of vegetative bacteria and heat-resistant psychrotolerant sporeformers into the cream layer during GS. There was an interaction ($P < 0.05$) of day of storage by pasteurization temperature on the shelf-life of GS and CS milks, with milks pasteurized at 72°C increasing in bacteria count faster than 80°C (experiment 1 and 2). Future work should focus on determining the chemical and biological basis for the mechanism of GS (i.e., rising) of bacteria and spores in raw and minimally pasteurized whole and skim milk. Once this mechanism is understood, it may be feasible to design a continuous-flow technology for removal of bacteria and spores from raw milk that can be done at low temperatures.

Key Words: gravity separation, shelf-life, pasteurized milk

T106 The influence of solids concentration and bleaching agent on bleaching efficacy and flavor of sweet whey powder. M. G. Jervis* and M. A. Drake, *North Carolina State University, Raleigh.*

Recent studies have demonstrated the impact of bleaching and bleaching agent on flavor and functional properties of whey protein ingredients. Fat had minimal effects on bleaching, but protein concentration at bleaching significantly impacted bleaching efficacy and flavor effects of different bleaching agents. It is not known if these parameters influence manufacture of sweet whey powder (SWP). The purpose of this study was to determine the effects of solids concentration and bleaching agent on the flavor and bleaching efficacy of SWP. Colored Cheddar whey was manufactured, fat separated and pasteurized. Subsequently, the whey (6% solids) was bleached, concentrated using reverse osmosis (RO) to 14% solids and then spray dried, or whey was concentrated prior to bleaching and then spray dried. Bleaching treatments included: Control (CT) (no bleaching, 50°C, 60 min), hydrogen peroxide (HP) (250 mg/kg, 50°C, 60 min), benzoyl peroxide (BP) (50 mg/kg, 50°C, 60 min), lactoperoxidase (LP) (20 mg/kg, 50°C, 30 min), and Maxibright (MB) (2 dairy bleaching units/ml, 50°C, 30 min). The experiment was repeated in triplicate. Sensory properties and volatile compounds of SWP were evaluated by a trained panel and gas chromatography mass spectrometry, respectively. Bleaching efficacy (norbixin destruction) and benzoic acid were measured using high performance liquid chromatography. Differences in bleaching efficacy, sensory and volatile compound profiles and benzoic acid were observed with different bleaching agents ($P < 0.05$) consistent with previous studies. Solids concentration impacted bleaching efficacy of HP ($P < 0.05$) but not other bleaching agents. SWP from whey bleached with HP or LP following RO had increased cardboard and fatty flavors and higher concentrations of lipid oxidation compounds compared to SWP from whey bleached prior to RO. These results indicate that solids concentration impacts bleaching efficacy of HP and influences off flavors associated with specific bleaching agents in SWP.

Key Words: sweet whey powder, bleaching, flavor

T107 Detection of fat and protein differences between mid-infrared instruments used for milk producer payment testing. M. C. Adams* and D. M. Barbano, *Cornell University, Ithaca, NY.*

The USDA Federal Milk Marketing Orders are responsible for ensuring milk component testing accuracy for producer payment. Currently, there are 2 ways this can be achieved: through split-sampling or statistical analysis of routine testing data. The former is ideal, as the same sample can be measured in 2 labs. However, this is not always practiced due to duplicate sampling costs. Our objective was to determine the least significant differences (LSD) necessary to detect differences in mid-infrared (MIR) spectrophotometric payment results at various confidence levels ($P = 0.0001$ to 0.10). This robust statistical method could be used when split-sampling is not practical. Two MIR instruments' fat and protein results from 4 months (153 to 197 producers in a month) were analyzed. Models for each component during each month were constructed (i.e., Fat_{July} = producer + instrument + instrument × producer + error) using the general linear model statement (PROC GLM) of SAS software. The analyses of variance indicated that "producer" was significant ($P < 0.0001$) in all 8 models, "instrument" was significant ($P < 0.05$) in most models, and "instrument × producer" was not significant ($P > 0.05$) in any of the models. "Instrument" LSD values for fat ranged from 0.0108% to 0.0148% for the 4 months ($P = 0.05$). "Instrument" LSD values for protein ranged from 0.0045% to 0.0089% for the 4 months ($P = 0.05$). In addition to these models, the differences between instruments for each producer were plotted as function of fat or protein concentration and regression was used to estimate the slopes of the best-fit lines. Surprisingly, the slopes of the best-fit lines were different ($P < 0.001$) from 0 for all 4 months for both fat and protein. This indicated that systematic differences in the MIR calibrations across component concentrations could lead to underpayment or overpayment to producers at the extremes of the concentration range, even though the means for the 2 instruments may not be different. Given the present trend toward fewer farms producing larger volumes of milk, small errors in test values could amount to large payment errors over time.

Key Words: mid-infrared, payment, statistics

T108 Measuring consumer emotional response to flavored and unflavored milk. E. Arnade*, S. Duncan, J. Dunsmore, R. Rudd, and S. O'Keefe, *Virginia Tech, Blacksburg.*

Flavored milk in school food service settings has received significant media attention because of higher caloric content, mostly from high fructose corn syrup, and questions about contributions to childhood obesity. The goal of the experiment was to characterize emotional response to unflavored (white) vs. flavored (chocolate) milk as compared to reported behavior and hedonic preference for a young adult population to better understand the current sentiment and/or disconnect between intake and liking. Panelists consumed chocolate and white milk (1% fat) and selected emotional terms from a list (n = 43 terms) describing the way they felt immediately post-consumption of each product sample. Panelists completed demographic, knowledge and

attitudes, and beverage consumption questionnaires, and rated each sample using a 9-point hedonic scale. Frequency, similarities (shared) and differences (unique) in emotional terms selected across and between samples were compared. Chocolate milk received a statistically higher ($P = 0.0017$) mean acceptability score than white milk, 7.0 ± 1.5 and 5.7 ± 2.4, respectively (overall; n = 52). Gender segmentation showed a statistically higher ($P = 0.0047$) mean acceptability score for chocolate milk than white milk within females (n = 34); no statistical difference in acceptability scores were shown within males (n = 18). Emotional term analysis identified 14 frequently used terms as well as shared terms (calm, good) across samples. Unique terms were identified between the chocolate (satisfied, happy, warm, nostalgic, and joyful) vs. white (disgusted) milk. Gender segmentation showed that females (n = 31) differentiated between the samples with many more unique terms than males (n = 17), while males had a greater number of shared terms among the samples than females, suggesting that female and male emotional response may differ. Emotional response may provide an added value understanding for the acceptability of flavored and unflavored fluid milk, suggesting an opportunity to foster the current positive response to flavored milk by providing rationale for promotion and continued access to low-fat flavored milk options.

Key Words: milk, emotion

T109 Oxidative stability evaluation of milk from cow fed with dried distillers grains with solubles by sensory and chemical analysis. G. Li*, E. Testroet, S. Clark, and D. Beitz, *Iowa State University, Ames.*

Feeding dried distillers grains with solubles (DDGS) to dairy cows has been loosely implicated in formation of oxidized off flavors in milk. The purpose of this study was to examine the impact of feeding DDGS to dairy cows on the oxidative quality of the milk by sensory and chemical analysis. Twenty-four cows were divided into 2 groups, fed a total mixed ration, with 3 incorporation levels of DDGS (0%, 10%, 25%). Each group received each of the diets, such that they served as their own controls. Milk was collected 3 times (on days 14, 21, 28) during the feeding periods. For each treatment, pooled fresh milk was divided into 3 fortification options (no vitamin, 0.06% vitamin E, 0.06% vitamin C) then HTST pasteurized. Milk fat (%), SNF (%), and protein (%) were measured by LactiCheck. A 10-member descriptive analysis panel evaluated the milk samples on seven specific descriptors on days 1, 3, and 7 of storage. Chemical analyses [peroxides, free fatty acids (FFA)] were taken from the same milk with SafTest kits. Milk fat decreased significantly ($P < 0.0001$) from 3.3% to 2.7% in both 10% and 25% DDGS groups, while SNF and protein increased ($P < 0.1$), storage day effect ($P > 0.1$), or fortification effect ($P > 0.05$) on oxidized off-flavors. However, for the 25% diet treatment milk with vitamin C, higher light oxidized ($P < 0.05$) and metal oxidized ($P < 0.0001$) flavor scores were found. Though statistically significant, the milks did not exhibit definite oxidized flavor; the scores were lower than 1.5 on a 15-cm line scale. All peroxide and most of the FFA measurements were below detection level, with the exception of a couple of samples that had slightly elevated FFA; the elevated results were not observed in their replicates. With no apparent oxidation in any milk from any treatment, the sensory and chemical analyses support the conclusion that feeding of DDGS at 10% and 25% levels did not decrease the oxidation stability of milk. Spontaneous oxidation is a complex process that cannot be blamed on DDGS alone.

Key Words: milk, dried distillers grains with solubles, sensory evaluation

T110 Role of exopolysaccharide-producing starters in biofilm formation on dairy separation membranes. N. Garcia-Fernandez*, A. N. Hassan, and S. Anand, *Midwest Dairy Foods Research Center, Dairy Science Department, South Dakota State University, Brookings.*

The objective of this research was to evaluate the role of exopolysaccharides (EPS) produced by lactic starters in biofilm formation on dairy separation membranes. Exopolysaccharides are thought to play a role in biofilm formation and stability. We hypothesized that EPS-producing starters used in cheese making would increase the risk of biofilm formation on whey separation membranes. Two different EPS^+ starters and their isogenic EPS^- variants were used to study attachment of bacterial cells in the absence of growth (at 4ºC) and biofilm formation on Reverse Osmosis (RO) membranes. M17 broth and whey protein concentrate 35 solution (10% w/w) were used as growth media for biofilm formation under static conditions. *Streptococcus thermophilus* ST3534 (EPS^+) and ST5842 (EPS^-) were provided by Chr. Hansen. *Lactococcus lactis* ssp. *cremoris* JFR^+ (EPS^+) was isolated from a retail dairy product and an EPS^- mutant (JFR^-) was selected in our laboratory. Plasmid profile analysis revealed the absence of a plasmid in JFR^-. Five (2 × 2 cm) pieces of RO membrane were used in each experiment. Bacterial cells were allowed to attach and form biofilm on the retentate side only. A stomacher was used to recover cells attached to the membrane and the viable cell counts were estimated. Each experiment was repeated three times. Results showed significantly greater ($P < 0.05$) counts (cfu/cm^2) of ST3534 cells in biofilm than those of ST5842 whilst counts of cells attached to the membrane in the absence of growth did not differ ($P > 0.05$) between the isogenic pair. Interestingly, JFR^+ counts were significantly lower ($P < 0.05$) than those of JFR^-. These findings indicate that EPS produced by ST3534 may have a role in building up the three dimensional structure of the biofilm rather than assisting in the attachment to the membrane at the initial steps of biofilm formation while EPS produced by JFR^+ interfered with both cell attachment and biofilm formation. In conclusion, EPS produced by starter cultures vary in their role in bacterial attachment and biofilm formation, likely, due to variations in their molecular characteristics and interactions with the membrane.

Key Words: biofilm, exopolysaccharide, membrane

T111 Solubility and antihypertensive activity of whey protein hydrolysate subjected to Maillard-induced glycosylation. K. Ruud*, Q. Wang, and B. Ismail, *University of Minnesota, St. Paul.*

The interest in the utilization of biologically active whey protein hydrolysates (WPH) in functional foods and beverages, specifically, has significantly increased over recent years. While bioactive WPH potentially may impart physiological benefits such as antihypertensive activity, maintaining quality and shelf-life stability is a major hurdle that hinders its application in beverages. We have recently demonstrated whey protein solubility and thermal stability enhancement upon partial Maillard-induced glycosylation over a broad pH range. Our objective was to evaluate the effect of limited and controlled Maillard-induced glycosylation on the solubility, thermal stability, and antihypertensive activity of WPH. Whey protein hydrolysate (DH 5.2%) was reacted with dextran (10 kDa) at $a_w = 0.49$ and at 60°C for up to 60 h to produce partially-glycosylated WPH (PGWPH). Extent of glycosylation was assessed by monitoring absorption at 304 nm and by determining % amino-groups blockage. Extent of browning was monitored at 420 nm. The antihypertensive activity was determined by measuring the angiotensin converting enzyme (ACE) inhibitory activity following an in vitro assay. For determination of solubility and thermal stability, PGWPH samples and their controls were prepared in solutions (5% wt/

vol) at various pH values and subjected to heat treatment at 80°C for 30 min. Difference UV spectroscopy confirmed that glycosylation was initiated after 48 h of incubation. Partial glycosylation with only up to 2% amino-group blockage and minimal browning were maintained after 60h of incubation. Solubility and thermal stability of PGWPH were enhanced especially around the pI of whey protein. The antihypertensive activity of PGWPH was preserved maintaining an IC_{50} similar to or greater than that of WPH. Our results indicated that partial glycosylation has the potential to improve the solubility and thermal stability of WPH over a wide range of pH, while maintaining its bioactivity.

Key Words: whey protein hydrolysate, Maillard-induced glycosylation, antihypertensive activity

Graduate Student Competition: ADSA Production Division Poster Competition, MS Division

T113 Effect of dietary unsaturated fatty acids on ruminal fermentation in dairy cows. J. E. Freitas Jr.*[1], M. D. S. Oliveira[2], B. C. Venturelli[1], E. F. Jesus[2], R. Gardinal[1], G. D. Calomeni[1], J. R. Gandra[1], V. G. C. Lacuna[1], V. P. Bettero[2], C. S. Takiya[1], R. V. Barletta[1], and F. P. Rennó[1], *[1]University of São Paulo, Pirassununga, São Paulo, Brazil, [2]State University Julio de Mesquita, Jaboticabal, São Paulo, Brazil.*

The aim of this study was to evaluate the ruminal fermentation in dairy cows supplemented with unsaturated fatty acids sources. Eight Holstein cows in the mid lactation (80 ± 20 d in milk; mean SD) cannulated in the rumen and abomasums (580 ± 20 kg of weight; mean ± SD) with milk yield of 25 kg/d were assigned randomly into two 4 × 4 Latin squares, fed the following diets: (1) control (C); (2) refined soybean oil (inclusion of 3% in the total dry matter); (OS); (3) whole soybean raw (WS) (inclusion of 16% in the total dry matter); and (4) calcium salts of unsaturated fatty acids (CSFA) (inclusion of 3% in the total dry matter). Data were analyzed using PROC MIXED of SAS 9.1 according with the orthogonal contrasts (C vs SO + WS + CSFA); (SO vs WS + CSFA) and (WS vs CSFA). Dietary treatments did not affect total molar proportions of ruminal volatile FA. However, cows fed WS, SO and CSFA had a slow molar proportion of butyrate than those fed the CO diet. Cows fed SO had a higher ruminal pH than those fed the WS and CSFA diets (5.76; 5.87; 5.78 and 5.76 to diets CO, SO, WS and CSFA respectively). However, cows fed CO had a higher NH_3-N concentration than those fed the WS, SO and CSFA diets (43.1; 36.4; 36.9 and 33.3 mg/dL to diets CO, SO, WS and CSFA respectively). Unsaturated fatty acids increased ruminal molar proportions of acetate and propionate (1.2 and 3.3% respectively) and decreased ruminal molar proportions of butyrate in 10.1%. It is concluded that the supplementation of unsaturated fatty acids, alter ruminal fermentation and have positive effect on ruminal energetic efficiency

Key Words: oil soybean, abomasum, whole soybean

T114 Effects of nutritional prepartum supplementation upon maternal-kid behavior (1). N. E. Hernandez-Macias*[1], V. Contreras-Villarreal[1], O. Angel-Garcia[1], J. M. Guillen-Muñoz[1], P. A. Robles-Trillo[1], G. Arellano-Rodriguez[1], R. Rodriguez-Martinez[1], M. Mellado[1], C. A. Meza-Herrera[2], and F. G. Veliz[1], *[1]Universidad Autonoma Agraria Antonio Narro, Torreon, Coahuila, Mexico, [2]URUZA-UACh, Bermejillo, Durango, Mexico.*

This study aimed to evaluate the effect of either 15 or 30 d of prepartum nutritional supplementation upon maternal-kids behavior under grazing-semiarid rangeland conditions in northern México (26 N). A total of 23 goats with similar body weight and condition were divided in three experimental groups: (1) Control Group (CG; n = 7) was non-supplemented, (2) G15 Group (G15, n = 8) was supplemented from 15-d pre- up to 7-d postpartum; goats were supplemented prior grazing (0800) with a 500 g of a mixture of 20% manure, 37% rolled corn, 37% bran, 4% treacle and 2% salt); (3) G35 group (G35, n = 8) received the same supplement as G15 but from 35-d pre- up to 7-d postpartum. To evaluate kids' ability to differentiate their mother from an alien kid's at 8 h postkidding, a discrimination test was carried out, which is a double election test to evaluate their preference for his mother. The test lasted 5 min. Recorded behaviors included: high and low bleating per kid, number of visits to the "Contact Zone" and time spent in each zone. Data were subjected to the Student t-test (MYSTAT). Table 1 shows the behavioral variables considered. No differences ($P < 0.05$) were observed among experimental groups for the studied behavioral doe-kids variables. The last may have occurred because does depicted a intermediate body condition and were facing similar management conditions. Therefore, results suggest that does-kids facing such physiological and environmental scenarios do not require any additional supplementation to enhance or stimulate a closer relationship between does and their kids.

Table 1. Results of the discrimination test performed 8 h after birth

	Events (no.)		Time (min)		High bleating (no)		Low bleating (no.)	
	Own	Alien	Own	Alien	Own	Alien	Own	Alien
CG	0.3±0.2^{a,x}	0.3±0.2^{a,x}	0.3±0.2^{a,x}	0.3±0.2^{a,x}	2.1±1.5^{a,x}	1.0±0.7^{a,x}	0.8±0.8^{a,x}	0.2±0.2^{a,x}
G15	0.2±0.2^{a,x}	0.2±0.2^{a,x}	6.2±6.9^{a,x}	0.2±0.2^{b,x}	1.8±1.9$^{a-x,}$	0.4±0.4^{a,x}	0.4±0.4^{a,x}	0.1±0.1^{a,x}
G30	0.8±0.2^{b,x}	1.1±0.3^{b,x}	19.6±11.2^{a,x}	15.7±7.7^{b,x}	2.9±0.9^{a,x}	2.1±0.7^{b,x}	3.4±1.9^{a,x}	0.3±0.2^{a,x}

^{a,b}Statistical differences between groups at $P < 0.05$.
^{x,y}Statistical differences between own and alien kid at $P < 0.05$.

Key Words: goat, behavior, supplementation

T115 Use of estradiol to induce reproductive activity in anestrous goats. V. Contreras-Villarreal*[1], O. Angel-Garcia[1], J. M. Guillen-Munoz[1], P. A. Robles-Trillo[1], M. A. de Santiago-Miramontes[1], G. Arellano-Rodriguez[1], R. Rodriguez-Martinez[1], M. Mellado[1], C. A. Meza-Herrera[2], and F. G. Veliz[1], *[1]Universidad Autonoma Agraria Antonio Narro, Torreon, Coahuila, Mexico, [2]URUZA-UACh, Bermejillo, Durango, Mexico.*

Use of estradiol for sexual activity induction was evaluated in anestrous goats. Mixed breed anovulatory adult goats (n=16) were divided into 2 groups (n=8) with homogeneous body condition score and body weight; four mixed-breed bucks were also used. Does grazed from 1000h to 1600h. Group 1 (IM+E2) received 25 mg i.m. progesterone and 24h later received 1 mg i.m. estradiol (estradiol cyclopentil propionate). Group 2 (Spo+E2) was treated during 7 days with an intravaginal sponge impregnated with 20 mg cronolone; at sponge removal, goats received 1 mg i.m. estradiol; does were penned and kept there during 5-d, and were fed with alfalfa hay ad libitum, 200 g commercial mix (14% CP, per animal/d) while trace mineral salt blocks and water ad libitum. Estral activity was evaluated by introducing a male in each experimental group 15 min (morning) and 15 min (afternoon). Females depicting signs of heat were moved to a different pen with two males. Follicular activity was evaluated with a transrectal ultrasonographic scanning (TUS) from -7 d up to +7 d from estradiol administration. Forty-five days after estrus detection, goats were evaluated for pregnancy by TUS. Number and size of ovulatory follicles and size of the corpus luteum for each group were compared with a Student T; the percentage of females depicting estrus, ovulation and pregnancy were compared with a chi^2. Reproductive response from both experimental groups is presented on Table 1. Mixed-breed anestrous goats from northern Mexico (26°N) treated with estradiol positively responded to estral activity induction although depicted a reduced ovulation rate. Therefore, estradiol may have not been able to stimulate follicles enough for oocyte maturation and ovulation.

Table 1. Reproductive response of mixed-breed anestrous goats receiving either an i.m. progesterone or intravaginal sponges impregnated with progesterone and estradiol.

	Group	
Sexual response	IM + E2	Esp + E2
Estrus (n)	8/8[a]	8/8[a]
Ovulation (n)	4/8[a]	5/8[a]
Pregnancy (n)	3/5[a]	3/5[a]
Ovarian follicles (n)	0.63 ± 0.22[a]	0.88 ± 0.23[a]
Ovarian follicles size (mm)	0.8 ± 0.03[a]	0.8 ± 0.03[a]
Corpus luteum size (mm)	0.825 ± 0.07[a]	0.762 ± 0.26[b]

[a,b]Different superscript within variables denote differences $P < 0.05$.

Key Words: estradiol, anestrous, goat

T116 Effects of nutritional prepartum supplementation upon maternal-kid behavior (2). N. E. Hernandez-Macias*[1], V. Contreras-Villarreal[1], O. Angel-Garcia[1], J. M. Guillen-Munoz[1], P. A. Robles-Trillo[1], G. Arellano-Rodriguez[1], R. Rodriguez-Martinez[1], M. Mellado[1], C. A. Meza-Herrera[2], and F. G. Veliz[1], *[1]Universidad Autonoma Agraria Antonio Narro, Torreon, Coahuila, Mexico, [2]URUZA-UACh, Bermejillo, Durango, Mexico.*

This study aimed to evaluate the effect of either 15 or 30 d of prepartum nutritional supplementation upon maternal-kids behavior under grazing-semiarid rangeland conditions in northern México (26°N). A total of 23 goats with similar body weight and condition were divided in three experimental groups: (1) Control Group (CG; n = 7) was non-supplemented, (2) G15 Group (G15, n = 8) was supplemented from 15-d pre- up to 7-d post-partum; goats were supplemented prior grazing (0800) with a 500 g of a mixture of 20% manure, 37% rolled corn, 37% bran, 4% treacle and 2% salt); (3) G35 group (G30, n = 8) received the same supplement as G15 but from 30-d pre- up to 7-d postpartum. To evaluate mother ability to differentiate their kids from an alien at 4h postpartum, a Discrimination Test was carried out, which is a double election test to evaluate their preference for her kid. The test lasted 5 min. Recorded behaviors included: high and low bleating per mother, number of visits to the "Contact Zone" and time spent in each zone. Data were subjected to the Student t-test. Table 1 shows the behavioral variables considered. No differences ($P < 0.05$) were observed among experimental groups for the studied behavioral doe-kids variables. The last may have occurred because does depicted a intermediate body condition and were facing similar management conditions. Therefore, results suggest that does-kids facing such physiological and environmental scenarios do not require any additional supplementation to enhance or stimulate a closer relationship between does and their kids.

Table 1. Results of the discrimination test realized to the mothers at 4 h postpartum.

	Events (no.)		Time (min)		High bleating (no)		Low bleating (no.)	
Group	Own	Alien	Own	Alien	Own	Alien	Own	Alien
CG	1.0±0.4[a,x]	0.9±0.3[a,x]	40.7±19.5[a,x]	57.3±36.5[a,x]	3.8±1.9[a,x]	3.0±1.5[a,x]	15.8±6.8[a,x]	16.4±6.1[a,x]
G15	0.7±0.5[a,x]	0.4±0.3[a,x]	9.7±4.9[b,x]	6.0±3.7[a,x]	2.6±2.5[a,x]	3.3±3.0[a,x]	1.8±1.2[a,x]	1.5±1.1[b,x]
G30	1.3±0.5[a,x]	0.9±0.2[a,x]	25.1±11.5[ab,x]	11.9±5.9[a,x]	8.6±4.0[a,x]	4.6±2.3[a,x]	6.3±2.8[a,x]	4.4±2.0[ab,x]

[a,b]Statistical differences between groups at $P < 0.05$.
[x,y]Statistical differences between own and alien kid at $P < 0.05$.

Key Words: goat, behavior, supplementation

T117 Effects of tamoxifen on estrogen and progesterone receptor expression in prepubertal female calves. H. L. M. Tucker*[1], C. L. M. Parsons[1], S. Ellis[2], and R. M. Akers[1], *[1]Dairy Science Department, Virginia Polytechnic Institute and State University, Blacksburg, [2]Animal and Veterinary Sciences Department, Clemson University, Clemson, SC.*

We have reported that ovariectomy (OVX) of prepubertal calves reduces mammary development in the period before puberty would have occurred. This was accompanied by increases in expression of estrogen receptor (ER), IGF-I axis molecules and expression of extracellular matrix proteins. Our purpose was to determine if the effects of OVX were dependent on expression of estrogen and/or progesterone (PR) receptors by use of the anti-estrogen tamoxifen. Sixteen Holstein calves were randomly assigned to one of two treatment groups: tamoxifen-injected (TAM) or control (CON). Calves were injected daily from 28 d to 120 d of age with 0.3 mg/kg tamoxifen or carrier. At 120 days calves were sacrificed and udders removed. Weight of trimmed parenchymal tissue (left rear quarter) was dramatically lower ($P < 0.0003$; 16.1 vs. 34.8 g) in TAM calves. Parenchymal samples from three regions of the left rear quarter (lower, middle and outer regions) were processed for immunohistochemical staining for ER and PR. Ductal areas within parenchymal sections were identified as stratified or unstratified. Epithelial cells were classified as ER positive, PR positive, dual labeled or unlabeled. The orientation of labeled cells was also characterized based on position within the epithelial layer (luminal, medial, or basal). Overall, the proportion of neither ER nor PR labeled cells was impacted by treatment but the percentage of dual labeled cells was higher (38.4% vs. 34.1%) in CON calves ($P < 0.05$). However, imaging analysis indicated a markedly higher intensity of ER expression in CON calves but no difference for PR staining intensity. The proportion of both ER and PR labeled cells was different when comparing stratified vs. unstratified ductal regions ($P \leq 0.001$). While treatment with the anti-estrogen tamoxifen reduced mammary parenchymal mass similarly to OVX, the mechanism(s) involved appear to differ. This suggests that the impacts of ovariectomy are only partially explained by alterations in ER expression. Ongoing analysis is focused on determining intensity of ER expression as well as effects of tamoxifen on other mammogenic pathways.

Key Words: tamoxifen, ovariectomy, estrogen receptor

T118 Effect of fatty acids n-3 and n-6 supplementation on blood parameters of Holstein cows during transition period and early lactation. R. Gardinal*[1], J. R. Gandra[1], G. D. Calomeni[1], L. C. Verdurico[1], R. D. Mingoti[1], R. V. Barletta[1], J. E. Freitas Jr.[1], C. E. Araújo[1], T. H. A. Vendramini[1], E. Ferreira de Jesus[2], and F. P. Rennó[1], *[1]Department of Nutrition and Animal Production, Faculty of Veterinary Medicine, University of São Paulo, Pirassununga, São Paulo, Brazil, [2]Department of Animal Science, State University Julio de Mesquita UNESP, Jaboticabal, Jaboticabal, São Paulo, Brazil.*

The aim of this study was to evaluate effect of n-3 and n-6 supplementation on blood parameters of Holstein cows during transition period and early lactation. Forty-eight Holstein cows were divided in 4 experimental groups in randomized design. Animals were assigned to receive 1 of 4 treatments: (1) control (C; n = 12), without fat sources in pre and postpartum; (2) flaxseed (FS; n = 12), fed 60 and 80 g/kg of DM of flaxseed in pre and postpartum; (3) whole raw soybeans (WS; n = 12), fed 120 and 160 g/kg of DM of whole raw soybeans in pre and postpartum; (4) calcium salts of unsaturated fatty acids (CSFA; n = 12; Megalac-E), fed 24 and 32 g/kg of DM of calcium salts of unsaturated fatty acids in pre and postpartum. Experimental diets were fed from 35 d before the estimate calving until 84 d of lactation, formulated to meet nutritional requirements of each period. Blood samples were

taken −21, −14, −7 days in relation to prediction of birth, at birth and +7, +14, +21, +28, +35, +42, +84 days postpartum. Glucose (GLU), total cholesterol (CHOL), triacylglycerides (TRI), non-esterified fatty acids and β-hydroxybutyrate concentrations were measured. Data were analyzed using the PROC MIXED of SAS 9.1 with fixed dietary effect, time effect, interaction between diet and time. Data were analyzed by orthogonal contrasts C vs. WS+CSFA+FS (C1); FS vs. WS+CSFA (C2); and WS vs. CSFA (C3). In the prepartum, animals supplemented with fatty acids had higher ($P < 0.05$) concentration of TRI (C1) (25.0 vs. 40.4, respectively). Concentration of GLU was higher ($P < 0.05$) in group FS, C2 (70.7 vs. 62.4, respectively). WS group had higher concentration ($P < 0.05$) of CHOL compared to CSFA group (C3) (137.9 vs. 103.1, respectively). In the postpartum, animals supplemented with fatty acids had higher ($P < 0.05$) concentration of CHOL (C1) (142.0 vs. 165.1, respectively). Concentration of GLU was higher ($P < 0.05$) in group FS (C2) (67.2 vs. 58.4, respectively). Blood parameters of Holstein cows fed with source of n-3 and n-6 in the transition period and early lactation were positively influenced.

Key Words: fat source, blood parameter, transition period

T119 Ruminal dynamics and neutral detergent fiber digestibility of dairy cows fed with different sources of unsaturated fatty acids. R. Gardinal*[1], J. E. Freitas Jr.[1], M. D. S. Oliveira[2], B. C. Venturelli[1], E. F. Jesus[2], G. D. Calomeni[1], L. C. Verdurico[1], V. G. C. Lacuna[1], V. P. Bettero[2], T. H. A. Vendramini[1], R. V. Barletta[1], and F. P. Rennó[1], *[1]Department of Nutrition and Animal Production, Faculty of Veterinary Medicine, University of São Paulo, Pirassununga, São Paulo, Brazil, [2]Department of Animal Science, State University Julio de Mesquita – UNESP, Jaboticabal, Jaboticabal, São Paulo, Brazil.*

The aim of this study was to evaluate the ruminal dynamics, NDF concentrations and digestibility of dairy cows fed with different sources of unsaturated fatty acids. Eight Holstein cows in mid-lactation (80 ± 20 d in milk, mean SD) cannulated in the rumen and abomasums (580 ± 20 kg of weight, mean ± SD) with milk yield of 25 kg/d were randomly assigned into two 4 × 4 Latin squares, fed the following diets: (1) control (C); (2) refined soybean oil (inclusion of 3% in the total dry matter); (SO); (3) whole raw soybean (WS) (inclusion of 16% in the total dry matter); and (4) calcium salts of unsaturated fatty acids (CSFA) (inclusion of 3% in the total dry matter). Milk yield and dry matter intake were measured daily throughout the experimental period. The marker NDFi was used to determine the abomasal dry matter flow. Ruminal contents were evacuated manually through the ruminal cannula at 4.5 h after feeding on d 20, and at 2.0 h before feeding on d 21 of each period. Fractional rates of fatty acids biohydrogenation and passage by the rumen were calculated utilizing the model that accounts for transfer of fatty acids among ruminal pools. The potentially digestible neutral detergent fiber (pdNDF) was calculated by the difference (1.0 − NDFi). Data were analyzed using PROC MIXED of SAS 9.1 according with the orthogonal contrasts (C vs. SO + WS + CSFA) (SO vs. WS + CSFA) and (WS vs. CSFA). Animals fed with WS diet showed higher NDF intake ($P < 0.05$) than those fed with CSFA diet (5.25 vs. 4.65 kg/d, respectively). There was a lower pdNDF intake ($P < 0.05$) by the animals fed with WS diet relative to the animals fed with CSFA diet (2.41 vs. 2.70 kg/day, respectively). The cows fed with C diet had lower ruminal digestibility of pdNDF ($P < 0.05$) compared to the cows fed with SO, WS and CSFA diets, contrast one (1.41 vs. 1.79; 2.02; 1.88, respectively). The use of diets containing raw soybean and calcium salts provided better ruminal digestibility of pdNDF (kg/d) in dairy cows in mid-lactation.

Key Words: linoleic acid, whole raw soybean, ruminal fermentation

T120 Follicular dynamics of Holstein cows fed with supplemental sources of n-3 and n-6 fatty acids during transition period and early lactation. G. D. Calomeni*[1], J. R. Gandra[1], R. Gardinal[1], J. E. Freitas Jr.[1], L. C. Verdurico[1], E.F. Jesus[2], C.S. Takiya[1], R.D. Mingotti[1], T. H. A. Vendramini[1], R. V. Barletta[1], and F. P. Rennó[1], *[1]Department of Nutrition and Animal Production, Faculty of Veterinary Medicine, University of São Paulo, Pirassununga, São Paulo, Brazil, [2]Department of Animal Science, State University Julio de Mesquita – UNESP Jaboticabal, Jaboticabal, São Paulo, Brazil.*

The aim of this study was evaluate the effect of supplemental sources of n-3 and n-6 fatty acids in follicular dynamics of dairy cows fed during the transition period and early lactation. Forty-eight Holstein cows were assigned into 4 experimental groups in randomized designed. The animals were randomly assigned to receive one of 4 treatments: (1) control (C), without fat sources in the pre and postpartum, (2) flaxseed (FS), 60 and 90 g/kg of DM of flaxseed in the pre and postpartum, respectively; (3)whole raw soybeans (WS), 120 and 160 g/kg of DM of whole raw soybeans in the pre and postpartum; (4) calcium salts of unsaturated fatty acid (CFSA; Megalac-E), 24 and 32 g/kg of DM of calcium salts of unsaturated fatty acid in pre and postpartum. The experimental diets were fed from 35 d before the estimate calving, and provided until 84 d of lactation, formulated to meet the nutritional requirements of each period. Ovaries of all cows were examined daily by ultrasonography beginning on day 14 and continuing until day 72 postpartum. Were examined by scanning: the total number of follicles (TNF), size of follicles, number and area (mm^2) of corpus luteum. Follicles were classified by size into 5 classes: (1) <3mm (CLA1), (2) 3-5mm (CLA2), (3) 6-9 mm (CLA3), (4) 10-15 mm (CLA4) and (5) >15 mm (CLA5). Data were analyzed using PROC MIXED of SAS 9.1, with the effect of treatment, period and interaction as fixed effects, and animal has random effect. The data were analyzed by orthogonal contrasts C vs. WS+CSFA+FS (C1); WS vs. CSFA (C2); and FS vs. WS+CFSA (C3). We observed an effect ($P < 0.05$) of treatment only for TNF and number of CLA1. Effect of period was observed for TNF, number of CLA3 and CLA5. There was interaction ($P < 0.05$) between the fatty acids sources and period for TNF, number of CLA2 e CLA3. Analyzing the orthogonal contrasts effect of C1 was observed for TNF (10.4 vs. 14.5) and number of CLA1 (1.27 vs. 4.21). The supplemental sources of n-3 and n-6 fatty acids influenced follicular dynamics of dairy cows fed during transition period and early lactation.

Key Words: fat source, follicular dynamics, transition period

T121 Ruminal dynamics of dairy cows fed with different sources of unsaturated fatty acids. G. D. Calomeni*[1], J. E. Freitas Jr[1], R. Gardinal[1], M. D. S. Oliveira[2], B. C. Venturelli[1], E. F. Jesus[2], C. S. Takiya[1], V. G. C. Lacuna[1], V. P. Bettero[2], T. H. A. Vendramini[1], R. D. Mingoti[1], F. Zanferrari[1], R. V. Barletta[1], and F. P. Rennó[1], *[1]Department of Nutrition and Animal Production, Faculty of Veterinary Medicine, University of São Paulo, Pirassununga, São Paulo, Brazil, [2]Department of Animal Science, State University Julio de Mesquita – UNESP Jaboticabal, Jaboticabal, São Paulo, Brazil.*

The aim of this study was to evaluate the ruminal dynamics of dairy cows fed with sources of unsaturated fatty acids. Eight Holstein cows in the mid lactation (80 ± 20 d in milk; mean SD) cannulated in the rumen and abomasums (580 ± 20 kg of weight; mean ± SD) with milk yield of 25 kg/d were assigned randomly into two 4 × 4 Latin squares, fed the following diets: (1) control (C); (2) refined soybean oil (inclusion of 3% in the total dry matter); (OS); (3) whole soybean raw (WS) (inclusion of 16% in the total dry matter); and (4) calcium salts of unsaturated fatty acids (CSFA) (inclusion of 3% in the total dry matter). Milk yield and the dry matter intake were measured daily throughout the experimental

period. The marker iNDF was used to determine the abomasal dry matter flow. Ruminal contents were evacuated manually through the ruminal cannula at 4.5 h after feeding on d 20, and at 2.5 h before feeding on d 21 of each period. Turnover rate in the rumen, passage rate from the rumen, and ruminal digestion rate of each component (%/h) were calculated. Data were analyzed using PROC MIXED of SAS 9.1 according with the orthogonal contrasts (C vs. SO + WS + CSFA); (SO vs. WS + CSFA) and (WS vs. CSFA). There was no effect of unsaturated fatty acids sources on dry matter and NDF digestions rates. Although, cows fed with WS diet submitted lower ($P < 0.03$) digestion rate of potentially digestible NDF (pdDNF) than cows fed with CFSA diet (1.21; 1.30; 0.89; 1.34%/h, to diets CO, SO, WS and CSFA respectively). Ruminal turnover rate for pdNDF ($P < 0.01$) was greater for animals fed the WS diet than did cows fed the CFSA diet (2.13; 2.48; 2.82; 1.91%/h, to diets CO, SO, WS and CSFA respectively). There was no effect of the diets on the passage rate, ruminal turnover rates of dry matter, organic matter, NDF and iNDF and rate of passage of dry matter, NDF, and iNDF. The supplementation of unsaturated fatty acids alter the ruminal dynamics of dairy cows

Key Words: ruminal turnover rate, dairy cow, unsaturated fatty acids

T122 Effect of different fatty acid profiles on milk fat depression in dairy cattle fed diets below 4% fat. C. M. Stoffel* and L. E. Armentano, *Department of Dairy Science, University of Wisconsin-Madison, Madison.*

High dietary C18:2 (linoleic acid) levels can result in incomplete biohydrogenation of fatty acids (FA) in the rumen leading to reduced milk fat secretion. The goal of this study was to identify the effect of different dietary FA profiles at FA levels below 4% of TMR dry matter (DM). Twenty-four primiparous and 36 multiparous lactating cows were paired (within parity) to form 30 experimental units. Pairs were fed 6 diets in five 6 × 6 balanced Latin squares with 21-d periods, using data from the last 5 d. There were two control diets: a corn control diet (CC; 29% corn silage, 16% haylage, 19% corn grain, 8% distillers grain, DM basis) containing 3% ether extract; and a low oil control (LOC; 9% corn silage, 35% haylage, 20% corn starch, and 8% corn gluten meal, DM basis) containing 2% ether extract. Starch in LOC was replaced with 1.75% diet DM of a 50/50 blend of corn oil and high linoleic safflower oil (CO), high oleic sunflower oil (OO), palm oil (PO), or 1.84% diet DM MegaLac (ML, Church and Dwight Company, Inc., Princeton, NJ) to create 4 treatment diets. Milk fat yield and concentration was significantly lower for CO than for PO. Milk yield was significantly lower for LOC than all other diets except ML. There were no treatment by parity or treatment by production effects on any of these parameters. The underperformance of the LOC versus the other diets suggests that it is useful to feed some fat in the diet. However, while adding free oils to the LOC diet increased milk yield, only palm oil increased milk fat yield.

Table 1.

Item	CC	LOC	CO	OO	PO	ML
C18:2 from oil, % Diet DM	—	—	1.15	0.18	0.16	0.11
Milk, kg/d	43.5^{ab}	39.7^{c}	42.7^{ab}	43.1^{ab}	43.5^{a}	40.7^{bc}
Fat, kg/d	1.49^{a}	1.38^{ab}	1.29^{c}	1.38^{ab}	1.48^{a}	1.39^{ab}
Fat, %	3.50^{a}	3.50^{a}	3.02^{c}	3.26^{ab}	3.41^{a}	3.44^{a}
Protein, kg/d	1.36^{a}	1.26^{b}	1.33^{ab}	1.34^{ab}	1.35^{a}	1.25^{b}

$^{a-c}$Means in a row with different superscripts differ ($P < 0.05$, Tukey-Kramer post hoc comparisons).

Key Words: fatty acid, milk fat depression, biohydrogenation

T123 Increasing dietary cation-anion difference improves feed efficiency in lactating dairy cows. M. E. Iwaniuk* and R. A. Erdman, *University of Maryland, College Park.*

Feed costs in the dairy industry have doubled during the last five years and dairy producers are keenly interested in factors that will improve dairy feed efficiency (FE). The most common index of dairy FE is 3.5% fat-corrected milk (FCM) per unit of dry matter intake (DMI). Increasing dietary cation-anion differences (DCAD) has been shown to increase milk production, FCM, and FE while optimizing DMI. However, the optimal DCAD concentration for maximum production and dairy FE has yet to be determined. The objective of this experiment was to determine the optimal DCAD concentration for maximal FE in early lactation dairy cows. Eight primiparous and 12 multiparous Holstein cows averaging 89 (±25) days in milk were used. Cows were individually fed a basal diet consisting of 60% corn silage and 40% concentrate (dry matter basis). Experimental treatments consisted of 250 (basal), 300, 350, and 400 mEq/kg DCAD which were applied in a 4 × 4 Latin square design with 3-week experimental periods. Potassium carbonate was added to the basal diet to provide the respective DCAD concentrations. DCAD had no effect on milk production or DMI. However, milk fat percent was increased linearly ($P = 0.014$) by DCAD resulting in an increased ($P = 0.054$) FCM. This resulted in a 0.08 unit increase in dairy FE ($P = 0.027$). As the maximum FE occurred at the highest DCAD concentration, the optimal DCAD could not be determined, but it would be at least 400 mEq/kg DM. The results confirm earlier studies suggesting that altering DCAD could be used to increase FE in dairy cows and reduce feed costs.

Table 1.

	DCAD, mEq/kg					$P <$	
Item	250	300	350	400	SEM	Linear	Quadratic
Milk, kg/d	38.9	38.4	39.2	38.7	1.560	0.943	0.917
Fat, %	2.58	2.82	2.75	2.89	0.179	0.014	0.529
3.5% FCM, kg/d	32.8	33.7	34.3	34.7	1.410	0.054	0.745
DMI, kg/d	21.7	22.1	22.3	22.0	0.500	0.247	0.156
FCM/DMI	1.52	1.54	1.54	1.60	0.510	0.027	0.350

Key Words: dairy cow, DCAD, potassium carbonate

T124 Sodium bicarbonate is more effective than potassium carbonate as a DCAD source for improving feed efficiency in lactating dairy cows. M. E. Iwaniuk* and R. A. Erdman, *University of Maryland, College Park.*

Increasing dietary cation-anion differences (DCAD) has been shown to increase milk production (MP), 3.5% fat-corrected milk (FCM), and feed efficiency (FE) while optimizing dry matter intake (DMI) in lactating dairy cows. Either sodium (Na) or potassium (K) can be used to increase DCAD in lactating dairy cow diets; however, cation supplementation with potassium carbonate (K_2CO_3) is 4× more expensive than cation supplementation with sodium bicarbonate ($NaHCO_3$). The objective of this study was to determine the relative efficacy of K_2CO_3 versus $NaHCO_3$ on dairy FE. Eight primiparous and 12 multiparous Holstein cows averaging 95 (±75) days in milk were used. Cows were individually fed a basal diet consisting of 65% corn silage and 35% concentrate (dry matter basis). Experimental treatments consisted of a basal diet containing 250 mEq/kg DCAD, and the addition of 150 mEq/kg DCAD using four ratios (mEq/kg basis) of K:Na: 100:0, 67:33, 33:67, and 0:100 using K_2CO_3 and $NaHCO_3$, respectively. Treatments were applied in a 4 × 4 Latin square design with 3-wk experimental periods. Cation source had no effect on DMI, MP, or FCM production. However, cation source had

a significant effect on milk fat where replacement of K with Na resulted in a linear increase in milk fat percent ($P = 0.005$). Dairy FE, defined as FCM/DMI, was highest ($P = 0.04$) when Na was the sole cation source. This change was primarily a result of increased milk fat percent that increased FCM. These results suggest that Na was more effective than K as a cation supplement to improve dairy FE.

Table 1.

	K:Na[1]					$P <$	
Item	100:0	67:33	33:67	0:100	SEM	Linear	Quadratic
Milk, kg/d	37.5	37.3	36.3	37.9	1.280	0.903	0.219
Fat, %	3.06	3.20	3.20	3.36	0.169	0.005	0.885
3.5% FCM, kg/d	34.6	35.2	34.3	36.7	1.060	0.132	0.262
DMI, kg/d	22.3	22.3	22.1	22.0	0.460	0.598	0.851
FCM/DMI	1.56	1.58	1.55	1.67	0.040	0.036	0.125

[1]All diets contained an overall DCAD concentration of approximately 400 mEq/kg.

Key Words: dairy cow, DCAD, feed efficiency

T125 Quality of corn silage inoculated with *L. buchneri* and *P. pentosaceus*. K. N. Kaletsch*[1], S. H. Ward[1], J. K. Ward[2], J. D. Davis[2], and A. J. Geiger[1], *[1]Department of Animal and Dairy Sciences, , Mississippi State, [2]Department of Agriculture and Biological Engineering, Mississippi State.*

Corn was harvested on July 21–22, 2012, using a 1.9-cm forage chopper with kernel processor. Corn was 35% DM and treated with 5×10^5 cfu/g of *Lactobacillus buchneri* and *Pediococcus pentosaceus* (B500) or not (CON). Treatment was applied as silage was loaded into bags using a Kelly Ryan Bagger with a 2.74 m tunnel. 22,959 and 25,290 kg of wet silage was loaded into CON and B500 bag, respectively. Temperature sensors were placed in the bags and data was logged every 4 h for 120 d. Samples were collected every 6 h for 48 h, every 24 h for 5 d, then weekly for 5 wk, and again at 90 and 120 d. Samples were analyzed for pH then subjected to proximate analysis. Samples were pooled by week (1-6), 90 and 120 d, analyzed for mold and mycotoxins. MIXED procedure of SAS (Cary, NC) was used to analyze the main effects of treatment, day, and their interaction. Significance was declared at $P < 0.05$. Interaction of treatment and day was significant for all measures of proximate analysis and pH. DM was lower in B500 compared to CON (39.1 vs. 40.2%, respectively; $P < 0.01$). DM increased in CON from 40% on d 60 to 45% on d120 and decreased in B500 from 35% on d 60 to 25% on d120. Ash content was greater in CON compared to B500 (5.0 vs.4.9%, respectively; $P < 0.04$). IVDMD was greater in CON compared to B500 (72.7 vs. 60.9%. respectively, $P < 0.01$). On d7, 8, and 50 CON had greater NDF (53.6, 52.3, 52.7%, respectively) and ADF (25.9, 29.3, 28.8%, respectively) than B500 (NDF: 43.5, 50.1, 46.9%, respectively; ADF: 17.1, 24.3, 27.3%; respectively; $P < 0.01$), otherwise B500 had greater NDF and ADF content. CP was lower in B500 than CON on d7, 40, and 50 (7.0 vs. 7.3%; 7.5 vs. 7.8%; 8.5 vs. 9.6%; respectively, $P < 0.01$), but greater on other days. In 24h, pH of CON decreased faster compared to B500 (4.5 to 3.9 vs. 3.9 to 3.8, respectively; $P < 0.01$). B500 had lower pH on d1, but the reverse was observed in subsequent days. Greater spoilage was noted in B500 as time progressed. Mold count exceeded 6×10^6 cfu/g by d 120 in B500 compared to CON (<50,000 cfu/g). Inoculation was more effective in nutrient preservation than CON, but after d60 data indicated increased spoilage of inoculated silage.

Key Words: silage, inoculant, dairy

T126 Effect of stocking density in the prepartum period on innate immune parameters and hemogram of dairy cows. A. Dresch*[1], J. Moraes[1], P. Silva[2], H. Hooper[1], C. Spies[1], P. Lau[1], K. Lobeck[2], K. Machado[1], M. Ballou[3], M. Endres[2], and R. Chebel[1], *[1]Department of Veterinary Population Medicine, University of Minnesota, St Paul, [2]Department of Animal Science, University of Minnesota, St Paul, [3]Department of Food and Animal Sciences, Texas Tech University, Lubbock.*

Objectives were to evaluate the effect of prepartum stocking density on innate immune parameters and hemogram of Jersey cows. Within each replicate (n = 4), 2 pens were assigned to 80% stocking density (80D, n=38) and 2 pens were assigned to 100% stocking density (100D, n=48). Nulliparous and parous animals were housed separately. Pen was considered the experimental unit (n=8/treatment). A sub-sample of animals randomly selected to represent each pen (n=48/treatment) had blood sampled weekly from 14 d prepartum to 14 d postpartum. Polymorphonuclear leukocyte (PMNL) phagocytosis (PHAGO) and oxidative burst (OB) and expression of CD18 and L-selectin were determined by flow cytometry, and complete blood count was performed. Animals were examined for metritis at 4, 7, 10, and 14 d postpartum. Dichotomous data were analyzed by logistic regression using the PROC GLIMMIX and continuous data were analyzed by ANOVA using the PROC MIXED procedure. Pen was included as the random effect. Treatment was nested within pen and replicate and cows were nested within treatment. Stocking densities were 74.0 and 94.3% (±0.3) of headlocks and 80.7 and 102.8% (±0.4) of stalls for 80D and 100D, respectively. The incidence of metritis was 33.3 and 11.8% for nulliparous animals and 16.7 and 22.2% for parous animals in the 80D and 100D treatments, respectively. Treatment did not affect percentage of PMNL PHAGO+ ($P = 0.71$) and the intensity of PHAGO ($P = 0.79$). Similarly, treatment did not affect percentage of PMNL OB+ ($P = 0.84$) and intensity of OB ($P = 0.84$). Treatment tended to affect percentage of PMNL CD18+ (80D = 98.8 ± 0.3 vs. 100D = 99.5 ± 0.3%; $P = 0.12$). Intensity of CD18 expression by PMNL, however, was not affected by treatment ($P = 0.47$). Percentage of PMNL L-selectin+ was not ($P = 0.93$) affected by treatment. Similarly, intensity of L-selectin expression by PMNL was not ($P = 0.66$) affected by treatment. The ratio of granulocyte:lymphocyte was not ($P = 0.96$) affected by treatment. Stocking density did not affect innate immune parameters, indicating that 100% stocking density during the prepartum period may not affect health of dairy cows.

Key Words: stocking density, dairy cow, immune response

T127 Effects of residual feed intake classification on feed efficiency, ultrasound, and feeding behavior traits in growing Santa Gertrudis heifers. J. A. Ramirez*[1], G. E. Carstens[1], J. G. Moreno[1], L. O. Tedeschi[1], J. C. Bailey[1], J. Jorgenson[2], and D. D. DeLaney[2], *[1]Texas A&M University, College Station, [2]King Ranch, Kingsville, TX.*

Objectives of this study were to evaluate the effects of residual feed intake (RFI) classification on performance, efficiency, carcass ultrasound and feeding behavior traits in growing heifers. Santa Gertrudis heifers (n = 220) with initial BW of 282.3 ± 98 kg were used in this study. Feed intake and feeding behavior traits were collected for 70 d using a GrowSafe system while consuming a forage-based diet (ME = 2.04 Mcal/kg DM). RFI was computed by regression of DMI on mid-test $BW^{0.75}$ and ADG, and heifers classified into low and high RFI (± 0.05 SD) groups. A 2-population distribution model was fit to $\log_{10}$-transformed non-feeding interval lengths to estimate meal criterion (MC) and compute frequency and duration. RFI was positively correlated ($P < 0.001$) with DMI (r = 0.77) and F:G (r = 0.68), but not with initial BW or ADG. RFI was positively correlated ($P < 0.05$) with bunk visit

(BV) frequency (r = 0.50) and duration (r = 0.44), and meal frequency (r = 0.13) duration (0.32). RFI was negatively correlated with meal criterion (r = −0.33). The R^2 of the base RFI model (ADG, mid-test $BW^{0.75}$) was 0.42, which increased to 0.65 with the inclusion of feeding behavior traits (BV frequency and duration, MC, meal frequency and duration). Low RFI heifers had 25 and 26% lower ($P < 0.0001$) DMI and F:G compared to high RFI heifers. Heifers with low RFI had lesser ($P < 0.001$) BV frequency (60.5 vs. 75.4 ± 1.7 events/d) and duration (80.2 vs. 99.5 ± 4.1 min/d) and higher ($P < 0.01$) MC (11.65 vs. 9.45 ± 0.61 min) compared to high-RFI heifers. Between-animal variation in RFI was not associated with differences in ultrasound measurements of carcass composition in this study. However, variation in feeding behavior traits account for 23% additional variance in DMI beyond that associated with ADG and mid-test $BW^{0.75}$. The longer MC observed in low-RFI heifers suggests that these heifers take longer to initiate a subsequent meal compared to high-RFI heifers, and demonstrate the heifers with divergent RFI have distinctive feeding behavior patterns.

Key Words: feeding behavior, residual feed intake

Graduate Student Competition: ADSA Production Division Poster Competition, PhD Division

T129 Hepatic gluconeogenesis in dairy cows as affected by dietary starch level and supplementation with monensin during early lactation. M. M. McCarthy*[1], T. Yasui[1], S. H. Pelton[1], C. M. Ryan[1], G. D. Mechor[2], and T. R. Overton[1], *[1]Cornell University, Ithaca, NY, [2]Elanco Animal Health, Greenfield, IN.*

The objectives of this study were to determine the effects of postpartum dietary starch level and supplementation with monensin (M) on rates of in vitro hepatic gluconeogenesis and oxidation from propionate. Primiparous (n = 17) and multiparous (n = 37) Holstein cows were fed a high starch (HS) or low starch (LS) early lactation diet with 0 or 450 mg/d M by topdress in a 2 (starch) × 2 (M) factorial arrangement. Prior to parturition all cows received a common controlled energy diet ad libitum with a daily topdress of either 0 or 400 mg/d M, depending on early lactation treatment assignment. From parturition until d 21 cows were fed HS TMR (26.2% starch, 34.3% NDF, 22.7% ADF, 15.5% CP) or LS TMR (21.5% starch, 36.9% NDF, 25.2% ADF, 15.4% CP) with a daily topdress of 0 or 450 mg/d M. Biopsies were obtained on d 7 (± 4) postpartum and liver slices used in an in vitro incubation system to determine liver capacity to convert [1-^{14}C]propionate to CO_2 and glucose. Interactions of starch × M were not significant. There was no effect of starch or M treatment on liver capacity to oxidize propionate to CO_2, and effects of starch on gluconeogenesis were not significant. Cows fed M tended (P=0.14) to have greater capacity to convert propionate to glucose than controls. Primiparous animals had greater capacity for oxidation and gluconeogenesis from propionate than multiparous animals (P = 0.04 and 0.01, respectively). In vitro incubation with insulin (10 n*M*) tended to decrease propionate oxidation to CO_2 (P = 0.10) but had no effect on propionate conversion to glucose. The ratio of rates of conversion of radiolabeled propionate to glucose and CO_2 provide an index of the efficiency of propionate utilization for gluconeogenesis; M supplementation increased the ratio of glucose to CO_2 (P = 0.05), which indicates that cows fed M have a greater propensity to convert propionate to glucose. Overall, primiparous cows had greater capacity to both oxidize and convert propionate to glucose than did multiparous cows and M increased hepatic capacity to convert propionate to glucose relative to CO_2.

Key Words: early lactation, gluconeogenesis, monensin

T130 Effect of postruminal propionate infusion on expression of key genes for gluconeogenesis in the liver of lactating dairy cows. Q. Zhang*, H. A. Tucker, K. E. Boesche, J. E. Sibray, S. L. Koser, and S. S. Donkin, *Purdue University, West Lafayette, IN.*

Propionate is the major precursor for gluconeogenesis in ruminants. Glucose demand during lactation is met through increased availability of gluconeogenic precursors, including propionate, as a consequence of greater feed intake. This experiment evaluated the effect of increased postruminal propionate supply on hepatic expression of phosphoenolpyruvate carboxykinase-cytosolic (PEPCK-C), phophoenolpyruvate carboxykinase – mitochondria (PEPCK-M) and glucose-6-phosphatase (G6P), three rate-limiting enzymes for gluconeogenesis in bovine liver. Six multiparous mid-lactation Holstein cows were utilized in a replicated 3 × 3 Latin square. Periods consisted of a 6-d acclimation and washout phase followed by 8-h infusion. Solutions delivered 1.67 mol propionate, 0.84 mol glucose, or an equivalent volume of water over 8-h period. On the day of infusion, blood samples were collected at 0,2,4,6, and 8-h relative to the start of infusion for blood propionate, glucose, and insulin analysis and liver biopsy samples were collected at the end of infusion for mRNA analysis. Plasma propionate tended to increase at 8-h relative to start of infusion with propionate infusion (0.059 m*M* vs. 0.044 m*M* vs. 0.037 m*M* for propionate, glucose and water, respectively; P = 0.07). Plasma glucose was not affected by treatments (P > 0.1). Serum insulin was increased (P < 0.05) 1.47-fold by glucose and1.74 fold by propionate compared to water infusion. There was a tendency for PEPCK-C expression to differ (P = 0.1) among treatments (1.45 vs. 0.65 vs. 1.33 arbitrary units, for propionate, glucose and water, respectively). Propionate tended to increase PEPCK-C expression compared to isocaloric glucose infusion (P = 0.1). Expression of PEPCK-M and G6P mRNA were not affected by treatments (P > 0.1). These data indicate in vivo effects of propionate to alter hepatic gene expression in mid-lactation dairy cows that is tempered by a commensurate increase in serum insulin concentration.

Key Words: propionate, gluconeogenic gene expression, lactating dairy cow

T131 Regulation of pyruvate carboxylase expression by fatty acid cocktails in Madin-Darby bovine kidney cells. K. E. Boesche*, S. L. Koser, and S. S. Donkin, *Department of Animal Sciences, Purdue University, West Lafayette, IN.*

Pyruvate carboxylase (PC) catalyzes oxaloacetate synthesis, a key reaction for both gluconeogenesis and fatty acid oxidation. Activity of this enzyme is linked to PC mRNA and is increased during feed restriction and transition to lactation, metabolic states when non-esterified fatty acids (NEFA) are elevated in blood. Saturated fatty acids, including C18:0, decrease expression of PC while intracellular signals related to unsaturated fatty acid metabolism act to increase PC expression in Madin-Darby bovine kidney (MDBK) cells. The objective of this study was to determine dominance of control of PC mRNA expression in MDBK cells with copresence of saturated and unsaturated fatty acids. MDBK cells were cultured to 80% confluence and exposed to fatty acid treatments for 24h. Single fatty acid treatments consisted of 1.0 m*M* of either C16:0, C18:0, or C18:3n-3 *cis*. Fatty acid cocktails (1 m*M* total) were supplied as increasing concentrations of C18:3n-3 *cis* (0.25 m*M*, 0.5 m*M*, 0.75 m*M*) combined with decreasing concentrations of either C16:0 (0.75 m*M*, 0.5 m*M*, 0.25 m*M*) or C18:0 (0.75 m*M*, 0.5 m*M*, 0.25 m*M*). Saturated fatty acid treatments of either 1.0 m*M* C16:0 or 1.0 m*M* C18:0 decreased (P < 0.05) PC expression by 72.2% and 92.9%, respectively. Cells exposed to 1.0 m*M* C18:0 had significantly lower (P < 0.05) PC expression when compared to C18:0 treatment combined, at any level, with C18:3n-3 *cis*. While the lowest evaluated concentration (0.25 m*M*) of C18:3n-3 *cis* proved enough to ameliorate PC expression with exposure to 0.75 m*M* C18:0, only the highest inclusion level of C18:3n-3 *cis* (0.75 m*M*) with C16:0 (0.25m*M*) could recover PC expression to levels similar to control. Data indicate that C18:3n-3 *cis* is a more potent alleviator of PC depression caused by C18:0 than similar effects resulting from C16:0 exposure. The activation of PC mRNA by unsaturated fatty acids may play a critical role in setting the capacity for fatty acid oxidation.

Key Words: fatty acid, gluconeogenesis, pyruvate carboxylase

T132 Lying time, lameness and leg injuries on freestall farms in China. Y. Liang*[1,2], Y. Wang[3], G. I. Zanton[2], M. A. Vazquez-Anon[2], D. M. Weary[1], and M. A. G. von Keyserlingk[1], *[1]Animal Welfare Program, University of British Columbia, Vancouver, Canada, [2]Novus International Inc., St. Louis, MO, [3]Novus International Inc., China.*

The aim of the study was to describe variation in lying time, lameness, and leg injuries among Holstein herds in two prominent dairy regions in China: Beijing (14 herds) and Huadong (25 herds). One trained individual evaluated one group of high production cows in each of the herds. Cows were gait scored using a 5-point Numerical Rating System where 1 and 2 are considered non-lame, ≥3 clinically lame, and ≥4 severely lame. Hock injuries were scored on a scale of 1 to 5 (1=healthy and 5=severe swelling or severe lesion). Knee injuries were based on a 1 to 3 scale (1=healthy, 2=hair loss and 3=evident swelling). The analyses were descriptive and all results are presented as means ± standard deviation. Herd size in the Beijing region averaged 807 ± 701 milking cows (range 184 to 2444) and 1737 ± 2115 cows (range 160 to 8873) in Huadong. Lying times and lameness were similar in the two regions: lying time averaged 11.3 ± 0.54 h/d (range 10.3 to 12.3 h/d) and 11.4 ± 1.01 h/d (range 9.1 to 13.1 h/d); prevalence of clinical lameness averaged 29 ± 10.5% (range 15% to 46%) and 29 ± 13.7% (range and 6% to 51%); and prevalence of severe lameness averaged 10 ± 7.7% and 8 ± 6.0% in Beijing and Huadong, respectively. Knee and hock injuries were less prevalent in Beijing versus Huadong: prevalence of swollen knees averaged 4 ± 4.1% versus 16 ± 9.2%; prevalence of hock injuries (≥2) averaged 37 ± 11.3% and 41 ± 24.6; and prevalence of severe injuries (score ≥4) averaged 1 ± 1.2% and 7 ± 10.7% in Beijing and Huadong, respectively. Previous work on North American farms has demonstrated that the use of deep bedding is highly protective for leg injuries. We therefore suggest that the lower rates of knee and hock injuries in Beijing were likely associated with most farms in this region using deep-bedded stalls, but more work is now required to identify farm management factors associated with injuries and other indicators of cow comfort on farms in these regions of China.

Key Words: lying time, hock injuries, knee injuries

T133 Colostrum replacer feeding regimen, addition of sodium bicarbonate, and milk replacer: The combined effects on absorptive efficiency of IgG in neonatal calves. R. G. Cabral*[1], M. A. Cabral[1], C. E. Chapman[1], D. M. Haines[2], and P. S. Erickson[1], *[1]University of New Hampshire, Durham, [2]Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, SK, Canada.*

Eighty Holstein and Holstein cross dairy calves were blocked by birth date and randomly assigned to 1 of 8 treatments within each block. The objective of this experiment was to examine the effect of colostrum replacer (CR) feeding regimen, supplementation of CR with sodium bicarbonate ($NaHCO_3$), and provision of a milk replacer (MR) feeding on IgG absorption. Calves were offered CR containing 184.5 g/L of IgG in either 1 feeding at 0 h (within 30 minutes of birth), with or without 30 g of $NaHCO_3$, with or without a feeding of MR at 6 h, or 2 feedings of CR (123 g/L of IgG at 0 h with or without 20 g of $NaHCO_3$ and 61.5 g/L at 6 h with or without 10 g of $NaHCO_3$), with or without a MR feeding at 12 h. Blood samples were obtained at 0, 6, 12, 18, and 24 h after birth and were analyzed for IgG via radial immunoassay. Results indicated that CR feeding regimen, MR treatments, and the interactions CR*Na, CR*MR, and CR*Na*MR were not significant for 24 h serum IgG, apparent efficiency of absorption (AEA), or area under the curve (AUC). Serum IgG at 24 h ($P < 0.0001$), AUC ($P < 0.0001$) and AEA (P = 0.0002) were decreased with addition of $NaHCO_3$ compared to calves not receiving $NaHCO_3$ (12.6 g/L vs. 16.08 g/L; 236.67 g/L·h vs. 314.50 g/l·h; and 24.8% vs. 31.07% respectively). There was a trend ($P = 0.09$) for a Na*MR interaction in reference to AUC indicating that feeding MR without $NaHCO_3$ supplementation (295.2 g/L·h) or not feeding MR with $NaHCO_3$ (229.2 g/L·h) is not beneficial compared to feeding neither MR nor $NaHCO_3$ (333.8 g/L·h), or feeding MR with $NaHCO_3$ (244.1 g/L·h). These data indicate that supplementation of CR with $NaHCO_3$ is not beneficial to IgG absorption and feeding MR within 6 h of CR feeding does not impact IgG absorption.

Key Words: colostrum replacer, sodium bicarbonate, milk replacer

T134 Serotonin (5-HT) increases gene expression of fatty acid enzymes and activates pAMPK in the mammary gland of transition rats. J. Laporta*, S. Weaver, C. Cronick, K. E. Merriman, T. L. Peters, and L. L. Hernandez, *University of Wisconsin-Madison, Madison.*

Fatty acids are fundamental to energy production and storage, cellular structure and are critical to the synthesis of milk fat. The role of serotonin (5-HT) in regulating milk protein gene expression in the mammary gland is established, however little is known regarding 5-HT's role in fatty acid metabolism in the mammary gland. Serotonin is synthesized in a two-step reaction from the amino acid L-tryptophan (L-TRP). The rate-limiting step is catalyzed by tryptophan hydroxylase (TPH1) to form 5-hydroxytryptophan (5-HTP), and 5-HTP is then converted directly into 5-HT. To explore the role of 5-HT in mammary gland fatty acid synthesis and energy expenditure during the transition period (9 d pre to 9 d postpartum) we fed 30 rats (n=15 per diet) 2 diets: (I) control (CON) and (II) 5-HTP (0.2% total diet). Blood was collected on d 9 of lactation to measure circulating 5-HT. Total RNA was isolated from mammary gland tissues collected on d 9 of lactation to measure the expression of peroxisome proliferator-activated receptor gamma (PPARG), leptin (LEP) and fatty acid synthase (FASN) by real time RT-PCR. Additionally, total protein was extracted from mammary glands to measure phosphorylated 5′ AMP-activated protein kinase (pAMPK, which regulates metabolic energy balance and metabolism of glucose and fatty acids) by western blot, and 5-HT by ELISA. Feeding 5-HTP effectively increased serum 5-HT concentrations over time ($P < 0.0003$). Mammary gland gene expression of PPARG, LEP and FASN was markedly up-regulated in the 5-HTP fed dams on d 9 of lactation ($P < 0.034$). Additionally, 5-HT concentrations were increased in the mammary gland of 5-HTP fed rats compared to CON ($P = 0.0083$). Finally, 5-HTP fed dams had significantly increased pAMPK compared to CON animals ($P = 0.006$). These results suggest the possibility that 5-HT is involved in regulating fatty acid and energy metabolism during the transition from pregnancy to lactation in the mammary gland of rats. However, the physiological significance and the mechanism of action regulating these findings needs to be further investigated.

Key Words: fatty acid, serotonin, lactation

T135 Effect of induced subclinical hypocalcemia (SCH) on physiological parameters and function of immune cells in dairy cows. N. Martinez*, L. D. P. Sinedino, R. S. Bisinotto, E. S. Ribeiro, G. C. Gomes, F. S. Lima, L. F. Greco, J. P. Driver, C. A. Risco, and J. E. P. Santos, *University of Florida, Gainesville.*

Objectives were to create a model to induce SCH [blood ionized calcium (Ca^{2+}) NC, 0.9% NaCl i.v. plus 43 g of oral Ca at 0 and 12 h) or an induced SCH (SCHI, 5% EGTA at pH 7.4, i.v.) in a crossover design. The infusion lasted 24 h. The sequence of treatments was either NC-SCHI or SCHI-NC. A 6-d period between treatment administrations was used to minimize carryover effects. Heart and respiratory rates, rectal temperature, and rumen contractions were measured during and after infusion at 6 to 12-h intervals. Ionized Ca, K, Mg, and blood pH were evaluated

at 0 h, hourly during the infusion period, and at 24, 48 and 72 h after the infusion to monitor Ca^{2+}. In addition, DMI, neutrophil function, and white blood cell differential count (WBC) were evaluated at 0, 24, 48 and 72 h after treatments. Data were analyzed using PROC GLIMMIX of SAS. Infusion of a 5% EGTA solution successfully induced SCH in SCHI cows (0.78±0.01 vs. 1.27±0.01 mM Ca^{2+}) during 23 h. There were no differences in heart and respiratory rates, rectal temperature, and WBC between SCHI and NC cows. On the infusion day, SCHI cows had lower ($P < 0.01$) K (2.92 ± 0.07 vs. 3.47 ± 0.07 m*M*) and higher ($P < 0.01$) Mg (0.94 ± 0.03 vs. 0.68 ± 0.03 m*M*) in blood. The decrease in blood Mg was likely caused by supplemental oral Ca in NC. SCHI cows had reduced ($P < 0.01$) DMI on the day of infusion (5.1 vs. 10.0 kg/d) and decreased ($P = 0.01$) rumen contractions every 2 min (1.7 vs. 2.7) in the second half of the infusion period. Cows in SCHI had a reduced ($P < 0.01$) percent of neutrophils with phagocytosis (79.9 ± 8.8 vs. 119.2 ± 13.0, % baseline) and oxidative burst (80.2 ± 17.9 vs. 140.3 ± 17.9, % baseline), evident at 24 h after the end of the infusion. A 5% EGTA solution successfully induced SCH in dairy cows. Subclinical hypocalcemia reduces DMI, rumen contractions and neutrophil function and it is suggested to be linked with peripartum immunosuppression.

Key Words: dairy cow, neutrophil, subclinical hypocalcemia

T136 Modification of AOAC method to measure total starch in animal feeds. S. D. Ranathunga*, J. L. Anderson, K. J. Herrick, and K. F. Kalscheur, *South Dakota State University, Brookings.*

Various methods are currently available to measure total starch in animal feeds. The ease of use, time spent on analysis, and cost per assay may vary between methods. The AOAC method 996.11 (1996) has been recognized as an accurate, repeatable, and efficient method to measure total starch. The objective of this study was to determine if an alternative starch method would be more economical and alleviate technical difficulties associated with the AOAC method. Modification of the AOAC method was done by combining the AOAC method with the acetate buffer method by M. B. Hall (2009) and using alpha-amylase (1200 liquefon units/assay) and amyloglucosidase (400 units/assay) concentrations from different sources (Ankom Technology Inc. and Sigma-Aldrich Inc.). The modified method was performed in sealable vessels. Nine samples including pure corn starch, TMR, concentrate mixture, alfalfa, corn silage, dried distillers grains with solubles, ground corn, dried fecal, and dried rumen samples were analyzed using the two methods. Two technicians performed two runs of each method. All samples were analyzed in duplicate within each run. The effect of method, technician, and run was analyzed using Tukey's test. Starch concentrations of the analyzed samples were not different between the two methods (pure corn starch = 101, TMR = 27.9, concentrate mixture = 33.3, alfalfa = 2.62, corn silage = 22.7, dried distillers grains with solubles = 4.51, ground corn = 72.7, fecal sample = 2.2 and rumen sample = 1.67% with SE of 0.15%). The average starch concentration for all samples (29.8% with ± 0.07% SE) was not affected by method ($P = 0.24$), technician ($P = 0.49$), nor run ($P = 0.59$). The average time spent to analyze 18 samples was around 3 h for both methods. Average cost per sample assayed with the modified method was $0.76 compared with $3.30 for the AOAC method. Therefore, the modified starch assay could be considered a more cost effective and less technically difficult method compared with the AOAC starch method.

Key Words: AOAC method 996.11, starch, feed analysis

T137 Concentrations of luteinizing hormone and ovulatory responses in dairy cows before timed AI. S. L. Pulley*[1], D. H. Keisler[2], and J. S. Stevenson[1], *[1]Kansas State University, Manhattan, [2]University of Missouri, Columbia.*

Our objective was to determine the incidence of spontaneous and GnRH-induced LH surges and ovulatory responses in lactating dairy cows enrolled in a timed AI (TAI) program. Cows were assigned randomly at calving to 2 treatments: 1) Pre10 (n = 37): two 25-mg injections of $PGF_{2\alpha}$ (PG-1 and PG-2) 14 d apart (Presynch); or 2) PG3G (n = 33): one 25-mg injection of PG 3 d before 100 µg GnRH (G-1), with a PG injection administered at the same time as PG-2. Cows were enrolled in a TAI protocol 10 d after PG-2 (Ovsynch; injection of GnRH 7 d before [G-2] and 56 or 72 h after [G-3] PG-3 with TAI at 72 h after PG-3). Blood was collected to determine LH at: (1) G-1: 0 to 80 h after PG-2 and hourly from 72 to 78 h (G-1 at 72 h); (2) G-2: 0 to 6 h after G-2; and (3) G-3: 0 to 80 h after PG-3 and hourly from 56 to 62 or 72 to 78 h for cows injected with GnRH (G-3) at 56 or 72 h after PG-3. Ovaries were scanned before injections and pregnancy per TAI (P/TAI) was diagnosed 31 d post-TAI by ultrasonography. The PG3G cows had increased ($P < 0.01$) incidence of induced LH surges in response to G-1 than Pre10 cows (75.8 vs. 0%). Proportion of cows with spontaneous (43.2 vs. 24.2%) or no LH surge (56.8 vs. 0%) was greater ($P < 0.01$) in Pre-10 than PG3G cows, respectively. An induced LH surge occurred in all cows at G-2 regardless of treatment. More ($P < 0.05$) cows had induced LH surges after G-3 at 56 (100%) than after 72 h (88.6%). Ovulation rate at G-1 was greater ($P = 0.003$) in PG3G (90.9%) than Pre10 (59.5%) cows, but did not differ at G-2 (PG3G = 51.5%; Pre10 = 61.2%). At G-3, ovulation was more ($P < 0.05$) likely in Pre10 than PG3G cows (94.6 vs. 84.9%) and after G-3 at 56 than 72 h (94.3 vs. 85.7%). The P/TAI for PG3G vs. Pre10 (56.7 vs. 37.8%) and for 56- vs. 72-h G-3 injections (54.5 vs. 38.2%) did not differ. We conclude that more PG3G cows had LH surges at G-1 compared with Pre10. Consistent with our earlier report, PG3G cows had increased ovulation rates at G-1 and greater ($P = 0.069$) progesterone at G-2 (4.1 vs. 2.7 ± 0.5 ng/mL) than Pre10 cows.

Key Words: Presynch, LH surge, pregnancy

T138 Discovery of genomic markers for gut health in dairy calves. G. Liang*[1], N. Malmuthuge[1], H. Bao[1], X. Sun[1], P. Stothard[1], T. B. McFadden[2], P. J. Griebel[3], and L. L. Guan[1], *[1]Department of Agricultural, Food and Nutritional Science, Edmonton, AB, Canada, [2]Divison of Animal Sciences, University of Missouri, Columbia, [3]Vaccine and Infectious Disease Organization, University of Saskatchewan, Saskatoon, SK, Canada.*

Enteric diseases significantly impair the health and productivity of both beef and dairy cattle. Moreover, it is well known that calf gut health is a critical determinant of a cow's lifelong performance and efficiency. MicroRNAs (miRNAs) are a large family of small, non-coding RNAs that have emerged as key regulators of gene expression involved in numerous biological processes including innate and adaptive immunity. We hypothesized that miRNAs regulate development of gut immune function and innate immune responses to enteric pathogens in pre-weaned dairy calves. In this research, expression profiles of miRNA and their potential target genes in the gut were characterized using next-generation sequencing analysis of small intestine tissues (ileum, mid-jejunum and distal-jejunum) collected from healthy calves at 1 week (n = 6), 3 week (n = 6), or 6 week (n = 6) postpartum. In total, 103,452,564 high-quality small RNA tags were obtained, of which 75,903,402 tags were mapped to a known bovine miRNA database (miRBase 19). The results showed that 495 known miRNAs were identified in distal-jejunum, 472 in mid-jejunum and 455 in ileum. Moreover, 141 candidate novel miRNAs were also detected from these tissues. Further analysis revealed that the expression pattern of some miRNAs known to be involved in regulation of immune

functions differed between calves of different ages and among different regions of the small intestine. For example, miRNAs of the bta-miR-29 and bta-miR-146 families, which may regulate immune responses and TLR signaling, respectively, were differentially expressed across the three ages. In addition, members of the bta-miR-10 and bta-miR-196 families, which may play crucial roles in the development of the intestinal mucosal immune system of dairy calves by regulating intercellular junctions, were differentially expressed. In conclusion, we have identified several miRNAs that were differentially expressed during the early life of dairy calves. These miRNAs may play a role in development of the gut immune system and therefore may be useful as molecular diagnostic markers to predict host response and susceptibility to enteric infections and diseases.

Key Words: dairy calf, gut health, microRNA

T139 Effects of an adjustable fan and mister cooling system with different motor size and water output on core body temperature (CBT) of lactating dairy cows. S. D. Anderson*[1], J. D. Allen[2], R. J. Collier[1], and J. F. Smith[1], *[1]The University of Arizona, Tucson, [2]Northwest Missouri State University, Maryville.*

Evaporative cooling in arid environments is effective in reducing heat stress on dairy cows during periods of high temperature. The FlipFan Dairy Cooling System (FLFN) is an adjustable fan and mister cooling system which is available in either 0.50 HP (372.85 W) or 0.75 HP (559.27 W) versions. In this study, water output of 0.50 HP FLFN ranged from 0.42 to 1.26 L/min per fan under 1,379 to 1,551 kPa of pressure, and 0.75 HP FLFN had water output of 0.40 to 3.14 L/min per fan under 689 to 6895 kPa of pressure. Misters in both systems automatically turned off when relative humidity (RH) exceeded 65%. Our objective was to determine if FLFN operated at 0.75 HP was more effective than 0.50 HP FLFN at lowering CBT of multiparous, lactating Holstein cows (46.7 ± 0.75 kg/milk per d, 143 ± 6 DIM) on a commercial dairy in Arizona. Twenty four cows were measured continuously in a switchback design for 8 d. Cows were housed in 1 of 2 pens with 12 study cows/pen. Pen served as the experimental unit. The study consisted of 4 2-d periods in which the first day served as an acclimation period, whereas data collected on the second day was used for statistical analysis. All cows were subjected to each cooling treatment twice. Mean daily dry-bulb temperature was 30.0 ± 0.80°C and ranged from 24.0°C to 36.3°C. Mean daily RH was 55.5 ± 2.16% and ranged from 39.9% to 73.2%. Mean daily temperature-humidity index (THI) was 78.8 ± 0.78 and ranged from 72.7 to 84.3. Mean 24-h CBT was lower ($P < 0.001$) for cows cooled by 0.75 HP FLFN compared to 0.50 HP FLFN (38.69°C vs. 38.84°C). Furthermore, mean hourly CBT was lower ($P < 0.001$) at all times of day for cows cooled by 0.75 HP FLFN. No treatment × time interaction was detected ($P = 0.3219$). Results suggest that 0.75 HP FLFN has greater cooling capacity as measured by lower CBT. However, additional work will be required to determine what situations warrant the additional electrical and water cost to operate the 0.75 HP FLFN. There may be different conclusions for different climates, stage of lactation, and parity.

Key Words: heat stress, adjustable fan, water output

T140 The effect of induced ascites syndrome on blood gas parameters and internal organ weights in broilers. M. Naghous[1], A. Pakdel[2], R. V. Torshizi[3], and H. Bazdidi*[1], *[1]Dept. of Animal Science, Faculty of Agriculture, Birjand University, Birjand, Iran, [2]Dept. of Animal Science, University College of Agriculture & Natural Resources, University of Tehran, Karaj, Iran, [3]Dept. of Animal Science, Faculty of Agriculture, Tarbiat Modares University, Tehran, Iran.*

In order to evaluate the effects of induced ascites syndrome on blood gas parameters and internal organ weights, 149 male birds and 200 females birds were randomly selected from a commercial broiler strain and rearing under two normal and induced ascites condition. Several traits including body weight gain, feed intake (FI), food conversion ratio (FCR) between 23 and 54 d of age were evaluated. Moreover the blood gas parameters and hematocrit value were evaluated at 21, 35 and 54 d of age. At the end of experiment all the birds were slaughtered and the internal organs like liver, heart and spleen were inspected. There was no significant difference between two groups based on FCR and Body weight gain, while in the broiler males, FI was significantly different ($P < 0.05$). The result showed that liver and spleen weights were not significant different between two treatment in both sex. Right ventricle to total ventricle ratio (RATIO) of the male birds in the induced ascites treatment (T2), was higher than that of male birds in the control treatment (T1) ($P < 0.01$). However RATIO of females was not significantly different. The blood gas parameters including PH, $pvCO_2$, total CO_2, and pvO_2, were not significantly different between both groups of T1 and T2 in both sex However the O_2 saturation at 35 and 54 d of age in T1 group was higher than that of T2 group ($P < 0.05$). The results of current study indicated that O_2 saturation could be a useful measure for predicting ascites syndrome.

Key Words: ascites syndrome, blood gas parameter, broiler

T141 The relationship between growth curve and ascites syndrome in broilers. M. Naghous[1], A. Pakdel[2], R. V. Torshizi[3], and H. Bazdidi*[1], *[1]Dept. of Animal Science, Faculty of Agriculture, Birjand University, Birjand, Iran, [2]Dept. of Animal Science, University college of Agriculture & Natural Resources, University of Tehran, Karaj, Iran, [3]Dept. of Animal Science, Faculty of Agriculture, Tarbiat Modares University, Tehran, Iran.*

Ascites syndrome is a metabolic disorder in broilers. Birds that selected for higher body weight (BW) and lower feed conversion ratio (FCR) are more susceptible to this syndrome. The aim of present study was to investigate the relationship between growth curve and ascites syndrome in broilers. The BW at 1, 4, 7, 10, 14, 17, 21, 28, 35, 42, 49 and 54 d of age were measured on 299 male birds kept under normal (T1) and more susceptible condition to ascites syndrome (T2). The birds were chosen randomly from two sire lines A & B of a commercial broiler strain. These lines (A & B) were primarily selected for lower FCR and higher BW, respectively. Mortality in the induced ascites condition (T2) was higher than normal condition (T1) in both lines (mean 5.2% vs. 21.8%). Moreover right ventricle to total ventricle ratio of the induced T2 was higher than that of T1 ($P < 0.01$). The results of growth curve parameters in the sire line A showed that mature index and age at the inflection point between two treatments were significantly different ($P < 0.05$), but hatch weight, mature weight and weight at the inflection point weren't significantly different. The birds in T2 reached to the age at inflection point 1.55 d earlier than birds in T1, but weight at inflection point was similar in both treatments. The growth rate in T2 was higher than that of T1 until 35 d of age, but later on the growth rate was lower in T2 in compared to T1 ($P < 0.05$). Growth curve parameters in the sire line B showed that hatch weight, mature index, mature weight, weight and age at the inflection point between two treatments weren't significantly different. The growth rate in T2 was higher than that of T1 until 35 d of age, but later on the growth rate was lower in T2 in compared to T1. The results of current study indicated that induced ascites condition changed linear phase of growth in the male broiler chickens with lower FCR.

Key Words: ascites, low FCR, high body weight

T142 Performance, gut morphology and meat quality characteristics of broilers fed diets with probiotics supplementation. M. D. Olumide*, O. A. Adebiyi, and D. E. Bamisaye, *University of Ibadan, Ibadan, Oyo State, Nigeria.*

Large amounts of antibiotics have been used to control diseases and improve performance in livestock. However, due to growing concerns about antibiotics resistance and drug residues on carcass meat, bans had been placed on antibiotic growth promoters in many countries in the world. There is an increasing interest in finding alternatives to these antibiotics in poultry production. One alternative is beneficial bacterial-derived probiotics feed supplements. A total of 150 day-old Arbor Acre broiler chicks were distributed randomly into 5 treatments with 3 replicates (10 birds/replicate) in a completely randomized design. Treatments include: Control (0.00 g/kg), T1 (0.02 g/kg), T2 (0.04 g/kg), T3 (0.06/kg), and T4 (0.08 g/kg) of probiotics feed supplement. Data on performance, carcass quality and gut morphology were obtained. Data taken were subjected to statistical ANOVA procedure of SAS, 2010. No significant ($P > 0.05$) difference was observed in the final weight gain for all the birds on the respective treatment. Meat quality characteristics revealed significant ($P < 0.05$) differences in cooking loss, thermal shortening, cold shortening and water holding capacity of meat cuts from breast, drumstick and thigh areas. Birds fed the T4 diet had the lowest mean values for cooking losses (16.23%), thermal shortening (20.17%), cold shortening (0.20%) and water holding capacity (47.00%) for the thigh muscle when compared with birds on other treatments. Birds fed diet supplemented with 0.08 g/kg probiotics (T4) had a significant villus height and crypt depth compared to the others. Therefore, it can be concluded from this study that supplementing diets of broiler birds with 0.08 g/kg probiotics improves significantly the performance, meat quality and improve nutrient absorption of broilers.

Key Words: probiotic, broiler performance, gut morphology

T143 Evaluating the effectiveness of *Bacillus subtilis* (DMF) and yeast cell wall (YCW) in the performance of broiler chickens. M. Aronovich*[2], L. A. M. Keller[1], J. R. Sartori[3], J. E. Butolo[5], and A. N. Andrade[4], *[1]University Federal Rural of Rio de Janeiro (UFRRJ), Seropédica, RJ, Brazil, [2]Agricultural Development Company of the Rio de Janeiro State (PESAGRO), Niteroi, RJ, Brazil, [3]Universidade Estadual de São Paulo (UNESP), Botucatu, SP, Brazil, [4]Lesaffre Feed Additives (SAF), Rio de Janeiro, RJ, Brazil, [5]JEB Instituto de Biociências, São Paulo, SP, Brazil.*

Probiotics are live microorganisms that may confer a health benefit leading to increased performance. Lactic acid bacteria, bifidobacteria and certain yeasts are the most common types of microorganisms used. The functional capacity of the digestive tract of broilers during the first weeks of life can be considered a factor possible limiting to health and productivity. The focus of this study was determine if the use of *B. subtilis* and yeast cell

wall (Safmannan) offer benefits in production compared to antibiotic-based growth promoters (Virginiamycin). For this study 3,600 day-old male birds (Cobb) were acquired and randomly distributed in 5 treatments of 70 experimental units: Basal Ration (negative control); Basal Ration (positive control with growth promoter Virginiamycin-10g/ton); Basal Ration with *B. subtilis*-2g/ton; Basal Ration with *B. subtilis*-4g/ton; Basal Ration with Safmannan-500g/ton. Birds were observe daily and evaluated at d 0 (start), 21, 35 and 42 of treatment. The intestines of euthanized birds were collected and sectioned (duodenum, jejunum and ileum) for histopathological evaluation. All results were subjected to ANOVA with further tests of differences using Tukey analysis. Mean values for weight, weight gain, feed consumption, feed efficiency and mortality for treatment were not different from control values though tendencies towards reduced mortality were present for bacterial probiotics (Table 1). The data suggest that live culture *B. subtilis* probiotic treatment may be more beneficial towards reduced mortality than other tested options though more study is needed.

Table 1. Mean weight (MW), weight gain (WG), mean of feed consumption, feed conversion and mortality during the experimental period of 0 to 21 days

Treatment	MW and WG/ bird (kg)		Average consumption of feed (kg)	Feed conversion	Mortality (%)
T1- Negative Control	0.768	0.720	1.141	1.582	0.29
T2- Positive Control	0.773	0.725	1.144	1.574	0.57
T3- B. subtilis (2g/ton)	0.765	0.717	1.143	1.593	0.29
T4- B. subtilis (4g/ton)	0.760	0.713	1.142	1.602	0.14
T5- Safmannan (500g/ton)	0.780	0.732	1.142	1.556	0.49
P-value	0.0795	0.0759	0.0935	0.0755	0.0591

Key Words: *Bacillus subtilis*, *Saccharomyces cerevisiae*, food additive

T144 In vitro anthelmintic activity of crude aqueous extracts of *Pithecellobium dulce* and *Lysiloma acapulcensis* againts gastrointestinal nematodes in small ruminants. A. Olmedo[1], R. Rojo*[1], J. Arece[3], A. Salem[2], E. Morales[2], F. Aviles[1], J. Hernández[1], B. Albarrán[1], and F. Vázquez[1], *[1]Centro Universitario UAEM Temascaltepec, Temascaltepec, Estado de México, México, [2]Facultad de Medicina Veterinaria y Zootecnia, UAEM, Toluca, Estado de México, México, [3]Estación experimental Indio Hatuey, Central España Republicana, Matanzas, Cuba.*

An experiment was conducted to evaluate the effect two lyophilized aqueous extract of tree leaves of *Lysiloma acapulcensis* and *Phitecellobium dulce* on an in vitro assessment of hatching eggs, larval development and migration of gastrointestinal nematodes of small ruminants. Treatments were extracts from both species at different concentrations (0, 12.5, 25.0 and 50.0 mg/mL) and albendazole and levamisole were used as positive control (1%). A general lineal model test was used to determine the dose effect of each plant extract in the assays. The extracts of *L. acapulcensis*, compared with extracts of *P. dulce* showed better inhibition effect ($P < 0.05$) on the hatching of eggs (Table 1). Larval development in both extracts showed larvicidal effect ($P < 0.05$) on all larvae exposed to different doses of the extract. In the larval migration assay, we found a similar effect with levamisole doses of 25 and 50 mg/mL of the extract of *L. acapulcensis*. The extract of *P. dulce* presented a lower larvicidal effect ($P < 0.05$) of levamisole and the extract of *L. acapulcensis*. Aqueous extracts of both species have antiparasitic effect in small ruminants, and could be used as biological alternative to control gastrointestinal nematodes in sheep and goats under subtropical conditions.

Table 1. Mean inhibition (%) of egg hatch, larval development and migration of gastrointestinal nematodes by *L. acapulcensis* (LA) and *P. dulce* (PD) aqueous extracts

Treatment[1]	Eggs hatching	Larval development	Larval migration
PBS	96.68^{a}	86.38^{b}	79.31^{a}
LEV1.25			4.64^{gf}
LEV2.50			6.67^{ef}
LEV5.0			2.94^{g}
ALBZ	30.50^{e}	1.28^{c}	
DMSO	68.12^{b}	100.00^{a}	
LA 1.25	38.01^{de}	0.00^{c}	12.04^{cd}
LA2.50	32.58^{e}	0.00^{c}	8.98^{de}
LA5.00	47.40^{cde}	0.00^{c}	9.19^{de}
PD1.25	62.73^{bc}	0.00^{c}	13.95^{bc}
PD2.50	59.60^{bc}	0.00^{c}	11.96^{cd}
PD5.00	56.32^{bcd}	1.27^{c}	16.11^{b}
SEM	4.56	1.77	0.76

$^{a–e}$Different letters in the same column indicate significant difference ($P < 0.05$) between means.
[1]LEV = levamisole, ABZ = albendazole 1%; DMSO = dimethyl sulfoxide; LA = *Lysiloma acapulcensis*; PD = *Phitecellobium dulce*.

Key Words: biological control, nematode, small ruminant

T145 Anthelmintic and immunomodulating effects of *Moringa olifera* extracts in goats. M. Worku*, K. Gyenai, H. Ismael, and J. Reddy, *North Carolina Agricultural and Technical State University, Greensboro.*

Gastrointestinal parasites pose a serious threat to the US goat industry due to inefficacy of existing anthelmintic drugs. Alternative anthelmintics are being sought from plants such as *Moringa oleifera* (moringa). The objective of this study was to evaluate the effect of aqueous extracts of dried moringa leaves on adult Boer goats infected with gastrointestinal parasites. Following initial screening for infection goats were assigned to three groups of five each (n = 15). Powdered moringa leaves were soaked in hot or cold water with stirring. Sterile filtered extracts were prepared. Goats were drenched daily with 10 ML of the hot (Treatment I) or cold extract (Treatment II) daily for a 4 week period, a control group of five age matched goats received sterile water (Treatment III). Body weight, FAMACHA score, packed cell volume (PCV), white blood differential count (WBC), total white blood cell count (TWBC) and *Haemonchus* and coccidia fecal egg counts were determined once a week, for a 4 week period. Serum was evaluated for 8 pro-inflammatory cytokines using a commercial ELISA(Sygnosis). There was no treatment effect on coccidia egg counts, FAMACHA score, and PCV or body weight. Moringa treatment increased mononuclear cells and decreased *Haemonchus* eggs per gram feces. The hot extract had a greater anthelmintic effect than the cold extract and higher TWBC ($P < 0.05$). The hot extract increased and the cold extract decreased cytokine concentrations compared to controls. Aqueous extracts from moringa affect cell-mediated immunity in goats and may aid in the reduction of parasite burden in a species specific manner.

Key Words: goat, moringa, anthelmintic

T146 Sericea lespedeza diets modulate gene expression and rumen microbial diversity in goats. A. Abdalla, M. Worku*, H. Mukhtar, and N. Whitley, *North Carolina Agricultural and Technical State University, Greensboro.*

Sericea lespedeza (SL) is considered high-quality, low input forage that suppresses gastro-intestinal parasites in goats. The objective of this study was to evaluate the impact of a diet containing SL on goat rumen micro flora, and on transcription of markers of innate immunity in goats. Samples were collected from 16 Female goats fed a diet of 75% SL (n = 9) and a control group (n = 7), 0% SL. Rumen contents were collected at slaughter and stored at −20°C. Microbial DNA was isolated from frozen rumen samples using the QIAamp DNA kit (Qiagen) to test for the presence of bifidobacteria. General microbial 16S rDNA and targeted genus specific PCR primers for *Bifidobacteria* were used to amplify specific DNA. Amplified samples and DNA markers were separated by electrophoresis on a 2% agarose gel, stained with ethidium bromide and visualized. Denaturing gradient gel electrophoresis of PCR-amplified 16S rRNA gene segments was used to profile microbial populations in rumen fluid. Pooled serum samples collected from goats on SL or non-treated animals were used to determine total protein using the BCA assay. Blood collected in PAX gene tubes was used to isolate RNA. The concentration and purity of RNA were determined using a Nanodrop spectrophotometer. Quantitative real time PCR was used to evaluate expression of cytokine (TNF, IL8, INF and IL-10) and receptor (CD14, TLR 2, TLR4) genes. Data was analyzed by GLM of SAS 9.2. Variations were observed in microbial DGGE profiles indicating an impact of diet. Six animals out of the seven in the control group 0% SL showed *Bifidobacteria* genus specific band of 523 bp. Rumen samples from treated animals did not show any specific bands. SL decreased transcription of all cytokine genes (18% TNF, 24%IL8, 37%INF and 53%IL-10) and increased transcription of receptor genes (12%CD14, 21%TLR2, 6%TLR4). These differential effects of SL on goat innate immunity and rumen microbial diversity need further evaluation to maximize the benefits of feeding SL to goats.

Key Words: diet, sericea lespedeza, immunity

T147 Influence of probiotics on innate immune response in goats. K. Gyenai*[1], M. Worku[1], M. Tajkarimi[2], and S. Ibrahim[1], [1]*North Carolina Agricultural and Technical State University, Greensboro,* [2]*University of North Carolina at Greensboro, Greensboro.*

Immunostimulants can induce nonspecific resistance against parasites. The use of probiotics to control development of animal gastrointestinal parasites could help reduce the risks of infestation or complement anti-parasite treatments. In this study, we investigated the effects of probiotic administration on gastrointestinal parasites coccidia, *Haemonchus contortus* epg and markers of infection. Three month-old male Spanish Boer kid-goats (n=6) were used. A cocktail of probiotic mix including *Bifidobacterium longum* and *Bifidobacterium breve, Lactobacillus acidophilus, Lactobacillus reuteri* and *Lactobacillus rhamnosus* were used. Treatment animals were drenched daily with 10 CUF/ml of probiotic once a day, a control group age matched received sterile water for a 4 week period. Body weight, fecal egg count, FAMACHA scores, packed cell volume (PCV), and white blood cell differential count (WBCDC) was determined once a week, for a 4-wk period. Denaturing gradient gel electrophoresis (DGGE) was used to monitor fecal bacteria using bacteria 16S rDNA primers. Pro-inflammatory cytokines, prostaglandin (PGE) and immunoglobulin E levels in serum were evaluated using commercial ELISAs. Analysis of variance and GLM was used to evaluate differences between probiotic drenched and control. Results showed no significant difference in PCV, body weight, WBCDC, FAMACHA score, PGE and IgE levels between probiotic drenched and control. However, epg were increased significantly ($P < 0.05$) for probiotic drenched 100, 90 and 120% at wk 2, 3 and 4 for *Haemonchus* and 70% for coccidia at week 3 respectively. An increase of 50 to 300% in proinflamatory cytokines was observed for probiotic drenched over control at weeks 2, 3 and 4 with GM-CSF been highest. Results from PCR-DGGE analysis showed increased fecal microbial DNA for probiotic drenched, with no difference in band pattern and staining intensity. Although increase in fecal egg count levels initiated an increase in cytokine levels probiotics had no immunostimulatory effect against coccidia or *Haemonchus*. This study supports the idea that use of probiotics in ruminants may be impacted by lack of microbial retention in the rumen. Further studies on establishment and retention are needed.

Key Words: cytokine, goat, probiotic

T148 Evaluation of the protective effect of pelleted beet pulp as a substitution for ground corn fed to dairy cows during a subacute ruminal acidosis challenge. Y. Guo*, Y. Zou, S. Li, Z. Cao, X. Xu, and Z. Yang, *State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing, China.*

Eight multiparous Holstein dairy cows (568.5±34.7 kg of BW; 164±15 DIM), 4 of them fitted with rumen cannulas, were assigned to the following experimental treatments during 4 successive periods designed: (1) control (W0); (2) TMR containing 10% finely ground wheat (FGW) (W10); (3) TMR containing 20% FGW (W20); and (4) the W20 diet was amended with 10% BP as a replacement for 10% ground corn (BP10). Each period consisted of a 12-d period of adaptation to the diets, followed by 5 d (d 13-17) for sample collection. Average ruminal pH was lower ($P <0.01$) during SARA (W20 treatment) than during the weeks of adaptation (5.94 versus 6.37). The substitution of BP for corn increased the daily mean ruminal pH by 0.11 pH units and the minimum ruminal pH by 0.22 pH units compared with the W20 treatment, and no ruminal pH values <5.6 were found during the BP10 treatment. Ruminal concentrations of total volatile fatty acid, propionate, butyrate, valerate, and isovalerate increased ($P < 0.01$) with the W20 treatment compared with the W0 and W10 treatments. The cows fed the BP10 diet had a higher ($P < 0.01$) molar percentage of acetate and a lower ($P < 0.01$) molar percentage of butyrate compared with the W20 treatment. The diets had no effect on the DMI and the milk yield, but the milk fat percentage, yield, and 3.5% FCM were reduced ($P < 0.01$) in the W20 and BP10 treatments. The cows fed the W20 diet had greater ($P < 0.05$) milk concentrations (g/100 g of FA) of C11:0, C13:0, C15:0, C14:1, C16:1, C17:1, C18:2n6c, C20:3n6, and lower ($P < 0.05$) concentrations of C18:0 compared with cows receiving the W0 diet. These results indicate that an increase in the concentration of odd-chain FA in milk could be a good candidate for the diagnosis of SARA and that the substitution of pelleted BP for ground corn could regulate rumen fermentation patterns and lower the risk of SARA.

Key Words: beet pulp, dairy cow, subacute ruminal acidosis

T149 Milk components predicted by mid-infrared spectrometry as indicators of the udder health status of the dairy cow. C. Bastin*, A. Lainé, and N. Gengler, *University of Liège, Gembloux Agro-Bio Tech, Animal Science Unit, Gembloux, Belgium.*

Mastitis affects milk composition. Hence, early detection of mastitis could be based on indicators present in milk. The objective of

this research was therefore to investigate components predicted by mid-infrared (MIR) analysis of milk as early indicators of the udder health status of the dairy cow. First, mastitis data collected in 26 herds from the Walloon Region of Belgium were merged with test-day data including milk composition data collected as a part of milk recording. Out of 762 mastitis events, 243 were associated with records from a test-day occurring before the infection (from 30 to 50 days before the event) and with records from a test-day occurring during the infection (from 10 days before to 10 days after the event). Milk components investigated were somatic cell score (SCS), somatic cell count (SCC), titratable acidity recorded as Dornic degree and the content in milk of fat, protein, urea, lactose, lactoferrin, minerals (Na, Ca, P, Mg, K), and 17 individual and groups of fatty acids. Paired t tests were performed on the dataset and showed significant differences before and during mastitis for SCC, SCS, titratable acidity and contents in milk of protein, lactoferrin, K, and lactose. While SCC, SCS, lactoferrin and protein increased during the infection, titratable acidity, K, and lactose decreased. These changes could be related to disease-combating response of the cow, reduced secretory activity and alteration of blood-milk barrier. This preliminary research substantiated the opportunity of using MIR-predicted milk components as mastitis indicators. Future research needs to be conducted on larger dataset and will further investigate the changes in milk composition before, during, and after mastitis. Also, differences in milk composition between cows that have experienced mastitis at least once during the lactation and healthy cows will be examined.

Key Words: mid infrared, mastitis, milk

T150 Gliotoxin occurrence in pre- and postfermented corn, sorghum and wet brewer's grains silage in Sao Paulo, Brazil. L. A. M. Keller*[1,2], M. Aronovich[3], L. R. Cavaglieri[4], and C. A. R. Rosa[1,2], *[1]University Federal Rural of Rio de Janeiro (UFRRJ), Seropédica, RJ, Brazil, [2]Conselho Nacional de Pesquisas Científicas (CNPq), Belo Horizonte, MG, Brazil, [3]Agricultural Development Company of the Rio de Janeiro State (PESAGRO), Niteroi, RJ, Brazil, [4]Universidad Nacional de Río Cuarto (UNRC), Rio Cuarto, Cordoba, Argentina.*

Silage is an important feed source for beef cattle in Brazil is a widespread practice to preserve forages. Poor storage conditions can lead to mold contamination and mycotoxin production. The aim of this study was to determine total fungal counts and the relative density of *A. fumigatus* in silage samples intended for bovines before and after fermentation in farms located in São Paulo State, Brazil, to monitor the natural occurrence of gliotoxin in silage samples (pre- and post-fermentation) and to evaluated the ability of strains of *A. fumigatus* to produce gliotoxin. A total of 300 samples were taken, immediately after opening of the silos (3-5 months) and during the ensiling period of years 2009 to 2012. Fungal counts were done by surface-spread method and the toxigenic ability of isolates strains was evaluated *in vitro* condition. Gliotoxin natural contamination was determined both by TLC and HPLC. All post fermented samples had total number of moulds that exceeded 1×10^4 cfu g^{-1} and *Aspergillus* sp. was the most prevalent genus in all materials evaluated (Table 1). Toxigenic *A. fumigatus* strains isolated produced more than one mycotoxin as shown by TLC. More than 50% of the samples showed contamination with gliotoxin with concentrations that exceeded the levels that are known to induce immunosuppressive and apoptotic effects in cells (level range 0.1 to 32 µg g^{-1}). The present data suggest that care should be taken because gliotoxin and the fungal levels contamination of in feedstuffs. Can could affecting productivity and present a health risk for the herd.

Table 1. Isolation frequency of *Aspergillus* spp. (%) and relative density of *Aspergillus fumigatus* (%)

		Aspergillus spp.		*A. fumigatus*	
Sample	Silage	No. of strains/total	Isolation (%)	No. of strains/total	Relative density (%)
Corn	Prefermented	52/136	38	18/55	32
	Postfermented	203/354	57	69/209	33
Sorghum	Prefermented	18/44	41	12/47	26
	Postfermented	42/84	50	19/44	43
Wet brewer grains	Prefermented	6/22	27	2/7	29
	Postfermented	12/40	30	5/19	26

Key Words: *Aspergillus fumigatus*, mycotoxin production, fungi

T151 Evaluation of β-hydroxybutyrate blood concentration in early lactation in a grazing Jersey herd and its effect on milk yield and reproduction. A. Saborio-Montero* and J. M. Sanchez, *University of Costa Rica, Animal Nutrition Research Center, San Jose, Costa Rica.*

The aim of this study was to analyze blood BHBA concentration in a commercial grazing Jersey herd in Costa Rica (9°55' N, 83°51' W, 2350 m of altitude), measured in 117 cows (24% primiparous, 76% multiparous) at 8±3 and 30±3 days in milk (DIM), to determine its relationship with actual milk yield, milk yield at 305d, open period length, services (AI) per conception and calving interval. The study was carried out from September, 2010 to August, 2012. The close-up period diet was based on grazing 30d regrowth kikuyu grass (*Kikuyuocloa clandestina*) and 4 kg of grain mixture (14% CP, 1.7 Mcal of NEL/kg, 35% starch, 0.2% Ca) per cow daily. The fresh period diet consisted of the same pasture and 4 to 6 kg of a concentrate mixture (20% CP, 1.9 Mcal NEL/kg, 48% starch, 1% Ca). Blood samples were taken from the coccygeal vessels of 117 and 114 cows at 8 ± 3 and 30 ± 3 DIM, respectively. Each sample was analyzed in situ for BHBA concentration using an electrochemical cowside test (Abbott Diabetes Care). Milk yield and reproductive data was registered weekly. Statistical significance was declared at $p<0.05$. BHBA concentration in multiparous cows at 8 ± 3 DIM (0.71 mmol/L) differed ($P < 0.01$) from those at 30 ± 3 DIM (1.03 mmol/L). BHBA concentration at 8 ± 3 DIM in primiparous cows was correlated to open period length (0.554, $P < 0.01$) and services per conception (0.486, $P < 0.05$). A lineal regression ($R^2 = 0.31$, $P < 0.05$) indicated that the open period length with a blood BHBA concentration of zero would be 57 days, and for each 0.1 units of increment in blood BHBA , the open period increases 10.2 days. Another lineal regression ($R^2 = 0.24$, $P < 0.05$) showed that the number of services per conception with a blood BHBA concentration of zero would be on average 1.24 and for each unit of increment in blood BHBA , 2.28 services per conception would be necessary in primiparous cows. No other traits were associated with blood BHBA concentration. Data suggest that elevated blood BHBA concentration at 8 ± 3 DIM may be an early indicator of future reproductive problems in primiparous grazing dairy cows.

Key Words: β-hydroxybutyrate, grazing cows, ketosis

T152 Evaluation of the accuracy of an electronic beta-hydroxybutyrate meter using fresh and stored whole blood and serum from dairy cows. J. L. Gordon*, S. J. LeBlanc, and T. F. Duffield, *University of Guelph, Guelph, Ontario, Canada.*

The purpose of this study was to determine the accuracy of an electronic handheld BHBA meter (Precision Xtra (PX); Abbott) under various

conditions. This meter was previously validated for measurement of BHBA in whole blood in cattle at time of collection, but it is unclear how this device will perform using stored whole blood or serum. Blood was collected into tubes without additive (NA, red top), with EDTA (purple top), or sodium heparin (NaHep, green top) from the same cows at the same time. All BHBA measurements were performed using one meter, test strips from one lot, and by one individual. Blood from all tubes was tested immediately for BHBA at the time of collection. EDTA and NaHep tubes were placed in a refrigerator (4°C) and tested 1 and 7 days after collection. Serum harvested from NA tubes was tested using the PX and submitted to a diagnostic lab to measure BHBA via colorimetric enzymatic reaction (gold standard). Subclinical ketosis (SCK) was defined as BHBA ≥1.2 mmol/L. In 98 samples collected from 80 cows, there was near perfect agreement among measurements taken from all 3 tube types at the time of collection ($R^2 = 0.99$, $P < 0.0001$). The correlation was high between the lab serum BHBA and fresh whole blood meter BHBA at time of collection ($R^2 = 0.98$, $P < 0.0001$) and within tubes tested over time compared to the time of collection of the same tube (EDTA: day+1 $R^2 = 0.97$, $P < 0.0001$, day+7 $R^2 = 0.82$, $P = 0.0003$; NaHep: day+1 $R^2 = 0.97$, $P < 0.0001$, day+7 $R^2 = 0.84$, $P = 0.0002$). The correlation between serum tested on the PX and in the lab was high ($R^2 = 0.98$, $P < 0.0001$). Using a threshold of 1.2 mmol/L, the sensitivity of SCK diagnosis using the PX to measure whole blood at the time of collection, whole blood on day+1 and serum was 93%, 100%, and 100% and the specificity was 96%, 86%, and 74% respectively. This suggests that the PX can be used to accurately measure BHBA in whole blood with various additives, even after storage. The PX is also an accurate tool for diagnosis of SCK in whole blood, but lacks specificity for SCK diagnosis in serum.

Key Words: Precision Xtra, β-hydroxybutyrate, ketosis

T153 Application of sodium chlorate to reduce coliform bacteria in rumen and feces of sheep: 1. Effects on ruminal and fecal coliforms. C. Arzola*[1], R. Copado[1], F. Rodriguez[1], C. Rodriguez-Muela[1], J. Salinas[2], A. Corral[1], O. Ruiz[1], and H. Gaytan[1], *[1]Universidad Autonoma de Chihuahua, Chihuahua, Chih., Mexico, [2]Universidad Autonoma de Tamaulipas, Cd. Victoria, Tamaulipas, Mexico.*

The use of chlorate is being investigated as a non-antibiotic alternative to control certain pathogenic bacteria capable of reducing chlorate to the autocytotoxic compound chlorite, but the lowest effective dose has not yet been clearly established. The objective of this study was to evaluate the efficacy of sodium chlorate administered orally as a regulator of total coliform populations in ewes. A 30% sodium chlorate product or a sodium chloride placebo was administered to twelve lactating Dorper × Blackbelly or Pelibuey crossbred ewes averaging 65 kg body weight. The ewes were acclimated to a balanced diet formulated to meet NRC requirements for production. Ewes were randomly assigned (4/treatment) to each of three treatments administered twice daily by oral gavage for 5 consecutive days: a control (Group 1) consisting of 3 g NaCl/animal/d, a 1× treatment (Group 2) consisting of 0.9 g of $NaClO_3$/animal/d, and a 3× treatment (Group 3) consisting of 2.7 g $NaClO_3$/animal/d; the latter was intended to approximate a lowest known effective dose. Ruminal samples collected by stomach tube and freshly voided fecal samples were collected daily beginning 3 days before treatment initiation and for 6 days thereafter. Contents were cultured quantitatively to enumerate total coliforms. There were no significant differences in colony forming units per gram (cfu) in the feces between treatment groups ($P = 0.832$). There were differences ($P < 0.02$) in ruminal cfu per gram between groups (4.1, 4.3 and 5.0 log10/g contents in Groups 1, 2 and 3, respectively) which tended to increase in cfu from the beginning until the 5th day of treatment ($P < 0.05$). Overall, we did not obtain the expected results with oral administration of $NaClO_3$ with the applied doses. By comparing the trends in coliform populations in the rumen contents in all treatments, there was an increase over the days. The opposite trend occurred in the feces, due mainly to differences among rumen contents and feces in Group 3 treated ewes ($P = 0.06$), suggesting that low chlorate doses used here were suboptimal for the control of coliforms in the posterior gastrointestinal tract.

Key Words: *E. coli*, coliforms, chlorate

T154 Sodium chlorate to reduce the carriage of coliforms in rumen and feces of sheep: 2. Effects on ruminal and fecal bacterial diversity. R. Copado*[1], C. Arzola[1], S. V. R. Epps[2], F. Rodriguez[1], C. Rodriguez-Muela[1], J. Salinas[3], A. Corral[1], O. Ruiz[1], and H. Gaytan[1], *[1]Universidad Autonoma de Chihuahua, Chihuahua, Chih., Mexico, [2]Department of Veterinary Integrative Bioscience, Texas A&M University, College Station, TX, USA., [3]Universidad Autonoma de Tamaulipas, Cd. Victoria, Tamaulipas, Mexico.*

Sodium chlorate is being investigated as a potential intervention to reduce the carriage of certain pathogenic bacteria in food-producing animals, but the minimal effective dose has not yet been clearly established. In this study, the effect of low potentially suboptimal oral chlorate administration to ewes was assessed by comparing the diversity of prominent bacterial populations in their gastrointestinal tract. Twelve lactating Dorper × Blackbelly × Pelibuey crossbred ewes averaging 65 kg body weight were acclimated to a balanced diet formulated to meet NRC production requirements. Ewes were randomly assigned (4/treatment) to receive a control (Group 1) treatment consisting of 3 g NaCl/animal/d, or either of two chlorate treatments (Group 2) or (Group 3) consisting of 0.9 g or 2.7 g $NaClO_3$/animal/d, respectively. Treatments were administered twice daily in equal amounts via oral gavage for 5 consecutive days. Ruminal and fecal samples were collected daily beginning 3 days before and ending 6 days after initiation of treatments and were subjected to denaturing gradient gel electrophoresis of the 16s rRNA gene sequence amplified from total population DNA. For populations of ruminal microbes, between group similarity coefficients varied from 23.0 to 67.5% and from 39.4 to 43.3% during pre-treatment and treatment periods, respectively. During the treatment period, within group similarity varied across days, ranging from 39.4 to 90.3%, 43.3 to 86.7% and 67.5 to 92.4% for Groups 1, 2 and 3, respectively. For fecal microbes, between group similarity coefficients varied from 38.0 to 85.2% and 38.0 to 94.2% during pre-treatment and treatment periods, respectively. Within group similarity coefficients for fecal populations during treatment were most varied for Group 1 (38.0 to 67.9%), intermediate for Group 3 (75.6 to 92.0%) and least varied for Group 2 (80.6 to 90.6%). We concluded, however, that the observed heterogeneity within and between groups before and after treatment provided little if any evidence of an effect of chlorate treatment on prominent ruminal or fecal microbial populations.

Key Words: coliform bacteria, DGGE, chlorate

T155 Effects of spray-dried whole colostrum and spray-dried plasma on veal calf health and performance. D. Wood*, R. Blome, and J. Sowinski, *Animix, Juneau, WI.*

Study objective was to evaluate effect on veal calf health and performance from supplementing whole spray-dried colostrum (SDC) and spray-dried plasma (SDP). Auction-sourced Holstein bull calves (n=120; app.1 wk of age) were randomly placed in individual, raised,

slatted stalls. Treatment pairs were equally placed within each row, i.e. calves in stalls 1 and 2 were fed supplemental SDP/dry fat blend, calves in stalls 3 and 4 were supplemented SDC, and calves in stalls 5 and 6 were supplemented WPC/dry fat blend (control). Each respective supplement contained 50% CP 20% fat. SDC contained min. 18% and SDP est. 11% IgG. Serum total protein averaged 4.68 g/dL (83% <5.5 g/dL) and there was no difference between groups. Calves were fed liquid milk replacer (all-milk, 17% CP 19% fat) and supplemented 50 gram (g)/feeding (2X/day) of respective supplement for weeks 1 to 6, then 40 g/feeding week 7, 20 g weeks 8 to 9, 10 g week 10 and 5 g weeks 11 to 12. Calves were harvested 19.9 weeks. Accounting for total solids intake, calves started on 26:20 (CP:Fat), increased to 1,330 g/day (d) of 20:19 by 28d and 1,871 g/d 18:19 by 56d. Milk replacer was medicated to 56d. Calves received no dry feed. Incidence of morbidity during the combined room-filling period (4 d) and the first week the barn was full, was lower in SDC (17%, $P < 0.028$) and SDP (19.5%, $P < 0.054$) vs. control (42%). During week 7 when feeding rate was reduced, incidence of morbidity was greater for SDC vs. control ($P < 0.048$). Average individual calf treatment costs were $4.26, $8.91 and $9.78/calf for SDP, SDC and control respectively. SDP tended ($P < 0.10$) to reduce medical treatment costs verses control. Data was analyzed using F-test for variances and student t-test comparing two means. Mortality/culls were 4.8% each for both SDP and SDC and 13.2% for control. In conclusion, SDC and SDP reduced morbidity during typical stressful first weeks of life in low-colostrum status, co-mingled auction-sourced calves treated prophylactically with antibiotics. Some difficulty was noted in weaning calves off SDC. No differences in ADG were noted.

Key Words: calf, colostrum, plasma

T156 Growth and health costs used to evaluate OmniGen-AF feeding strategies in Jersey heifer calves reared on a commercial dairy. A. E. Holland*[1], J. D. Chapman[1], L. O. Ely[2], and Y. Q. Wang[3], *[1]Prince Agri Products Inc., Quincy, IL, [2]University of Georgia, Athens, [3]OmniGen Research LLC, Corvallis, OR.*

The objectives were to determine growth, treatment costs and immune parameters in Jersey heifer calves fed diets supplemented with OmniGen-AF (OG) from birth to weaning or to 160 d of age. Newborn calves were randomly assigned to three groups: G1 controls (n = 50) no OG fed d 1 to 160 either in the milk replacer or pasteurized milk (MR) or starter feed (SF) or heifer TMR, G2 (n = 53) OG fed d 1 to 90 via MR (10 g/h/d) and SF (2 g/lb. of feed) only, G3 (n = 53) OG fed d 1 to 160 via MR, SF, and TMR (3 g/lb. DM). Each calf was housed in a hutch and body weights (BW), hip heights (HH), body condition scores (BCS), and blood were taken on d 1, 50, 90, and 160. Blood samples were analyzed for neutrophil L-selectin (NLS) and interleukin 8 receptor (IL8) mRNA using quantitative RT-PCR. Medications used and costs/treatment were recorded on each calf. Differences were tested using PROC GLM (SAS). Birth weights and HH of G1 (26.1 kg, 71.6 cm), G2 (26.3 kg, 71.1 cm) and G3 (25.6 kg, 70.9 cm) at start were not different. Average daily gain (ADG) for G1 (0.2 kg) from d 5 to 50 differed ($P < 0.05$) from G2 (0.30 kg) and G3 (0.30 kg). ADG were not different between groups at d 90 or 160. BW between groups at d 60 was not different. HH gains in G2 (25.7cm) and G3 (26.0cm) calves were greater ($P < 0.05$) than G1 (24.1 cm) at d 160. BCS at d 50 and 90 were not different between groups; however at d 160, G1 (3.04) and G2 (3.07) were different ($P < 0.05$) from G3 (2.92). Treatments differed between groups ($P < 0.05$), with G1 calves treated 2.3× more often than G2 and 4.7× more often than G3. Total medication costs/treated calf for G1 ($9.80) differed ($P < 0.05$) from G2 ($8.53) and G3 ($7.25). NLS levels were similar for all groups to d 50; however G2 and G3 at d 90 had NLS levels 2.5 times greater than G1. G3 NLS levels were 2 to 4 times greater than G1 and G2 at d 160. IL8 levels differed ($P < 0.05$) between groups at d 1, 90, and 160. Results from this study demonstrated that supplementing OG to pre- and postweaned calves improved growth and health resulting in reduced medication costs.

Key Words: calves, health, OmniGen-AF

T157 Ex vivo and in vitro effects of *Lactobacillus rhamnosus* in the control of gastrointestinal infections in calves. F. Fàbregas*[1], S. Genís[1], A. Bach[1,2], and A. Arís[1], *[1]Department of Ruminant Production-IRTA, Caldes de Montbui, Spain, [2]ICREA, Barcelona, Spain.*

The objective of this study was to assess the potential of *L. rhamnosus* to modulate the inflammatory response against gastrointestinal infections and its protective effect on intestinal cells. Jejunal bovine Peyer patches explants of 1 cm^2 were obtained from a 2-mo calf immediately after sacrifice. Tissue fragments were ex vivo cultured in 6-well plates with Krebs media. Explants were treated with 2×10^9 cfu/well of *L. rhamnosus* or control media (n = 6) for 1 h and infected for additional 8 h with 10^7 cfu/well of *Escherichia coli* EPEC at 37ºC at 5% CO_2. Supernatant and tissue samples were taken to analyze cytokines involved in inflammatory response by qRT-PCR and ELISA. To assess the effect of *L. rhamnosus* on the integrity of intestinal cells, a primary culture of jejunal epithelial cells was established and seeded at 5×10^4 epithelial cells/well. Primary cells were treated with 1, 2, 5, 10, 25, 50 and 100 MOI of *L. rhamnosus* or control media (n = 6), and incubated during 24h at 37°C at 5% CO_2 to further analyze the cell viability by lactate dehydrogenase assay (LDH). Data were analyzed using ANOVA. The EPEC infection caused an inflammatory response by increasing ($P < 0.05$) the levels of pro-inflammatory cytokines IFN-γ, IL-6, IL-1β, and TNF-α, and decreasing ($P < 0.05$) the levels of anti-inflammatory cytokines TGF-β and IL-10. *Lactobacillus rhamnosus* down-regulated the basal tissue inflammation level and the inflammatory response against EPEC by decreasing ($P < 0.05$) the levels of pro-inflammatory cytokines IFN-γ, IL-6, IL-1β, TNF-α, whereas the anti-inflammatory cytokines were unaffected. The LDH levels were less ($P < 0.05$) in *L. rhamnosus*-treated cultures at MOI = 25 (0.55 ± 0.10 mU/mL), MOI = 50 (0.75 ± 0.12 mU/mL), and MOI = 100 (0.58 ± 0.06 mU/mL) than in control cultures (24.72 ± 3.21 mU/mL). In conclusion, *L. rhamnosus* has a positive effect on ex vivo and in vitro bovine intestinal cultures, regulating not only the inflammatory response triggered by an infection, but also modulating the basal inflammatory response and enhancing cell viability.

Key Words: *Lactobacillus rhamnosus*, immunity, intestinal infection

T158 Application of intravaginal lactic acid bacteria improved reproductive performance of Holstein dairy cows. Q. Deng[1], J. F. Odhiambo[2], U. Farooq[1], T. Lam[1], S. Sharma[1], S. M. Dunn[1], Y. Wang[1], M. Gänzle[1], and B. N. Ametaj*[1], *[1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada, [2]Department of Animal Science, University of Wyoming, Laramie.*

The objective of this investigation was to test whether intravaginal infusion of lactic acid bacteria (LAB) around calving can improve reproductive performance in periparturient dairy cows. One hundred pregnant Holstein dairy cows were assigned (based on parity, body condition score, and milk yield) to 3 treatment groups at 2 wk before the expected day of parturition as follows: (1) 1 mL of LAB infused intravaginally on wk -2 and -1, and 1 mL of carrier (i.e., sterile skim milk) on wk +1 relative to the expected day of parturition (TRT1);(2) 1 mL of LAB

infused intravaginally on wk −2, −1, and +1 (TRT2); and (3) 1 mL carrier infused intravaginally on wk −2, −1, and +1 (CTR). Lactic acid bacteria were a mixture of *Lactobacillus sakei* FUA3089, *Pediococcus acidilactici* FUA3138, and *Pediococcus acidilactici* FUA3140 frozen in sterile skim milk with a cell count of 10^8 to 10^9 cfu. Insemination and pregnancy diagnosis records were analyzed retrospectively for all the cows enrolled in this experiment for 12 consecutive months. Data were analyzed with GLIMMIX procedure of SAS. Results showed that cows in the TRT1 had higher (46.9 ± 8.8% vs. 38.2 ± 8.3%, $P = 0.48$), while cows in the TRT2 had lower (28.0 ± 9.0% vs. 38.2 ± 8.3%, $P = 0.42$) first service conception rate than those in the CTR. Cumulative pregnancy rates up to five services were 84.4 ± 6.4%, 72.0 ± 9.0% and 76.5 ± 7.3% in TRT1, TRT2 and CTR, respectively ($P = 0.61$). Cows in TRT1 and CTR required less than 2, while those in the TRT2 required more than 2 services per conception. Consequently, cows in the TRT1 had shorter days open than those in the CTR (82.7 ± 8.0 vs. 109.7 ± 8.1 d, $P < 0.01$), but cows in the TRT2 had longer days open than those in the CTR (137.4 ± 8.4 vs. 109.7 ± 8.1 d, $P < 0.01$). In conclusion, the LAB treatment had distinct effects on reproductive performance. Cows benefited from 2 prepartum doses of LAB (TRT1) for shorter days open. However, the additional postpartum dose (TRT2) did not confer any benefit. The reason for this discrepancy is not clear at present and deserves further inquiry.

Key Words: dairy cow, lactic acid bacteria, reproductive performance

T159 Application of intravaginal lactic acid bacteria modified prostaglandin production of periparturient Holstein dairy cows. Q. Deng[1], J. F. Odhiambo[2], U. Farooq[1], T. Lam[1], S. Sharma[1], S. M. Dunn[1], Y. Wang[1], M. Gänzle[1], and B. N. Ametaj*[1], *[1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada, [2]Department of Animal Science, University of Wyoming, Laramie.*

The objective of this study was to test whether intravaginal infusion of lactic acid bacteria (LAB) around calving could modify prostaglandin production in periparturient dairy cows. One hundred pregnant Holstein dairy cows were assigned randomly (based on parity, body condition score, and milk yield) to 3 groups at 2 wk before the expected day of parturition as follows: (1) 1 mL of LAB infused intravaginally on wk -2 and -1, and 1 mL of carrier (i.e., sterile skim milk) on wk +1 relative to the expected day of parturition (TRT1); (2) 1 mL of LAB infused intravaginally on wk −2, −1, and +1 (TRT2); and (3) 1 mL carrier infused intravaginally on wk −2, −1, and +1 (CTR). Lactic acid bacteria were a mixture of *Lactobacillus sakei* FUA3089, *Pediococcus acidilactici* FUA3138 and FUA3140 with a cell count of 10^8 to 10^9 cfu. Blood samples from 10 cows in each group were used to quantify the concentrations of 15-keto-13,14-dihydro-$PGF_{2\alpha}$ (PGFM) and PGE_2 with enzyme immunoassay kits. Data were analyzed with MIXED procedure of SAS. Results showed that LAB treatment elevated serum PGFM relative to CTR, which were 1346.08 ± 172.21, 1600.02 ± 192.68, and 980.86 ± 220.37 pg/mL in TRT1, TRT2 and CTR, respectively ($P = 0.08$). Overall PGFM increased sharply from wk −1, peaked at parturition and dropped to the prepartum level by wk +2 ($P < 0.01$). Concentrations of serum PGE_2 were 384.97 ± 56.80 pg/mL in TRT1, 687.69 ± 65.21 pg/mL in TRT2 and 471.29 ± 58.52 pg/mL in CTR ($P < 0.01$). Serum PGE_2 dropped at parturition and wk +1, and then increased at wk +2 and +3 ($P < 0.01$). No significant difference was detected among groups regarding the ratio PGFM/PGE_2, but it increased sharply at parturition, and then decreased to a basal level by wk +2 ($P < 0.01$). In conclusion, cows in TRT2 had highest concentrations of both PGFM and PGE_2, while TRT1 had intermediate PGFM and lowest PGE_2, translating into higher PGFM/PGE_2 ratio in TRT1 and intermediate ratio in TRT2 relative to CTR. These findings suggest that postpartum infusion of LAB exerted a distinct effect on prostaglandin production from the prepartum infusion.

Key Words: dairy cow, lactic acid bacteria, prostaglandin

T160 The effect of late pregnancy supplementation of ewes with trace mineral on ewe hematology and lamb vigor. M. Mallaki*, M. A. Norouzian, A. A. Khadem, and M. M. Bardzardi, *The University of Tehran, Tehran, Iran.*

The present study was conducted to evaluate the effect of parenteral supplementation of cobalt, copper and iron in late pregnancy on ewe hematology parameters and lamb vigor. Twenty ewes were allocated to one of two groups (n = 10). In the test group, on d 120 of pregnancy, cobalt, copper and iron were injected at a dose of 0.1 mL/kg BW (Fercobsang, France, cobalt gluconate 5 mg/100 mL, copper gluconate 0.5 mg/100 mL and ferrous citrate 1000 mg/100 mL). Ewes in control group received equal amounts of normal saline as placebo. Blood samples were taken from the jugular vein at the beginning of the study (day 0, 40 ± 5 pre-partum, before injection of trace elements, and saline) and at 24 and 72h postpartum. Group had no significant effect on ewe hematological parameters ($P > 0.05$). There were no significant effects of parenteral mineral supplementation on lamb birth weight, rectal temperature and weaning weight after birth. Lamb viabilities are reported as scores as these gave a true representation of the effects of treatment on underlying measurements. However, there were no differences between groups in lamb vigor and sucking assistance score. It seems that using of additional trace elements in late pregnancy could be effective in deficiency situations.

Key Words: ewe hematology parameter, lamb viability, trace element

T161 From animal breeding to bio-medical research: Day-blind sheep as an animal model for restoration of visual function using gene therapy. E. Gootwine*[1], R. Ofri[2], E. Averbukh[3], H. Honig[1], A. Rosov[1], R. Ezra-Elia[2], A. Obolensky[3], E. Yamin[3], W. W. Hauswirth[4], and E. Banin[3], *[1]Institute of Animal Science, the Volcani Center, Bet Dagan, Israel, [2]Koret School of Veterinary Medicine, Hebrew University of Jerusalem, Jerusalem, Israel, [3]Hadassah Hebrew University of Jerusalem Medical Center, Jerusalem, Israel, [4]University of Florida, Gainesville.*

We reported on novel hereditary recessive day-blindness in sheep caused by a mutation in the *CNGA3* gene (Genomics 95:101–104, 2010). Mutations in this gene can also cause achromatopsia in humans. Culling carrier rams eliminated the birth of affected lambs in a commercial sheep flock. Following establishment of a day-blind sheep population, different types of adeno-associated viral (AAV) vectors carrying the intact human or mouse *CNGA3* gene under the control of a red-green Opsin promoter were delivered unilaterally into the subretinal or vitreal space of affected sheep. Animals were electrophysiologically and behaviorally assessed preoperatively and up to 12 months after treatment. Cone function was measured by electroretinography (ERG) following light adaptation (10 min, 30 cd/m^2). Responses to flash and flicker (10 to 80 Hz) stimuli were recorded at 4 intensities (1 to 10 cd × s/m^2). Behavioral assessment included scotopic (night time) and photopic (day time) maze testing, where passage times and number of fence collisions were recorded. Age-matched normal and non-treated day-blind sheep were similarly assessed as controls. Cone function was significantly depressed in affected sheep prior to surgery. Following surgery, there was significant improvement in eyes treated by either the human or the mouse *CNGA3* gene. Behaviorally, there were no differences between day-blind and normal controls in scotopic testing. While untreated affected animals failed to navigate the maze under photopic conditions, the ability of the day-blind treated sheep to navigate the

photopic maze improved dramatically, approaching that of normal controls. The electrophysiological and behavioral improvement in operated sheep persisted for at least 1 year post-op without affecting animals' health. The long-term electrophysiological and behavioral improvement in this naturally-occurring large animal model following gene therapy may pave the way to application of a similar treatment in human achromatopsia patients.

Key Words: sheep, achromatopsia, gene therapy

T162 OmniGen-AF supplementation improves leukocyte responses and hematology of multiparous peripartum cows. C. R. Nightingale*[1], M. D. Sellers[1], A. R. Pepper-Yowell[1], J. D. Chapman[2], D. L. O'Connor[2], and M. A. Ballou[1], *[1]Texas Tech University, Lubbock, [2]Prince Agri Products Inc., Quincy, IL.*

Objectives of the current study were to determine if supplementing OmniGen-AF (Prince Agri Products Inc.) during the peripartum period improved leukocyte responses and hematology of multiparous dairy cows. Forty-seven multiparous Holstein cows were randomly assigned to two treatments (Control; n = 24, Treatment; n = 23). Treatment cows were supplemented with 2 oz/cow/day of OmniGen-AF from dry-off through 28 d in milk of the subsequent lactation. On d −60 (dry-off), −30, 0, 14, and 28 relative to calving, peripheral blood samples were collected for measurement of hematology and leukocyte responses, which included: neutrophil surface L-selectin (CD62L) protein expression, neutrophil oxidative burst capacity in response to an *Escherichia coli*, plasma haptoglobin concentrations, and whole blood secretion of tumor necrosis factor-α and interferon-γ when co-cultured with lipopolysaccharide and phytohemagglutinin-P, respectively. A linear mixed model was fitted with the effects of treatment, time, and treatment × time, using baseline (−60 d) measurements as a covariate. Baseline measurements were not different between treatments for all variables ($P > 0.22$). Hemoglobin concentrations and hematocrit percentages decreased ($P < 0.01$) on d 14 and were lower among Control cows from d −30 to 28 (10.5 vs. 10.9 ± 0.12 g/dL and 33.5 vs. 34.3 ± 0.31%, for hemoglobin and hematocrit, respectively; $P < 0.01$). Neutrophil L-selectin protein concentrations were greater in Treatment cows on d 0 (769 vs. 431 ± 84.6 GMFI; $P < 0.01$). In contrast, neutrophil oxidative burst intensity was elevated among Control cows on d 0 (373 vs. 259 ± 28.1 GMFI; $P < 0.01$). Plasma haptoglobin concentrations were also elevated among Control cows on d 14 (1.6 vs. 1.2 ± 0.09 optical density; $P < 0.01$). These data indicate that supplementing OmniGen-AF attenuates the peripartum suppression of neutrophil L-selectin, hemoglobin concentrations, and hematocrit percentage. Moreover, treatment cows did not have an elevated neutrophil oxidative burst at parturition or haptoglobin concentrations on d 14, suggesting OmniGen-AF improved health status during this period.

Key Words: immune, OmniGen-AF, peripartum

T163 Water treatment by magnetic field on production and blood gas level in dairy cow. G. B. Neto*[1], N. J. Ramos[1], P. M. Graça[1], J. R. E. Filho[2], M. C. M. Coelho[2], and S. S. Luz[3], *[1]Agencia Paulista de Tecnologia dos Agronegocios, Ribeirão Preto, São Paulo, Brazil, [2]Faculdade de Ciencias Agrarias e Veterinarias da Universidade Estadual Paulista, Jaboticabal, São Paulo, Brazil, [3]Faculdade de Zootecnia e Engenharia de Alimentos da Universidade de São Paulo, Pirassununga, São Paulo, Brazil.*

Data suggest that the properties of magnetically treated water are different from the ones of untreated water. This fact is usually attributed to the weaknesses in or breaking of intermolecular interactions (hydrogen bonds) and nucleation processes (effect of impurity, frequency and growth of nuclei). Water treatment by magnetic field is an attractive but still controversial issue as might apply to animal production. The purpose of the present study was to investigate the effects of water treatment by magnetic field on milk production and blood gas and ionic character. The treatment of water was performed using a commercial magnetic conditioner (Sylocimol) designed to generate a strong magnetic monopole field. These devices were inserted into the water troughs (500 L); the strength of the static magnetic field was 32,400 Gauss. A completely randomized design was used. Twenty-six Jersey cows were allotted into two groups: control (C; n=13) and group consuming magnetic water (MW; n = 13) for 75 days to compare the milk production and blood gas level and Na ion concentration ([Na]). Blood samples were collected by caudal auricular artery using a blood sampling kit for blood gas analysis (3 ml ventilated syringes with 23 G 1 in needle, containing freeze-dried lithium heparin). All the samples were immediately analyzed in a calibrated blood gas analyzer set at the body temperature of cows. No significant difference was found on daily milk yield. However, higher pH and lower pCO2 levels were found in arterial blood of MW compared to C. Lower [Na] and [Cl] were associated with lower osmolality in MW compared to C. The test results suggested that animals consuming water conditioned by magnetic field technology have blood characteristics different from those consuming unconditioned water.

Table 1. Magnetic treatment of water on milk production and blood gas and ion content

	Control	Test	CV	MSE	Pr > F
Daily milk yield (kg/cow)	10.30	11,.40	21.14	2.309	0.357
Osmolality (mOsm/kg)	280.1[a]	273.3[b]	1.45	4.03	0.0007
pHt	7.41[b]	7.45[a]	0.28	0.02	0.0004
pO_{2t} (mmHg)	101.48	110.43	18.72	19.83	0.326
pCO_{2t} (mmHg)	42.47[a]	37.97[b]	7.58	3.05	0.002
Na (mmol/L)	141.10[a]	136.97[b]	1.55	2.16	0.0002
Cl (mmol/L)	101.89	99.25	1.95	1.96	0.0161

[a,b]Means not bearing the same superscript letters within rows are significantly different ($P > 0.05$).

Key Words: bovine, blood gas partial pressure, pH

T164 Evaluation of chlorine stability in a novel teat dip disinfectant system. L. L. Timms*[1], M. Pawlak[2], and C. Durham[2], *[1]Iowa State University, Ames, [2]Zurex Pharmagra, Middleton, WI.*

Objective was to evaluate chlorine stability of a novel germicidal product as well as dilutions developed for pre and post milking teat dipping with different additives. Initial base germicidal compound (ECAlogix System) was designed to have 8000 ppm chlorine. A teat dip cup filled with initial solution was placed in milking parlor and served as base control over time (all trials - never used for dipping). Pre (500 to 1000 ppm) and post (1000 to 2000 ppm) milking teat dips were made, used, and tested (trial 1: 14 days). 1000 ppm and 2000 ppm pre and post dips, respectively from trial 1, were chosen to evaluate different emollient levels (trial 2 – 21 days) and subsequent trial against commercial dip products (trial 3 – 49 days). Additives for prototype pre and post dips for trials 1-3 were PREP and POST, PREP/PRE-POST and POST+ / PRE-POST (different emollient levels), and PREP and POST/POST-Blue, respectively. Pre and post milking teat dips were made in 1 gallon quantities (last ~ 1 week). A single dip cup was used for each dip in each trial. Chlorine concentrations in all products were tested every 2-3 days by drawing directly from teat dippers used in the milking parlor. Samples

were tested in duplicate using a chloride titration kit (10 drops of 50% Potassium iodide; 3 drops of 50% sulfuric acid; 5 drops of 1% starch solution; drops of thiosulfate solution until sample turned colorless). Chlorine levels of pre dips (500 and 1000ppm + PREP), post dips (1000 and 2000 ppm + POST) and stock solution (8000 ppm) were stable and not significantly different within any product across Trial 1. In trial 2, pre (1000 ppm) and post (2000 ppm) dips with additives PREP and POST+, respectively, were stable and not significantly changed (21 d) while dips with PRE-POST additive resulted in significant reductions to 200 ppm chlorine within 24 h post mixing. In trial 3, pre (1000 ppm) and post (2000 ppm) dips with additives PREP and POST (same as trial 1), respectively, were stable and not significantly changed (49 d) while post dips with POSTBlue showed significant reductions to 200 ppm chlorine within 24 h post mixing. This novel technology shows excellent chlorine stability over time and importance of measuring potential effects of different solution additives.

Key Words: chlorine, teat dip, disinfection

T165 Development and evaluation of experimental chlorine technology pre and postmilking teat dips on teat end and teat skin condition and health. L. L. Timms*[1], M. Pawlak[2], and C. Durham[2], *[1]Iowa State University, Ames, [2]Zurex Pharmagra, Middleton, WI.*

Objectives were to evaluate pre and post teat dip formulations using a novel chlorine disinfectant technology (ECAlogix System) and their effect on teat health and integrity. There were 2 trials with 3 pens (10, 11, and 12) in both trials. Trial 1 (2 wk) was designed to evaluate maximal chlorine concentrations; trial 2 (3 wk) assessed emollient levels. Pen 12 (48 cows) had all teats dipped with current herd commercial pre and post dips (hydrogen peroxide pre and lactic acid barrier post- herd sentry pen). Pen 11 (48 cows) was pre-dipped in a half udder design and all teats post dipped with herd commercial product. Trial 1 compared 500 and 1000 ppm chlorine pre-dips. Trial 2 compared 1000 ppm predips with different emollient levels. In trials 1 and 2, Pen 10 (24 cows) was pre-dipped with commercial herd product and post dipped in a half udder design. Trial one compared 1000 and 2000 ppm. Trial 2 compared 2000 ppm postdips with different emollient levels. Teat skin (1 = normal, 2 = slightly dry; 3 = chapped) and teat end (1 to 1.5 = normal; 2 to 3 = smooth ring; 3.5 to 4 = rough ring; 4.5 to 5 very rough ring) scoring was performed twice per week. Mixed procedure of SAS with repeated measured (mixed model with quarter within cow as a repeated measure) were used to analyze average teat skin score (TSS), average teat end scores (TES), and % rough teats, with $P < 0.05$ considered significant. Prior to trial initiation, all pens had similar TSS (1.08; 3 to 16% scoring 2), with pen 10 having slightly lower TES and % rough teats (2; 50%) compared to pens 11 and 12 (2.5; 60%). Trial 1 showed no overall change in TSS, TES, and % rough teat ends for pen 12 (sentry) and 11 (prototype pre dips) with no differences between 500 and 1000 ppm chlorine pre-dips in Pen 11. Pen 10 (prototype post dips) showed significant improvements in TSS (1.01, < 1% score 2), TES (1.7), and % rough teat ends (30%), with no differences between 1000 and 2000 ppm chlorine post dips. Trial 2 showed similar results to trial 1 (improved teat integrity with prototype chlorine post dips) with no additional benefits seen to extra emollient addition to either pre or post chlorine dips. No adverse effects were seen at any chlorine concentration.

Key Words: chlorine, teat dipping

T166 Evaluation of experimental chlorine technology pre and post milking teat dips vs. a commercial hydrogen peroxide pre dip and iodine barrier post milking teat dip on teat end and teat skin condition and health. E. Smith[1], L. L. Timms*[1], M. Pawlak[2], and C. Durham[2], *[1]Iowa State University, Ames, [2]Zurex Pharmagra, Middleton, WI.*

Objectives were to evaluate (using half udder design model) a novel chlorine predip and postdip combination (ECAlogix System) versus a control commercial hydrogen peroxide premilking teat dip and iodine barrier postmilking teat dip on overall teat end and teat skin condition and health. There were 3 pens (10, 11, and 12) in the trial (7 weeks). Pen 12 (48 cows) had all teats dipped with current herd pre and post dips (herd sentry pen). Pen 11 (48 cows) and Pen 10 (24 cows) had left side teats dipped with commercial herd pre and post dips while right teats were dipped with 1000 ppm chlorine predip and 2000 ppm chlorine post dips (experimental prototypes). Teat skin (1 = normal, 2 = slightly dry; 3 = chapped) and teat end (1 to 1.5 = normal; 2 to 3 = smooth ring; 3.5 to 4 = rough ring; 4.5 to 5 = very rough ring) scoring was performed two times per week. Mixed procedure of SAS with repeated measured (mixed model with quarter within cow as a repeated measure) were used to analyze average teat skin score (TSS), average teat end scores (TES), and % rough teats, with $P < 0.01$) TSS, TES, and % rough teats than control dipped teats within 10 days of trial initiation (1.01, 2.0, 30 to 40% vs. 1.03, 2.6, and 60%, respectively) and maintained this improved teat integrity through the trial. Prototype chlorine teat dips were stable and provided significantly better teat skin and teat end health and integrity compared to commercial products.

Key Words: chlorine, postmilking teat dipping, premilking teat dipping

T167 Supplementation of organic selenium and its effect on productive and reproductive performance in grazing dairy cows in Costa Rica. J. Sanchez-Salas*[1], J. A. Elizondo-Salazar[1], C. Orozco-Vidaorreta[2], and E. Viquez-Matei[3], *[1]Estacion Experimental Alfredo Volio Mata. Facultad de Ciencias Agroalimentarias, Universidad de Costa Rica, [2]Alltech, Inc, Costa Rica, [3]Alimentos Balanceados, Cooperativa de Productores de Leche Dos Pinos, Costa Rica*

The objective was to evaluate the effect of supplementation of selenized yeast derived from a specific strain of *Saccharomyces cerevisiae* (CNCM I-3060) on productive and reproductive performance and on selenium concentrations in milk of grazing dairy cows. Multiparous Holstein cows (n=40) with an average body weight of 607 ± 62 kg and a body condition score of 3.1 ± 0.2 before parturition were randomly assigned to one of two treatments. Treatment 1 consisted of a basal diet supplying 0.7 mg of Se/kg dry matter. Treatment 2 consisted of the same basal diet supplemented with 3.0 mg of Se from d 5 to 56 of lactation. Milk production, milk composition, SCC, and Se content of milk from individual cows were determined at d 5, 14, 28, 42, and 56 of lactation. Blood samples from each cow were also taken during the same days to measure glutathione peroxidase (GSH-Px) and Se concentration. To evaluate reproductive performance the ovaries were examined by transrectal ultrasonography at d 22 and 57 postpartum. Days open, days to conception and services per conception were also recorded. Milk production (41.7 vs. 40.2 on d 56), milk composition, and SCC did not differ between treatments ($P > 0.05$) during the trial. Selenium supplementation increased ($P < 0.01$) Se apparent efficiency of transfer into milk (9.9 vs. 7.9%) and Se content of milk (20.5 vs. 12.7 µg/L). Selenium supplementation did not alter ($P > 0.05$) GSH-Px (220.3 vs. 199.0 U/g Hb) or Se concentration in blood (184.2 vs. 166.4 µg/L). There were no treatment effects on animal reproductive performance. Considering that 35% of Costa Rican population is Se deficient and taking into account the increase in Se content in milk, milk derived from cows supplemented with selenized yeast could contribute to a person's daily intake of Se.

Key Words: selenium, trace mineral, grazing cattle

T169 Inhibition of nuclear factor kappa B in duodenal mucosa of piglets by a grape seed and grape marc meal extract. D. K. Geßner[1], A. Fiesel[1], M. Lohölter*[2], B. Eckel[2], and K. Eder[1], *[1]Institute of Animal Nutrition and Nutrition Physiology, Universität Gieesen, Germany, [2]Dr. Eckel GmbH, Niederzissen, Germany.*

Enteric infections and the development of gut disorders commonly observed in piglets after weaning have negative effects on digestive capacity of the intestine, feed consumption, and growth of animals. The underlying molecular mechanism of this is an activation of nuclear factor kappa B (NF-κB), which leads to an increased expression of pro-inflammatory target genes. Studies in rodent models have shown that polyphenols have the ability to suppress inflammatory processes in the intestine by inhibiting NF-κB. The present study investigated the hypothesis that feeding a grape seed and grape marc meal extract (GSGME) as a dietary supplement has the potential to suppress the inflammatory process in the duodenum of piglets by modulating the activity of NF-kB polyphenols. Twenty-four crossbred (Danzucht × Pietrain) piglets, 6 weeks of age, were randomly assigned to a control group and a treatment group and fed a nutritionally adequate basal diet, based mainly on wheat, barley and soy bean meal for a period of 4 weeks. The control group received the basal diet; the treatment group received the basal diet supplemented with 1% of GSGME (AntaOx, Dr. Eckel GmbH, Niederzissen, Germany). There were no differences in average daily gains and daily feed intake between the two groups. However, the gain:feed ratio was increased in the treatment group ($P < 0.05$). Additionally, the treatment group had a lower activity of NF-κB and lower expression levels of NF-κB target genes such as TNFa, IL-8 and MCP-1 in the duodenal mucosa ($P < 0.05$). Moreover, the villus height:crypt depth ratio in the duodenum was increased in the pigs fed the GSGME, suggesting an increased absorptive capacity. In conclusion, the present study shows that a polyphenol rich GSGME has an anti-inflammatory effect in the small intestine of piglets. It is suggested that feeding of polyphenol rich plant extracts might provide a useful dietary strategy to inhibit inflammation in the intestine frequently occurring in piglets.

Key Words: grape seed and grape meal extract, anti-inflammatory, piglets

T170 Degradation of ergopeptines by *Rhodococcus erythropolis* MTHt3. M. Thamhesl*[1], E. Apfelthaler[2], E. Kunz-Vekiru[2], I. Schöner[3],H. Schwartz[3], F. Berthiller[3], R. Krska[2], G. Schatzmayr[1],and W.-D. Moll[1], *[1]Biomin Research Center, Tulln, Austria, [2]Christian Doppler Laboratory for Mycotoxin Research, Department for Agrobiotechnology (IFA-Tulln), University of Natural Resources and Life Sciences, Vienna, Tulln, Austria, [3]Christian Doppler Laboratory for Mycotoxin Metabolism, Department for Agrobiotechnology (IFA-Tulln), University of Natural Resources and Life Sciences, Vienna, Tulln, Austria.*

Ergot alkaloids are secondary metabolites produced by ergot fungi (*Claviceps* species) in cereals and endophytes (*Epichloë*, *Neotyphodium*, and *Balsania* species) in grasses. Ergot poisoning occurs predominantly in livestock after consumption of endophyte infected grasses and leads to reduced animal performance. Diverse strategies on pasture and animal management or feed treatments have been investigated. Ergot degrading microorganisms, which can be applied as feed additives and are active in the gastrointestinal tract, may be a technological solution to ameliorate the problem. The objective of this research was to isolate ergot alkaloid-degrading microorganisms from natural habitat. Strain MTHt3 was isolated from soil and identified by phylogenetic analysis based on 16S rRNA as member of the species *Rhodococcus erythropolis*. In comparison to a number of tested *R. erythropolis* strains the ability to metabolize ergopeptines was unique for strain MTHt3. In a degradation experiment with an extract from ground sclerotia (acetonitrile/water; 1:1; v/v; 2 hours at room temperature) strain MTHt3 was capable of converting all detected ergopeptines (ergotamine, ergovaline, ergocryptine, ergocristine, ergocornine, and ergosine) to ergine and cyclic dipeptides (diketopiperazines). Ergine was further de-amidated to lysergic acid. Cyclic dipeptides were completely catabolized by strain MTHt3, but not utilized by *R. erythropolis* type strain DSM 43066. Characterization of strain MTHt3 showed that conversion of ergopeptines to ergine occurred in a broad pH and temperature range whereas deamination of ergine to lysergic acid was strongly influenced by pH and temperature. Lysergic acid has lower vasoconstrictive activity compared to ergopeptines and simple lysergic acid amides. Hence, metabolization of ergot alkaloids to lysergic acid by *R. erythropolis* MTHt3 may reduce toxicity. Application as feed additive of strain MTHt3, however, seems to be difficult due to characteristics of the strain. Isolation of responsible enzymes combined with enzyme engineering and application as feed enzymes can be an alternative approach to reduce effects of ergot alkaloid-contaminated fodder on animals.

Key Words: ergot alkaloid, degradation

T171 The impact of grazing toxic tall fescue on bull growth, fat deposition and blood flow. S. K. Duckett*[1], G. E. Aiken[2], H. M. Stowe[1], M. C. Miller[1], S. M. Calcatera[1], M. D. Owens[1], J. G. Andrae[1], and S. L. Pratt[1], *[1]Clemson University, Clemson, SC, [2]ARS-Forage-Animal Production Research Unit, Lexington, KY.*

Tall fescue is utilized extensively in the Southeastern United States; however, most tall fescue contains an ergot alkaloid producing fungal endophyte. Consumption of ergot alkaloids (EA) results in the syndrome known as tall fescue toxicosis. The objective of this study was to evaluate growth, fat deposition, and blood circulation for bulls grazing an EA containing toxic tall fescue (Toxic) compared to a novel non-toxic (NT) endopyhte, which lacks EA. Angus bulls (n = 21) were stratified by BW and BCS and allotted to graze either KY31 or NT for 155 days. Body weights were taken on d 0 and d 140. Body condition scores were taken on d 0, 35, 84, 112, and 140. Doppler ultrasound was conducted on the caudal and testicular arteries to evaluate blood flow and real-time ultrasound conducted on the loin and rump to determine subcutaneous fat deposition, intramuscular fat (IMF) and muscle depth (MD) on d 8, 57, 106 and 155. GLIMMIX procedures were used to perform an ANOVA to test for the main effects of treatment (TRT), day, and TRT × day interaction for all parameters. TRT × day combination means were generated and compared using Fisher's LSD test. No difference in BW ($P = 0.43$) was observed on d 0; however, by d 140 BW was decreased ($P = 0.04$) in the Toxic bulls (546.2 ± 16.6 kg) compared to the NT bulls (595.9 ± 16.6 kg). The gain in BW was increased in NT bulls compared to bulls grazing Toxic ($P = 0.0001$; 105.8 ± 8.9 versus 33.8 ± 8.1 kg, respectively). No difference was observed for TRT ($P = 0.3$) or TRT × day interactions ($P = 0.08$) for BCS. No differences were observed for IMF ($P = 0.8$) or fat thickness ($P \geq 0.06$) due to TRT; however, the rump MD was decreased in bulls grazing Toxic compared to NT ($P < 0.001$). Luminal area was reduced from 9.7 ± 0.9 to 4.8 ± 0.8 mm^2 for the caudal artery ($P = 0.001$) and 10.3 ± 0.8 to 5.0 ± 0.8 mm^2 for the testicular artery ($P = 0.01$) for NT compared to Toxic bulls, respectively. These data support previous research demonstrating the negative effects of ergot alkaloids on BW and blood flow.

Key Words: fescue toxicosis, bull, ultrasound

T172 Finishing residual feed intake is positively correlated with backgrounding growth of metabolically imprinted Angus-sired steers. J. K. Smith*, S. P. Greiner, and M. A. McCann, *Virginia Polytechnic Institute and State University, Department of Animal and Poultry Sciences, Blacksburg.*

Backgrounding is commonly utilized within the beef industry to achieve economical weight gains while providing feeders with a continuous cattle supply. Previous research has indicated implications of early growth dynamics on finishing (FIN) performance and carcass traits. The objective of this study was to identify relationships between FIN residual feed intake (RFI) and early growth performance or carcass traits of conventionally weaned (CW; n = 22; weaned at 204 ± 18 DOA; d 204) or metabolically imprinted (MI; n = 21; weaned at 104 ± 18 DOA; d 104) Angus-sired steers that were MI via concentrate supplementation (100 d) immediately following weaning. Upon completion of the MI feeding period, MI and CW calves were commingled and backgrounded for a minimum of 153 d prior to being finished on a concentrate- and corn silage-based ration for 92 ± 6 d after a 21 day adaptation period. Average daily metabolic BW gain (ADMG) was calculated throughout the early (EG; d 104 to 204), backgrounding (BG) and FIN growth phases. ADFI was measured and used to calculate FIN RFI. Cattle were harvested in groups upon reaching a common subcutaneous fat thickness (BFT) of 1 cm. Pairwise correlations between RFI and growth or carcass measurements were determined using the Multivariate and Pairwise Correlations procedure of JMP. When evaluated irrespective of weaning regimen, RFI was correlated ($P < 0.05$) with ADMG during the EG and BG phases, ribeye area and yield grade, and tended ($P < 0.10$) to be correlated with BFT with respective r values of -0.37, 0.51, -0.30, 0.46 and 0.27. Within weaning regimen, RFI was correlated ($P < 0.05$) with ADMG during the BG phase, ribeye area, yield grade and BFT for MI steers with respective r values of 0.54, -0.42, 0.60 and 0.51, but was not correlated ($P > 0.10$) with growth or carcass traits for CW steers. These results suggest relationships between FIN RFI and pre-finishing growth that were unique to MI cattle in this experiment. Targeting MI cattle for low ADMG during the BG phase may improve FIN feed efficiency through decreasing RFI.

Key Words: metabolic imprinting, residual feed intake, beef

T173 Early metabolic imprinting for improved feed efficiency of backgrounded Angus-sired steers. J. K. Smith*, S. P. Greiner, and M. A. McCann, *Virginia Polytechnic Institute and State University, Department of Animal and Poultry Sciences, Blacksburg.*

Previous research has indicated the ability of energy supplementation early in life to metabolically imprint cattle for improved growth and carcass traits. The objective of this study was to evaluate the effect of metabolic imprinting (IMP) on finishing (FIN) average daily residual feed intake (RFI) of Angus-sired steers. Calves born in the fall of 2009 (FB) and spring of 2010 (SB) were stratified by sire and age before being randomly assigned to a metabolically imprinted (MI; weaned at 104 ± 18 d of age; n = 21) or conventionally weaned (CW; weaned at 204 ± 18 d of age; n = 22) treatment group. Following weaning, MI calves were adapted to and received a concentrate-based ration in a feedlot setting for 100 d. Upon completion of the MI feeding period, previously unsupplemented CW calves were commingled with MI calves and backgrounded for a minimum of 153 d prior to being finished on a concentrate- and corn silage-based ration for 92 ± 26 d following a 21 d adaptation period. ADFI was collected using a Calan Broadbent feeding system and used to calculate average daily TDN intake (TDNI). Cattle were harvested in groups upon reaching a common 12th rib subcutaneous fat thickness (BFT; 1 cm). Predicted average daily metabolic BW (MBW) gain was regressed against predicted mid-finishing MBW and TDNI using the Fit Y by X procedure of JMP to express RFI in kg of TDN. While analysis of a compiled FB and SB dataset using the Fit Model procedure of JMP revealed no effect ($P > 0.10$) of IMP on finished MBW, HCW, BFT, ribeye area (REA), KPH and yield grade (YG), IMP resulted in lower RFI ($P < 0.05$; −0.299 vs. 0.246 kg TDN) and greater marbling score ($P < 0.05$; 542 vs. 595) when compared to conventional weaning. Although not associated ($P > 0.10$) with carcass measurements of CW steers, RFI was associated ($P < 0.05$) with BFT ($R^2 = 0.26$) and YG ($R^2 = 0.36$) of MI steers, with a tendency ($P < 0.10$) toward an association with REA ($R^2 = 0.17$). These results indicate the ability of IMP to decrease the amount of TDN required by FIN cattle to reach a common carcass endpoint. Economic savings in FIN TDN may be capable of offsetting a portion of IMP feed costs.

Key Words: metabolic imprinting, residual feed intake, beef

T174 Comparison of serial and parallel beef fabrication methods in a traceable supply chain. T. Foster*[1], D. Buskirk[1], and J. Schweihofer[2], *[1]Michigan State University, East Lansing, [2]Michigan State University Extension, East Lansing.*

Traceability of meat attributes from small and mid-sized farms through supply chains is recognized as a market barrier. Automatic identification and data capture technologies, such as radio frequency identification (RFID) and two-dimensional (2-D) barcodes, offer the feasibility of maintaining animal and product data through carcass fabrication. The objective of this study was to determine the influence of fabrication method on beef traceability system requirements. Individual animal identity of seventy-two (72) beef carcasses were maintained during either serial or parallel processing of carcass quarters. Each carcass quarter was labeled with a 2-D barcode containing the animal's unique RFID ear tag number at harvest. Nine carcasses were processed on alternating days of processing by one of two methods for eight days of processing. Carcasses were serially fabricated (SER) resulting in creation of all wholesale cuts of a single carcass before moving on to the next, or parallel fabricated (PAR) by processing 10 hindquarters, followed by 10 forequarters, 8 hindquarters, and 8 forequarters. The major difference between processing method was that beef from only one animal was on a cutting table for SER, whereas beef from multiple carcasses was on a cutting table for PAR. In-process, 5.1 × 2.5 cm "child" labels were generated by scanning the 2-D barcode on the parent carcass label with a handheld mobile computer and wirelessly printed with a mobile printer. Tracking of SER and PAR carcass quarters were accomplished by creating in-process labels for lugs and individual wholesale cuts, respectively. The amount of time required to fabricate each carcass was similar ($P > 0.05$) for SER (2 hours 35 minutes) and PAR (2 hours 49 minutes). The mean number of in-process labels generated per carcass for SER was 3.7 and for PAR was 30.9 ($P < 0.01$). The amount of time required for generating labels for SER (2 minutes 16 seconds) was less than that for PAR (8 minutes 45 seconds) ($P < 0.01$). Logistics of traceability was less complex for SER than PAR and did not significantly add to the time of processing beef carcasses.

Key Words: radio frequency identification, two-dimensional, beef traceability

T175 Effect of supplement and resynchronization protocol on body weight, body condition score, and estrus appearance of Charolais cows grazing Buffelgrass in Northeastern Mexico. E. Garza Brenner*[1], H. Bernal Barragán[1,3], E. Gutiérrez Ornelas[1,3], F. Sánchez Dávila[1], A. S. Juárez Reyes[2,3], and E. Olivares Sáenz[1], *[1]Universidad Autónoma de Nuevo León, San Nicolás de los Garza, Nuevo León, México, [2]Universidad Juárez del Estado de Durango, Durango, México, [3]Red Internacional de Nutrición y Alimentación Animal, México.*

The effects of type of supplement and resynchronization protocol on condition and reproductive performance were evaluated using 32 Charolais cows grazing Buffelgrass (*Cenchrus ciliaris* L.), supplemented daily with 1 kg of either dried distillers grains with solubles (DDGS) or 50% DDGS:50% dried citrus pulp (DDGS:DCP) during 30 d. Estrus was synchronized by inserting on d 0 a controlled internal drug-releasing (CIDR) device, containing 1.38 g of progesterone, with retrieval on d 9; artificial insemination (AI) was conducted 12 h after estrus onset. Resynchronization started 5 d after AI, reinserting to each female its own CIDR device, for either 8 d (R8D) or 14 d (R14D). Body weight (BW) and body condition score (BCS) were registered at d 0, 9, 15, 23, and 30. Intervals from CIDR retrieval to estrus were registered by visual observation. Cows were blocked (age, parity, weight) and randomly assigned in a 2 × 2 factorial arrangement of treatments (two supplements: DDGS and DDGS:DCP, and two resynchronization protocols: R8D and R14D). Data were analyzed using two-way ANOVA (BW, BCS, intervals to estrus), and nonparametric test (Mann-Whitney for estrus appearance). Initial and final BW were similar (mean = 485 kg); however, on d 15 (487 vs. 464 kg) and d 23 (500 vs. 485 kg), cows receiving DDGS:DCP were heavier ($P < 0.05$) than those receiving DDGS. BCS changed ($P < 0.05$) from 4.7 (d 0) to 5.1 (d 30), but there was no effect ($P > 0.05$) of supplements. Fourteen out of 16 cows receiving DDGS:DCP, and 8 out of 16 cows receiving DDGS ($P < 0.05$), showed estrus. There was no effect ($P > 0.05$) of supplement on interval of CIDR retrieval to estrus onset (mean = 34.2 h). After resynchronization, 5 and 6 out of 16 cows for each protocol ($P > 0.05$) showed estrus, but it started later ($P < 0.01$) by R8D than R14D (141.9 vs. 27.8 h). In conclusion, Charolais cows grazing Buffelgrass and supplemented with DDGS:DCP had greater estrus appearance rate than those receiving DDGS. Length of resynchronization affected time, but not rate, of estrus appearance.

Key Words: dried citrus pulp, DDGS, resynchronization

T176 Influence of previous experience on performance and grazing behavior in beef heifers. G. A. Perry*, E. L. Larimore, and J. A. Walker, *Department of Animal Science, South Dakota State University, Brookings.*

Previous research has reported that grazing experience can impact performance when heifers are moved from a drylot to forage. The objective of this study was to determine the impact of prior grazing experience on weight change and activity when heifers were moved to spring forage. Angus-cross beef heifers were developed in a single pen following weaning. At the start of treatment (d 0) heifers were blocked by weight and allot to either remain in the drylot (n = 34) or were move to spring forage (n = 35). Body weights were collected on d 0, 9, 20, 41, 53, and 74. Pedometers were placed on 5 heifers per treatment on d 25 and measured numbers of steps taken, and amount of time standing and lying down. On d 44 all heifers were moved to spring forage, but were maintained in their respective group (12.1 ha/group). The statistical model included treatment, time, and their interaction. There was a treatment ($P < 0.01$), time ($P < 0.01$), and a treatment by time ($P < 0.01$) effect on ADG. Heifers moved to spring forage on d 0 had decreased ($P < 0.01$) ADG from d 0 to 9 compared to heifers that remained in the drylot. There was no difference between treatments in ADG from d 9 to 20 and from d 20 to 41. Following being moved to spring forage on d 44 the drylot group had decreased ($P < 0.01$) ADG from d 41 to 53 and from d 53 to 74 compared to the group that had previous grazing experience. From d 25 to 38, there was an effect of treatment ($P < 0.01$), time ($P < 0.01$), and a treatment by time ($P = 0.03$) on the number of steps taken each day, with heifers on forage taking more ($P < 0.05$) steps per d than heifers in the drylot. However, there was no effect of treatment on the amount of time a heifer spent standing or lying down per d. Following being moved to spring forage, heifers that remained in the drylot took more ($P < 0.05$) steps per d on d 44, 45, 46, and 47 compared to heifers that had previous grazing experience. However, there was no treatment effect on the amount of time a heifer spent standing and lying down per day. In summary, prior grazing experience can impact grazing behavior and heifer performance when heifers are moved to spring forage.

Key Words: heifer development, grazing behavior, ADG

T177 Immunocastration effect on performance in feedlot cattle. G. Z. Miguel*[1,3], R. O.Roça[2], C. T. Santos[3], M. H. de Faria[4], F. D. de Resende[4], G. R. Siqueira[4], J. M. Homem[3], A. D. Moreira[5], and B. R. C.

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Our objective was to determine the effect of immunocastration on performance of finishing cattle of 2 genetic groups (GG) and 3 sex conditions (SC). Thirty Nellore (NE) and 30 Nellore × Angus (NA) with average of 450 kg BW and 20 mo of age were evaluated during two periods: pre-feedlot and feedlot. The first period was defined from 130 to 90 d prior to harvest, while the second period was the last 90 d prior harvest. In the pre-feedlot period 10 NE and 10 NA were immunocastrated (IM) by vaccinating twice with Bopriva (anti-GnRH vaccine; Pfizer Animal Health) at 28 d and 1 d prior to transfer to feedlot. Surgical castration (CA) treatment was imposed on 10 animals from each GG, which occurred at 28 d before transferring to feedlot. Ten animals from each GG were kept intact (NC). During the pre-feedlot period the animals were raised on pasture and supplemented at 0.25% of BW, while during the feedlot period, the animals were fed ad libitum a high-grain diet formulated to contain 85% concentrate. In the feedlot the animals were finished in individual pens. Statistical analyses were performed according to a 2 × 3 factorial scheme (2 GG × 3 SC) in a completely randomized design. Data were analyzed using the MIXED procedure of SAS with initial weight as a covariate, and the means were compared by Student's t-test at 5% probability. As expected, NA animals had greater BW and ADG than NE ($P < 0.05$), but similar DMI and G:F ($P > 0.05$). Although IM and CA animals showed similar results for ADG, DMI and G:F ($P > 0.05$), IM had greater BW ($P < 0.05$). NC bulls had greater BW, ADG and G:F than the other SC ($P < 0.05$), but equivalent DMI ($P > 0.05$). Among IM treatments NA had greater BW, ADG and G:F than NE ($P < 0.05$). In this study NA animals and NC bulls were more efficient on high-grain diets due to greater BW and ADG. Additionally IM-NA animals had better performance than IM-NE with greater BW, ADG and G:F.

Key Words: sexual conditions, *Bos indicus*, beef cattle

T178 Correlations of visual scores and ultrasound carcass traits with economically relevant traits in Nellore cattle. R. C. Gomes*[1], P. H. Cancian[2], F. Manicardi[2], A. C. Ianni[2], M. N. Bonin[2], P. R. Leme[2], and S. L. Silva[2], *[1]Embrapa Beef Cattle, Campo Grande, MS, Brazil, [2]Faculdade de Zootecnia e Engenharia de Alimentos, Universidade de Sao Paulo, Pirassununga, SP, Brazil.*

Visual scores (VS) and carcass ultrasound have been used for genetic selection purposes in the Brazilian Nellore herd. However, the impacts on economically relevant traits, such as feed efficiency and the yield of commercial meat cuts, still lack investigation. The aim was to evaluate the correlations of VS and carcass traits evaluated by ultrasound (US), with feed efficiency (FE), hot carcass weight (HCW), dressing percentage (DP) and retail product yield (RPY). Fourty-two bulls and 44 steers were evaluated for both VS and US, in the postweaning phase (15 mo of age) and in the beginning of the finishing phase (21 mo of age). Cattle were ultrasound scanned for measuring backfat thickness (UBFT), rump fat thickness (URFT) and ribeye area (UREA). Visual scores of conformation (C), precocity (P) and muscling (M) were attributed individually. Gain-to-feed ratio (G:F) and residual feed intake (RFI) were measured in feedlot. HCW, DP and RPY were determined at harvest. Pearson correlation analyses were carried out. Bulls had greater HCW (321 vs. 292 kg; $P < 0.0001$) and RPY (74.5 vs. 71.8%; $P < 0.0001$) and lower finishing UBFT (0.58 vs. 1.60 mm, $P < 0.0001$) and URFT (1.96 vs. 3.64 mm; $P < 0.0001$) than steers. C and P did not differ across sex types ($P > 0.05$) in both phases, but bulls had greater M scores in the finishing phase (4.49 vs. 3.42, $P < 0.01$). Feedlot RFI and G:F were poorly correlated with postweaning VS and US in both sex types ($P > 0.05$). G:F was negatively correlated with finishing C ($r = -0.39$; $P < 0.05$), P ($r = -0.50$; $P < 0.01$) and M ($r = -0.50$; $P < 0.01$) in steers. DP was negatively correlated with postweaning P ($r = -0.31$; $P < 0.05$), M ($r = -0.32$; $P < 0.05$) and UREA ($r = -0.51$; $P < 0.01$) in steers. Finishing URFT was negatively correlated with RPY in bulls ($r = -0.41$; $P < 0.01$). Greater subcutaneous fat thickness in the beginning of the finishing phase may indicate cattle with lower retail product yield. The associations of visual scores and ultrasound carcass traits with feed efficiency and retail product yield are affected by age at evaluation and by castration, but are generally small.

Key Words: body composition, edible portion, feed conversion

Breeding and Genetics: Applications and Methods in Animal Breeding—Beef

T179 Genetic analysis of female weights via random regression and multiple trait models in a multibreed beef cattle population. B. Y. Coy[1,2], C. A. Martinez[1], C. Manrique[2], and M. A. Elzo*[1], *[1]University of Florida, Gainesville, [2]Universidad Nacional de Colombia, Bogota, Colombia.*

The objective was to obtain REML estimates of covariance functions and variance ratios for weights taken during the productive life of beef cows from a multibreed Angus-Brahman population using random regression models. The dataset contained 40,009 weights from 1,792 cows. Genetic analyses were performed using random regression models (RRM) with Legendre polynomials (LP). Reference heritabilities at birth, weaning, and 1, 2, 3, 4 and 5 years of age were estimated using 2-trait mixed models (MTM). Fixed effects for RRM were contemporary group (year-period of measurement), and cubic LP covariates for age of female, interactions between age of female and expected Brahman fractions of female and her dam, and direct and maternal heterozygosity. Random effects were cubic LP age covariates for direct and maternal additive genetic and direct permanent environment, and residual. Two-trait models for weights up to one year had contemporary group (year-period of measurement), age of female, expected Brahman fractions of female and her dam, and direct and maternal heterozygosity as fixed effects. Random effects were direct and maternal additive genetic, maternal permanent environment and residual. Two-trait models for weights taken after one year of age ignored maternal effects. Legendre polynomials behaved badly at extreme ages. The MTM direct heritability estimates were similar to RRM values, except for birth weight (0.3 ± 0.06 for MTM and 0.02 ± 0.02 for RRM). The RRM direct heritability increased from near zero at birth to 0.59 ± 0.05 at 764 d and then decreased to 0.39 ± 0.09 at 2,500 d of age. Maternal heritability reached its maximum value at 222 d (0.09 ± 0.02) and decreased towards 2,500 d (0.02 ± 0.05). Direct permanent environment variance ratios increased from 0.04 ± 0.02 at birth to 0.57 ± 0.08 at 2,500 d of age. Results suggested that this dataset should be reanalyzed using functions less sensitive at extreme age values such as splines to obtain reasonable estimates of variance ratios over the entire range of ages.

Key Words: cattle, multibreed, random regression

T180 Ranking of Nellore cattle at agricultural shows: Genetic and phenotypic parameters with production traits. M. E. Z. Mercadante*[1], E. A. Simielli Filho[1], J. A. V. Silva[2], T. R. Pinheiro[3], A. L. Grion[1], and L. A. Josahkian[4], *[1]Centro APTA Bovinos de Corte, Instituto de Zootecnia, Sertaozinho, Sao Paulo, Brazil, [2]Faculdade de Medicina Veterinária e Zootecnia, UNESP, Botucatu, Sao Paulo, Brazil, [3]AVAL, Goiania, Goias, Brazil, [4]ABCZ, Uberaba, Minas Gerais, Brazil.*

Although livestock judging does not use techniques of genetic evaluation and the population samples are not comprehensive in terms of the number of animals evaluated, agricultural shows exert an effect on breed improvement since the champion animals are rapidly disseminated in the population through semen or oocytes. Records (28,279) of 17,141 Nellore cattle participating in 26 agricultural shows, born from 1994 to 2009, from 764 sires, were used to estimate genetic and phenotypic parameters between animal rank in cattle judging and growth traits (yearling weight-YW, hip height-HH, body length-BL, heart girth-HG), scrotal circumference (SC) and ultrasound carcass traits (longissimus muscle area-LMA, backfat-BF, rump fat thickness-RF). Two traits were defined for animal rank in cattle judging: value 1 was attributed to animals ranked 1st to 3rd place within the age category and value 0 to the remaining animals (TOP3); and, value 1 was attributed to animals ranked 1st to 5th place within the age category and value 0 to the remaining animals (TOP5). TOP3 and TOP5 were evaluated from weaning to 36 months of age as repeated traits and YW, HH, BL, HG, SC, LMA, BF and RF were evaluated as single traits at 365 days of age. The (co) variance components were estimated by Bayesian inference under a two-trait threshold-linear animal model. The heritabilities posterior means estimated for TOP3 and TOP5 were 0.182 ± 0.010 and 0.260 ± 0.012, and the repeatabilities were 0.341 ± 0.007 and 0.400 ± 0.007. Genetic correlation between TOP3, TOP5 and YW were higher (0.941 ± 0.016 and 0.943 ± 0.014) than the estimates between TOP3, TOP5 and HH, BL, HG (from 0.535 ± 0.098 to 0.757 ± 0.038). Low genetic correlations were estimated between animal rank traits and SC (0.439 ± 0.072 and 0.382 ± 0.067) and carcass traits (from 0.341 ± 0.114 to 0.231 ± 0.145). The highest phenotypic correlations were estimated between TOP3, TOP5 and YW (0.485 ± 0.010 and 0.535 ± 0.009), followed by the phenotypic correlations with HG (0.379 ± 0.019 and 0.390 ± 0.018), suggesting that judges are most influenced by these two traits at the time of awarding prizes.

Key Words: *Bos indicus*, categorical trait, Zebu

T181 Genetic parameters and genetic trends for preweaning growth in an Angus-Brahman cattle population in the Colombian tropics. O. D. Vergara[1], M. A. Elzo*[2], R. M. Patino[3], A. Calderon[1], and R. Almanza[4], *[1]University of Cordoba, Monteria, Colombia, [2]University of Florida, Gainesville, [3]University of Sucre, Sincelejo, Colombia, [4]Gencaribe Hacienda Abastecedora de Carnes SA, Planeta Rica, Colombia.*

The objective of this research was to estimate genetic parameters and trends for birth weight (BW) and weaning weight adjusted to 270 d of age (WW270) in a beef cattle population composed of Angus and Brahman straightbred and crossbred animals located in a Colombian premontane humid forest. Data were from 561 calves born from 1999 to 2010. The 2-trait model included the fixed effects of contemporary group (year-season-sex), age of dam, breed direct genetic effects, breed maternal genetic effects, individual heterosis, and maternal heterosis. Random effects were calf direct genetic, dam maternal genetic, permanent environmental maternal, and residual. Variance components and genetic parameters were estimated by restricted maximum likelihood. Program AIREML was used to perform computations. Heritabilities estimates for additive direct genetic effects were 0.08 ± 0.005 for BW and 0.10 ± 0.006 for WW270. Maternal heritability was 0.04 ± 0.002 for BW and 0.08 ± 0.005 for WW270. 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 correlation between additive direct genetic effects for BW and WW270 (0.18 ± 0.03) indicated that genes affecting BW also affected WW270. The genetic correlations between direct and maternal additive effects were negative for BW (−0.51 ± 0.02) and for WW270 (−0.21 ± 0.03) suggesting that genes increasing weight would lower maternal ability. Calf weighted yearly means showed near zero trends during these years for direct and maternal effects for BW and WW270. This indicated that the intensity of selection applied to this multibreed population

was insufficient to influence direct and maternal genetic yearly EBV means during this 12-yr period. To make genetic progress for direct and maternal growth traits, a selection program that utilizes direct and maternal animal EBV to select replacement sires and dams will need to be implemented in this population.

Key Words: beef cattle, genetic parameters, genetic trends

T182 Population structure and relation among inbreeding coefficient and breeding values in Guzera beef cattle. D. G. F. Guidolin*[1,3], N. V. Grupioni[2,3], N. C. Tramonte[2,3], I. Urbinati[3,5], T. C. S. Chud[2,3], R. B. Lobo[4], and D. P. Munari[3,5], *[1]Coordenacao de Aperfeicoamento de Pessoal de Nivel Superior, CAPES, Brasilia, DF, Brazil, [2]Fundacao de Amparo a Pesquisa do Estado de Sao Paulo, FAPESP, Sao Paulo, SP, Brazil, [3]Universidade Estadual Paulista Julio de Mesquita Filho, UNESP, Jaboticabal, SP, Brazil, [4]Associacao Nacional de Criadores e Pesquisadores, ANCP, Ribeirao Preto, SP, Brazil, [5]Conselho Nacional de Desenvolvimento Cientifico e Tecnologico, CNPq, Brasilia, DF, Brazil.*

The aim of this study was to estimate population parameters and inbreeding coefficients and its relation with breeding values and with the index indicated for the Guzera breed (MGT). The reason to do that was to provide information for the breeding program hold by ANCP. For this we used pedigree data from 26,160 animals, born between 1943 and 2009, bred in 43 herds participant in the Guzerá Breeding Program (PAGRG). The population parameters estimated were average inbreeding coefficient (F), inbreeding per generation (DF), effective population size (Ne), generation interval, effective number of founders (Nf) and number of ancestors (Na). The traits studied were age at first calving (AFC), scrotal circumference at 365 and 450 days of age (SC365) and (SC450), body weight at 365 and 450 days of age (BW365) and (BW450). Ne presented equal to 78.59, indicated low genetic diversity in the herds studied. The generation intervals observed in the population is considered to be high, 9.1 years. The F observed was 0.93% and DF was 0.64%, this indicates that the inbreeding coefficient is increasing through the period studied. Although it was observed that the inbreeding coefficient does not influence animal performance. Despite the fact that inbreeding depression was not observed in this study, mating related animal is not recommended.

Key Words: parameter, selection, zebu

T183 Genetic parameters and trends for productive, reproductive and carcass traits in Guzera beef cattle. D. G. F. Guidolin*[1,3], N. V. Grupioni[2,3], N. C. Tramonte[2,3], P. A. Bernardes[3,5], G. B. Nascimento[1,3], G. Vargas[1,3], R. B. Lobo[4], and D. P. Munari[3,5], *[1]Coordenacao de Aperfeicoamento de Pessoal de Nivel Superior, CAPES, Brasilia, DF, Brazil, [2]Fundacao de Amparo a Pesquisa do Estado de Sao Paulo, FAPESP, Sao Paulo, SP, Brazil, [3]Universidade Estadual Paulista Julio de Mesquita Filho, UNESP, Jaboticabal, SP, Brazil, [4]Associacao Nacional de Criadores e Pesquisadores, ANCP, Ribeirao Preto, SP, Brazil, [5]Conselho Nacional de Desenvolvimento Cientifico e Tecnologico, CNPq, Brasilia, DF, Brazil.*

The objectives of this study were to estimate genetic parameters and genetic trends for traits evaluated by the Guzera Breeding Program (PAGRG), in order to provide support for the genetic improvement of the breed. Records on 18,491 animals from 43 farms were used. Traits studied were rib eye area (REA), fat thickness between the 12th and 13th rib (FT), rump fat thickness (RF), age at first calving (AFC), scrotal circumference at 365 (SC365) and 450 (SC450) days of age, gestation length (GL), mature weight of the cow (MWC), body weight at birth (BWB), 120 (BW120), 210 (BW210), 365 (BW365), 450 (BW450 days old) and cumulative productivity in females (CP). Genetic parameters and breeding values were estimated by restricted maximum likelihood, by one and two-trait analysis whose general model included additive genetic random effect and fixed effect of contemporary groups (CG), for CP, AFC, SC365 and SC450. For GL, BWB, BW120, BW210, BW365 and BW450, a maternal additive random genetic effect and the fixed effect (linear and quadratic) of the cow's age at calving were added to the base model. For carcass traits, the fixed effect (linear) of weight at ultrasound was included. Genetic trends were obtained by linear regression of average annual breeding values (obtained by one-trait analysis) on year of birth (1987 to 2009) The t statistic was used and the null hypothesis considered the regression coefficient as zero. Most traits showed sufficient additive genetic variation, except CP, FT and RF, which expressed low genetic correlations with other traits. The trend graphs indicate that genetic change is occurring in the average breeding value of animals over time, with the exception of CP, GL and the maternal genetic effect for BWB. The inclusion of RF in a selection index proposed by ANCP is recommended.

Key Words: zebu, heritability, breeding

T184 Genetic trend on growth traits in Hanwoo. Y.-S. Choi*[1], S.-W. Kim[1], K.-S. Kim[1], S.-K. Lee[1], D.-J. Yu[1], A.-A Yun[1], M.-J. Ku[1], D.-H. Park[1], J.-W. Lee[2], and W.-H. Kim[1], *[1]Livestock Research Institute Jeollanamdo Agricultural Research & Extension Service (JARES), Gangin-gun, Jeollanamdo, Republic of Korea, [2]Chonnam National University, Gwangju, Republic of Korea.*

The objectives of this study were to figure out factors affecting growth performance of Korean native cattle called Hanwoo and to analyze phenotypic correlations among carcass traits. Birth and weaning weights and carcass traits were considered for prediction of potential ability on growth. Linear model was used to analyze sex of calves, dam parity and age, birth year, birth season, slaughter season were used as fixed factors in this study. Birth and weaning weights by sex of calves were 27.32 ± 2.26kg and 83.84 ± 14.23kg in bull and 26.24 ± 3.08kg and 82.44 ± 14.34kg in heifer, respectively. Birth weight in bull was significantly heavier than those in heifer ($P < 0.05$). Carcass weight by the sex of calves was 399.07 ± 56.25 kg in steer and 302.16 ± 56.25 kg in cow. Eye muscle area was 87.37 ± 11.36 cm^2 in steer and 73.37 ± 13.02 cm^2 in cow. Birth weight by parity of dam was significantly different ($P < 0.05$). Birth and weaning weights at 4th parity was 28.86 ± 2.86 kg and 88.00 ± 14.29kg, respectively. Birth and weaning weights by birth season were not different. But carcass weight born in summer season was 386.85 ± 67.28 kg which was heavier than those of them born in spring season ($P < 0.05$). Backfat thickness by slaughter season was significantly different ($P < 0.05$). Carcass weight and eye muscle area slaughtered at winter were 379.38 ± 68.53 kg and 84.27 ± 14.20cm^2. Phenotypic correlation coefficient between carcass weight and eye muscle area was 0.84 in cow and 0.66 in steer. Other correlation coefficients of carcass traits were positive. Phenotypic correlation coefficient by birth season winter was negative between eye muscle area and backfat thickness and the other traits of correlation coefficient were positive 0.84 in cow and 0.66 in steer. Other correlation coefficients of carcass traits were positive. Especially phenotypic correlation coefficients between carcass weight and eye muscle area were 0.86 in spring, 0.81 in summer, 0.79 in fall, and 0.73 in winter, respectively. These results indicated that age of dam should be an important factor for better growth performance and eye muscle area could be used as a selection indicator to increase carcass weight.

Key Words: Korean native cattle, genetics, growth trait

T185 Genetic and phenotypic (co)variance component estimation of reproductive traits in a multibreed beef cattle population. Y. Mu*, T. Caldwell, G. Vander Voort, J. Jamrozik, R. Ventura, and S. Miller, *Centre for Genetic Improvement of Livestock, Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada.*

Accurate (co)variance estimates are necessary to optimize selection response in reproductive traits of economic importance for commercial beef cow/calf operations. The objective of this research was to determine the heritability of and relationship among 5 reproductive traits in a multi-breed beef cattle population. Records on 1369 cows from 505 sires and 1360 dams were collected between the years 2002 and 2011. Binary traits of first-service conception rate (FSCR) and pregnancy rate (PR), a categorical trait (number of service per conception, NS) were analyzed by a threshold model, while interval traits of gestation length (GL) and days to calving (DC) were analyzed using a linear model.Models included fixed effects of contemporary group (herd, year, breeding season and breeding method), age of cow, age of dam and linear regressions on breed proportions of Angus, Limousin, Charolais, Simmental, Gelbvieh and Piedmontese. Additive genetic and permanent environment due to repeated records on cows were included as random effects with service sire fitted in the threshold model as random univariate and bivariate animal models were fitted using ASReml (Gilmour et al, 2008). Estimates of heritabilities (repeatabilities) for FSCR, PR, NS, GL and DC were 0.121 (0.149), 0.143 (0.143), 0.016 (0.045), 0.211 (0.211) and 0.068 (0.096), respectively, which were relatively high compared to previous research. Genetic correlations between FSCR and PR, DC and GL were positive and high (r_G = 0.985 and 0.744). Furthermore, in addition to the negative correlation between the FSCR and GL (r_G = -0.562), the other traits appeared to be genetically independent. Phenotypically, reproductive traits were correlated with low to mediate correlation coefficients from -0.249 to 0.537. These parameters indicate genetic progress in reproductive traits of a multibreed beef cattle population would be possible.

Key Words: beef cattle, reproduction, genetic correlation

T186 Genetic analysis of a temperament trait in a Nellore cattle population in Brazil. F. L. Silva*[1], L. C. A. Regitano[3], F. Penagaricano[2], A. L. Paco[5], T. Sonstegard[4], L. L. Coutinho[1], M. A. Mudadu[3], M. M. Alencar[3], G. J. M. Rosa[2], and G. B. Mourao[1], *[1]ESALQ, USP, Piracicaba, SP, Brazil, [2]Department of Animal Sciences, University of Wisconsin, Madison, [3]Embrapa Pecuaria Sudeste, Sao Carlos, SP, Brazil, [4]USDA-ARS-ANRI-BFGL, Beltsville, MD, [5]UNESP, Jaboticabal, SP, Brazil.*

Temperament in cattle is generally assessed as the reaction of an animal to a stressful event, such as human handling. Flight speed (FS) is a temperament trait measured the time the animal takes to exit a squeeze chute over a given distance. A lower FS is indicative of a calmer animal, which is then easier to handle and manage. In addition, FS has been found to influence the productive performance of herds, due to its correlation with other traits such as carcass quality, daily gains, pregnancy rate and feed efficiency. However, almost nothing is known regarding the genetic landscape controlling FS variation in cattle. Thus, the objectives of this study were to identify genomic regions and biologically relevant pathways associated with FS in a Nellore cattle population in Brazil. The analysis included 599 Nellore males belonging to 34 paternal half-sib families born between 2007 and 2009 at the experimental farms Embrapa Cattle-Southeast and Embrapa Beef Cattle, and three additional farms in the State of Mato Grosso do Sul, Brazil. The genomic information consisted of 563,672 single nucleotide polymorphisms (SNPs). Associations between SNPs and FS were assessed using a series of linear mixed models, one for each SNP, including a random polygenic effect and a permanent environmental effect. These analyses were performed using the pedigreemm package in R. Gene set enrichment analysis also was conducted in order to find potential Gene Ontology (GO) terms related to this trait. Estimated SNP effects indicated some genomic regions that might be associated with FS, such as in chromosomes 5, 13 and 15. Additionally, we found a total of 28 GO terms significantly enriched with genes associated with FS. Interestingly, several of these functional categories are related to stress, such as cellular adhesion (GO: 0007155) and process of cellular response to toxins, physical stresses and inflammatory cytokines which occur by signaling via the stress-activated protein kinase (IPR017441). Results of this study shed some light regarding the genetic architecture underlying this trait in beef cattle. Financial support: FAPESP, EMBRAPA.

Key Words: beef cattle, gene ontology, GWAS

T187 The effects of winter hair coat shedding of Angus dams on adjusted weaning weight of calves. K. Fleetwood*[1], G. Hansen[1], T. Smith[2], J. Parish[2], and J. P. Cassady[1], *[1]North Carolina State University, Raleigh, [2]Mississippi State University, Mississippi State.*

Heat stress is a major concern for some beef cattle producers. Methods to select cattle that are resistant to the negative effects of heat stress are economically important for these producers. Decreases in feed intake, conception rates and milk production lead to reduced gains for cows and calves. A visual scoring method of how winter hair coat is shed may help identify cattle more resistant to heat stress. The objectives of the study were to collect hair coat shedding scores (HCS) on registered Angus dams throughout the Southeast, Missouri and Texas and to explore the relationship between HCS of the dam and adjusted weaning weight (WW) of her calf. Hair coat shedding scores were collected from 18 farms in 2011-2012 in North Carolina, South Carolina, Virginia, Tennessee, Kentucky, Missouri, Alabama, and Texas. Hair coat shedding scores were on a 1-5 scale with 5 being a cow with a full winter hair coat and a 1 being a slick summer coat. Two technicians independently scored each cow. Using the average of the two scores, cows were assigned to one of three categories for analysis. If a cow had an average HCS of less than 3, she was assigned to HCS1. If a cow had an average HCS between 3 or 4, she was assigned to HCS3. If a cow had an average HCS of 4 or greater, she was assigned to HCS5. Data were separated into two groups by calving season and analyzed separately. Regions were considered as Southeast, Missouri, and Texas. Data were analyzed in SAS using PROC GLM. There were no differences in HCS for cattle in Texas. However, for the lactating cows in Missouri and Southeast, calves from dams that were a HCS1 weighed, on average, 4.84 ± 1.62 kg ($P < 0.01$) heavier than calves from dams that were a HCS5. Calves from dams that were a HCS3 weighed, on average, 3.71 ± 1.72 kg ($P < 0.05$) heavier compared to calves from dams that were a HCS5. Calf WW did not differ between HCS1 and HCS3 dams. Regional differences observed in this project maybe due to forage differences such as the presence or absence of endophyte infected fescue. In conclusion, HCS can be a visual method to help producers determine if their cattle are suffering from heat stress.

Key Words: heat stress, beef

T188 Characterization and genetic selection for beef tenderness in polled Nellore cattle. C. U. Magnabosco*[1], E. C. Eifert[1], C. S. Prado[2], E. S. Miyagi[2], L. C. Moreira[2,1], L. M. Castro[2,1], A. F. Nakagawa[3], and R. D. Sainz[1,4], *[1]Embrapa, Brasília, DF, Brazil, [2]Universidade*

Federal de Goiás, Goiânia, GO, Brazil, [3]Guaporé Pecuária, Pontes e Lacerda, MT, Brazil, [4]University of California, Davis.

Brazil is the world's largest beef exporter, but receives low prices due to quality issues. The predominant Zebu breeds (80% Nellore) are well adapted to the tropics but generally lack tenderness. This project aims to establish the foundations for selection of Nellore animals of high genetic merit for tenderness. A base population was established by Guaporé Pecuária, using data from progeny tests of 25 sires representative of the Nellore breed and *inter se* matings of the animals with greatest potential for producing beef with high and low shear force (WBSF). A total of 82 bull calves from the third generation resulting from those matings were used in this study. Calves were born at the Guaporé Pecuária ranch in Mato Grosso, then transported to Embrapa for growing on pasture with supplementation and finally finished in a feedlot (40% corn silage + 60% concentrate, 14% CP). Calves were harvested at a minimum backfat of 4 mm in five lots after 54, 96, 104, 137 and 166 days on feed. Steaks were taken from the Longissimus muscle at the 12th rib, aged for 7 days and frozen pending measurement of shear force. Data were subjected to analysis of covariance, with Group as the main effect and age and weight at the beginning of finishing as covariates, using the GLM procedure (Minitab v. 16, State College, PA). Average initial weight of the animals was 215.3 ± 39.5 kg. There were no differences ($P > 0.10$) between Tender and Tough groups in ADG (1.443 ± 0.272 kg/d), final weight (529 ± 37.6 kg), dressing % (56.0 ± 1.38%), marbling score (Slight-) or pH (6.08 ± 0.30). There was a trend ($P = 0.072$) for greater fat thickness in the Tender group (7.3 mm) compared to the Tough group (6.5 mm). Animals in the Tender group produced beef with lower WBSF in comparison to animals in the Tough group (4.10 and 4.92 kg, respectively; $P = 0.05$). These data confirm that there is genetic variability in beef tenderness within the Nellore breed, and indicate that this trait will respond to genetic selection. Future studies will attempt to identify molecular markers to assist in genetic improvement programs for Zebu cattle.

Key Words: beef, tenderness, breeding

T189 Genetic association between heifers rebreeding and reproductive traits in Nellore heifers. R. B. Costa[1,2], A. P. N. Terakado*[1,3], and L. G. Albuquerque[1,3], *[1]Universidade Estadual Paulista (UNESP) - FCAV, Jaboticabal, SP, Brazil, [2]Fundacao de Amparo a Pesquisa do Estado de Sao Paulo (FAPESP), Sao Paulo, SP, Brazil, [3]Conselho Nacional de Desenvolvimento Cientifico e Tecnologico (CNPq), Brasilia, DF, Brazil.*

The aim of this study was to estimate genetic correlations between heifer rebreeding and other reproductive traits in Nellore heifers, and verify the possibility to include these traits as selection criteria in beef cattle breeding programs. Data from 231,473 Nellore females belonging to Agropecuaria Jacarezinho LTDA were used. Primiparous heifer rebreeding (PHR) was defined by assigning value 1 (failure) or value 2 (success) for heifers that did not calve or calved, respectively, given that they had previously calved. Early pregnancy occurrence (P16) was defined based on the conception and calving of the heifer, given that heifers entered the breeding season around 16 months of age. For heifers that calved before 31 months of age it was assigned the value 2 (success) and those who failed, the value 1 (failure). Age at first calving (AFC) and Days to first calving (DFC) were also analyzed. Genetic parameters were estimated by Bayesian inference in two-trait analyses, assuming a linear animal model for AFC and DFC and a threshold model for PHR and P16. For all traits, the additive direct effect was considered as random and the effect of contemporary group, as fixed. For PHR, the linear effect of the number of days between the first calving date and the second conception date was used as covariable. For P16, the linear effect of the covariable age of the heifer at the beginning of the breading season was used. Heritability estimates were 0.18 ± 0.02; 0.05 ± 0.01, 0.20 ± 0.03, and 0.56 ± 0.03 for PHR, DFC, AFC, and P16, respectively. Genetic correlation estimates between PHR and DFC (−0.59 ± 0.04), AFC (−0.68 ± 0.05), and P16 (0.72 ± 03) suggest that selection to improve any of these traits will result in an increase in re-conception rate.

Key Words: age at first calving, beef cattle, early pregnancy

T190 Evaluation of sire breed type on growth and carcass characteristics utilizing multigenerational Angus sired calves versus Charolais-sired calves. J. Bailey*, M. J. Canal, T. R. Howard, G. T. Gentry, and M. D. Garcia, *Louisiana State University, Baton Rouge.*

The objective of this study was to evaluate the effect of sire breed type on growth, performance, and carcass characteristics. This study compared the effects of sire breed type between calves sired by either multigenerational Angus sires or Charolais sires. A total of 132 calves were evaluated for growth performance traits were collected at the Central Research Stations in Baton Rouge, LA, and included birth weight, weaning weight, hip height, and average daily gain. Carcass quality and composition traits were also collected and included hot carcass weight (HCW), rib eye area (REA), back fat (BF), and marbling score (MARB). Analyses were conducted by breed using a means separation analysis with simple t-test procedures in SAS. Mean birth weights were significantly higher ($P < 0.05$) for Charolais-sired steers and heifers as compared to Angus-sired heifers. Charolais-sired steers had a significantly higher ($P < 0.05$) birth weight than Angus steers. Mean weaning weights however were significantly higher ($P < 0.05$) for Angus-sired steers and heifers as compared to Charolais-sired heifers. No significant differences were reported between the two groups for hip height, average daily gain, or hot carcass weight. Charolais-sired calves had a significantly larger ($P < 0.05$) rib eye area when compared to the Angus-sired calves. A significant difference ($P < 0.05$) was reported for back fat with the Angus-sired calves having a larger recorded measurement than the Charolais-sired calves. A significant difference ($P < 0.05$) was reported for marbling with the Angus-sired calves having a greater measurement than the Charolais-sired calves. The results of a larger rib eye area and lesser amount of marbling and back fat in the Charolais-sired calves as compared to the multigenerational Angus sired calves is in agreement with previous reports describing the differences in growth and carcass traits associated with each of these breeds.

Key Words: growth trait, carcass quality, carcass composition

T191 Genetic association between carcass, growth and visual scores traits in Hereford × Nellore cattle. A. P. N. Terakado*, R. B. Costa, D. R. Ayres, R. Carvalheiro, and L. G. Albuquerque, *Universidade Estadual Paulista (UNESP) - Faculdade de Ciencias Agrarias e Veterinarias, Jaboticabal, Sao Paulo, Brazil.*

The use of genetic evaluation is an important tool to increase farming profitability, allowing the identification and selection of superior genetically animals. The aim of this study was to estimate genetic associations among post-weaning daily gain (PWG), loin eye area (LEA) and backfat thickness (BT) measured by ultrasound, and visual scores of body structure (S), finishing precocity (F) and muscling (M) in Hereford × Nellore animals, to verify the possibility to include these traits as selection criteria in beef cattle breeding programs. Data from 231,354 animals from Conexao Delta G breeding program were used. The animals were scanned for LEA between the 12th and 13th ribs and for BT over the

longissimus muscle at a point 3/4 the length ventrally of LEA. Scores ranging from 1 to 5 were attributed to the traits S, F and M, with 5 corresponding to the highest expression of the trait and 1 corresponding to the lowest expression. For all traits, the individual and maternal breed compositions were considered as a fixed effects and the yearling age (linear and quadratic effects) as a covariate. For LEA and BT, it was considered the yearling weight (linear and quadratic effects) as a covariate. The genetic parameters were estimated by Bayesian inference in multi-trait analysis, under a linear animal model. Heritability estimates for PWG, LEA, BT, S, F and M were 0.13 ± 0.008; 0.20 ± 0.047; 0.09 ± 0.029; 0.16 ± 0.011; 0.16 ± 0.012 and 0.25 ± 0.012, respectively. Genetic correlations between PWG and visual scores ranged from 0.31 to 0.46, thus selecting to increase PWG will lead to genetic changes in the same direction in S, F and M. Otherwise, correlations between PWG and carcass traits were −0.22 (LEA) and −0.33 (BT), suggesting that selection for higher PWG will decrease LEA and BT. The genetic correlation estimates between S, F, M and carcass traits were practically null, −0.01 (S × LEA); 0.07 (S × BT); 0.08 (F × LEA); 0.05 (M × LEA) and 0.13 (M × BT), thus visual scores are not good indicators of those traits. However, a moderate genetic correlation was found between F × BT (0.44), this indicates that selection for F will increase BT.

Key Words: beef cattle, crossbred, genetic correlation

T192 Evaluation of growth and performance characteristics of crossbred calves sired by Charolais, Simmental, or Braunvieh sires. M. S. Mizell*, T. Page, K. Harborth, M. Canal, A. Canal, and M. D. Garcia, *Louisiana State University, Baton Rouge.*

The objective of the current study was to evaluate the growth and performance characteristics for a crossbred calf crop sired by three different paternal breeds of sires. The sire breeds consisted of Braunvieh, Charolais, and Simmental cattle that all originated from herds in the southeastern United States. The three sire types were mated to a population of crossbred cattle that are classified by the breed types comprising the MARC germplasm cycle 8 dams. A total of 44 Simmental calves, 34 Charolais calves, and 32 Braunvieh calves were calved at the LSU AgCenter Central Research Station and all had birth weights, weaning weights, and hip height measurements collected. Birth weight measurements were recorded within 48 hours of birth. Weaning weight and hip height measurements were recorded at weaning on approximately day 210 days of age. The average birth weight, weaning weight, and hip height for the Simmental heifers were 37.57 kg, 282.79 kg, and 113.77 cm. The average birth weight, weaning weight, and hip height for the Simmental steers were 40.01 kg, 307.24 kg, and 115.87 cm. The average birth weight, weaning weight, and hip height for the Charolais heifers were 34.98 kg, 266.67 kg, and 111.48 cm. The average birth weight, weaning weight, and hip height for the Charolais steers were 39.01 kg, 300.93 kg, and 115.14 cm. The average birth weight, weaning weight, and hip height for the Braunvieh heifers were 36.88 kg, 255.08 kg, and 111.53 cm. The average birth weight, weaning weight, and hip height for the Braunvieh steers were 35.28kg, 270.91kg, and 112.67 cm. Utilizing the mixed model procedure and the LSMEANS function of SAS it was observed that Simmental sired calves had a significantly higher birth weight ($P < 0.05$) than both the Braunvieh- and Charolais-sired calves. Simmental-sired calves also had a significantly ($P < 0.05$) higher hip height measurement than Braunvieh-sired calves but were not taller than Charolais-sired calves. No significant differences were reported between sire breeds for weaning weight.

Key Words: growth, birth weight, weaning weight

T193 An evaluation of 55 years of performance trends from the Dean Lee Research Station performance bull test. T. R. Howard, S. DeRouen, K. Harborth, K. Bondioli, and M. D. Garcia*, *Louisiana State University, Baton Rouge.*

The objective of this study was to evaluate genetic trends for bulls that have comprised the LSU AgCenter Dean Lee performance bull test that has been conducted for the past 55 years. The LSU AgCenter Performance bull test at the Dean Lee Research Station has collected data on yearling bulls on 112d of test for the last 55 years. To date 7,488 yearling bulls from 34 breeds have been evaluated for such traits, including birth weight (BW), initial weight, 112-day weight, average daily gain (ADG), adjusted yearling weight, and scrotal circumference (SC). The top 4 represented bull breeds with greater than 500 animals being tested were included in a Angus, Charolais, Hereford, and Simmental. In 1958, initial weights averaged 249.38 kg and 112-day weights averaged 362.19 kg. Initial weights and 112-d weights in 2011 averaged 332.52 kg and 510.49 kg, respectively. Analyses revealed that all growth traits for all animals regardless of breed demonstrated a linear increase across the years with BW and SC being the lone exceptions. Initial weight increased 1.61 kg/year, 112-d weight increased 2.63 kg/yr, ADG increased .0091 kg/day/year and adjusted yearling weight increased 3.67 kg/year while BW and SC decreased −0.44 kg/year and −0.23 cm/year respectively. The mixed model procedure of SAS and interval regression analyses were utilized to evaluate the positive slope increase observed for all traits over the past 55 years for the four highest represented breeds. Analysis of each individual breed's performance across all years indicated that the Simmental breed had the greatest increase ($P < 0.05$) in initial weight with 3.92 kg/year over Angus (1.92 kg/year), Charolais (0.12 kg/year), and Hereford (1.21 kg/year) ($P < 0.05$). Results for 112-day weight indicated that the Simmental breed made a greatest increase ($P < 0.05$) of 3.79 kg/year when compared to Angus (3.23 kg/year), Charolais (1.99 kg/year), and Hereford (2.24 kg/year). Charolais displayed the largest increase ($P < 0.05$) in ADG across all years with 0.02 kg/day/year while Angus, Hereford, and Simmental increased 0.01, 0.009, and 0.001 respectively.

Key Words: bull test, performance testing, genetic trend

T194 Multivariate heavy-tailed distribution modeling of residuals in estimation of genetic parameters of carcass traits in beef cattle. S. O. Peters[1,2], K. Kizilkaya[3,4], D. J. Garrick[3], R. L. Fernando[3], E. J. Pollak[5], M. De Donato[1,6], T. Hussain[1,7], and I. G. Imumorin*[1], *[1]Cornell University, Ithaca, NY, [2]Berry College, Mt Berry, GA, [3]Iowa State University, Ames, [4]Adnan Menderes University, Aydin, Turkey, [5]US Meat Animal Research Center, Clay Center, NE, [6]Universidad de Oriente, Cumana, Sucre, Venezuela, [7]University of Veterinary and Animal Sciences, Lahore, Pakistan.*

Evaluation of carcass quality and estimation of genetic parameters for carcass traits are of considerable importance in the genetic improvement for beef cattle. Assumption of normality of residuals in linear mixed models for carcass evaluation may make inferences vulnerable to the presence of outliers. Heavy-tail densities are viable alternatives to normal distributions. We compared estimates of genetic parameters by fitting Multivariate Normal (MN), Multivariate Student's-*t* (MS*t*) or Multivariate Slash (MS) and treating degrees of freedom (ν) as unknown for residuals in data of hot carcass weight (HCW), longissimus muscle area (REA) and 12th to 13th rib fat (FAT) traits in beef cattle. A total of 2,476 HCW, REA and FAT records were obtained from a large commercial operation in Nebraska between 2007 and 2008. The data set included pedigree information, contemporary groups, feed lot and breed types. Models included fixed effects of contemporary group of year and pasture and also feed lot type and sire breed. Deviance information criteria for

model comparisons favored MS*t* over MS and MN models respectively. The posterior means (PM) (and 95% posterior probability intervals, PPI) of *v* for the MS*t* and MS models were 5.90 ± 0.86 (4.37, 7.70) and 2.02 ± 0.17 (1.70, 2.38) respectively. Smaller values of posterior densities of *v* for MS*t* and MS models confirm that the assumption of normally distributed residuals is not adequate for the analysis of HCW, REA and FAT datasets. Posterior inference on additive heritabilities for HCW, REA and FAT using MN, MS*t*, and MS models indicated that they are similarly and moderately heritable and were comparable to those reported in literature. PM of genetic correlations for the HCW, REA and FAT were variable but positive except for the correlation between REA and FAT, which shows an antagonistic relationship. The 95% PPI estimates from MN and MS*t* models for HCW did not overlap indicating significant difference between PM estimates from MN or MS*t* models.

Key Words: cattle, genetic parameter, residual

T195 Heritability and correlations of immune response parameters in cattle treated for bovine respiratory disease. R. R. Cockrum*[1], S. E. Speidel[1], J. L. Salak-Johnson[2], C. C. L. Chase[3], R. K. Peel[1], R. L. Weaber[4], H. Van Campen[1], G. H. Loneragan[5], J. J. Wagner[1], P. Boddhireddy[6], M. G. Thomas[1], K. Prayaga[6], and R. M. Enns[1], *[1]Colorado State University, Fort Collins, [2]University of Illinois, Urbana, [3]South Dakota State University, Brookings, [4]Kansas State University, Manhattan, [5]Texas Tech University, Lubbock, [6]Zoetis, Kalamazoo, MI.*

We hypothesized that cattle vary in their innate immune response, which may serve as indicators of developing bovine respiratory disease (BRD). The objectives of this study were to determine the heritability and associative relationships among immune response parameters. Two contemporary groups of crossbred steer calves (n = 2869) were received approximately 83 d post-weaning (221.7 ± 24.34 kg) at a commercial feedlot in Southeastern Colorado. Upon receiving, jugular blood was collected via silicone-coated vacutainer tubes for immune response analyses. Immune response measures were collected at 227 d and 238 d for contemporary groups one and two, respectively. Heritability estimates for immunoglobulin G (IgG), immunoglobulin G1 (IgG1), immunoglobulin G2, (IgG2), IgG1 to IgG2 ratio (IgG1:IgG2), cortisol, and interleukin 8 (IL8) were estimated from a sire model using ASREML. Estimated heritability was low to moderate for the following immune response parameters: IgG (0.13), IgG1 (0.02), IgG2 (0.27), IgG1:IgG2 (0.13), cortisol (0.15), and IL8 (0.30). Furthermore, incidence of BRD as measured from observed clinical signs was heritable (0.21). Correlations among phenotypes and genotypes for traits of interest were calculated. There were low to high positive phenotypic correlations (0.12–0.87 ± 0.02; $P < 0.001$) between IgG, IgG1, IgG2, and IgG1:IgG2. Low negative phenotypic correlations ($P < 0.001$) were estimated between cortisol and IgG (−0.15 ± 0.02), IgG1 (−0.08 ± 0.02), and IgG1:IgG2 (−0.07 ± 0.02). Interleukin 8 had a low positive phenotypic correlation (0.04 ± 0.02; $P = 0.033$) with IgG. Moderate to high positive genetic correlations were observed between IgG1 and IgG2 (0.34) and cortisol (0.57), and a moderate negative genetic correlation was observed with IL8 (−0.36). Results from this study suggest that immune response parameters are heritable suggesting that immune response may be improved through genetic selection.

Key Words: bovine respiratory disease, cattle, immunity

T196 Genome-wide association study of cholesterol and poly- and monounsaturated fatty acids of beef from crossbred cattle. L. N. Schiermiester*, C. M. Ahlberg, J. T. Howard, C. Calkins, and M. L. Spangler, *University of Nebraska, Lincoln.*

Crossbred cattle of varying percentages of Angus, Simmental, and Piedmontese were used to investigate the proportion of phenotypic variation explained by the BovineSNP50 assay for the traits of cholesterol (CH), polyunsaturated fatty acids (PUFA), and monounsaturated fatty acids (MUFA). Steers and heifers (n = 239) were split into 4 groups and placed in a feedlot over a 2-year period between 2010 and 2012. After harvest, half-inch thick steaks were sampled from the eye of round (eye) and the longissimus dorsi (strip) and trimmed to a 1/8 inch of subcutaneous fat for nutrient analysis. All animals were genotyped with the BovineSNP50 assay and had a call rate above 97.5%. Illumina data analysis software was used to assign quality scores (GenCall) for each genotype. If genotypes were missing or a GenCall score was below 0.20, genotypes were replaced with the mean allele frequency across all animals. No SNP were culled based on minor allele frequency. A Bayes C algorithm was employed fitting group as a fixed effect using the GenSel software incuding a chain length of 150,000 samples with the first 50,000 being discarded as burn-in. In general, there was strong agreement between the posterior heritability estimates between the 2 cuts for all traits. The resulting posterior heritability (SE) estimates were 0.46(0.11), 0.52(0.06), 0.67(0.06), 0.71(0.08), 0.61(0.07), and 0.43(0.10) for eye CH, strip CH, eye PUFA, strip PUFA, eye MUFA, and strip MUFA, respectively. SNP were blocked into 1 Mb windows and the top 0.5% windows (n = 13) were compared across cuts within a trait. Of the windows in common between the 2 cuts for MUFA, 5 were on BTA2 and one on BTA19 (7–8 Mb). For PUFA, all 8 windows in common were on BTA2 and the one window in common for CH was also on BTA2. The influence of regions on BTA2 suggest that the Myostatin mutation (C313Y) segregating in some of these animals influences CH, MUFA and PUFA content of beef.

Key Words: beef cattle, genome-wide association study, fatty acids

T197 Genome-wide association study of protein and mineral content of beef from crossbred cattle. C. M. Ahlberg*, L. N. Schiermiester, J. T. Howard, C. Calkins, and M. L. Spangler, *University of Nebraska, Lincoln.*

Crossbred cattle of varying percentages of Angus, Simmental, and Piedmontese were used to investigate the proportion of phenotypic variation explained by the BovineSNP50 assay for the traits of protein, iron, potassium and sodium. Steers and heifers (n = 239) were split into 4 groups and placed in a feedlot over a 2-year period between 2010 and 2012. After harvest, half-inch thick steaks were sampled from the eye of round (eye) and the longissimus dorsi (strip) and trimmed to a 1/8 inch of subcutaneous fat for nutrent analysis. All animals were genotyped with the BovineSNP50 assay and had a call rate above 97.5%. Illumina data analysis software was used to assign quality scores (GenCall) for each genotype. If genotypes were missing or a GenCall score was below 0.20, genotypes were replaced with the mean allele frequency across all animals. No SNP were culled based on minor allele frequency. A Bayes C algorithm was employed fitting group as a fixed effect using the GenSel software incuding a chain length of 150,000 samples with the first 50,000 being discarded as burn-in. In general, there was strong agreement between the posterior heritability estimates between the 2 cuts for all traits. Posterior heritability estimates (SE) were 0.67(0.08), 0.75(0.06), 0.38(0.13), 0.33(0.09), 0.73(0.08), 0.64(0.08), 0.13(0.08), and 0.05(0.08) for strip protein, eye protein, strip iron, eye iron, strip potassium, eye potassium, strip sodium, and eye sodium, respectively. SNP were blocked into 1 Mb windows and the top 0.5% windows (n = 13) were compared across cuts within a trait. Windows in common between the 2 cuts for protein included 6 regions on BTA2. There was only one window in common between the 2 cuts for potassium and iron, both on BTA2. There were no windows in common between the 2 cuts for sodium. The influence of regions on BTA2 suggest that the Myostatin mutation (C313Y) segregating in some of these animals influences protein and the content of some minerals in beef.

Key Words: beef cattle, genome-wide association study, nutrient profile

T198 Association between single nucleotide polimorphisms and sexual precocity in Nellore heifers. I. C. Regatieri[1,3], R. Espigolan[1,3], R. B. Costa[1,3], F. Baldi[1], and L. G. Albuquerque*[1,2], *[1]Universidade Estadual Paulista (UNESP) - FCAV, Jaboticabal, SP, Brazil, [2]Conselho Nacional de Desenvolvimento Cientifico e Tecnologico(CNPq), Brasilia, DF, Brazil, [3]Fundacao de Amparo a Pesquisa do Estado de Sao Paulo (FAPESP), Sao Paulo, SP, Brazil.*

Reproductive traits, such as age at first calving (AFC) and occurrence of early pregnancy (OP), are used as selection criteria in beef cattle breeding programs since these traits affect production system profitability. The measure (r^2) of linkage disequilibrium (LD) is used in genome-wide association studies to detect genetic markers and major genes (QTL) that influence economically important traits. The aim of this study was to determine the extent of LD in the genome of Nellore cattle, and examine associations between single nucleotide polymorphisms (SNP) and AFC and OP, using a panel of high-density SNPs. Data from 1,182 Nellore born in 2007 and 2008, belonging to Agropecuaria Jacarezinho were used. A total of 13 contemporary groups (CG) consisting of farm, season and year of birth, with an average of 90 animals per CG were formed. For genomic-wide association, only autosomes were used and SNPs with minor allele frequency (MAF) below 0.05, and animals with Call Rate below 0.90 were excluded, totaling 431,885 SNPs. The model of analysis for both traits, AFC and OP, included the CG and SNPs (0, 1 and 2) as fixed effects. The Bonferroni correction was applied to adjust the limit of significance (1.16×10^{-7}). The average r^2 for all autosomes was 0.18 at a distance of 4.8 kb and the average MAF was 0.25 ± 0.13. The LD decreased as the distance between markers increased: 0.35 (1 kb) to 0.12 (100 kb). Eleven SNP showed significant effects on the traits and were distributed in 7 different chromosomes (BTA1, BTA4, BTA6, BTA11, BTA17, BTA21, and BTA22). Among these, 7 SNPs were associated with AFC and 4 with OP. Three SNPs were significant for both traits (BTA1, BTA21, and BTA22). Chromosome BTA21 showed 2 SNPs associated with OP. A total of 19 chromosomes showed potential QTL regions for AFC and OP. The most evident peaks of significant SNPs, that may suggest potential QTL regions, were located on chromosomes BTA4, BTA6, BTA8, BTA17, and BTA19.

Key Words: genome-wide association, linkage disequilibrium, quantitative trait loci

T199 Genome-wide associations study for Nelore and Angus Heifers with low and high ovarian follicle count. M. G. Favoreto*[1], B. Loureiro[1], R. L. Ereno[1], A. G. Pupulim[1], A. S. Carmo[2], J. Buratini[1],

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High variation of follicle numbers in cows during the estrus cycle can influence their reproductive performance. Animals with high follicle count (HFC) have a better reproductive performance when compare with low follicle count (LFC) animals (Mossa et al. 2012). Moreover animals with HFC can be more responsive to reproductive biotechniques such as superovulation, ovum pick-up and in vitro fertilization. Identifying these animals with superior genetic potential for fertility would be desirable to increase farm profitability. The SNP profile of 72 Nelore (32 HFC and 40 LFC) and 48 Angus heifers (21 HFC and 27 LFC) was determined using high-density SNP chip (BovineHD Illumina). Initial data cleanup was performed to remove poorly performing and nonautosomal probes from the analysis, considering as criteria for SNP or samples exclusion minor allele frequencies >0.02, call rates >0.98, significant deviations from Hardy-Weinberg equilibrium with $P < 10^{-5}$ and samples with call rate <0.90. Fast score test (qtscore) method, equivalent to the Armitage test, was used for case–control comparisons (GenABEL package). A total of 181 SNPs from the Nelore heifers and 201 from the Angus heifers met genome wide significance ($P < 10^{-4}$). The 181 SNPs from the Nelore heifers were associated on 23 different BTA chromosomes (UMD v3.1 assembly) and the 10 most significant SNPs ($P < 9.8 \times 10^{-5}$) were detected on BTA 1, 3, 7, 9, 14, 16 and 22. In the Angus population the 201 SNPs were associated on 29 different chromosomes and the highest significant SNP ($P = 1.2 \times 10^{-5}$) were located on BTA 3. This is the first time a high density SNP chip is used to identify polymorphisms in high and low follicle counts Nellore and Angus heifers. Results show biomarkers that can contribute to identification of animals with HFC. More analysis must be performed to determine which genes associated with reproduction are linked with those SNPs. This research was financed by FAPESP grant number 2011/5964-0. Scholarships for Loureiro, Ereno, Favoreto, and Pupulim were from FAPESP.

Key Words: GWAS, follicle, SNP

T200 An SNP association study evaluating modern Charolais sired calves versus multigenerational Angus sired calves for growth and carcass traits. J. Bailey*, M. S. Mizell, A. Canal, T. R. Howard, R. Hill, T. Page, and M. D. Garcia, *Louisiana State University, Baton Rouge.*

The objective of this study is to evaluate the association of single nucleotide polymorphisms with growth, performance, and carcass quality and composition characteristics in a population of cattle consisting of multigenerational Angus sired calves and modern characteristic Charolais sired calves. Previous studies have consistently indicated considerable differences in the growth and carcass quality and composition traits between the Angus and Charolais breeds. The data collected in the current study included growth and performance traits as well as raw carcass measurements. Specifically, birth weight (BW), weaning weight (WW), hip height (HH), and average daily gain (ADG) were the growth traits collected. Carcass quality and composition traits that were collected included hot carcass weight (HCW), rib eye area (REA), back fat (BF), and marbling score (MARB). Two candidate genes were selected based on their previous associations with carcass and growth traits. These genes were the calpastatin (CAST) gene located on BTA7 and the calpain 3 (CAPN3) gene located on BTA10. A total of 40 SNP were utilized for genotyping and subsequent association analyses. Calves were genotyped for 20 single nucleotide polymorphisms located equidistant across the CAST gene and for 20 single nucleotide polymorphisms located equidistant across the CAPN3 gene. Analyses to evaluate potential SNP association were conducted via the mixed model procedure of SAS and the LSMEANS function was utilized to determine significant difference in performance for specific traits between genotypes. Multiple SNP for production and carcass quality and composition traits were identified as significant ($P < 0.05$) or exhibited a trend ($P < 0.1$) for both candidate genes. Thus, identification of SNP associated with production and carcass traits in the current study require validation in association with the use of more SNP in other cattle populations.

Key Words: cattle, growth trait, carcass

T201 SNP associated with growth and performance of yearling bulls on a forage performance bull test. T. R. Howard, M. S. Mizell, K. Harborth, M. Canal, A. Canal, K. Bondioli, T. Page, and M. D. Garcia*, *Louisiana State University, Baton Rouge.*

The objective of the current study was to evaluate the association of single nucleotide polymorphisms (SNP) on 3 candidate genes for growth and performance traits in bulls participating in forage based performance bull test. Single nucleotide polymorphisms on 3 candidate genes including calpastatin (CAST), growth hormone (GH1), and insulin-like growth factor 1 (IGF-1) were utilized for association analysis. Single nucleotide polymorphisms were selected that were evenly distributed and represented the total length of the candidate gene. Of the 49 SNP genotyped, 20 were chosen for CAST, 9 for GH1, and 20 for IGF-1. These SNP were genotyped on 47 purebred Angus, Braford, and Brahman bulls on a forage based performance bull test. The measured traits included average daily gain, birth weight, final weight, hip height, intramuscular fat (IMF), ribeye area (REA), and scrotal circumference (SC). The mixed model procedure of SAS was utilized to evaluate associations of the 49 SNPs and measured traits. Associations were reported as significant if $P < 0.05$ and as a trend if $P < 0.1$. Seven SNP exhibited a trend for ADG (rs109022910, rs109199979, rs110266103, rs132665612, rs132951819, rs109327701 and rs110959643). No SNP for BW were significantly associated; however, 3 SNP (rs109327701, rs136939207, and rs137140434) displayed a trend. For finwt, 2 SNP (rs109275907 and rs132951819) were of significant and 7 SNP (rs109022910, rs109199979, rs109327701, rs110266103, rs110959643, rs132665612, and rs133980322) displayed a trend. Hip height and SC were both significantly associated with 1 SNP (rs133980322). Intramuscular fat exhibited a trend with 3 SNP (rs132951819, rs133980322, and rs137651874). No significant associations for REA were identified while 6 SNP (rs109022910, rs109199979, rs110266103, rs110959643, rs132665612, and rs137651874) displayed a trend. In total, one SNP within the GH1 gene was significantly associated with finwt, and 2 SNP within the IGF-1 gene were significantly associated with finwt, HH, and SC. Eleven different SNPs displayed trends associated with ADG, BW, finwt, HH, IMF, REA, and SC.

Key Words: forage performance bull test, SNP

T202 Genomic-polygenic evaluation of multibreed Angus-Brahman cattle for feed efficiency and postweaning growth using actual and imputed Illumina 50k SNP genotypes. M. A. Elzo*[1], M. G. Thomas[2], C. A. Martinez[1], G. C. Lamb[1], D. D. Johnson[1], I. Misztal[3], D. O. Rae[1], J. G. Wasdin[1], and J. D. Driver[1], *[1]University of Florida, Gainesville, [2]Colorado State University, Fort Collins, [3]University of Georgia, Athens.*

The objectives were to estimate the fractions of additive genetic variances for 4 postweaning feed efficiency and growth traits explained by 40,276 actual and imputed SNP genotypes, to compare EBV rankings from genomic-polygenic (GP), genomic (G), and polygenic (P) models, and to

determine EBV trends from Angus to Brahman in a multibreed population. Traits were residual feed intake (RFI), daily feed intake (DFI), feed conversion ratio (FCR), and weight gain (PWG). Phenotypes were from 807 bull, heifer, and steer calves measured at the Feed Efficiency Facility of the University of Florida from 2006 to 2010. Imputation from 2,899 SNP (Illumina 3k) to 46,909 SNP (Illumina 50k) was done with program findhap2 using a reference population of 828 Brangus heifers. Fixed effects for all models were contemporary group (year-pen), age of dam, sex of calf, age of calf, Brahman fraction of calf, and heterozygosity of calf. Random effects were additive SNP (GP and G models), additive polygenic (GP and P models), and residual. Software GS3 was used to compute variance components and heritabilities (option VCE; Markov Chain Monte Carlo), and EBV (option BLUP). Heritabilities were 0.31 for RFI, 0.38 for DFI, 0.25 for FCR, and 0.34 for PWG. The fractions of additive genetic variances explained by the 46,909 actual and imputed SNP were 0.46 for RFI, 0.36 for DFI, 0.47 for FCR, and 0.28 for PWG. These fractions were 3.0, 3.2, 1.9, and 1.8 times larger than those obtained for these 4 traits using 2,899 SNP from the Illumina3k chip. Rank correlations between EBV from GP and P and from GP and G models were high (0.89 to 0.98; $P < 0.0001$). Lower rank correlations existed between EBV from G and P models (0.69 to 0.81; $P < 0.0001$). Regressions of EBV on Brahman fraction were negative with the G model for DFI ($P < 0.0344$) and with all models for PWG ($P < 0.0171$ to $P < 0.0001$). This suggested that calves of similar EBV for RFI, DFI and FCR existed in all breed compositions, but EBV for PWG tended to decrease as Brahman fraction increased.

Key Words: cattle, imputation, multibreed

T203 Genetic parameters and single nucleotide polymorphism of feed utilization in beef cattle. D. Gonzalez-Pena*, N. V. L. Serão, J. E. Beever, D. B. Faulkner, and S. L. Rodriguez-Zas, *University of Illinois at Urbana-Champaign, Urbana.*

Three widely used indicators of feed utilization, residual feed intake (RFI), residual average daily gain (RADG), and residual intake gain (RIG) place different weights on the 2 main components of the system, input and output. Variation in intake and growth are at the center of RFI and RADG, respectively meanwhile RIG is an index of both indicators. The previous differences are expected to affect the total genetic variation and specific single nucleotide polymorphisms (SNPs) corresponding to each indicator. The aim was to estimate the genetic variation and co-variation of the 3 feed efficiency indicators and to uncover SNPs associated with these indicators that could explain the genetic variation. Phenotypic and genotypic measurements were available on approximately 1,300 Angus, Simmental and crossbred steers, assigned to 5 feeding treatments. The pedigree matrix included 3331 individuals across 3 generations. A model including a random animal effect and the fixed effects of breed composition, treatment, contemporary group, and age was implemented in Wombat to estimate the genetic parameters. The fixed effect of genotype was added to the model and fitted on a per-SNP basis using QxPak. The heritability estimates (standard errors) for RFI, RADG and RIG were 0.40 (0.10), 0.17 (0.07), and 0.40 (0.10), respectively and the genetic correlation were −0.43 (0.09), −0.99 (0.002) and 0.55 (0.08) for RFI with RADG, RFI and RIG, and RADG and RIG, respectively. Seven, 9, and 8 SNP were associated ($P < 0.0001$) to RFI, RADG and RIG, respectively. The RFI SNPs were annotated to genes including Ciliary neurotrophic factor receptor (CNTFR) and Transmembrane protein 40 (TMEM40). The RADG SNPs were associated to genes including KDEL Lys-Asp-Glu-Leu containing 1-like (KDELC2), ELMO/CED-12 domain containing 1 (ELMOD1), and PAK1 interacting protein 1 (PAK1IP1). The RIG SNPs were also annotated to KDELC2. In total, 24 SNP on 5 genes were associated with the 3 indicators. The genetic parameter and SNP estimates can support genome-enabled selection programs to improve feed utilization in the beef cattle industry.

Key Words: feed efficiency, genetic parameter, SNP

T204 Genomic variants and genetic parameters of feed efficiency from univariate and multivariate analyses. C. Zavala*, N. V. L. Serão, D. González-Peña, and S. Rodriguez-Zas, *University of Illinois at Urbana-Champaign, Urbana.*

Average daily gain (ADG) and dry matter intake (DMI) are 2 main components of feed efficiency in beef cattle. Univariate analysis of these components hinders the ability to evaluate the genetic correlation between them, the identification of genomic variants with pleiotrophic effects on both components, and could result in lower statistical power. The goals of this study were to assess the genetic variation and co-variation of ADG and DMI and to identify single nucleotide polymorphisms (SNPs) associated with these traits using multivariate analyses, and to compare the results to univariate analyses. Records from 1,321 feedlot steers across 5 farms and 4 years were analyzed. The steers pertained to one of 5 crosses between Angus and Simmental and received one of 5 diets. Univariate and bivariate animal models including the fixed effects of crossbreeding, diet, contemporary group, age and the random effect of animal were used to estimate the genetic parameters using Wombat. Similar univariate and multivariate models including a fixed SNP effect were evaluated using QxPak and a univariate linear model including all fixed effects was evaluated in PLINK. The heritability estimates (and standard errors) for ADG and DMI were 0.14 (0.06) and 0.24 (0.08), respectively and the genetic correlation was 0.30 (0.11). Seven SNPs were associated with ADG (P-value <0.0001) in the linear fixed effects model. Genes containing or in the proximity of the SNPs detected have functions associated with growth including calmodulin regulated spectrin-associated protein 1-like 1 (CAMSP1L1), Kruppel-like factor 6 (KLF6), Fanconi anemia, complementation group F (FANCF) and pseudo gene fucosidase α-L-1 tissue-like (FUCA1, LOC100140646). The bivariate mixed-effects analysis identified the highest number of variants (11 SNPs) and the DMI and ADG mixed effects analyses identified 9 and 8 associations, respectively. The total number of SNP detected was 28, mapping to 19 unique SNPs and 9 unique genes. These results can help in the identification of variants with favorable effect on both components of feed efficiency in beef cattle.

Key Words: SNP, heritability, multi-trait analysis

T205 Accuracy of genomic predictions in Nelore cattle with different marker densities. P. Boddhireddy*[1], R. B. Lobo[2], K. Prayaga[1], P. Barros[1], and S. DeNise[1], *[1]Zoetis Inc., Kalamazoo, MI, [2]Technical Centre of Genetic Evaluation (CTAG), Ribeirão Preto, Brazil.*

The objective of this study was to investigate the improvement in accuracies of genomic predictions associated with increasing the number of markers from 50,000 (50K) to 770,000 (770K) in the Brazilian Nelore breed. Expected progeny differences (EPD) for growth, reproductive, carcass, and conformation traits were available in the study. All animals genotyped with the BovineSNP50 BeadChip were imputed to 770K using FImpute software based on a reference data set with 763 records genotyped with the BovineHD BeadChip (770K). Genomic calibrations were performed using: 50K; 770K; and trait specific (770K_trait) SNPs. Trait specific SNPs were included if they were significantly associated ($P < 0.05$) in single point association analysis. The total number of informative markers from 50K and 770K platforms were 26,458 and 492,887, respectively. The number of informative markers in the 770K_trait sets ranged from 100K to 200K depending on the trait.

Sixty percent of the animals with the highest accuracy EPDs for each individual trait comprised training data sets, and the remaining animals were used for validation. Marker effects were estimated using BayesC as implemented in Gensel software. The training data set was clustered into 5 groups based on genotype similarity using an identical-by-descent strategy. Estimated marker effects were used to calculate direct genomic values (DGVs). A 5-fold cross validation was performed on the training data set. The average correlations across all traits, between DGVs and EPDs obtained with 50K, 770K and 770K_trait were 0.50, 0.50 and 0.59, respectively for the cross-validation, and 0.63, 0.63 and 0.62, respectively, for the external validation. Cross-validation correlations were higher when markers were pre-selected. However, the correlations observed for individual traits in the external validation were similar for 50K, 770K and 770K_trait data sets. The results demonstrate that increasing marker density from 50K to 770K did not improve genomic prediction accuracies as measured by correlations between DGVs and EPDs, supporting published results in dairy populations.

Key Words: Nelore, HD genotype, prediction accuracy

T206 Genomic evaluation and identification of a haplotype affecting fertility for Ayrshire dairy cattle. T. A. Cooper*, G. R. Wiggans, D. J. Null, and J. L. Hutchison, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

Genomic evaluation of dairy cattle in the United States has been available for Holstein, Jersey and Brown Swiss since 2009. As of February 2013, there were 1,100 genotyped Ayrshires in the North American database including 646 bulls with traditional evaluations allowing for the evaluation of this breed. Gains in reliability due to genomics were determined by comparing parent averages and genomic evaluations from August 2008 to January 2013 daughter performance for bulls born on or after January 1, 2000 who received a traditional evaluation by January 2013. The number of bulls tested ranged between 147 and 180 bulls by trait. The average gain in reliability over parent average for all traits was 8.2. The highest gains were found in milk yield (16.6), protein yield (16.9) and stature (16.2). These evaluations were calculated based on the North American population and may not be suitable to all red dairy cattle because linkage disequilibrium probably differs by population. There are 12 SNP in Ayrshire that can be used for breed determination because they are nearly monomorphic (>90%) in Ayrshire and have fewer than 30% of animals homozygous for that allele in Holstein, Jersey and Brown Swiss. There are fewer breed determining SNP in Ayrshire than in Holstein, Jersey and Brown Swiss, mostly due to the similarity of Ayrshire and Holstein. A haplotype affecting fertility was located on chromosome 17. This haplotype first originated in the genotyped population with Selwood Betty's Commander (b. 1953). The carrier frequency for genotyped Ayrshires is 23.2%. Sire conception rate was 3.0% lower for carriers of the haplotype as determined by 483 carrier by maternal grandsire carrier matings. Genomic evaluations of Ayrshire provide improved prediction over parent average, raising reliability by 8.2 over all traits.

Key Words: dairy cattle, genomic evaluation, fertility haplotype

T207 Regression metamodels of an optimal genomic testing strategy in dairy cattle when selection intensity is low. A. De Vries*[1], J. B. Cole[2], and D. T. Galligan[3], *[1]University of Florida, Gainesville, [2]Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD, [3]University of Pennsylvania, Kennett Square.*

Genomic testing of dairy cattle increases reliability and can be used to select animals with superior genetic merit. Genomic testing is not free and not all candidates for selection should necessarily be tested. One algorithm used to compare alternative genomic testing decisions is time-consuming and not easily applicable in practice. Therefore, the objective of this study was to develop regression metamodels that predict increases in estimated breeding value (EBV) of net merit ($NM) in selected animals based on the reliability of pre-ranking of animals, reliability of the genomic test, proportion of animals that are genomically tested, and selection intensity. First, the increase in EBV $NM in selected animals (>50% of the population) was calculated using Monte Carlo methods when all animals were pre-ranked for EBV $NM with reliabilities varying from 0 to 100% in increments of 10 percentage points (PP). After pre-ranking all animals, the genomic test was applied to all ranges of pre-ranked animals in 10 PP increments (n = 36,300 scenarios). Selection was applied after the second ranking and the gain in EBV $NM was recorded. For example, gain in EBV $NM with 20% pre-rank reliability, testing the 60 to 90 percentiles of the pre-ranked animals, 60% genomic test reliability, and 90% selection intensity was $80. Second, the SAS procedure glmselect was used to develop regression metamodels that predict gain in EBV $NM given 30 variables constructed from reliabilities, ranges of genomically tested animals, selection intensity and their logs, squares and reciprocals. Models constrained to 5, 10, 20, or 40 variables including 2-way interactions had RMSE of $14.90, $10.98, $6.47 and $5.11, respectively. The R-squared ranged from 94.4% to 99.4%. The same 4 models including 4-way interactions had RMSE of $12.20, $6.61, $3.62, and $2.45. The R-squared ranged from 96.3% to 99.9%. In conclusion, the larger metamodels accurately predicted gain in EBV $NM and can easily be implemented in decision support aids. The cost of genomic testing may be added to find the optimal range of pre-ranked animals that should be genomically tested.

Key Words: genomics, reliability, regression

T208 Prioritizing sequence polymorphisms for potential association with phenotype. W. M. Snelling*[1], G. L. Bennett[1], R. M. Thallman[1], A. K. Lindholm-Perry[1], L. A. Kuehn[1], T. G. McDaneld[1], S. D. Kachman[2], M. L. Spangler[2], H. Koshinsky[3], and T. S. Kalbfleisch[4,5], *[1]USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, [2]University of Nebraska, Lincoln, [3]Eureka Genomics Inc., Hercules, CA, [4]Intrepid Bioinformatics, Louisville, KY, [5]University of Louisville, Louisville, KY.*

The millions of SNP, insertions and deletions revealed by next generation sequencing (NGS), are certain to include polymorphisms responsible for phenotypic variation. Distinguishing causal from benign variants may allow genomic predictions that are robust across populations. While variants underlying phenotypic variation may never be known with certainty, classifying NGS variants according to expected effects on gene function may reveal likely candidates. Associations between phenotypes and available genotypes of markers flanking each variant may further indicate those likely to affect phenotype through altered gene function. Low-coverage NGS of 96 sires used in a 7-breed population of crossbred beef cattle revealed 10,028,578 variants. 1,309 were classified as having a high impact on protein coding genes, and 1,503 occurred in non-coding RNA, which may regulate protein coding genes. Potential impact of these variants on birth weight was assessed using 2,940 birth weight records from the 7-breed population, 3,812 records from a somewhat related 16-breed population, and imputed high-density SNP genotypes for both populations. Genomic heritability estimates (SE) in the 7-breed population were 0.38 (0.03) with 3,810 SNP flanking the high-impact and non-coding RNA variants, 0.25 (0.02) with 291 SNP surrounding 217 variants with the largest flanking SNP effects, 0.64 (0.03) with the full set of high-density SNP, and 0.38 (0.05) for the 300 high-density

SNP with the largest effects. Genetic correlations between 16-breed birth weights and genomic EBV predicted from 7-breed SNP effects were 0.42 (0.05) for the 3,810 SNP and 0.58 (0.05) for the 291 SNP around selected variants. Estimated birth weight-genomic EBV genetic correlations were 0.51 (0.04) for all high-density SNP and 0.48 (0.05) for the top 300. Genomic predictions with SNP flanking variants affecting gene function may be more robust than predictions based only on associations with phenotype. Further assessment of direct genotypes for the functional variants is needed. USDA is an equal opportunity provider and employer.

Key Words: cattle, DNA sequence variant, genomic prediction

T209 Accuracy of mixed model methods for genomic prediction and variance component estimation of additive and dominance effects using SNP markers. S. Wang, G. Hu*, C. Wang, and Y. Da, *Department of Animal Science, University of Minnesota, St. Paul.*

The accuracy of GREML and GBLUP methods for additive and dominance effects were evaluated using simulation data for various heritability levels of additive and dominance effects. SNP marker sets included 1K causal variants, 1K, 3K and 7K inter-QTL SNP markers, and 41K SNP marker with minor allele frequency > 0.05 including the 1K causal variants. Genomic additive and dominance relationship matrices using SNP markers were consistent with theoretical expectations. GREML and GBLUP using genome-wide SNP markers were able to capture small additive and dominance effects each accounted for 5 (10^{-5}) ~3 (10^{-4}) of the phenotypic variance. Accuracy of GREML and GBLUP increased as the heritability increased for both additive and dominance effects. GBLUP of total genetic values as summation of breeding values and dominance deviations had higher accuracy breeding values or dominance deviations. GREML was more sensitive than GBLUP to the true additive and dominance heritability levels and to the density of SNP markers. Low density of non-causal SNP markers (3K or less) had a tendency to underestimate additive and dominance variance components by GREML. The 41K that included the 1K causal variants overestimated the variance components for the phenotype with 1006 underlying QTL and performed better for the phenotype with 100 underlying QTL than lower density inter-QTL SNPs. Causal variants had the highest accuracy of GREML and GBLUP and adding whole genome SNP markers to the causal variants did not improve accuracy.

Key Words: genomic prediction, variance component, dominance

T210 Bias in genomic evaluations attributable to unknown parent group estimates. S. Tsuruta*, D. A. L. Lourenco, and I. Misztal, *University of Georgia, Athens.*

The objective of this study was to investigate bias in genomic evaluations due to unknown parent group estimates. Genomic (G)BLUP was predicted for final score in US Holsteins, 305-d milk yields in 3 parities in Israeli Holsteins, and multiple traits in pigs, using genomic and phenotypic combined data. The US Holstein data consisted of 10,167,604 records for 6,586,605 cows and 9,602,031 animals in pedigree including 34,506 genotyped bulls with 42,503 SNP; the Israeli Holstein data consisted of 1,205,801 records for 713,686 cows and 829,437 animals in pedigree including 1305 genotyped bulls with 30,359 SNP; the pig data consisted of 2,923,141 records for 884,250 pigs and 906,660 animals in pedigree including 4853 genotyped animals with 63,219 SNP. Original unknown parent groups (UPG) were defined based on year of birth by sex, year of birth by sex by breed, and year of birth for US Holstein, Israeli Holstein, and pig data, respectively. Genomic (G)EBV and UPG estimates were compared using original and refined UPG and separating additive genetic effects into those with UPG from pedigree and those without UPG from genotypes. The BLUP90IOD program using a single-step approach was used to estimate UPG effects and GEBV. The last UPG effect for US Holstein was significantly overestimated. The last UPG effects for Israeli Holstein bulls were overestimated. The UPG estimates in pigs were similar in original and refined UPG. For US Holstein, Israeli Holstein, and pig data sets, correlations between GEBV from original and refined UPG models were 0.99, 0.95–9.97, and 0.97–0.99, respectively. Those correlations between GEBV from original and 2 additive models were 0.91, 0.91–0.93, and 0.96–0.98, respectively. Refinement of UPG improved convergence in GBLUP by 4%, 55%, and 35% for US Holstein, Israeli Holstein, and pig data sets, respectively. Refinement of UPG is recommended to reduce bias in GEBV and improve computing speed in GBLUP.

Key Words: genomic evaluation, unknown parent group

T211 Accounting for heterogeneous pleiotropy in whole genome selection models. N. M. Bello*[1], J. P. Steibel[2], and R. J. Tempelman[2], *[1]Kansas State University, Manhattan, [2]Michigan State University, East Lansing.*

The additive genetic correlation between economically relevant traits is generally considered a critical factor determining the relative advantage of multi-trait models over single-trait models for whole genome prediction of genetic merit. Yet, the additive genetic correlation between traits may be considered an aggregate summary of between-trait correlations at the individual QTL level, thereby defining pleiotropic mechanisms by which individual genes have simultaneous effects on multiple phenotypic traits. Pleiotropic effects, in turn, may be gene specific and heterogeneous across the genome. In this study, we present a hierarchical Bayesian extension to bivariate genomic prediction models that accounts for heterogeneous pleiotropic effects across SNP markers. More specifically, we elicit a function of the SNP marker-specific correlation between traits as heterogeneous across markers following a square-root Cholesky reparameterization of the marker-specific covariance matrix that ensures necessary positive semidefinite constraints. We use simulation studies to demonstrate the properties of the proposed methods. We assess the relative performance of the proposed method by comparing prediction accuracy for genomic breeding values and for SNP marker effects for each of 2 traits across putative scenarios of homogeneous and heterogeneous pleiotropic genetic mechanisms. We also consider extensive model comparisons for cases of null and non-null additive genetic correlations under conditions of high and low heritability of the traits of interest. Overall, the relative advantage of genomic prediction bivariate models that account for heterogeneous pleiotropy relative to their univariate counterparts depended upon trait heritability and genetic architecture of the pleiotropic mechanisms and was of small magnitude (~1% net gain in predictive accuracy) when at all present. The trade-off between methodological and computational modeling complexity and net gain in prediction accuracy is also discussed.

Key Words: genomic selection, bivariate model, heterogeneous correlation

T212 Comparison of milk fatty acids composition from buffalo, camel, cow, goat, and yak. J. H. Yang, D. P. Bu*, J. Q. Wang, L. Ma, J. X. Zhang, and J. T. Chen, *Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Milk originated from different mammals has its own characteristic. The objective of this study was to investigate variation of FAs profile in milk from different dairy mammals. Milk samples collected from buffalo (n = 22), camel (n = 19), cow (n = 108), goat (n = 23) and yak (n = 22) were analyzed in this study. The FA methyl esters were determined via Agilent 6890 GC (Agilent Technologies, Hewlett Packard Co., Avondale, PA) fitted with a flame-ionization detector and expressed as grams per hundred grams. Data was processed through multi-comparison and principle component analysis (PCA), completed by SAS 9.0 (SAS Institute Inc., Cary, NC) and the Unscrambler 9.8 (Camo Software AS, Oslo, Norway), respectively. Results showed that composition (%) of camel milk contained the lowest C4-C12 (all below 0.90) and the highest C16:1 (3.51), C18 (21.30), C18:1 (35.58), c9c12C18:2 (2.66), c9t11C18:2 (1.85), C18:3 (1.81), C20:1 (0.22), C20:2 (1.52) and C20:3 (0.53). Goat milk had the highest C8 (2.92), C10 (10.24)and C12 (5.30). C4 (6.43) in buffalo milk and C14:1 (0.94) in cow milk were higher than in others, while yak milk highlighted FAs above 14 carbons without unsaturated bond like C15 (1.94), C17 (1.56), C20 (0.48) and C22 (0.35). Moreover, there was no difference in saturated FA (71.67–73.47%) and monounsaturated FA (MUFA, 24.10–25.39%) among bovine milk samples, whereas camel had maximum MUFA and polyunsaturated FAs. Short and median chain FA (sum of C4-C16:1) in buffalo (63.96), goat (62.67), cow (60.51), and yak (59.03) milk were higher than in camel milk (32.95). Scores and loading plots of PCA showed that high t11C18:1, c9C18:1, C18:0 in camel milk and high C8, C10, C12 in goat milk separated their samples from others, while buffalo, cow and yak milk clustered together for similar FA composition. It was suggested that camel milk highlight characteristic on long chain and unsaturated FA, and goat milk had special effects on short chain FA, while bovine milks exhibited much similarity.

Key Words: milk, fatty acid, different mammals

T213 Characterizing the relationship between peroxidase activity and enzymatic bleaching in fluid whey. R. E. Campbell*[1], P. D. Gerard[2], and M. A. Drake[1], *[1]North Carolina State University, Raleigh, [2]Clemson University, Clemson, SC.*

The carotenoid norbixin (annatto) is added to Cheddar cheese milk to impart desired color to cheese. Norbixin is also present in whey and is bleached using benzoyl or hydrogen peroxide. Due to increased regulations and off-flavors produced by these bleaching agents, alternative bleaching agents have been explored. Lactoperoxidase (LP), naturally in milk, or an external peroxidase (EP) may be used to bleach fluid whey or retentate with the addition of low concentrations (<50 ppm) of hydrogen peroxide. A working knowledge of enzyme activity and how activity relates to bleaching efficacy is required. The objective of this study was to characterize the relationship between enzyme activity and bleaching efficacy in fluid whey and whey protein retentate. A range of pH (5.5–6.5) and temperature (4–60°C) was evaluated. Colored Cheddar cheese whey was manufactured in triplicate from pasteurized whole milk and fat-separated pasteurized whey and whey protein retentate (10% solids, 80% protein) were manufactured. Subsequently, the effects of selected temperatures and pH in both fluid whey and whey protein retentate were evaluated for their effects on LP and EP activity and bleaching efficacy using a response surface model – central composite design (RSM-CCD) matrix. Peroxidase activity was determined using an established colorimetric method and bleaching efficacy was measured by quantifying norbixin destruction via high performance liquid chromatography. Across the pH and temperature ranges evaluated (5.5–6.5, 4–60°C), peroxidase activity associated with LP and bleaching efficacy increased with increasing temperature. The effects of pH were not as pronounced as temperature effects ($P < 0.05$). Increased peroxidase activity with the addition of EP was not evident while increased bleaching was observed, suggesting that peroxidase activity and bleaching are not necessarily linear. These results suggest that peroxidase activity is not always an accurate prediction of bleaching efficacy and that addition of exogenous EP may be beneficial to manufacturers to improve bleaching consistency across processing variables.

Key Words: whey protein, enzymatic bleaching, lactoperoxidase

T214 Factors that influence the required membrane area of a multi-stage microfiltration process to separate serum protein and lactose from micellar casein in skim milk. E. E. Hurt* and D. M. Barbano, *Northeast Dairy Foods Research Center, Department of Food Science, Cornell University, Ithaca, NY.*

Our objective was to determine how to minimize the microfiltration (MF) membrane area required to produce a micellar casein concentrate (MCC) from skim milk (SM). Several factors were studied. The 1st factor was feeding a MF system with ultrafiltered (UF) SM versus SM. Other factors (when UF SM was the MF feed) were the concentration of the UF SM, the number of MF stages and MF flux. To determine the effect of these factors on MF membrane area, a theoretical model based on a mass balance was developed. The model was based on previously measured performance of a 0.1µm ceramic uniform transmembrane pressure MF system producing a final MCC of 9% protein with ≥ 95% of the serum protein (SP) removed and <0.2% lactose from SM. The model was used to minimize the total mass of MF permeate removed by changing the concentration factor (CF) of the UF SM feeding the MF (if UF SM was the feed) and the CF and diafiltration factor for each MF stage. The MF permeate removed was converted to membrane area by specifying flux (54 kg/m^2 per h), processing time (18h) and mass of SM before UF (150,000 kg). It was assumed that 76% of the lactose had been removed from SM by UF. A 95% removal of lactose (equal to the SP removal) from this UF SM by MF would produce a MCC with <0.2% lactose. If the feed was UF SM, the MF membrane area required for a 5-stage process was 182 m^2 compared with 315 m^2 when SM was the feed. For 5-stages, increasing the UF SM CF from 1.0 to 1.7 decreased MF membrane area from 202 m^2 to 182 m^2. The UF SM CF that minimized MF membrane area for 2, 3, 4 and 5-stages was 0.8, 1.2, 1.5 and 1.7 respectively. Increasing the number of stages also decreased the required MF membrane area. When UF SM was used, increasing the number of stages from 2 to 5 decreased MF membrane from 297 m^2 to 182 m^2. Finally, for 5-stages, increasing the flux from 54 to 60 kg/m^2 per h decreased the MF membrane area from 182 m^2 to 164 m^2. Using UF SM, the UF SM CF, the number of MF stages and flux were all important factors for minimizing the membrane area of a MF system.

Key Words: microfiltration, micellar casein concentrate, optimization

T215 The impact of bleaching on functionality of whey protein isolate. T. J. Smith*, E. A. Foegeding, and M. A. Drake, *North Carolina State University, Raleigh.*

Whey protein is a highly functional food ingredient used in a wide variety of applications. A large portion of whey produced in the United States is derived from Cheddar cheese manufacture and contains annatto, and therefore must be bleached. We have demonstrated bleaching effects on whey protein flavor but bleaching effects on protein functionality have not been fully elucidated. The objective of this study was to compare functional properties of bleached and unbleached whey protein isolate (WPI). Cheddar whey was manufactured followed by addition of no bleach (control), hydrogen peroxide (HP, 250 mg/kg) or benzoyl peroxide (BP, 50 mg/kg) at 50°C for 1 h. WPI were then produced and spray dried. WPI were manufactured in triplicate. Functional properties were evaluated by measurement of foam stability, protein solubility, native PAGE, and the effect of sodium chloride (NaCl) concentration on gelation. In addition to functional properties, descriptive analysis and gas chromatography-mass spectrometry were performed to characterize flavor differences among treatments. Overrun and yield stress were not different between bleached and control WPI ($P < 0.05$). Foam stability of WPI was increased in both bleached treatments relative to the control ($P < 0.05$). Soluble protein loss at pH 4.6 was decreased by bleaching with either HP or BP ($P < 0.05$). The effect of NaCl concentration on gelation was also distinct with bleaching agent ($P < 0.05$). Lastly, native PAGE results suggested that both HP and BP contributed to protein degradation, which was likely a factor in the functional differences observed between unbleached and bleached WPI. These results suggest that chemical bleaching does have a significant effect on many of the functional characteristics of whey proteins.

Key Words: functionality, WPI, flavor

T216 Optimizing methods for improved raw milk analysis by NIR spectroscopy. T. J. Reuter*[1], X. Xiong[2], G. Rolland[2], and T. C. Schoenfuss[1], *[1]University of Minnesota, St. Paul, [2]BHI Labortechnik AG, Flawil, St. Gallen, Switzerland.*

Raw milk is hard to analyze by NIR because of excessive light scattering effects caused by large size variations in the fat component. How the sample is prepared and presented for NIR analysis could improve predictions of component quantities. In this study, sample presentation (static and dynamic) and fat particle size reduction by various homogenization processes were investigated for 160 diverse samples to predict 5 component quantities in raw milk (fat, moisture, ash, protein, casein) by FT-NIR. Spectra were acquired with a polarization inferometer in transflection in the wavelength range 1000 to 2500 nm, and preprocessed using standard normal variation scatter correction and Savitzky-Golay smoothing. The calibration models were created using PLS method. Excellent results were obtained for the standard errors of prediction following no homogenization (0.02, 0.02, 0.01, 0.01, and 0.01) for fat, moisture, ash, protein, and casein, respectively. Results from homogenization with sonicator and tube dispersion methods were not significantly improved from non-homogenized samples, but were still better compared with 2-stage valve homogenization for moisture and casein components (0.12 and 0.07, respectively) possibly because of whey protein denaturation that occurred during 2-stage processing. Relatively high sample temperatures during analysis could have led to more positive results for all component calibrations compared with reference values. For sample presentation, both the static and dynamic flow cell methods were shown to be very accurate based on the lowest standard errors of prediction (0.02, 0.02, 0.01, 0.01, and 0.01) for fat, moisture, ash, protein, and casein, respectively. The Petri dish presentation method was similarly accurate but may have been limited by the poor structural design of the transflectance cover, which allowed for sample dehydration and loss of reflected light.

Key Words: near-infrared spectroscopy, milk analysis, sample preparation

T217 The mechanism of resistance to plasmin activity through protein succinylation: A model study using β-casein. H. Bhatt*[2,1], A. Cucheval[1], C. Coker[1], H. Patel[3], A. Carr[2], and R. Bennett[2], *[1]Fonterra Research & Development Centre, Palmerston North, Manawatu, New Zealand, [2]Institute of Food, Nutrition and Human Health, Massey University, Palmerston North, Manawatu, New Zealand, [3]Dairy Science Department, South Dakota State University, Brookings.*

Plasmin-induced proteolysis is a major concern in the dairy industry, leading to defects in the texture and taste e.g., gelation and bitterness, of various milk systems. It is therefore important to control the activity of plasmin in milk systems. Several techniques have been investigated; the present work explores inhibition of the plasmin-catalyzed hydrolysis of β-casein, which is the primary target of plasmin action. As plasmin hydrolyses proteins on the carboxyl site of lysine-X and arginine-X bonds with a preference for the lysine-X bond, lysine residues on the β-casein backbone were targeted by succinylation. The target lysine sites were identified by liquid chromatography-tandem mass spectrometry to be Lys-28, 29, 99, 105 and 107. To get greater insight into the effect of different levels of succinylation on the hydrolysis of β-casein by plasmin, the reaction was monitored by quantifying the formation of the hydrolyzed product using sodium dodecyl sulfate PAGE and reverse-phase high performance liquid chromatography. This allowed the primary stage of the hydrolysis of β-casein, i.e., the formation of γ-caseins and proteose peptones, and the secondary stage, i.e., further hydrolysis of the γ-caseins and proteose peptones, to be distinguished. The results clearly indicated that succinylation affected both stages of hydrolysis negatively. Succinylated β-casein and proteose peptones became resistant to hydrolysis by plasmin. The following mechanism is proposed. The formation of succinyl-lysine renders the casein unrecognizable to the substrate-binding pocket of plasmin. Thus, the modified substrate cannot be positioned into the pocket and is not hydrolyzed by the catalytic triad of plasmin. These results indicate that succinylation may be useful for controlling the plasmin-induced hydrolysis of milk proteins and that the proposed mechanism may be useful as a base hypothesis for developing plasmin-resistant proteins by other means of modification.

Key Words: plasmin, succinylation, β-casein

T218 Effect of processing and storage temperatures on the physical stability of sodium-caseinate-stabilized emulsions. Y. C. Liang*[1,2], H. Patel[3], L. Matia-Merino[2], A. Q. Ye[4], G. Gillies[1], and M. Golding[2,4], *[1]Fonterra Research and Development Centre, Palmerston North, New Zealand, [2]Institute of Food, Nutrition and Human Health, Massey University, Palmerston North, New Zealand, [3]Dairy Science Department, South Dakota State University, Brookings, [4]Riddet Institute, Massey University, Palmerston North, New Zealand.*

Oil-in-water emulsions are an important basis of many food and nutraceutical products. Liquid beverages are processed at high temperature (e.g., retort or UHT processing) and maybe stored at different temperatures (e.g., at 40°C). There is little information on the effect of high heat treatment and high storage temperatures on the caseinate and droplet sizes, depletion potential, and creaming stability of caseinate-stabilized emulsions. This study investigated the influence of processing and

storage conditions on the structure and stability of caseinate-stabilized emulsions. Sodium caseinate was reconstituted to a 3% (wt/wt) solution. Corn oil (60% w/w) was mixed with the protein solution. The mixture was homogenized to yield a stock emulsion, which was then mixed with stock caseinate (20% wt/wt) to produce 30% oil-in-water emulsions containing 2 to 10% caseinate. The pH was adjusted to 6.8 ± 0.04 for all model emulsions. Each model emulsion was prepared at least in duplicates. The experimental data was analyzed by Student's *t*-tests, significant differences among the means were determined at a 95.0% confidence level. Heat-treated (120°C, 10 min) caseinate emulsions phase separated much more rapidly than unheated emulsions ($P < 0.05$). The droplet size was found to be unchanged after heating. The change in phase separation behavior can be attributed to the change in caseinate size because of the heat-induced polymerization of casein molecules. A small change in caseinate size resulted in a moderate change in the depletion interaction potential. In addition, unheated caseinate emulsions stored at 40°C phase separated much more rapidly than unheated emulsions stored at 20°C ($P < 0.05$). This change appeared to be influenced by the continuous phase viscosity. The formation of the droplet network and its rearrangement as a function of the caseinate concentration at 40°C were well reflected by small deformation rheology and Turbiscan curves. We show the interrelations between the formation of the droplet network and the processing conditions.

Key Words: caseinate, physical stability, depletion interaction potential

T219 Effect of reconstitution temperatures on the solubility of different protein fractions present in milk protein concentrates (MPC 80). H. Patel*[1,2], [1]*Dairy Science Department, South Dakota State University, Brookings,* [2]*Animal Sciences and Industry, Kansas State University, Manhattan.*

The solubility of high protein ingredients such as milk protein concentrates (MPC) influences important functional properties such as emulsification, foaming and gelling. The rate of solubility of MPC and different protein fractions present in MPC may vary depending on the reconstitution conditions. However, there is lack of reliable information on the solubility behavior of individual protein fractions during reconstitution process. Better understanding of such factors would help the manufacturers to identify optimum conditions for reconstitution. Considering this, the objective of present study was to study the order in which individual protein fractions are solubilize during reconstitution process. Five representative samples of MPC80 with similar protein (81–82%), lactose contents were obtained. Solutions (5% w/w) of these MPC were prepared by reconstituting MPC at 20, 40, 50 and 60°C. During reconstitution, the aliquots from each of this were withdrawn at different time interval (2, 10, 20, 30, 45 and 60 min). Percent solubility of these samples was analyzed using standard methods. The rate of solubility of different protein fractions was determined using PAGE under different reconstitution condition. The data were analyzed using SAS. Percent solubility of all MPC samples increased significantly ($P < 0.05$) with increase in the temperature and time of reconstitution up to 50°C and up to 30 min. The results of PAGE showed that the whey proteins were solubilized within initial 2 min of reconstitution process. The order of solubility of different proteins was found to be β-lactoglobulin = α-lactalbumin > α_{s1}-casein > β-casein > α_{s2}-casein > κ-casein. It required almost double time to reconstitute MPC at 20°C compared with 50°C. It was found that the disulfide interaction of casein and whey proteins were responsible for the poor solubility of some MPC samples. The manufacturers can use such insights for identifying processing conditions and, for achieving desired functionality of MPC in the final products.

Key Words: milk protein concentrate (MPC), solubility, polyacrylamide gel electrophoresis (PAGE)

T220 Comparison of the in vitro digestion of raw pasture milk and commercial HTST and UHT pasteurized milk. D. X. Ren[1,2], D. L. Van Hekken*[1], M. H. Tunick[1], and P. M. Tomasula[1], [1]*USDA, ARS, ERRC, Dairy and Functional Foods Research Unit, Wyndmoor, PA,* [2]*Zhejiang University, Institute of Dairy Science, College of Animal Science, Hangzhou, China.*

Consumption of raw milk from pasture-fed cows, typically purchased at local farms, is steadily increasing in the US because many consumers believe that high-temperature short-time (HTST) or ultrahigh temperature (UHT) pasteurization affects the digestibility of milk proteins and thus the bioavailability of their nutrients. The objective of this study was to compare the evolution of curd or clot size distribution with time during in vitro digestion of protein under simulated fasting gastro-intestinal conditions for commercial whole and skim milk treated by HTST or UHT pasteurization and raw whole and skim milk from pasture-fed cows. Milk digestion procedures followed the 2012 US Pharmacopeia with simulated gastric fluid (SGF) using pepsin and simulated intestinal fluid (SIF) using pancreatin. The in vitro protein digestibility of whole milk samples was greater than that of skim milk samples ($P < 0.05$), with milk fat acting as a barrier to the protein aggregation observed in skim milk samples. In a second series of experiments, the degradation kinetics of clots that formed upon initiation of SGF digestion were followed for 3 h using a light-scattering particle-size analyzer. The average clot sizes of the proteins upon initiation of digestion decreased in the order raw pasture > HTST > UHT milk with the clot sizes for skim milk (130.5, 128.3 and 52.9 μm, respectively) being larger than those for whole milk (98.5, 86.3 and 32.7 μm; $P < 0.05$). After 3 h of digestion, a single particle-size peak was observed for all samples. With the exception of the UHT milk samples, the clot sizes in skim milk samples averaged 38.5 μm and were larger than those in whole milk which averaged 29.3 μm ($P < 0.05$). Clot sizes of skim and whole milk UHT samples averaged 8.0 μm ($P < 0.05$), indicating that UHT milk was the most digestible since the smaller clot sizes offered increased surface area for enzyme contact. The results showed an inverse relationship between clot size and extent of in vitro digestibility. Moreover, the results indicated that raw pasture milk is as digestible as commercial HTST milk and not as digestible as commercial UHT milk.

Key Words: in vitro digestion, raw milk, pasteurized milk

T221 Computer simulation to predict energy use, greenhouse gas emissions and costs for production of extended shelf-life milk using microfiltration. P. M. Tomasula, W. C. F. Yee, A. J. McAloon, and L. M. Bonnaillie*, *USDA, ARS, ERRC, Dairy and Functional Foods Research Unit, Wyndmoor, PA.*

Extended shelf-life (ESL) milk has a shelf life between that of high-temperature short-time (HTST) and ultrahigh temperature (UHT) pasteurized milk. ESL milk is usually pasteurized at temperatures exceeding 125°C which may give the milk a cooked taste. ESL milk produced using crossflow microfiltration (MF) before HTST pasteurization at 72°C produces milk with the fresh taste of HTST milk and depending on raw milk quality, packaging and cold-chain handling, may have a shelf-life of up to 30 d. Little information is available on the additional energy use, greenhouse gas (GHG) emissions and operating costs of installing MF in an existing HTST processing plant. The objective of this study was to develop a model for milk MF and incorporate it into a computer simulation model of the fluid milk process that was recently

developed for processors to benchmark their current energy use, GHG emissions, and capital and operating costs. MF was modeled as 2 MF skids in series, each containing the housings for 1.4 µm membranes. In the simulator, skim milk leaves the separator at 55°C as the feed to the first skid. The retentate from the first skid fed the second MF skid. Permeates from both skids were blended with cream and pasteurized to produce 3.25% whole milk. Retentate (3% of the total feed stream) was added to the remaining cream stream and heated to 130°C before storage. Simulations conducted for medium–sized milk plants processing 27,300 L/h of milk showed GHG emissions, electricity and natural gas use were 88.6 gCO_2eq/kg milk, 0.38 MJ/L and 0.12 MJ/L using HTST pasteurization alone and 93.6 gCO_2eq/kg milk, 0.38 MJ/L and 0.14 MJ/L for the HTST/MF plant, showing the additional electricity and natural gas used by the MF process and for heating of the cream/retentate stream. The difference in operating costs between HTST and HTST/MF was estimated as 0.10 cents/L in agreement with literature estimates. This study demonstrates that computer simulation allows rapid assessment of process changes and evaluation of new technologies in an existing processing line without costly pilot testing.

Key Words: greenhouse gas, microfiltration, energy

T222 Effect of preheating temperature and time on the properties of evaporated milk. B. Chen*, A. Grandison, and M. Lewis, *University of Reading, Reading, Berkshire, UK.*

The objective of this study was to investigate the effect of different preheating temperature/time combinations on the properties of evaporated milk. Pasteurized whole milk was preheated at 85°C, 90°C and 95°C for 10, 20 and 30 min at each temperature. After evaporation to 28% total solids, different concentrations of disodium hydrogen phosphate and trisodium citrate were added (8 to 24 m*M*) and the density and heat stability of evaporated milk were measured after in-container sterilization. Heat stability was assessed by measuring the amount of sediment in the evaporated milk. Concurrently, pH, $Ca^{2+}$and viscosity were monitored at every processing stage. Overall, the pH and $Ca^{2+}$of raw milk was around 6.72 and 1.54 m*M*. Preheating caused only a small pH reduction and a fall in Ca^2 of about 0.30 m*M*, whereas sterilization caused a dramatic reduction in pH but an increase of Ca^{2+}. Also, viscosity of evaporated milk increased after preheating and also after evaporation but the most dramatic increase was brought about by sterilization. Higher preheating temperatures and longer preheating times resulted in evaporated milk with significantly lower pH and Ca^{2+}. The viscosity of evaporated milk without pre-heating was significantly higher than those which had been preheated. Addition of stabilizing salts significantly reduced the viscosity of evaporated milk. However, higher additions of up to 24 m*M* stabilizing salts sometimes resulted in a viscosity which was higher and above the range found for commercial samples. Adding increasing amounts of these stabilizing salts to evaporated milk increased pH, decreased Ca^{2+} and slightly increased the dry sediment. In addition, dialysis was used for measuring pH and Ca^{2+}at preheating temperatures. The pH of dialysates decreased as pre-heating temperature increased but Ca^{2+} did not change significantly. It was concluded that 85°C or 90°C for 10 min pre-heating were the best conditions for the evaporated milk manufacture to obtain a satisfactory viscosity.

Key Words: evaporated milk, preheating temperature and time, viscosity

T223 Predicting color change of skim milk during high pressure thermal processing. A. F. Devi[1,2], R. Buckow*[2], Y. Hemar[3], and S. Kasapis[1], *[1]School of Applied Sciences, RMIT University, Melbourne, VIC, Australia, [2]CSIRO Animal, Food and Health Sciences, Werribee, VIC, Australia, [3]School of Chemical Sciences, The University of Auckland, Auckland, New Zealand.*

The demand of extended shelf-life with fresh-like quality and retained nutrients has driven studies on high pressure treatment of milk. Inactivation of bacterial spores for milk sterilization purpose requires the incorporation of heat in the high pressure process. Currently, little is known about the influence of high pressure thermal (HPT) processing on physicochemical properties of milk. Therefore, the objective of this study was to develop a predictive model describing kinetics of color change (from white to caramel brown) of skim milk during HPT processing. Reconstituted skim milk (10% wt/wt) was treated under isothermal/isobaric conditions at 100 to 140°C and 0.1 to 600 MPa for up to 60 min. Its color was measured within 4 h after treatment using a chromameter and reported in CIE-Lab system. The total color change was calculated referring to the initial color of skim milk and represented as total color difference (ΔE_{ab}*). ΔE_{ab}* increased with time (t) and was described with an empirical equation: $\Delta E_{ab}^* = 38\ t/(k+t)$. Coefficient k varied with temperature and pressure, following a third order polynomial equation and reached the minimum value at 400 MPa. Consequently, ΔE_{ab}* was largely enhanced during HPT at 400 MPa. Meanwhile, ΔE_{ab}* increased progressively with temperature regardless of the applied pressure. Compared with atmospheric pressure, 60 min HPT treatment at 110°C and 200, 400, and 600 MPa increased ΔE_{ab}* by approximately 50, 200, and 100%, respectively. Selected images of processed skim milk, mathematical models, and pressure-temperature diagrams of color conversion as a function of pressure, temperature, and treatment time will be presented. The resultant knowledge can possibly help to identify suitable HPT process conditions for improved sensory quality of sterilized milk.

Key Words: high pressure processing, skim milk, color

T224 Feed substrates influence biofilm formation on reverse osmosis (RO) membranes and their cleaning efficacy. S. Marka* and S. Anand, *Dairy Science Department, Midwest Dairy Foods Research Center, South Dakota State University, Brookings.*

In recent times, there is a greater use of RO membranes for concentration of various feed materials such as whey and ultrafiltration (UF) permeate in the dairy industry. This study compares the influence of skim milk UF permeate and cheese whey on membrane biofilm formation. A resistant *Bacillus* sp., previously isolated from a membrane biofilm, was used to develop 48-h-old static biofilms on the RO membrane pieces using UF permeate and whey as feed substrates. Biofilms were analyzed for viable counts by swab technique and for microstructure using scanning electron microscopy (SEM). The membrane cleaning process included 6 sequential steps; alkali, surfactant, acid, enzyme, a second surfactant, and sanitizer application. The data were statistically analyzed. The SEM images showed a significant difference in the microstructure of biofilms for the 2 feed substrates. In the case of UF permeate biofilms, the bacilli were found to be adherent in small groups of random arrangement that were covered with a thin film of exopolysaccharide material having protrusions. On the other hand, the bacilli in whey biofilms were found to be in bigger groups with cells arranged in long chains covered with smoother and thinner films of exopolysaccharide material without any protrusions. Differences were also noticed in the resistance pattern of these 2 types of biofilms. The mean pre-treatment counts of the 48-h UF permeate biofilms were log 5.39, which were much higher than the whey biofilms pre-treatment counts of log 3.44. After 6 steps cleaning cycle, there were 2.6 log survivors of the *Bacillus* isolate on UF permeate biofilms, whereas only 1.82 log survivors were found in whey biofilms. In conclusion, the UF permeate substrate biofilms resulted in a higher

resistance to cleaning process as compared with the biofilms developed by whey substrate. The biofilm microstructure variations for the 2 feed substrates might have caused differences in their resistance to the CIP protocol. Further studies are in progress.

Key Words: whey and UF permeate, biofilm, reverse osmosis membrane

T225 Characterization of some changes in composition and physicochemical properties of casein micelles from cream to buttermilk. M. Looney*[1], Y. Pouliot[2], M. Britten[3], and R. Jiménez-Flores[1], *[1]Dairy Products Technology Center, California Polytechnic State University, San Luis Obispo, [2]STELA Dairy Research Center, Institute of Nutrition and Functional Foods (INAF), Laval University, Quebec City, QC, Canada, [3]Food Research and Development Center (FRDC), Agriculture and Agri-Food Canada, St-Hyacinthe, QC, Canada.*

It is well-documented that the poor coagulation properties of buttermilk are attributed to the changes that occur to the casein micelles during the butter-making process. It was hypothesized that churning is a critical step for the changes that occur in composition of the casein micelles. Raw cream was processed using a rotary churn at 18°C for approximately 30 min, and buttermilk was collected for analysis. Raw milk was skimmed at 10°C by centrifuging at 3,000 × *g* for 20 min. Cream, skim milk and buttermilk were centrifuged at 60,000 × *g* for 40 min twice using imidazole buffer at pH 6.8 to isolate the micellar content in the pellet. Variation in physical properties of the casein micelles was determined using a Malvern Zetasizer. Protein profiles of UP cream, skim milk, and buttermilk were analyzed using 1- and 2-dimensional gel electrophoresis technique. Experiments were performed using 3 different batches of UP cream, skim milk and buttermilk. Statistical analyses showed that processing the buttermilk significantly increased the surface charge ($P < 0.05$) of the micelle but had no significant effect on their size ($P > 0.05$). Our results also indicate that churning of cream promoted interactions between casein micelles and MFGM proteins as shown by the more complex 2D-gel electrophoresis pattern obtained for casein micelles sedimented from buttermilk.

Key Words: buttermilk, casein micelle, churning

T226 Investigation of the mechanism of membrane fouling in cold microfiltration of skim milk: A proteomics study. T. J. Tan* and C. I. Moraru, *Department of Food Science, Cornell University, Ithaca, NY.*

The main challenge in milk microfiltration (MF) is membrane fouling, which leads to a significant decline in permeate flux over time. This work aims to elucidate the mechanism of membrane fouling in cold MF of skim milk, by identifying and quantifying the milk proteins and minerals involved in the external and internal fouling of the membrane. Skim milk was subjected to MF using a 1.4 µm ceramic membrane, at a temperature of 6 ± 1°C, cross-flow velocity of 6 m/s and transmembrane pressure of 159 kPa, for 90 min. First, RO water rinses (20°C, 5 min) were conducted to collect the loosely attached external foulants (S1) and then loosely attached internal foulants (S2) from the membrane. After that, pressurized hot water extractions (70°C, 10 min) were performed to collect the strongly attached external foulants (S3) and the strongly attached internal foulants (S4). The collected foulants were analyzed for protein content using the Bradford method. The foulants were further analyzed by liquid chromatography coupled with tandem mass spectrometry for protein identification and relative quantitation of individual proteins. The mineral composition of the foulants was analyzed using Inductively Coupled Plasma Spectrophotometry and potentiometric titration. All experiments and analyses were carried out in triplicate. Significant differences among samples were determined by Tukey's HSD test at $P \leq 0.05$. The protein concentrations for S1, S2, S3, and S4 were 62.2 ± 10.1 µg/mL, 10.7 ± 1.0 µg/mL, 6.6 ± 0.7 µg/mL, and 1.0 ± 0.1 µg/mL, respectively. All major milk proteins were identified in the 4 foulants. α-Lactalbumin and BSA were found in higher levels in S4 than in the other foulants. This suggests that these proteins strongly attached to the internal pores of the membrane, which likely results in pore constriction and subsequent flux reduction. In general, the concentration for all mineral was very small (below 7.7 ppm) in all foulants, and likely they do not have a major contribution to membrane fouling. The knowledge generated in this study can be used to identify solutions to minimize membrane fouling and thus increase the efficiency of skim milk MF.

T227 Evaluation of thermization and CO_2 addition as methods of raw milk preservation. P. R. Rocha, V. P. Voltarelli, V. O. Gaino, C. M. V. B. de Rensis, and P. C. B. Vianna*, *Universidade Norte do Paraná (UNOPAR), Londrina/PR/Brazil.*

The aim of this study was to evaluate the use of thermization or dioxide carbon (CO_2) addition as methods of raw milk preservation before processing. Raw milk was divided into 3 treatments: (1) Control milk (without treatments), (2) thermized milk (65°C/20 s) and (3) CO_2 added raw milk (until pH 6.2). The samples were stored in plastic bottles hermetically sealed at 4 ± 1°C. Raw milk was evaluated upon receipt (d 0) for physicochemical composition, standard plate count and psychrotrophic bacteria count. Samples were randomly selected and evaluated after 3, 6, 10, 13 and 16 d for proteolysis and the same microbial counts evaluated at the reception. Decreased in casein as a percentage of true protein (CN/TP) was used as an index of proteolysis. Split-plot design was used with 3 replications and the results were evaluated by ANOVA and Tukey's test, at 5% significance level. The lag phase of psychrotrophic bacteria count was analyzed by Gompertz model. Raw milk presented typical whole milk composition and the standard plate count and psychrotrophic count were 3.1×10^4 cfu/mL and 3.1×10^2 cfu/mL, respectively. Standard plate count and psychrotrophic bacteria count increased during refrigerated storage for all the samples, however, this increase was significantly higher for control milk. Based on the initial standard plate count, the time required for control milk reaches the critical count regulated by Brazilian legislation (6.0×10^5 cfu/mL) was 10 d. For thermized and CO_2 added milk, microbiological counts remained below critical limits during the 16 storage days. The CO_2 addition and thermization extended the lag phase of psychrotrophic bacteria in ~2.2 and ~10.3 times, respectively, when compared with raw milk control. Proteolysis significantly increased during refrigerated storage for all samples. However, in this study, the increased proteolysis could not be related to greater psychrotrophic count of raw milk control. The results showed that both CO_2 addition and thermization are effective and can be used to preserve the quality of raw milk before processing and to prevent quality problems in dairy products.

Key Words: raw milk, carbon dioxide, thermization

T228 Utilizing clean label starches in yogurts processed with challenging temperature and homogenization pressures. B. Roa*, A. Perez, E. Yildiz, I. Potrebko, T. Shah, and L. Carr, *Ingredion Incorporated, Bridgewater, NJ.*

Formulating yogurts with thermally inhibited, clean label starches has often been challenging because of the harsh processing conditions

manufacturers utilize. This is the case when manufactures use high temperature and homogenization pressures, which degrade the integrity of many existing clean label starches. The loss of starch integrity affects the functionality and ultimately the texture of finished yogurt product. This presentation will focus primarily on the next generation clean label starch that extends the functionality of clean label starches in yogurts processed with demanding temperature/pressure parameters. The next generation clean label starch performance was compared with existing clean label starches and chemically modified counterparts, over a range of different parameters including upstream/downstream homogenization configurations. The downstream yogurts were processed over a pasteurization range of 185 to 195°F and 0 to 2610 psi total homogenization pressure. The upstream yogurts were processed over a preheat range of 140 to 170°F and 725 to 3625 psi total homogenization pressure. Based on instrumental characterization results from the Brookfield DV-II+ Viscometer and SMS TA-XT2 Texture Analyzer, the next-generation clean label starches were able to be processed with up to 1450 psi more total homogenization pressure at certain temperatures than with previously available clean label starches, while still providing the desired texture effect. Using a downstream homogenization configuration with 2610 psi total pressure, the next generation clean label sample had a viscosity of 5100 cps compared with the previously available clean label starch sample's viscosity of 1674 cps. The instrumental characterizations also demonstrated that the enhanced functionality of the next generation clean label starches yielded process tolerance comparable to highly inhibited chemically modified starches. Based on the results of this work, the next generation clean label starch was able to be processed with very demanding parameters, while still providing functionality in terms of viscosity and overall texture.

Key Words: yogurt, starch, processing

T229 Proteomic evaluation of milk fat globule membrane proteins and bovine health status. M. Vaiente*, L. Tomanek, M. Yeung, and R. Jimenez-Flores, *California Polytechnic State University, San Luis Obispo.*

Proteins associated with the milk fat globule membrane (MFGM) have been associated with many biological functions in the dairy cow. These proteins are also purported to confer nutritional and health benefits to human. However, there is little information about the effect of the health of the cow on the composition and expression of these membrane proteins. Since the overabundance of casein and whey in milk interfere with typical MFGM protein analysis, a contemporary proteomic approach offers an ideal solution. To this end, this study was aimed to observe and measure changes in the MFGM proteins collected from cow with different health status. MFGM fractions and somatic cell pellets were extracted from raw bovine milk collected from 3 healthy cows at the dairy farm on campus. These were separately pooled to form a MFGM sample and a somatic cell sample. Similarly, the samples were pooled from 3 cows exhibiting suboptimal health, indicated by elevated levels of somatic cell count. To generate the MFGM and somatic cell proteome maps, 2D gel electrophoresis was conducted and the gel images were analyzed using Delta2D program. Spot intensities were compared between samples derived from healthy and suboptimally healthy cow by using permutation ANOVA ($\alpha = 0.02$) available within Delta2D. The proteomes were also visualized using principal components analysis to explore differences between the proteomes and bovine health status. The proteome maps for somatic cells and MFGM proteins show differentially protein expression and distinct characteristics, including numerous putative novel proteins. Unique proteins were selected for MALDI-TOF mass spectrometry analysis and identification. Our results suggest that cow lactation physiology is markedly different under varying health status and lead to changes in the MFGM proteome. The outcome of this study further helped generate specific hypotheses to test the interaction between bovine health and individual protein species, and the role of these proteins in human health.

Key Words: milk fat globule membrane, proteomics, somatic cell

T230 Production of sodium chloride nanoparticles by nanospray drying method. M. Moncada*[1], K. Aryana[1,2], C. E. Astete[3], and C. Sabliov[3], *[1]School of Animal Sciences, Louisiana State University Agricultural Center, Baton Rouge, [2]Department of Food Science, Louisiana State University Agricultural Center, Baton Rouge, [3]Biological and Agricultural Engineering, Louisiana State University Agricultural Center, Baton Rouge.*

Reduction in sodium intake decreases blood pressure and could prevent hypertension; hypertension is a major risk factor in the development of cardiovascular diseases. One alternative to reduce sodium content without replacing sodium chloride (NaCl) in foods by other food additives is to reduce the particle size of salt without modifying its chemical composition to produce nanosalt. Reducing the particle size of sodium chloride crystal would increase dissolution rate in saliva leading to a more efficient transfer of the ions to the taste buds and hence a saltier perception of foods. The goal of this study was to develop nanosalt by using a nanospray drying method. The processing parameters were optimized to ensure formation of the smallest size nanosalt, as measured by scanning electron microscopy (SEM) and dynamic light scattering. A sodium chloride solution (3% wt/wt) prepared in deionized water was processed by nanospray drying (Nanospray dryer B-90, Büchi Corporation). The sodium chloride solution was sprayed through 2 different nozzle sizes (4 and 7 μm) at 20, 10, 5 and 3% (wt/wt). The gas flow (125 L/min), pressure (38 mbar), head temperature (95°C) and spray percentage (90%) were kept constant in all treatments. The resulting nanoparticles were analyzed by SEM to visually analyze shape and size. Of the 3 concentrations studied, the lower concentration (3% wt/wt) provided the smallest size nanosalt. Three replicates were conducted at this concentration, and particle size distribution from each nozzle size was analyzed using ANOVA of SAS. There was a significant ($P < 0.05$) difference in NaCl particle sizes using 4 and 7 μm nozzles. The NaCl solution subjected through the 4-μm nozzle had the smallest sodium chloride nanoparticle size (500–700 nm). The outcomes from these trials showed that smaller sodium chloride nanoparticles were produced when utilizing a 4-μm nozzle in the Nanospray dryer B-90 with a 3% (wt/wt) NaCl solution. Studies are on the way to test the nanosalt on the physicochemical, microbiological and sensory characteristics of surface-salted cheese crackers.

Key Words: nanosalt

T231 Physiochemical property, microstructure and probiotic survivability of nonfat goat milk yogurt using heat-treated whey protein concentrate as fat replacer. T. H. Zhang[1], J. McCarthy[2], G. R. Wang[2], Y. Liu[2], and M. R. Guo*[2], *[1]Jilin University, Changchun, Jilin, China, [2]University of Vermont, Burlington.*

Low-fat and probiotic dairy foods are getting popular in the United States. A nonfat goat milk yogurt containing probiotics (*Lactobacillus acidophilus* and *Bifidobacterium* spp.) was developed using heat-treated whey protein concentrate (HWPC) as a fat replacer and pectin as thickening agent. The yogurt was analyzed for chemical composition, water-holding capacity (syneresis), microstructure, changes in pH and viscosity, mold, yeast and coliform counts, and probiotic survivability during storage at 4°C for 10 wk. The results showed that the nonfat goat milk yogurt made with 1.3% of HWPC (12% WPC solution heated at 85°C for 30 min at pH 8.5), and 0.35% pectin had high viscosity 1650 ± 40.2 mPa·s and low syneresis (4%). The pH value of the yogurt was decreased significantly during the first week ($P < 0.05$), but there was no significant decrease after wk 2 ($P > 0.05$). Counts for mold, yeast, and coliform were negative the 10-wk study. *Bifidobacterium* spp. remained stable and was $>10^6$ cfu/g during the 10-wk storage. However, the population of *Lactobacillus acidophilus* dropped to $<10^6$ cfu/g after 4 wk of storage. Microstructure analysis of the non-fat goats' milk yogurt by scanning electron microscopy revealed that HWPC interacted with casein micelles to form a more comprehensive network in the yogurt gel. The results indicated that HWPC could be used as a fat replacer for improving the consistency of nonfat goat milk yogurt and other products alike.

Key Words: goat milk, nonfat yogurt, heated whey protein

T232 Do dairy cattle classified as high immune responders yield nutritionally better milk compared with average and low immune response cows? K. Fleming*, M. Corredig, D. Hodgins, F. Miglior, and B. Mallard, *University of Guelph, Guelph, Ontario, Canada.*

It is known that some dairy cattle have an enhanced immune response that is capable of defending against a wide array of infectious pathogens. These High immune response (HIR) cows have more robust and balanced antibody-mediated and cell-mediated immune responses compared with Average (A) or Low (L) immune responders. In this study, it is hypothesized that HIR cows produce higher quality milk with elevated contents of nutritionally valuable components. The presence of Lactoferrin (LF) is the focus of this work. Milk (n = 5) and colostrum (n = 9) samples from Holstein cattle classified as High, A or L immune responders were analyzed. Cows had previously been classified using a patented HIR test system. Milk and colostrum samples were collected at d 5 and d 0 relative to calving, respectively. Concentrations of LF were measured using a bovine LF enzyme-linked immunosorbent assay kit (Bethyl Laboratories, Inc.). Preliminary results indicate that there is substantial biological variation of LF concentrations in milk and colostrum among cows. Values range from 0.023 to 0.24 mg/mL in milk and 0.066–1.7 mg/mL in colostrum with net differences of approximately 0.22 mg/mL and 1.6 mg/mL, respectively. These values and the moderate heritability of LF provide the potential to naturally improve the nutrition of foods by implementing selective breeding programs. Quantification of LF concentrations as well as other nutritionally valuable components (i.e., glycosphingolipids) in additional samples is currently underway. Data will be analyzed with statistical analysis software using a generalized linear model upon completion of component measurement and subsequent matching of cows to immune response categorization. Overall, consumption of functional foods such as higher quality milk with elevated contents of nutritionally important components would provide one potential solution to improve the health of individuals.

Key Words: lactoferrin (LF), high immune response (HIR), milk quality

T233 Physicochemical and sensory properties of milk supplemented with dispersible nanopowdered oyster shell during storage (II). Y. K. Lee*, M. A. Mijan, and H. S. Kwak, *Sejong University, Seoul, South Korea.*

The present study was carried out to investigate the dispersibility of nanopowdered oyster shell (NPOS), Zn-activated nanopowdered oyster shell (Zn-NPOS) or powdered oyster shell (POS) and to determine the effect on the physicochemical and sensory properties of the oyster shell-added milks during storage at 4°C for 16 d. For dispersing, 20% (w/v) oyster shell samples were added in distilled water and mixed at 800 rpm for 2 h, and then 0.5% polyglycerol monostearate (PGMS) was added and mixed again at 800 rpm for 24 h. The sizes of NPOS, Zn-NPOS and POS were measured as 257 nm, 389 nm, and 180 μm, respectively. The pH values of all the milk samples ranged from 6.62 to 6.89 during the storage. The thiobarbituric acid (TBA) of NPOS- and Zn-NPOS-added milks increased to 0.36 and 0.37, respectively, but POS-added milk was higher TBA than that of samples (0.44) at d 16. In color, L* and a* values in the milks were not significantly influenced from all treated milks ($P > 0.05$). However, b* value was significantly increased during storage ($P < 0.05$). The sensory attribute revealed that NPOS- and Zn-NPOS (0.5, 1.0 and 1.5%)-added samples were significantly increased in yellowness, calcite and astringency scores, but fishy smell, bitterness and sandy were not changed during 16 d ($P < 0.05$). However, POS-added sample was significantly increased in yellowness, calcite, astringency, bitterness and sandy scores during the storage ($P < 0.05$). Base on the data obtained from this study, it is concluded that the dispersible nanosized oyster shell could be added to milk without significant adverse effects on the physicochemical and sensory properties.

Key Words: milk, nanopowdered oyster shell, sensory properties

T234 Comparison of physicochemical properties in nanopowdered red ginseng and powdered red ginseng (I). K. H. Choi*, M. A. Mijan, and H. S. Kwak, *Sejong University, Seoul, South Korea.*

Red ginseng is known to have several health benefits, such as antiinflammtory, anticancer, and antioxidative activities, In addition, red ginseng contains some distinct functional ingredients, such as Rg_3, Rg_5 and Rk_1 ginsenoside, which are not found in white ginseng. However, low bioavailability was attributed previously to their poor oral absorption. Nanotechnology may be capable of enhancement of the bioavailability for red ginseng. Therefore, this study was carried out to compare the physicochemical properties of nanopowdered red ginseng (NRG) with powdered red ginseng (PRG) and to determine the quantitation measurement of ginsenosides in NRG. To study the physicochemical properties of the NRG, the size of particles, proximate composition, pH, tapdensity, color, and water or oil holding capacities were measured. In the result, sizes of NRG and PRG were 200.6 ± 13.7 nm and 120.810 ± 1.171 μm, respectively under the particle size analyzer, and similarities were observed between NRG and PRG in proximate composition. But, the pH value was decreased from 5.6 to 5.4 when the concentrations were increased from 2 to 8%, and tap densities were 0.3030 and 0.6667 g/cm^3 in NRG and PRG, respectively. Color of NRG was significantly different from PRG, and water- and oil-holding capacities were 2 to 3 times higher in NRG than in PRG ($P < 0.05$). In quantitative analysis, total ginsenosides of NRG

(4,609.30 mg/kg) was 30% higher than that of PRG (3,335.71mg/kg). In conclusion, NRG was significantly different from PRG in most properties and nanosizing markedly increased the total ginsenosides of red ginseng. Considering these results, NRG is worth to make functional cheese.

Key Words: nanopowdered red ginseng, physicochemical property, ginsenoside

T235 Isolation of lactic acid bacteria from Xin Jiang fresh cheese and the studies of property. L. Zhang, Y. Zhang*, and X. Xu, *College of Food Science and Engineering, Harbin Institute of Technology, Harbin, China.*

Sixteen lactobacillus and 6 lactococcus were screened from traditional fermented fresh domestic acid-coagulated cheese. Then, the acid production ability, sticky production ability, fragrance production ability, textural property, the content of diacetyl, proteolysis and lipolysis capacity of these screened strains was analyzed. The strains that had the fastest production of acid were C63M and C34M. The higher production of sticky was C63M, C34M, and C61–2M. The higher content of diacetyl was C34M and C103M, which were 7.47 ± 0.01 and 6.62 ± 0.01 μg/mL separately. The higher proteolysis capacity were found in strains C104 and C61–2M, the free amino acid of these 2 strains were 469.42 mg/L and 390.68 mg/L separately. These selected 5 strains showed almost no lipolysis capacity but had good textural properties. Combined these 5 strains each other and fermented milk to make fresh acid-coagulated cheese. One group was selected for have good characteristics. Then the inoculate rate were studied. The results showed that cheese have the fastest yield with 5% inoculate, the amount was 56.79%. And the cheese moisture, texture property and its sensory evaluation are also good.

Key Words: acid-coagulated cheese, lactic acid bacteria, quality

T236 Effects of mineral content of bovine drinking water: Does iron affect milk quality? G. R. Mann, S. E. Duncan*, S. F. O'Keefe, K. A. Knowlton, A. D. Dietrich, R. E. James, C. Martel, and X. Feng, *Virginia Polytechnic Institute and State University, Blacksburg.*

Water is an important nutrient for dairy cattle; however, influences of water chemistry on milk synthesis are not well described. High mineral concentrations (>0.3 mg/kg Fe and other metals) may be from natural sources in ground water, run-off from contaminating sources, drought, or water storage systems. This study evaluated the effects of added iron in bovine drinking water on milk composition and oxidative stability. Ferrous lactate treatments corresponding to 0, 2, 5, and 12.5 mg/kg drinking water concentrations were delivered through the abomasum at 1 L/d to 4 lactating dairy cows over 4 periods (1 wk infusion/period), in a Latin square design. On d 6 of infusion milk was collected, processed (homogenized, pasteurized), and analyzed. Mineral content (Fe, Cu, P, Ca) was measured by inductively coupled plasma mass spectrometry. Oxidative stability of whole processed milk was measured by thiobarbituric acid reactive substances (TBARS) assay for malondialdehyde (MDA) and sensory analysis (triangle test) within 48 h of processing and after 7 d of refrigerated storage. Significant sensory differences ($P < 0.05$) between processed milks from cows receiving iron treatment and the control infusion were observed. No differences in TBARS (1.46 ± 0.04 mg/kg MDA) or mineral content (0.22 ± 0.01 mg/kg Fe) were noted. A case study of raw milk from cows receiving water with naturally high (1.4 mg/kg) and low (0.02 mg/kg) iron content revealed no significant differences ($P > 0.05$) in mineral composition (0.23 ± 0.06 mg/kg Fe) or analytical measures of oxidation (0.77 ± 0.03 mg/kg MDA). While iron added directly to milk causes changes in oxidation of milk, high levels of iron given to cattle in drinking water did not have such an effect.

Key Words: milk, oxidation, iron

T238 Tetracycline residues in pasteurized goat milk. R. Attaie* and A. Mora-Gutierrez, *Prairie View A&M University, Prairie View, TX.*

Twelve milking does, 5 La Monchs, 5 Alpines, and 2 Nubians were randomly selected from the milking herd of the International Goat Research Center at Prairie View A&M University. The objective was to determine the residual amount of tetracycline in the milk of treated goats after pasteurization. The tolerance limit of this antibiotic in milk for human consumption is 300 ppb. The selected goats were treated with recommended doses of tetracycline and then the milks of treated animals collected and analyzed. The residual amount of tetracycline was quantified for each milking time until the level went below the tolerance limit. High-performance liquid chromatography was used to quantify the residual amount of tetracycline in milk. Milk samples containing antibiotic residues were deproteinized by 1 *N* hydrochloric acid and addition of 15 mL acetonitrile. The sample was filtered and concentrated by using sample concentrator to approximately less than 1 mL. The samples were adjusted to exactly 1 mL using deionized water. The samples were filtered (0.45 μm) before injection into reversed-phase HPLC using isocratic procedure. For analysis, a Wakosil II C_{18} column was used with mobile phase of 0.02 *M* H_3PO_4 and 0.01 Na decanesulfonate:acetonitrile (35%:65%) at the rate of 1 mL/min using UV detector at 380 nm. The HPLC procedure was able to detect the tetracycline residues at levels less than the tolerance level in goat milk. Furthermore, it was determined that pasteurization significantly reduced the level of tetracycline residues in goat milk compared with fresh or 72 h aged goat milk.

Key Words: tetracycline residues, goat milk, high-performance liquid chromatography

T384 Assessment of consumer perceptions, preferences, and behaviors with fluid milk from different packaging. M. Paterson*[1], S. Clark[1], and M. Bozic[2], *[1]Iowa State University, Ames, [2]University of Minnesota, St. Paul.*

The objective of this study is to understand consumers' "intellectual" (beliefs or expectations) and actual sensory perceptions about fluid milk. Seven sessions, composed of approximately 10 consumers in each, were carried out. All sessions began with explanation of a consent form and process for the experiment; panelists filled out a survey about demographics and milk purchasing/consumption behaviors. Consumers were blindly served 2 pairs of milk samples (2% and skim; from 1/2 gallon translucent plastic and paperboard containers) and asked to indicate preference and acceptability for each sample using a 7 point scale. A panel of 9 judges was trained to evaluate milk quality attributes on a 15cm line scale; all samples tasted by consumers were simultaneously evaluated by the trained panel. All milk was from the same source, processed on the same day, and evaluated within 5 to 7 d of packaging; milk had only been stored in the dairy warehouse; none of the milk was exposed to a lighted dairy case. Only 2 participants (3%) indicated preference for glass in the surveys; 7% indicated preference for paperboard, and 90% indicated preference for plastic packaging. However, upon tasting, consumers did not have a preference for 2% milk from translucent plastic over paperboard, or for skim from translucent plastic over paperboard ($P > 0.05$). These findings were in agreement with their acceptability scores, which were 4.6 for skim in plastic, 4.7 for skim in paperboard, 5.0 for 2% in plastic and 5.0 for 2% in paperboard ($P > 0.05$). Trained panelists did not detect oxidized off flavor in skim milk from translucent packaging (4.7) or paperboard (3.5), or 2% milk from translucent plastic (3.6) or paperboard (1.6) ($P > 0.05$). These results confirm that trained panelists and consumers cannot distinguish fresh milk from different packaging before exposure to lighted dairy cases. Additionally, purchasing behavior is not necessarily linked to actual sensory experience. A future paper will discuss the relationship of these findings with consumer perceptions about milk after exposure to UV light.

Key Words: milk, packaging, consumer perceptions

T239 Evaluation of sensory properties of goat milk ice creams formulated with three different levels of caprine milk fat. C. McGhee, B. P. Gupta*, J. Jones, and Y. W. Park, *Fort Valley State University, Fort Valley, GA*.

Ice cream is a very popular frozen dairy food around the world. Although many studies have been reported on bovine milk ice cream, the scientific literature on caprine milk ice cream has been almost nonexistent. A study was conducted to evaluate sensory characteristics of goat milk ice creams manufactured with 3 fat levels of goat milk and a commercial powdered mix containing 0.25% fat. Three batches of 3 different low fat ice creams were produced as skim (0.46%; SIC), 2.0% (2IC) and whole (3.65%; WIC) goat milk ice creams formulated with the commercial ice cream mix. The Sani Serv ice cream machine (A5223P, Mooresville, IN) was used to make soft-serve ice creams. Upon manufacture, all experimental fresh ice creams were stored in a freezer at −18°C for 0, 2, 4 and 8 weeks. Sensory characteristics of all ice creams were evaluated by an 8-member sensory panel, using ADSA collegiate ice cream scorecards. Flavor traits were determined by normal range of flavor score 1–10, where excellent 10 (no criticism), good 8–9, fair 6–7, and poor 5 or less, respectively. Body and texture, and color properties were assessed by normal range of 1–5 scores, where 5 indicated no criticism. The results showed that there were no significant differences in all sensory characteristics of flavor, body and texture, and color traits between 0 to 8 weeks storage periods for the 3 goat ice creams, except a few cases of flavor and body and texture. No detectable color changes were found in all 3 types of ice creams. For flavor properties, the sweet and whey flavors between 0 and 2–8 weeks for 2IC and WIC were appeared to be different, while no differences in flavors were observed in SIC. For body and texture traits, increases in weak body in WIC, and increases in sandiness and sogginess were occurred in 2IC from 0 to 8 weeks. The 2IC showed a slight improvement in weak body as the storage time advanced. It was concluded that very few changes occurred in sensory properties of all 3 types of goat milk ice creams up to 8 weeks frozen-storage.

Key Words: goat milk, ice cream, sensory property

T241 Influences and mechanisms of heat-related processes during manufacture of milk powder on coagulation quality of milk. X. Han*, L. Zhang, and W. Wang, *Harbin Institute of Technology, College of Food Science and Engineering, Harbin Institute of Technology, Harbin, China.*

Thermal processing during milk powder production changed not only the nutritional characteristics of milk but also its technological characteristics. The purpose of this study is to analyze the effects of the conventional heat sterilization during the manufacture of milk powder on the milk coagulation properties (rennet-induced coagulation and acid-induced coagulation). The texture of rennet-induced gel and acid-induced gel during different heat treatment of milk were analyzed. And the protein distribution of milk serum heat-induced changes in casein micelle size, surface hydrophobic and calcium ion activity were also detected. The results showed the heating parameters have the good regression relationship with the variables of coagulations. The coefficients of determination R^2 were greater than 0.88. The hardness of gel were decreased when heat the raw milk at 70°C for 15 s, while 90°C for 8 min decreased by 37.27% compared with the raw milk. The changes in serum protein aggregates (SPA) were also affected by different heat treatments. The protein aggregates caused by the thermal denaturizing of milk protein can be performed as part of the casein micelles in the solidification process, or as a "bridge" between the micelles, thus contributing to the process of acid curd. However, the protein aggregates did not act such a role in the rennet-induced gel according to the data in the experiment. And the size of SPA increased with the increase of heating temperature and time, ranging from ~30 nm at low-intensity heat treatment increased to ~100 nm at high-intensity treatment. By the test of rennet coagulation with SPA addition the inhibition effect was not found, suggesting the inhibition of heating on rennet coagulation was not derived from SPA. The rennet coagulation of milk was influenced by the properties of casein micelles and calcium ion. Thus, the combined (positive and negative) effects of heat induced changes of SPA and the properties of casein and calcium ion activity led to the reduced ability of rennet coagulation.

Key Words: milk powder, protein aggregate, rennet gel

T242 Light-protective packaging effectiveness to enhance sensory and nutrient stability of extended shelf life milk and n-3 enriched milk. D. Johnson, S. E. Duncan*, W. N. Eigel, and S. F. O'Keefe, *Virginia Tech, Blacksburg.*

Modification of milk composition with n-3 (omega-3) fatty acids increases risk of product oxidation, which can be accelerated by light. Effectiveness of light protection additives (LPA) incorporated into high density polyethylene (HDPE) packaging in limiting light-induced oxidation of extended shelf-life milk (2% total fat) and n-3 fatty acid enriched milk (2% total fat) was studied. Packaging effectiveness was determined by assessing changes to packaged milk flavor, oxidation, and riboflavin concentration throughout a 35-d shelf life study. Extended shelf-life fluid milk, with and without n-3 fatty acids, was stored in a lighted dairy case (average light intensity: 2200 lx; 4°C). HDPE packaging included no LPA (control; translucent appearance); light-protected (foil overwrap over no LPA control); and 3 LPA levels (low, medium, high) for the experimental treatments. Over the study period, riboflavin concentration in the 2% milk decreased 11% and 29% in the light-protected control and the high LPA packages respectively. Thiobarbituric acid reactive substances assay (TBARS) of more than 1.3 μmol of malondialdehyde (MDA) indicated significant change in flavor; the high LPA package provided effective protection for the 2% milk. In n-3 milk, the high LPA package provided greater protection of sensory quality and riboflavin than the other packages; however, riboflavin decreased by 28% through the 35-d study even in the light-protected control representing a higher loss rate than observed in milk without n-3 lipids. The n-3 milk packaged in the no LPA-HDPE package exceeded MDA of 3.0 μmol by d 7, suggesting the milk would not be of sufficient sensory quality for consumer acceptance. Conversely, the high LPA package protected riboflavin and controlled MDA development most effectively of the LPA packages studied in the n-3 enriched milk beverage. Packaging innovation and design, including light protection material incorporation, can provide improved protection of milk flavor and nutrient content. Product composition influences packaging light protection effectiveness.

Key Words: n-3, packaging, oxidation

T243 Properties of whey protein isolate-maltodextrin conjugates as affected by powder acidity during the Maillard reaction. W. Wang* and Q. Zhong, *The University of Tennessee, Knoxville.*

A challenge of producing shelf-stable high protein (>4.2% wt/vol) beverages using whey proteins is the protein denaturation and aggregation during heating that result in turbidity and possibly gelation. Our previous studies showed that transparent dispersions of whey protein isolate (WPI) glycated

with maltodextrin (MD) were heat stable at pH 3.0–7.0. Glycation was achieved by heating powders spray-dried from a neutral pH solution with equal mass of WPI and MD – the Maillard reaction. However, the undesired brown color and health-concerning advanced Maillard reaction products are to be reduced. In this study, WPI and MD were dissolved at equal mass in water, adjusted to pH 4–7, hereafter referred as "mixture pH – m-pH," and spray-dried. The obtained powder was incubated at 80°C, 65% relative humidity for 1, 2, and 4 h to prepare conjugates. The resultant conjugates were prepared at 5% (wt/vol) protein in deionized water, adjusted to pH 4–7, hereafter referred as "solution pH – s-pH," 0–100 mM NaCl and 5% (wt/wt) sucrose. After heating at 138°C for 1 min, the absorbance at 600 (Abs_{600}) and 420 nm (Abs_{420}) was measured as indicators of turbidity and color formation, respectively. A darker brown color, higher Abs_{420} and lower Abs_{600} were observed for conjugates glycated for a longer time, with all conjugates prepared by 4-h glycation being transparent at all s-pH. For samples glycated for 2 h, a lower m-pH corresponded to a lighter color but was generally less heat stable; the m-pH 6.0 treatment was the most heat stable, with only the pH 5.0 and 0 m*M* NaCl sample showing turbidity. The m-pH 6.0 treatment corresponded to the highest degree of glycation assessed based on free amino group concentration and the highest denaturation temperature according to differential scanning calorimetry. The transparent samples after heating had mean particle diameters as small as ~13 nm. The combination of m-pH 6 and 2-h glycation was concluded as the most desirable treatment in terms of both heat stability improvement and color reduction. This study suggests that the quality of glycated WPI can be improved by controlling m-pH.

Key Words: whey protein, heat stable, conjugate

T244 Caseinomacropeptide index for cheese whey detection in pasteurized milk, Brazil. P. R. Lobato[1], M. E. R. Fortini[1], R. S. Conrrado[1], M. M. O. P. Cerqueira[1,2], L. M. Fonseca*[1,2], M. O. Leite[1,2], R. Rodrigues[1], M. R. Souza[1], and C. F. A. M. Penna[1], *[1]Department of Food Technology and Inspection, School of Veterinary Medicine, Universidade Federal de Minas Gerais (UFMG), Belo Horizonte, MG, Brazil, [2]CNPq, Brasilia, DF, Brazil.*

Cheese whey is a high nutritive by-product of the cheese industry. However, due to its low commercial value, its use to adulterate milk is a well known and hard to detect in practice. Caseinomacropeptide (CMP) index determination by high performance liquid chromatography with gel filtration (HPLC-GF) is officially used in Brazil to investigate whey addition to milk, and it should be no more than 30 mg/L. If CMP index is 30 to 75 mg/L, milk can be used only for specific dairy products, and above 75 mg/L, only for animal feeding. The objective of this study was to evaluate the CMP index method by HPLC-GF to detect fraudulent addition of whey to retailed pasteurized milk in Minas Gerais, a state responsible for about 30% of Brazilian milk production. Fifty-six samples of several brands of pasteurized milk were collected from randomly chosen retail stores, and kept under refrigerated conditions until analysis in the Laboratory of Chromatography, School of Veterinary Medicine, Universidade Federal de Minas Gerais, Brazil. CMP index ranged from 30 to 75 mg/L for 1.8%, and above 75mg/L for 30.4% of the samples. Based on CMP index, only 67.9% of the samples were compliant to the standards, with CMP index below 30 mg/L. Fraudulent addition of cheese whey to pasteurized milk was aggravated in some regions with up to 90% of occurrence, and it was brand related. The levels of cheese whey found in pasteurized milk in the current study indicate lower nutrient levels in the final product. It is concluded that quality monitoring in the milk collection must be emphasized and stricter plant inspection is necessary to keep milk integrity in Brazil. Routine CMP index determination by HPLC-GF might play an important role to monitor cheese whey fraudulent addition to pasteurized milk.

Key Words: food adulteration, CMP index, cheese whey

T245 Milk mineral harvest from dairy streams using filtration technology. L. Mealy*, C. Marella, A. Biswas, and L. Metzger, *Midwest Dairy Foods Research Center, South Dakota State University, Brookings.*

Milk minerals harvested from dairy processing streams have applications in several areas including use as a supplement in a wide variety of foodstuffs. Dairy stream demineralization methods are employed in commercial lactose isolation and can also be used as a pretreatment for other filtration processes to minimize membrane fouling. The objective of this research was to investigate the potential of wide pore ultrafiltration membranes for removal of minerals from skim milk ultrafiltration permeate. Filtration experiments were conducted using a lab scale plate and frame filtration unit. Pre-production water flux rates were obtained at 27°C (80°F). Subsequently, 2000 mL of feed was added to the balance tank and processed at 49°C (120°F) until a 5× volume reduction was achieved. After a rinse of 2000 mL water at 49°C, post-product water flux values were obtained at 27°C. Membrane performance evaluation was based on the flux obtained during the filtration process, percent flux recovery after production and rinsing as well as by mineral retention. In this study, 3 feeds that varied in mineral content (0.91, 0.97 and 1.04%) were standardized to 11.03% total solids and concentrated using [polyethersulfone (PES) membrane with a molecular weight cut off (MWCO) of 20 kDa, and 2 polyvinyledefluoride (PVDF) membranes with a MWCO of 30 and 40 kDa, respectively]. Significant differences in both product flux values and ash recovery were seen between feed - membrane pairs analyzed. The PVDF membrane with MWCO 40 kDa exhibited the highest product flux rate of 117 LMH and ash retention of 41%. Future work will focus on using these membranes for industrial scale applications.

Key Words: milk mineral, ultrafiltration

T246 Characterization of whey protein films incorporated with oregano essential oil (*Origanum vulgare*). S. P. L. F. de Oliveira[1], I. M. B. Dianin[1], A. P. Bilck[1], C. M. V. B. de Rensis[1], L. C. Bertan[2], and P. C. B. Vianna*[1], *[1]Universidade Norte do Paraná (UNOPAR), Londrina/PR/Brazil, [2]Universidade Federal da Fronteira Sul (UFFS), Laranjeiras do Sul/PR/Brazil.*

The aim of this study was to evaluate the characteristics properties (visual appearance, thickness, water vapor permeability and water solubility) of the whey protein films incorporated with oregano essential oil. The films were produced by casting technique from whey protein isolate and added of oregano oil at 4 concentrations: 0% (control film), 0.5%, 1.0% and 1.5% (vol/vol). The whey protein isolate was dispersed in distilled water, added with glycerol (3%) and heated at 90°C/30 min in water bath. The oregano oil was added to the solutions before heating. The film solution was spread on Petri dishes (90 cm of diameter) and dried for 24 h at room temperature. The films were removed from the plates with a spatula and stored at controlled humidity (52%) at 25°C/48 h before analysis. The results were evaluated by ANOVA and Tukey's test at 5% significance level. Generally, films presented transparent and homogeneous, with a slight yellow color. The films were more flexible with increasing oregano oil concentration. The films thickness ranged from 0.013 mm to 0.015 mm, and the control film showed significantly thinner than the films added with 0.5 and 1.0% of oregano oil. The water vapor permeability decreased significantly in added oregano oil films when compared with control film. However, increasing the concentration of oregano oil caused no significant changes in water vapor

permeability. The solubility ranged from 14.0% to 20.2%, with the control film significantly more soluble than 1.5% added oregano oil. Probably the hydrophobic characteristic of oregano oil influenced the decrease in water vapor permeability and solubility of the films suffered its addition. The results indicate that whey protein isolate is a good matrix for production of biodegradable films and addition of oregano essential oil, even in small quantities positively affected the characteristics of the films. The oregano essential oil can also confer antimicrobial properties for these films.

Key Words: whey protein, film, oregano oil

T247 Effect of Sicilian pasture feeding management on content of α-tocopherol and β-carotene in cow milk. V. M. Marino*[1], I. Schadt[1], S. Carpino[1], M. Caccamo[1], S. La Terra[1], C. Guardiano[1], and G. Licitra[1,2], *[1]CoRFiLaC, Ragusa, Italy, [2]DISPA, Catania, Italy.*

This study was performed to evaluate α-tocopherol and β-carotene content of pasture milk under ordinary Sicilian farming conditions. Fourteen dairy farms were allocated into 2 balanced groups on the basis of cultivated (CULT) and spontaneous (SPO) pasture type feeding. Bulk milk per farm was collected 4 times from February through April with 3-wk intervals. Pasture botanical and diet composition, diet nutritional quality, milk yield and composition were estimated each time. Pasture intake levels were calculated based on feed analyses and hay and concentrate amounts fed and, on milk yield and chemical composition using CPM Dairy. In accordance to pasture intake the farms were split into a low pasture (LPI; < 29.5% DMI) and a high pasture intake group (HPI; > 29.5% DMI). Milk samples per farm were analyzed for α-tocopherol and β-carotene contents. Spontaneous milk had higher levels ($P < 0.05$) of α-tocopherol and β-carotene in milk (0.7 and 0.3 mg/L, respectively) and in milk fat (19.0 and 7.5 mg/kg fat, respectively) compared with CULT (0.5 and 0.2 mg/L milk; 14.6 and 4.9 mg/kg fat, respectively). High pasture intake compared with LPI increased α-tocopherol in milk fat (18.0 and 16.0 mg/kg fat, respectively; $P < 0.05$). However, only in SPO but not in CULT milk, HPI increased α-tocopherol ($P < 0.05$) and β-carotene ($P < 0.01$) in milk and β-carotene in milk fat ($P < 0.05$) (0.8, 0.3 mg/L milk and 8.4 mg/kg milk fat, respectively) compared with LPI (0.6, 0.2 mg/L milk and, 6.6 mg/kg milk fat, respectively). All results may be explained by the different botanical composition of both pasture types. Spontaneous pasture compared with CULT contained more Asteraceae, Fabaceae, Cruciferae, Euphorbiaceae and Malvaceae. Milk and milk fat α-tocopherol levels were higher at the test-d 1, 2 and 4 compared with 3 ($P < 0.01$). At HPI milk fat β-carotene content was higher at the first 2 test-days compared with the others ($P < 0.05$). These differences are probably related to plants' biological stage. On Sicilian dairy farms highest milk α-tocopherol and β-carotene content may be obtained feeding SPO pasture at high levels.

Key Words: milk, fat-soluble vitamin, pasture

T249 Whey permeate used as salt substitute in processed foods. S. Chizonda*, E. M. Dixon, Y. Jiang, and J. C. Allen, *North Carolina State University, Raleigh.*

Whey permeate (WP) from ultra-filtration of whey and milk is considered a low-priced by-product in cheese and whey protein production. WP contains lactose (80–89%) fat, moisture, soluble non-protein nitrogen and minerals. WP minerals help provide salty taste even if Na content is low. The objectives of this study were to utilize WP as a salt substitute to decrease Na and Cl content and increase K, Ca, and Mg content in several food products. People who consume significant quantities of such products might decrease hypertension risk. Furthermore, with increasing demand for cheese and whey protein, there will be more WP available and a need to find new ways to utilize it. Powdered WP was analyzed with ICP for 7 minerals (Na, K, Ca, Mg, Fe, Zn, Cl). The saltiness intensity of WP and NaCl in aqueous solution were determined by a trained descriptive panel (n = 12) to calculate the equivalent concentrations of salt and permeate for salty taste. WP was used as a salt substitute based on the salty taste equivalencies in reformulating canned cream soup base, fresh cream soup base, smoked sausage, and bread. Consumer panels evaluated the products. Fresh WP soup was ranked in salty taste slightly lower and canned soup slightly higher than soup with 50% of salt omitted. However, the fresh and retorted soup formulations made from permeate actually contained only 11% and 19% as much Na as the full-salt recipe, respectively. Sausages made with 25% WP salt substitution were not different than the 100% salt sausage in overall liking, flavor, saltiness, texture, firmness, juiciness or deformability ($P < 0.05$). WP sausages had lower water activity and pH than the 100% salt sausage, and lower ingredient cost. The foods made with WP were lower in Na and Cl and had higher K, Ca, and Mg levels. The WP foods had higher saltiness than the actual sodium content's contribution to the taste, but not as high as predicted from the salty taste of the permeate in aqueous solution, suggesting mineral interaction with other food ingredients. This research showed the feasibility of using WP as a salt substitute in several processed food products.

Key Words: whey permeate, sodium reduction, processed food

T250 Application of a rising plate meter to estimate forage yield on dairy farms in Pennsylvania. A. N. Hafla*, K. J. Soder, M. Rubano, and R. Stout, *USDA-Agricultural Research Service-Pasture Systems and Watershed Management Research Unit, University Park, PA.*

Accurately assessing pasture forage yield is necessary to budget feed expenses. The rising plate meter (RPM) is a rapid method of estimating dry matter (DM) forage yield but calibrations and equations provided by manufactures may be unreliable. The objective of this study was to evaluate the ability of a RPM to accurately estimate pasture forage yield on dairy farms with multiple plant species and determine the best calibration equation. The 3 PA farms in this study used rotational grazing with lactating dairy cows. Forage mass was estimated in each pasture, a day before grazing, using 45 measurements from a FILIPS RPM (n = 180–225 per farm). To measure forage DM yield, 15 clippings (n = 60–75 per farm) of 1 m × 10 cm were taken alongside RPM measurements. Visual estimates of botanical composition were made to assess species diversity. Equations for estimating pasture forage mass were determined by regressing measured DM yield on the corresponding RPM value. Four calibration equations based on measurements were evaluated: (1) pooled from all farms (2) by farm (3) by season (summer or fall) and (4) by farm and season. Two equations provided by the RPM manufacturer were also evaluated: a default and seasonal equation. Equations were evaluated by regression procedures (PROC REG, SAS) and estimated standard error of prediction (SEP). Measured DM forage yield was 1209, 896, and 2,246 kg/ha for farms 1, 2 and 3, respectively. Grasses made up 23, 44, and 63% of pasture composition; legumes composed 48, 25, and 20%, for the 3 farms. Manufacturer equations had the greatest SEP (32 and 38% of measured forage yield, respectively) and low r^2 (0.58 and 0.51, respectively). Error levels for calibration equations 1, 2 and 4 were greater than the 10% level considered acceptable by previous studies (12 to 21%). The equation considering season had the lowest SEP (9%) and a high r^2 (0.76). Our results indicate that manufacturer equations are unreliable for estimating forage yield on farms in PA in pastures with multiple species. Calibration equations should be developed and adjusted for each season to ensure the greatest accuracy.

Key Words: forage yield, grazing, rising plate meter

T251 Case study: Dairies utilizing ultra-high stock density grazing in the Northeast. K. J. Soder*[1], M. Hautau[2], A. N. Hafla[1], M. D. Rubano[1], B. Moyer[2], and R. Stout[1], *[1]USDA-ARS, University Park, PA, [2]The Pennsylvania State University, University Park.*

Ultra-high stock density (UHSD) grazing has recently gained interest in the dairy industry. However, little research exists to support anecdotal claims that forage and soil improvement occur through trampling high proportions (75+%) of mature forage into the soil by grazing dense groups of cattle on small paddocks (550,000+ kg per 0.4 ha) with long (60–90+ days) rest periods. Furthermore, UHSD may not be appropriate for northeastern dairies. A case study was conducted to evaluate grazing management of dairies that are early adopters of self-defined UHSD grazing. Data, collected on 4 dairy farms in PA and NY during the 2012 grazing season, included: forage and soil nutrient analyses, stock density, botanical composition and pasture stratification. Data were analyzed using the MIXED procedure of SAS. Least squares means are presented. Pasture area ranged from 80 to 250 ha with 60 to 270 lactating cows. Milk yield ranged from 9 to 18 kg/cow. Stock density ranged from 37,800 to 180,444 kg/ha with an average 39 (±7) day rest cycle. Forage consumed ranged from 50 to 70% of total forage available. Cows averaged 75% (±18) consumption above 20 cm of growth with lower layers averaging 53% (±11) consumption. Soil mineral content and pH were within recommended levels. Forage crude protein averaged 20% (±3.5; DM basis) in June and 29% (±3.7) in Oct. Neutral detergent fiber decreased from 52% to 34% (DM basis) from June until Oct. Forage net energy for lactation increased from 1.34 to 1.61 Mcal/kg DM between the 2 grazings, resulting from grazing at a less mature state in the autumn. Dairies in the Northeast took a modified approach to current UHSD definitions by grazing forages slightly more mature than that recommended in rotational grazing systems, and slowing the rotation to allow plants to mature (but not nearly as mature as what has been anecdotally reported in other UHSD situations) to increase forage DM available as well as improve nutrient balance (e.g., protein and fiber) in forage to better meet nutritional needs. Data from this case study will help identify needed areas to compare this grazing strategy with more traditional methods.

Key Words: dairy, grazing, ultra-high stock density

T252 Feed efficiency by dairy cows in China: A farm survey result. C. Wang*[1,2], J. X. Liu[2], N. B. Wei[1], Q. M. Xu[1], and H. P. S. Makkar[3], *[1]Zhejiang Agriculture and Forestry University, Hangzhou-Lin'an, China, [2]Institute of Dairy Science, Zhejiang University, Hangzhou, China, [3]Animal Production and Health Division, FAO of the United Nations, Rome, Italy.*

This work was conducted to evaluate feed efficiency and economic profits under different dairy systems in China. Twenty-three farms across China were selected for survey on the basis of differences in management systems and animal numbers. Three dairy systems were defined: (i) Smallholder subsistence farms (SH): < 10 cows per farm and farm is owned by one person or one family; (ii) Peri-urban farms (PR): > 100 cows herd per farm, with good management practices; and (iii) Cooperative farms (CO): usually >100 cows per farms but the cows in the farm are owned by several different person and kept collectively in a farm. Data were statistically analyzed by using GLM procedure of SAS. Though statistical significance was not observed, numerically more concentrates were used in PR than other 2 systems (Table 1). Human edible grain was the most used feedstuff in all the systems with higher percentage in SH than in the other 2 systems where farmers used more cottonseed, extruded soybeans, and by-products. Milk production per cow ranked across groups as PR > CO > SH ($P < 0.01$). Average feed efficiency for lactating cows was significantly higher in PR than that in CO or SH system ($P < 0.01$), with highest value (1.51 kg milk/kg DMI) in PR and lowest value (0.93 kg milk/kg DMI) in SH system recorded for single farm. Nitrogen utilization efficiency was higher in PR than in CO or SH system, with little difference between CO and SH systems. Overall, although the milk produced per USD ($) worth of feed was similar in different systems, the economic profitability and ecological benefit were higher in PR system because of the higher sales price, high nitrogen conversion, and less use of human edible grains.

Table 1. Production and economic profits for different systems of dairy farms

Item	PR	CO	SH	SEM	*P*-value
Concentrate, % DM	53.9	49.4	44.4	3.04	0.28
Grains, % DM	27.1	29.2	35.1	2.32	0.10
Milk yield, kg/d/cow	27.0[a]	22.3[b]	17.2[c]	1.00	<0.01
Feed efficiency, kg milk/kg DMI	1.36[a]	1.17[b]	1.06[b]	0.028	<0.01
Nitrogen conversion[1]	0.273[a]	0.244[b]	0.229[b]	0.004	<0.01
Milk yield, kg/$	2.63	2.47	2.68	0.060	0.20

[ab]Means within same row with different superscripts differ ($P < 0.05$).
[1]Milk protein yield/CP intake.

Key Words: feed efficiency, dairy system, economic benefit

T253 Silage management on high-producing dairy farms in Brazil. R. C. Amaral*[1], T. Gama[1], I. De Oliveira[2], and T. F. Bernardes[2], *[1]DeLaval, Campinas, São Paulo, Brazil, [2]University of Lavras, Lavras, Minas Gerais, Brazil,*

Silage management on dairy farms is important to reduce the dry matter losses and maintain the quality of silage during the year. Most of the research on silages in Brazil has been performed in laboratory-scale silos, but limited research has been conducted on farm-produced silages. The objective was to assess the silage management practices in high producing dairy farms. A survey was carried out on 13 high producing dairy farms in 5 Brazilian States. All farms had Holstein cows, which average of 1,818 milking cows/farm. A questionnaire was applied to identify the silage management, regarding the harvest, silo type and feed-out management. The data were collected during a spring (August until November) in 2012. Silages samples were taken at 2 locations across the feed-out face (3 samples on the top and 3 samples on the center) to determine pH of the silages. The silage from top was measured to determine the spoilage silage and silage color. All data were tabulated in an Excel spreadsheet. The number of responses, mean, minimum value, maximum value, and standard deviation were calculated. The average milk production was 24,211.9 kg/d/farm and 31.4 kg/d/cow. For a silage harvest, 76.5% of the farms used contracted harvest and 23.5% used their own machines. One-hundred percent used self-propelled harvesters. Seventy one percent of the farms used a Penn State Particle Size Method to determine the distribution and the particle size of the forage, 6.0% used a ruler and 24.0% did not use any method. In these farms, 70.6% used inoculants in the ensiling process (75.0% homolactic and 25.0% heterolactic inoculant). The trench silo represented the major silo type (82.3%), followed by 11.3% of pile silo and 5.9% pressed bag. In the feed-out phase 58.8% of the farms used milling cutter and 41.2% wheel loader. Silage pH <4.0 was found in 64.7% of center silage samples and 47.1% on the top. Higher pH on top can explain the presence of spoiled silage of 4.4 cm average depth on top for 47.1% of the farms.

Key Words: corn silage, dairy nutrition, silage quality

T254 Modelling the effect of white clover protein degradability on milksolids production and nitrogen excretion. E. N. Khaembah*[1], P. Gregorini[1], P. C. Beukes[1], and G. P. Cosgrove[2], *[1]DairyNZ, Hamilton, Waikato, New Zealand, [2]AgResearch, Palmerston North, Manawatu, New Zealand.*

There is a positive correlation between dietary white clover (WC) content and milk production; however, utilization of WC-rich diets may be limited by increased urinary nitrogen (UN) excretion resulting from rapid ruminal degradation of WC proteins. Increasing the dietary fraction of rumen undegradable protein (RUP) has the potential to increase protein passage to the small intestine, thus improving protein utilization. Model simulation provides a tool to evaluate the effect of the RUP fraction in dietary WC on milk production and UN excretion. This study used the DairyNZ Whole Farm Model (with Molly cow model) to evaluate a Waikato dairy system with 2–7 year old Friesian cows (stocking rate = 3.0 cows/ha) for whole-farm productivity and N partitioning, over the 2004/2005 milking season. The control diet (standard perennial ryegrass (PR)/WC containing 15% WC) was compared with mixed PR (60%) and WC (40%) diets containing 0.3, 0.4 and 0.5 RUP fraction of WC (treatments 1, 2 and 3, respectively). Model adjustments were made to allow 22% extra dry matter intake (DMI) on WC of the treatment diets. Pasture silage was fed during feed deficits. Model outputs were DMI, milksolids (fat + protein) production, N intake and N in milk, urine and feces. There was greater DMI from treatment diets compared with the control (4.6 vs. 4.4 t DM/cow/lactation). Milksolids (kg/ha) production was 1179, 1260, 1264, 1269 for the control and treatments 1, 2 and 3, respectively. Dietary N intake was 14 kg/cow/lactation greater on treatment diets relative to the control. Nitrogen excretion (kg/cow/lactation) for the control and treatments 1, 2 and 3 were 26.9, 28.8, 28.9, and 29.1 in milk, 76.8, 87.5, 86.8, 86.2 in urine, and 33.6, 35.4, 35.9 and 36.3 in feces, respectively. Under this study's assumptions, increasing dietary WC content increased MS production, but also increased UN excretion. Increasing RUP of WC protein only slightly reduced UN excretion. This model-derived outcome indicates that breeding for decreased protein degradability would offer only limited prospects for reducing UN excretion from WC-rich diets.

Key Words: white clover, protein degradability, nitrogen partitioning

T255 Effect of cow genotype and level of supplementation at pasture on milk performance of animals under a simplified rotational grazing system. A. I. Roca-Fernandez*[1,2], L. Delaby[2], S. Leurent[3], Y. Gallard[3], and M. E. Lopez-Mosquera[4], *[1]Agrarian Research Centre of Mabegondo, La Coruña, Galicia, Spain, [2]INRA Agro-Campus Ouest UMRPL, Saint Gilles-Rennes, Bretagne, France, [3]INRA Experimental Farm Le Pin au Haras, Borculo-Exmes, Normandy, France, [4]University of Santiago de Compostela, Lugo, Galicia, Spain.*

Milk performance of 2 cow genotypes, Holstein-Friesian (F, n = 178) vs. Normande (N, n = 174), managed at 2 levels of concentrate supplementation at pasture, low (0 kg DM/cow/day, n = 174) vs. high (4 kg DM/cow/day, n = 178), was studied in 4 groups (F0, F4, N0 and N4) applying a 2 × 2 factorial design. A simplified rotational grazing system, with a mean residence time per cycle of 10 d, was examined at Pin au Haras farm (France) during 2001–2005. The objective of this work was to determinate the maximum milk yield (MY max.) and the milk yield drop (Dm) in each grazing cycle for both cow genotypes in both grazing feeding regimens. Data were analyzed using PROC MIXED in SAS. MY and peak of MY per lactation were higher ($P < 0.001$) in Holstein-Friesian (7,591 and 36.2 kg/cow, respectively) than in Normande cows (6,214 and 29.2 kg/cow, respectively), with lower ($P < 0.001$) body weight (BW) and body condition score (BCS) in Holstein-Friesian (659 kg and 2.18, respectively) than in Normande cows (695 kg and 2.83, respectively). Supplemented cows showed higher ($P < 0.001$) MY and peak of MY (7,567 and 35.0 kg/cow, respectively) than cows without supplementation (6,238 and 30.4 kg/cow, respectively), with higher ($P < 0.001$) BW and BCS in supplemented cows (702 kg and 2.85, respectively) than in cows without it (652 kg and 2.15, respectively). Supplemented cows had higher ($P < 0.001$) MY max. but lower ($P <$

0.001) Dm (24.9 and –5.3 kg/cow, respectively) than those cows without it (21.2 and –6.1 kg/cow, respectively). MY max. and Dm were higher ($P < 0.001$) in Holstein-Friesian (25.1 and –6.4 kg/cow, respectively) than in Normande cows (21.0 and –4.9 kg/cow, respectively). Milk protein and fat content were higher ($P < 0.001$) in Normande (34.5 and 40.6 g/kg DM, respectively) than in Holstein-Friesian cows (31.5 and 36.4 g/kg DM, respectively). To choose an appropriate cow genotype for an efficient milk performance at grazing is an important goal for adjusting food supply to animal demand by considering cow lactation stage and level of supplementation at pasture.

Key Words: cow genotype, simplified rotational grazing system, supplementation

T256 Effect of forage proportion on milk fatty acids profile of Holstein-Friesian cows under Galician conditions (NW Spain). A. I. Roca-Fernández*[1], A. González-Rodríguez[1], O. P. Vázquez-Yáñez[1], and J. A. Fernández-Casado[2], *[1]Agrarian Research Centre of Mabegondo, La Coruña, Galicia, Spain, [2]Agrarian and Fitopathologic Laboratory of Galicia, La Coruña, Galicia, Spain.*

The aim was to investigate the effect of forage proportions: S, 100% silage (50% grass + 50% maize); G/S, 50% grazing + 50% silage; and G, 100% grazing (80% perennial ryegrass + 20% white clover) on profiles of milk fatty acids (FA) from autumn calving Holstein-Friesian cows (n = 60) in NW Spain. From March to August, weekly milk samples were collected from individual cows for FA determination, measured by gas chromatography-mass spectrometry. There were differences in saturated FA, with higher levels in S ($P < 0.001$, 65.85 g/100 g) and G/S ($P < 0.001$, 65.34 g/100 g) than in G (61.95 g/100 g). Those differences were mainly due to C14:0, C16:0, C18:0 and to a minor extent to C6:0-C12:0. Lower content of short chain FA (C6:0-C10:0) was found in G ($P < 0.05$, 10.15 g/ 100 g) than in G/S (11.31 g/100 g). The lowest content of medium chain FA (C12:0-C16:0) was found in G (40.75 g/100 g) compared with S ($P < 0.001$, 44.68 g/100 g) or G/S ($P < 0.001$, 43.99 g/100 g). The highest content of long chain FA was found in G (38.50 g/100 g) compared with S ($P < 0.01$, 35.41 g/100 g) or G/S ($P < 0.001$, 34.78 g/100 g) due to C18:0, C18:1, C18:2 and C18:3. The highest level of unsaturated FA was found in G (27.45 g/100 g) compared with S ($P < 0.01$, 25.06 g/100 g) or G/S ($P < 0.001$, 24.75 g/100 g). The levels of oleic and linoleic acid were higher in G (23.70 and 3.13 g/100 g) than in S ($P < 0.001$, 21.81 g/100 g for oleic acid; $P < 0.001$, 2.86 g/100 g for linoleic acid) and in G/S ($P < 0.01$, 21.49 g/100 g of FA for oleic acid; $P < 0.001$, 2.76 g/100 g of FA for linoleic acid). Highest levels of mono- and polyunsaturated FA were found in G (23.70 and 0.75 g/100 g) compared with S ($P < 0.001$, 21.81 g/100 g for MUFA; $P < 0.001$, 0.26 g/100 g for PUFA) or to G/S ($P < 0.001$, 21.49 g/100 g for MUFA; $P < 0.001$, 0.25 g/100 g for PUFA) due to C18:1, C18:2 and C18:3. Linolenic and conjugated linoleic acid (g/100 g) differed ($P < 0.001$) between groups, with higher contents in G (0.62 and 1.14 g/100 g) than in S (0.40 and 0.49 g/100 g) or in G/S (0.50 and 0.82 g/100 g).

Key Words: dairy cow, forage proportion, milk fatty acids profile

T257 Effect of forage proportion on sward characteristics and milk performance of Holstein-Friesian cows under Galician conditions (NW Spain). A. I. Roca-Fernández*, A. González-Rodríguez, and O. P. Vázquez-Yáñez, *Agrarian Research Centre of Mabegondo, La Coruña, Galicia, Spain.*

A trial was carried out to investigate the effect of forage proportions (S, 100% silage; G/S, 50% grazing + 50% silage; G, 100% grazing) on sward characteristics and milk performance of autumn calving Holstein-Friesian cows (n = 60). On average, the G/S and G groups completed 4–5 rotations with 139 grazing days. The G group had less grazing days per rotation ($P < 0.001$, 27.9 d) than the G/S group (34.8 d). The G/S group was allocated to greater herbage mass (kg DM/ha) ($P < 0.05$, 3,347) than the G group (3,069). The G/S group had higher herbage allowance (kg DM/cow/day) ($P < 0.05$, 23.94) than the G group (19.34). Lower herbage utilization (%) was found in the G/S (40.1) than in the G group (89.2). The G group showed higher ($P < 0.01$) crude protein (G, 144 vs. G/S, 118 g/kg DM), carbohydrates (G, 182 vs. G/S, 148 g/kg DM) and digestibility (G, 785 vs. G/S, 756 g/kg DM) than the G/S group but lower acid (G, 271 vs. G/S, 289 g/kg DM) and neutral (G, 525 vs. G/S, 573 g/kg DM) detergent fiber. Pre- and post-grazing heights were lower in the G (16.4 and 4.7 cm) than in the G/S group (17.3 and 7.2 cm). Total intake (kg DM/cow/day) was lower in the S (21.2) than in the G/S ($P < 0.05$, 22.8) and G ($P < 0.01$, 23.6) groups. Pasture intake (kg DM/cow/day) was higher in the G (17.3) than in the G/S group ($P < 0.001$, 9.6). Silage intake (kg DM/cow/day) was higher in the S (14.9) than in the G/S group ($P < 0.001$, 6.9). Cows in the S group showed the highest ($P < 0.01$) body weight (631 kg) and body condition score (3.2) than those in the G/S (600 kg and 2.9) and G (580 kg and 2.7) groups. Milk yield was higher in the S (23.3 kg/cow/day) than in the G/S ($P < 0.001$, 21.5 kg/cow/day) and G ($P < 0.01$, 22.6 kg/cow/day) groups. The highest milk protein was found in the G (3.16 g/kg) compared with the S ($P < 0.001$, 3.03 g/kg) and G/S ($P < 0.01$, 3.06 g/kg) groups. Milk fat was higher ($P < 0.05$, 4.18 g/kg) in the S than in the G group (3.96 g/kg). Higher milk protein content was achieved in cows fed with higher proportion of forage in its diet due to higher crude protein levels in the swards.

Key Words: forage proportion, sward characteristics, milk performance

T258 Stocking strategies and stocking rate to enhance forage utilization, gain per animal, and gain per unit land area from rye-ryegrass pastures. F. Rouquette Jr.*, J. Kerby, G. Nimr, and K. Norman, *Texas A&M AgriLife Research, Overton.*

Small grain pastures (PAS) in the Southeastern United States have a bimodal DM production trait with a minor peak in the fall, and a major DM peak during mid-February to mid-May. Climatic conditions create erratic monthly DM that challenges management of stocking strategies (STRG) for stocker cattle. During a 3-year season (2008–2009, 2009–2010, 2011–2012), bermudagrass [*Cynodon dactylon* (L.) Pers] was overseeded with 112 kg/ha 'Maton' rye (*Secale cereale* L.) plus 34 kg/ha 'TAM 90' annual ryegrass (*Lolium multiflorum* Lam.). Two replicate PAS of all STRG included stocking initiation at a normal or early (RLY) date of late December and a delayed (DLA) date of late January. The RLY PAS consisted of 2 fixed (FIX) stocking rates (STK) of low (LO) and medium (ME) and 2 variable (VAR) STK. For the RLY FIX PAS, the STK were 3.7 hd/ha for LO and 6.2 hd/ha for ME. Forage allowance (kg forage DM/kg BW) was 1.6 to 2.1 on LO and 1.2 to 0.7 on ME. The 2 RLY VAR STRG included an initial LO STK until mid-late March, then increased to ME and high (HI). The DLA PAS had FIX STK of ME and HI. Six 1/2 Simmental stockers (3 steers and 3 heifers) at 250 kg were used on each replicate PAS each year (total = 202 hd). The ADG and gain/ha were assessed via PROC MIXED with STRG and Year as Fixed, and rep as random effects. Year affected STRG for ADG. The RLY FIX LO with respective gains of 1.53, 1.60, and 1.22 kg/hd for the 3 years had highest ($P < 0.01$) ADG. In contrast, the DLA FIX HI STK had the lowest ($P < 0.01$) ADG for the 3 years at 0.69, 1.15, and 0.94 kg/hd. The greatest ($P < 0.01$) gains/ha were from RLY FIX ME with 1162, 1504, and 1329 kg/ha, respectively, for years 1–3

using STK of 5.9, 8.2, and 8.4 hd/ha. Lowest gain/ha ($P < 0.01$) resulted from DLA FIX HI with gains of 663, 975, and 627 kg/ha for years 1–3. The STRG of increasing STK to maximize forage utilization on PAS during the last 60 d of stocking lowered ADG which also reduced gain/ha. The actual, season-long STK was not as important a STRG as was the timing of stocking intensity.

Key Words: small grain, stocking rate, stocking strategy

T259 Effects of supplement or fertilizer on forage quality, and performance of stocker cattle grazing warm-season pastures in South Mississippi. J. D. Rivera*[1] and R. W. Lemus[2], *[1]South MS Branch Experiment Station, Mississippi Agriculture and Forestry Experiment Station, Poplarville, [2]Department of Plant and Soil Sciences, Mississippi State University, Starkville.*

Crossbred (*Bos taurus* × *Bos indicus*) beef steers (BW = 224 kg; n = 54) were used over 2-yr to examine the efficacy of nitrogen fertilizer compared with feed supplementation on forage quality, animal production, and nitrogen cycling. Steers were weighed, and assigned to graze six 4-ha paddocks of mixed warm-season perennials (bermuda and bahiagrass) for an average of 126 d. Paddocks were randomly assigned to 1 of 3 treatments: no fertilizer and no supplement; 1.1 kg of dried distillers grains per steer/d and no fertilizer; or fertilizer (68 kg N per ha) and no supplement. Cattle were individually weighed every 28 d, and an individual fecal sample was collected. Pasture clippings were taken weekly and pooled for nutrient analysis for each 28 d period. Data were analyzed as a randomized complete block with year and block as random effects and pasture as the experimental unit. Supplement increased BW ($P < 0.04$) at d 56, 84, 112 and for the overall grazing period. No differences ($P > 0.10$) were noted regarding BW in steers that grazed fertilized pastures or non-fertilized pastures at any point in the study. Supplement also increased ($P < 0.05$) ADG d 56, 84, 112, and for the overall study compared with grazing alone (regardless of fertilizer). Moreover, ADF in forage samples was reduced ($P < 0.07$) in pastures that were fed a supplement or fertilized at d 56, 84 and for the overall study. In addition, forage CP was increased ($P < 0.06$) by supplementing or fertilizing at d 56, 112 and for the overall study, and pasture TDN at d 56, 84 and overall was increased ($P < 0.07$) by supplementing or fertilizing. In year 1, fecal N increased at d 28 ($P < 0.05$) for supplemented cattle compared with their counterparts, increased at d 56 ($P < 0.09$) for both supplement and fertilizer groups, and increased at d 84 for the fertilizer group. Overall fecal N was increased ($P < 0.08$) using either supplement or fertilizer application. Results suggest that supplementing cattle grazing warm-season pastures will improve performance compared with fertilization with no negative consequence to pasture quality.

Key Words: beef cattle, warm-season pasture, supplement

T260 Nutritional assessment and productive response in tropical sheep fed with conserved agricultural byproducts in Ecuador. A. Sánchez-Laiño*[1,2], J. Avellaneda-Cevallos[1,2], D. Zambrano-Gracia[1], E. Torres-Navarrete[1,2], L. Montenegro-Vivas[1], and I. Espinoza-Guerra[1], *[1]Facultad de Ciencias Pecuarias, Quevedo, Los Ríos, Ecuador, [2]Dirección de Investigación Científica y Tecnológica, Quevedo, Los Ríos, Ecuador.*

The nutritional value of corn, rice, and soybean stover (CS, RS and SS) stored dry (12–14% moisture), after ammonification (3% urea), or stored as silage (10.12% molasses+1.0% urea) was determined using 18 tropical sheep. A factorial arrangement 3 (agricultural byproducts) × 3 (conservation methods) within a completely randomized design was applied. The ensiled CS, when compared with RS and SS stored dry and after ammonification, registered the highest ($P < 0.01$) in vivo digestibility coefficient (IVDC) for dry matter (DM: 59.8%); organic matter (OM: 64.9%); ether extract (EE: 60.2%); crude protein (CP: 43.3%); crude fiber (CF: 71.9%); nitrogen free extract (NFE: 50.8%); neutral detergent fiber (NDF: 69.7%); acid detergent fiber (ADF: 62.0%); total digestible nutrients (TDN: 49.8%) and metabolizable energy (ME: 1768 kcal/kg DM). Forty tropical sheep (3 months of age) were used for fattening. A factorial arrangement (3 × 3) + 1 control diet based on *Panicum maximum* Jacq was used within a completely randomized block design. Feed consumption (FC), weight gain (WG), feed conversion ratio (FCR) and carcass yield (CY) were assessed. Profitability was determined by the cost-benefit ratio. With ensiled CS, higher WG (184.3 g/animal/d), FCR (6.08), and CY (49.3%) were obtained. The highest profitability was obtained when ensiled CS (60.8%) and ammoniated SS (60.04%) was provided. The conserved agricultural byproducts enhanced performance compared to the grazing control ($P < 0.01$). According to these results, it is concluded that preservation methods increase the digestibility of the agricultural byproducts and the productive response in tropical sheep documents their value as a staple food for ruminants during the dry season.

Key Words: ruminant, digestibility, byproduct

T261 Effect of Next Enhance with or without Rumensin on performance of growing steers grazing cool-season annual pasture. P. Beck*[1], H. Gray[1], B. Stewart[1], and T. Wistuba[2], *[1]University of Arkansas Division of Agriculture, Hope, [2]Novus International Inc., St. Charles, MO.*

Ionophores have been proven to increase daily gains of growing steers on pasture. Essential oils (such as garlic oils and cinnamon extracts) have recently been found to have ruminal effects with potential to improve performance of growing beef steers. This research was conducted to determine the effects of Next Enhance (NE, 250 mg/d, Novus International Inc.) and Rumensin (R, 200 mg/d, Elanco Animal Health) supplementation on performance of growing steers grazing cool-season annual pasture. In the spring of 2012 (Exp. 1), 24 – 0.8 ha bermudagrass pastures that had been interseeded to either a mixture of cereal rye and annual ryegrass or oats and annual ryegrass the previous fall were stocked with 4 mixed breed beef steers per pasture (average BW 215 ± 4.8 kg) in early March for an 84 d grazing period. In the fall of 2012 (Exp. 2), 20 – 1.6 ha bermudagrass pastures that had been interseeded to cereal rye and annual ryegrass with 4 mixed breed beef steers per pasture (average BW 217 ± 6.7) in mid-November for an 84-d grazing period. Mineral premixes including the treatment materials were blended with soybean hulls and offered to steers in respective pastures 5-d/wk at a rate of 0.9 kg/steer each feeding. Steer BW were collected following a 16-h fast on 28-d intervals. Animal performance data for each year were analyzed as RCBD with a 2 × 2 factorial arrangement of treatments using the mixed procedure of SAS. There were no interactions between R and NE for steer BW or performance in either Experiment ($P \geq 0.17$). Over the 84-d spring grazing period in Exp. 1, NE increased ($P = 0.03$) steer BW by 10 kg, and steer ADG was increased ($P = 0.05$) by 0.06 kg/d, whereas there was no effect of R on steer BW or ADG ($P \geq 0.93$). In Exp. 2, NE had no effect on steer BW ($P = 0.83$) or ADG ($P = 0.77$), whereas R additions increased ($P = 0.05$) ADG by 0.09 kg/d. These results indicate that NE and R have potential to improve performance of steers grazing high quality pastures but additional research is needed to elucidate these effects.

Key Words: beef steer, cool-season annual pasture, Next Enhance

T262 Calf response to summer legumes as a creep grazing option in bermudagrass pastures. R. M. Martin*[1], R. S. Walker[2], G. Scaglia[3], B. Buckley[4], M. W. Alison[5], K. J. Han[6], G. Gentry[7], and W. D. Pitman[2], *[1]LSU Agcenter School of Animal Sciences, Baton Rouge, [2]LSU AgCenter Hill Farm Research Station, Homer, [3]LSU AgCenter Iberia Research Station, Jeanerette, [4]LSU AgCenter Red River Research Station, Bossier City, [5]LSU AgCenter Macon Ridge Research Station, Winnsboro, [6]LSU AgCenter Southeast Research Station, Franklinton, [7]LSU AgCenter Dean Lee Research Station, Alexandria.*

Nutritive value of bermudagrass (*Cynodon dactylon*) pastures can limit growth of nursing calves. Summer legumes with high nutritive value have been evaluated for use by creep grazing in Florida and Georgia with contrasting results. Thus, calf responses to creep grazing and legume species were evaluated at 4 Louisiana locations from mid-summer to weaning. Each location included pastures with a creep-grazed summer annual legume treatment (CREEP) and a control with similar cattle, grass, and stocking rate but no legume. Legume creeps were planted on 10% of the pasture areas available. Legume species and grazing duration differed among locations with only alyceclover (*Alysicarpus vaginalis*) at the Iberia Research Station, aeschynomene (*Aeschynomene americana*) and cowpea (*Vigna unguiculata*) at the Dean Lee Research Station, cowpea and soybean (*Glycine max*) at the Red River Research Station, and all 4 of the legumes at the Hill Farm Research Station with 83, 96, 60, and 82 grazing d, respectively. Pasture size of 2.5 to 8 ha differed among locations with 2 replications per location except at Hill Farm, which had 3 replications. Initially, grazing was limited by novelty of the legumes and, at Dean Lee, accumulated legume growth (>1 m height and 15,000 kg/ha) despite 17% crude protein concentration of leaves of cowpea and aeschynomene, which was grazed very little. All legumes were heavily grazed at the Hill Farm and Red River with legume availability of approximately 3,000 kg/ha in mid season declining through August and likely limiting legume intake through September. At Iberia, alyceclover provided about 40% of creep swards dominated by bermudagrass, and grass dominance of the novel alyceclover may have limited intake and calf gains. CREEP calves gained more (76 vs. 71 kg per head, $P = 0.062$) at all locations except Iberia where legume accessibility was limited. Earlier grazing of legumes and increased legume availability in September should further increase calf weaning weights with creep grazing; however, creep grazing required substantially more intensive management than did the control treatment.

Key Words: cattle, creep grazing, summer legume

T263 Responses to creep feeding protein to calves for cow-calf pairs grazing limpograss pastures during summer in Florida. A. D. Aguiar*[1], J. M. B. Vendramini[1], J. D. Arthington[1], L. E. Sollenberger[2], M. Hersom[2], J. D. Sanchez[1], and W. L. Ladeira[1], *[1]Range Cattle Research Education Center, Ona, FL, [2]University of Florida, Gainesville.*

Limpograss (*Hermatria altissima* [Poir] Stapf and C.E. Hubb) is a warm-season grass routinely used by cow-calf (*Bos* sp.) producers in South Florida; however, limpograss has low CP concentration, which may limit animal performance. The objective of this study was to test the effects of creep feeding protein supplements to calves on performance of cow-calf pairs grazing limpograss pastures during the summer. The experiment was conducted in Ona, FL from June to August 2012. Treatments were calves receiving 0, 200, or 400 g/d of soybean meal on creep feeding in randomized incomplete block design with 3 replicates for 0, and 200 g/d and 2 replicates for 400 g/d. Twenty-four cow-calf pairs (434 ± 49 and 182 ± 27 kg, respectively) were randomly distributed in 8 limpograss pastures (experimental units; 1.0 ha/pasture; 3 cow-calf pairs/pasture). Cows and calves weights were recorded every 28 d. Herbage mass (HM) and nutritive value was measured every 14 d. The data were analyzed using PROC MIXED with treatment and months as fixed effects, and replicates and its interactions as random effects. There was no difference in HM (mean = 6,645 kg/ha, $P = 0.41$, SE = 686), herbage allowance (HA; mean = 3.4 kg DM/kg LW, $P = 0.67$, SE = 0.4), CP concentration (mean = 10.9%, $P = 0.29$; SE = 0.9), and IVDOM (mean = 50.3%, $P = 0.56$; SE = 3.4) between treatments. Herbage mass and HA decreased from June to July from 8,300 to 5,500 kg/ha and 4.5 to 2.9 kg DM/kg LW, respectively. Conversely, there was an increase in HM from July to August from 5,500 to 6,300 kg/ha. There was a linear ($P = 0.03$) effect of treatments in calf ADG (mean = 0.29, 0.48, and 0.60 kg/d for C, 200 and 400, respectively, SE = 0.07); however, there was no effect of the treatments ($P = 0.47$) on cows ADG (0.07, 0.38, 0.19 kg/d for C, 200, and 400, respectively, SE = 0.15). Both levels of soybean meal supplemented to calves in this study increased ADG of calves grazing limpograss pastures.

Key Words: cow-calf, creep-feeding, performance

T264 Heifer growth and reproductive performance following two levels of fall pasture allocation. B. L. Bailey[1], T. C. Griggs[2], and K. M. Krause*[1], *[1]Division of Animal and Nutritional Sciences, West Virginia University, Morgantown, [2]Division of Plant and Soil Science, West Virginia University, Morgantown.*

The objective of this study was to compare heifer growth and reproductive performance following 2 patterns of gain during the fall grazing season. Three 5-ha fields were selected as blocks in a randomized complete block design for application of grazing treatments. All fields contained cool-season grass-legume mixtures. Spring-born heifers (yr 1, n = 72; yr 2 n = 64; yr 3 n = 67) of primarily Angus background and 246 kg mean BW were allocated to 2 grazing treatments during the fall period each replicated 3 times per year. The fall grazing treatment consisted of daily herbage dry matter (DM) allocation of 3.5 (LOW) or 7.0 (HIGH) % of BW. During the winter feeding period haylage (5.9 kg DM/hd/d, yr 1; 5.4 kg DM/hd/d, yr 2; 5.6 kg DM/hd/d, yr 3) and soybean hulls (1.7 kg DM/hd/d, yr 1; 1.5 kg DM/hd/d, yr 2; 1.8 kg DM/hd/d, yr3) was fed. Heifers were grazed continuously (as one group) throughout the spring and summer during all years. Heifers were synchronized and artificially inseminated (A.I) utilizing a single sire each year. A cleanup bull was used for 35 d. Mean ADG was greater for HIGH heifers (0.40 kg/d) than LOW heifers (0.12 kg/d) during the fall grazing period ($P < 0.0001$). During the winter feeding period, ADG were 0.30 kg/d and 0.39 kg/d ($P < 0.05$) for LOW vs. HIGH heifers. During the spring grazing period, ADG were 1.38 kg/d and 1.30 kg/d ($P = 0.17$) for LOW vs. HIGH heifers. Mean ADG was greater for LOW heifers (0.74 kg/d) than HIGH heifers (0.67 kg/d) during the summer grazing period ($P < 0.05$). Proportion of heifers that reached puberty at the onset of the breeding season did not differ (33% and 34%, $P = 0.82$ for LOW vs. HIGH), although LOW heifers had lower BW at the time of breeding (335 kg vs. 355 kg, $P < 0.05$ for LOW vs. HIGH). No treatment differences occurred for overall pregnancy rates by A.I., (34% vs. 44%, $P = 0.18$) bull (39% vs. 33%, $P = 0.43$), or overall (73% vs. 77%, $P = 0.55$) for LOW vs. HIGH heifers. We interpret these results to indicate that delaying the majority of weight gain until late in heifer development may decrease costs of winter feeding without detrimental effects on reproductive performance.

Key Words: heifer, grazing, reproductive performance

T265 Stocker steer performance on tall fescue or meadow fescue alone or in binary mixture with white clover. M. R. Schaefer*, K. A. Albrecht, and D. M. Schaefer, *University of Wisconsin-Madison, Madison.*

An evaluation of meadow fescue (*Festuca pratensis* L.) in pastures has not been reported in the USA since the early 1900s. This research was conducted to determine effects of either meadow fescue (MF) or tall fescue (TF, *Festuca arundinacea* L.) in binary mixture with white clover (*Trifolium repens* L.) or these species as N-fertilized monocultures on forage and animal performance in Upper Midwest pastures. Treatments were replicated 3 times, and data were collected over 3 grazing seasons. There was no attempt to reseed legume-containing swards. One hundred 80 crossbred beef steers (*Bos taurus*, 257 kg) were rotationally grazed across all pastures using a variable stocking rate to detect treatment differences. White clover persisted similarly ($P < 0.05$) in either grass pasture, and fraction of white clover in the sward decreased as the trial progressed (45, 24, and 14% for years 1, 2, and 3, respectively). The poor persistence of white clover may be attributed to below average rainfall and accentuates the need for a legume adapted to a variety of climatic conditions. Swards containing TF had greater available forage (3200 and 2800 kg/ ha) and lower in vitro true digestibility (82.2 and 84.6%), neutral detergent fiber digestibility (66.5 and 70.6%), and steer ADG (0.84 and 0.98 kg/d) than meadow fescue ($P < 0.05$). Adding white clover to MF and TF swards increased all forage quality variables, steer ADG (0.98 and 0.84 kg/d), animal gain per hectare (780 and 680 kg/ha) ($P < 0.05$) and tended to lower available forage ($P < 0.10$) compared with monoculture pastures. Even though MF containing swards had greater steer ADG, TF had an increased stocking rate ($P < 0.05$) which resulted in similar gain per hectare (720 and 750 kg/ha for TF and MF respectively). Data collected suggests that both grass species are suitable for inclusion in Upper Midwest pastures. The addition of a legume to either grass species increased ADG and gain per hectare, both of which have positive economic implications.

Key Words: fescue, grazing, beef

T266 Bovine lateral saphenous veins exposed to ergopeptine alkaloids do not relax. J. L. Klotz[1], A. Pesqueira*[2], A. F. Branco[3], and D. L. Harmon[2], *[1]USDA-ARS, Forage-Animal Production Research Unit, Lexington, KY, [2]Department of Animal and Food Sciences, University of Kentucky, Lexington, [3]Universidade Estadual de Maringa, Brazil.*

The ergot alkaloid, ergovaline has demonstrated a persistent binding and sustained contractile response in several vascular models. It was hypothesized that different alkaloids isolated from endophyte- (*Neotyphodium coenophialum*) infected tall fescue (*Lolium arundinaceum*) will contribute to this response differently. The objective was to compare contractile-response patterns of single additions of $1 \times 10^{-4} M$ lysergic acid (LSA), lysergol (LYS), ergonovine (ERN), ergotamine (ERT), ergocristine (ERS), ergocryptine (ERP), ergocornine (ERO) and $1 \times 10^{-6} M$ ergovaline (from a tall fescue seed extract; EXT). Lateral saphenous veins were collected from 6 Holstein steers (397 ± 28 kg) immediately after slaughter, sliced into cross-sections, and suspended in myograph chambers containing oxygenated Krebs-Henseleit buffer (95% O_2/5% CO_2; pH = 7.4; 37°C). Treatments were added at 0 min and buffer was replaced in 15-min intervals for a 120-min incubation. The maximum tension (g) and time interval to reach maximum tension were determined for each compound. Percent relaxation and rate of relaxation were determined following maximum tension for each treatment. Contractile response data were normalized to a reference addition of 1×10^{-4} *M* norepinephrine and analyzed as a CRD with repeated measures using mixed models of SAS. All compounds tested produced significant contractile responses ($P < 0.05$). Ergoline alkaloids, LSA, LYS, and ERN reached maximum tension in less time the remaining compounds ($P < 0.05$) and began to relax immediately with LSA having the greatest percent relaxation ($P < 0.05$). The EXT and ergopeptine alkaloids, ERT, ERS, ERP, and ERO all had slower developing contractile responses with a longer interval until maximum tension was achieved. Maximal responses to these alkaloids, however, all persisted for the remainder of the 120-min experiment with negligible relaxation occurring. Persistence of contractile response caused by ergopeptine alkaloids is thought to be the primary contributing factor to vasoconstriction in animals demonstrating signs of fescue toxicosis.

Key Words: bovine, ergot alkaloid, vasoconstriction

T267 Effect of fescue toxicosis on ruminal kinetics, nitrogen and energy balance in Holstein steers. A. F. Koontz*[1], D. H. Kim[1], A. P. Foote[1], J. L. Klotz[2], K. R. McLeod[1], and D. L. Harmon[1], *[1]Department of Animal and Food Sciences, University of Kentucky, Lexington, [2]USDA-ARS, Forage-Animal Production Research Unit, Lexington, KY.*

This study was designed to examine alteration of ruminal kinetics, as well as N and energy balance during fescue toxicosis. Six ruminally cannulated Holstein steers (BW = 217 ± 7 kg) were weight-matched into pairs and pair-fed throughout a crossover design experiment with a 2 × 2 factorial treatment structure. Factors were endophyte (infected, E+ vs. uninfected, E-) and feeding level ($1.8 \times NE_m$, H vs. $1.1 \times NE_m$, L). During each period after 8 d of diet adaptation one steer per pair was ruminally dosed with ground endophyte-infected fescue seed (E+), the other with ground endophyte-free fescue seed for the remainder of the period. In situ degradation of ground alfalfa was determined on d 13–16. Total fecal and urinary collections were performed on d 17–21, with animals placed into indirect calorimetry head-boxes during d 20 and 21for determination of heat production (HP) using the Brower equation. Liquid and particulate passage rates were evaluated using Cr:EDTA and iADF respectively on d 22 and 23. There was no difference ($P > 0.9$) in DMI/$kg^{0.75}$ between endophyte treatments, and DMI/$kg^{0.75}$ was different ($P < 0.01$) between H and L intake by design. Animals on H feeding had higher ($P < 0.01$) water, N, and energy intakes. Energy and N excretion, as well as retained N, DE, ME, RE, and HP were higher ($P < 0.03$) for H v L. There were no differences in retained N, DE, ME, or HP ($P > 0.15$) between endophyte treatments. Neither rate nor extent of in situ degradation was altered by intake level or endophyte treatment ($P > 0.3$). Dry matter percentage and DM weight of rumen contents were increased ($P < 0.01$) by E+ dosing. Particulate passage was decreased by both L feeding ($P < 0.01$) and endophyte ($P = 0.02$). Ruminal liquid passage rate increased ($P = 0.03$) with H feeding. Total VFA concentration increased with both H feeding ($P < 0.01$) and E+ dosing ($P < 0.01$). Despite these differences, the N and energy balance data indicate that reduced weight gain during fescue toxicosis is primarily a function of reduced intake which may be driven by a reduction in ruminal particulate passage rate.

Key Words: bovine, energy, fescue

T268 The fatty acid profile and retention time in the rumen in cattle grazing tropical grasses. D. F. A. Costa*[1], P. Isherwood[1], S. Quigley[1], S. R. McLennan[2], J. De Souza[3], J. Gibbs[4], X. Q. Sun[5], and D. P. Poppi[1], *[1]The University of Queensland, Gatton, Queensland, Australia, [2]The University of Queensland, Brisbane, Queensland, Australia, [3]University of Sao Paulo, Piracicaba, Sao Paulo, Brazil,*

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The objectives of this study were to examine the fatty acid (FA) profile in the rumen fluid (RF) and relate the extent of biohydrogenation (BH) to the retention time (RT) of fluid in the rumen. Four rumen cannulated steers (790 ± 17 kg BW) grazing pastures of C3 ryegrass *Lolium multiflorum* and C4 species, signal grass *Brachiaria decumbens*, stargrass *Cynodon dactylon* and speargrass *Heteropogon contortus*. Each pasture was grazed for 21d followed by 3d collection. On d 22 CrEDTA was used to estimate RT (182 mg Cr/100 kg BW injected via cannula) and RF samples collected at 0, 4, 8, 12, 16, 24, 28, 32 and 48 h after dosing for Cr analysis and at 0, 8 and 16h for FA profile by gas chromatography. One way model analysis was used for RT and repeated measures procedure for FA profile, both carried out using GLM procedure. Speargrass had a longer RT than ryegrass (8 vs. 11 h) while signal and stargrass grasses had intermediate values (10h) with the differences not expected to results in differences in extent of BH due to RT. Palmitic and stearic acids in RF were much higher than in forage plucked samples (PS) but all grasses had similar total saturated fatty acid (TSFA) with a greater degree of saturation for ryegrass. A higher CLAc9,t11 content in RF of steers grazing ryegrass resulted from the higher linolenic concentration in PS but linoleic concentration in RF was lower for those steers. Total unsaturated FA (TUFA) content of RF was reduced markedly compared with the TUFA of the forage with some small differences between forages.

Table 1. Fatty acid profile in PS and in RF samples

FA, % total FA	Ryegrass		Signal		Stargrass		Speargrass	
	PS	RF	PS	RF	PS	RF	PS	RF
C16:0	15.3	30.6^{ab}	19.6	34.2^{c}	21.2	34.0^{c}	21.0	29.1^{a}
C18:0	1.2	7.4^{a}	1.4	6.5^{a}	1.6	7.4^{a}	1.8	7.1^{a}
C18:2n-6	10.3	3.9^{a}	17.5	5.6^{b}	13.4	5.5^{b}	17.8	5.6^{b}
C18:3n-3	61.0	5.5^{b}	47.1	4.3^{ab}	50.8	4.9^{b}	35.1	3.5^{a}
CLAc9, t11	0.1	0.6^{b}	0.0	0.2^{a}	0.0	0.2^{a}	0.2	0.3^{a}
TSFA	18.7	58.5^{a}	25.1	64.2^{b}	25.8	64.8^{b}	30.2	57.1^{a}
TUFA	76.5	29.7^{bc}	69.6	28.6^{bc}	68.9	27.1^{ab}	59.7	23.8^{a}

Key Words: fatty acid, tropical forage

T269 Effects of forage type and season on rumen parameters of grazing cattle. D. F. A. Costa*[1], P. Isherwood[1], S. Quigley[1], S. R. McLennan[2], and J. De Souza[3], *[1]The University of Queensland, Gatton, Queensland, Australia, [2]The University of Queensland, Brisbane, Queensland, Australia, [3]University of Sao Paulo, Piracicaba, Sao Paulo, Brazil.*

The objective of this study was to evaluate the effects of forage type and season on retention time (RT) and rumen function of grazing cattle. Four rumen cannulated steers (790 ± 17kg BW) grazing pastures (herbage mass 2600–6200 kg DM/ha) of C3 ryegrass *Lolium multiflorum* and C4 grasses kikuyu *Pennisetum clandestinum*, speargrass *Heteropogon contortus* in the wet season and the latter grass and a legume leucaena *Leucaena leucocephala* in consortium with *Panicum maximum* in the dry season. Each grazing run consisted of 21d followed by 3d collection period. On d 22 CrEDTA was used to estimate RT (182 mg Cr/100 kg BW via cannula) and rumen fluid (RF) samples collected at 0, 4, 8, 12, 16, 24, 28, 32 and 48h after dosing for Cr analysis. Diet crude protein (CP) and dry matter digestibility (DMD) were estimated by fecal NIRS. NH_3N concentration in RF was determined at 0, 8 and 16h. Volatile fatty acids (VFA) concentration was from bulked RF from 0, 8 and 16h and determined by gas liquid chromatography. Speargrass treatment in dry season had the lowest CP and DMD, which was associated with less NH_3N and VFA concentration and a much longer RT. Despite the season of the year speargrass diet had the highest Acetic:Propionic (A:P). Total VFA was intermediate for grasses on wet season and highest for leucaena grass mix. Ryegrass had higher CP and DMD but a similar NH_3N to kikuyu and leucaena/grass mix. The RT of all wet season grasses, including the C3 ryegrass, was similar (even though some small quantitative significant differences) and similar to a leucaena/grass mix in the dry season. Only dry season speargrass had very long RT.

Table 1. Crude protein and DMD estimated by fecal NIR, rumen NH_3N and VFA concentration, A:P and RT of liquid phase in the rumen

Parameter	Ryegrass	Kikuyu	Speargrass (wet)	Speargrass (dry)	Leucaena	SEM
CP (g/kg)	200^{e}	176^{d}	99^{b}	39^{a}	135^{c}	0.56
DMD (g/kg)	68^{d}	62^{c}	59^{b}	49^{a}	58^{b}	0.84
NH_3N (mg/L)	113^{bc}	130^{c}	29^{a}	9^{a}	147^{c}	20.1
Total VFA (mmol/L)	95^{b}	93^{b}	96^{b}	70^{a}	114^{c}	7.4
A:P	3.3:1^{b}	2.5:1^{a}	6.8:1^{d}	6.9:1^{d}	5.3:1^{c}	2.1
RT (h)	8.3^{a}	10.1^{ab}	11.3^{ab}	19.8^{c}	13.4^{b}	1.9

$^{a–d}$Different superscripts across the rows indicate significant difference between treatments ($P < 0.05$).

Key Words: tropical grass, rumen parameter

T270 Interactions between grazing management and a low level of energy supplementation on ingestive behavior of beef cattle. L. R. D. Agostinho Neto*, J. R. R. Dorea, V. N. Gouvea, D. F. A. Costa, A. V. Pires, M. G. M. F. Santos, and F. A. P. Santos, *University of Sao Paulo, Piracicaba, Sao Paulo, Brazil.*

The objective of this trial was to evaluate the effect of 2 pregrazing canopy heights and 2 levels of energy supplementation on ingestive behavior of Nellore steers grazing intensively managed tropical grass during the rainy season. Treatments were a control (mineral supplementation) and a low level of energy supplementation (0.3% BW of fine ground corn) combined with 2 pregrazing canopy heights (25 and 35 cm). Eight 48-mo-old rumen-cannulated steers (343 kg BW ± 5.97) were assigned to 2 4x4 Latin squares and allocated in 2 ha of *Brachiaria brizantha* pasture. Ingestive behavior was evaluated through a 24-h observation period in which grazing, rumination and resting activities were monitored every 5 min. Bite and ingestion rates were also evaluated Grazing time decreased when 25 cm of canopy height and energy supplementation were used (78.3 and 39.7 min, respectively). The rumination time was not affected by energy supplementation and pre-grazing canopy height. However, resting time increased when the grazing management was 25 cm. Energy expenditure for maintenance could be reduced by this fact, resulting in an increased animal performance. The pregrazing canopy height of 25 cm increased ingestion rate what possibly is related to a higher harvest efficiency, but no further effects were observed for energy supplementation. A higher bite rate was also observed for the 25 cm grazing management also indicating a higher harvest efficiency and consequently more dry matter intake. The pregrazing canopy height of 25 cm was determinant to improve harvest efficiency, but there was little influence of low level of energy supplementation on ingestion behavior.

Table 1. Grazing, rumination and resting time, ingestion and bite rate

	Management, cm		Supplementation, % of BW		*P*-value			
	25	35	0	0.3	M	S	M × S	SEM
Grazing time, min/d	386	465	445	406	*	*	NS	20.29
Rumination time, min/d	385	384	379	389	NS	NS	NS	19.73
Resting time, min/d	608	530	554	584	*	NS	NS	18.33
Ingestion DM rate, g DM/min	16.72	9.21	13.34	12.59	*	NS	NS	1.85
Bite rate, bite/min	34.23	22.78	28.20	28.80	*	NS	NS	3.28

Key Words: ingestive behavior, tropical pasture

T271 Interactions between grazing management and a low level of energy supplementation in beef cattle. L. R. D. Agostinho Neto[1], J. R. R. Dorea*[1], V. N. Gouvea[1], D. F. A. Costa[1], A. V. Pires[1], L. G. R. Pereira[2], and F. A. P. Santos[1], *[1]University of Sao Paulo, Piracicaba, Sao Paulo, Brazil, [2]Empresa Brasileira de Pesquisa Agropecuaria, Juiz de Fora, Minas Gerais, Brazil.*

The objective of this trial was to evaluate the effect of 2 pregrazing canopy heights and 2 levels of energy supplementation on voluntary intake and ruminal parameters of Nellore steers grazing intensively managed tropical grass. Treatments corresponded to control (mineral supplementation) and a low level of energy supplementation (0.3% of BW of fine ground corn) combined with 2 pregrazing canopy heights (25 and 35 cm), with a common stubble height of 15 cm for all treatments. Eight 48-mo-old rumen-cannulated steers (300 kg BW ± 5.97) were assigned to two 4 × 4 Latin squares and allocated in 2 ha of *Brachiaria brizantha* pasture. Chromium oxide was used as an indigestible marker. Concentration of purine derivatives in the urine was used to estimate microbial synthesis. Forage intake decreased for 35 cm of canopy height and for use of energy supplementation (1.03 of substitution rate). The total and energy intake were not affected by energy supplementation. However, grazing management of 35 cm decreased both total and energy intake. Ruminal pH was affected only by grazing management, but remained above 6.0. Concentration of NH_3N decreased with grazing management and energy supplementation whereas microbial synthesis was not affected by either. The N retention decreased when the pre-grazing canopy height was 35 cm. Interactions between management and supplementation were not significant. Pre-grazing canopy of 35 cm affects intake and may result in lower animal performance; these effects were more significant on voluntary intake than responses to a low level of energy supplementation.

Table 1. Forage and total intake, ruminal parameters, microbial synthesis and nitrogen retention

	Management, cm		Supplement, % BW		*P*-value		
Item	25	35	0	0.3	M	S	SEM
Forage DMI, %BW	1.86	1.32	1.79	1.38	*	*	0.14
DMI, %BW	2.01	1.47	1.79	1.68	*	NS	0.14
Digestible DMI, %BW	1.34	0.93	1.13	1.15	*	NS	0.08
Substitution rate	0.00	0.00	0.00	1.03	NS	*	0.25
pH	6.39	6.52	6.46	6.44	*	NS	0.14
$N\text{-}NH_3$,mg/dL	11.22	9.77	11.28	9.70	*	*	1.10
Microbial synthesis, g/d	457.07	411.25	425.01	443.32	NS	NS	62.35
N retention, %N intake	45.96	21.07	39.55	40.48	*	NS	5.04

* = significant, NS = not significant.

Key Words: tropical pasture, energy supplement

T272 Effects of resistant starch in milk replacer on fecal volatile fatty acids and pH and performance in neonatal Holstein calves. C. C. Williams*, B. F. Jenny, B. L. Fisher, A. H. Dolejsiova, E. L. Chartier, and E. Eckelkamp, *LSU AgCenter, Baton Rouge, LA.*

Resistant starch (RS) may help in preventing intestinal disturbances in calves. Thirty female Holstein calves were assigned to 1 of 3 treatments at 2 d of age to study effects of adding commercial resistant wheat starch to milk replacer (MR) on growth and health. Treatments were 0, 4, or 8g RS mixed into reconstituted MR. Calves were housed in hutches and fed MR until 56 d of age. MR was fed once daily according to body weight (BW), 10% of BW containing 15% solids. Initial amount of MR fed was based on birth weight and was increased at 7, 14, 21, and 28 d according to BW change and then held constant until weaning at 56 d. An 18% crude protein calf starter was offered ad libitum beginning on d 29 throughout the duration of the trial. Water was offered ad libitum beginning on d 3. Calves remained in hutches until d 70 to determine post weaning performance. BW was determined at birth and weekly throughout the trial. Wither height (WH), hip height (HH) and hip width (HW) were measured on d 7, 14, 28, 42, 56, and 70 of age. Feed intake and fecal scores were recorded daily. Fecal samples were collected weekly beginning at d 7 for analysis of pH and volatile fatty acids (VFA). Blood was collected on d 14, 28, 42, 56, and 70 for analysis of hematocrit (HCT), plasma urea nitrogen (PUN) and total protein (TP). Effects of treatment, week, and their interactions were analyzed using the MIXED procedure of SAS. HCT, PUN and TP did not differ ($P > 0.05$) and were within normal ranges suggesting no major metabolic problems. There was no effect ($P > 0.05$) of treatment on BW, HH, HW, WH, or fecal scores. There was a week effect ($P < 0.01$) for grain intake, with all calves increasing intake throughout the duration of the study. There was a week effect ($P < 0.01$) for fecal scores, with calves having lower fecal scores at the end of the study compared with the beginning. There was no effect ($P > 0.05$) of treatment on fecal pH or concentrations of VFA. Overall, incorporation of RS in the milk replacer of neonatal dairy calves did not show any significant effects on growth or gut health of Holstein dairy calves.

Key Words: dairy calf, resistant starch, milk replacer

T273 Effects of a simplified feeding program on growth and rumen development of dairy calves C. Julien*[1,2], B. Gestes[1,2], C. Lacroux[3], C. Bayourthe[1,2], and F. Enjalbert[1,2], *[1]INRA, UMR1289 TANDEM, Tissus Animaux Nutrition Digestion Ecosystème et Métabolisme, Castanet-Tolosan, France, [2]Université de Toulouse, INPT ENSAT, INP-ENVT, UMR1289 TANDEM, Castanet-Tolosan, France, [3]UMR INRA ENVT 1225, Interactions Hôte Agent Pathogène, Ecole Nationale Vétérinaire de Toulouse, 23 Chemin des Capelles, Toulouse, France.*

The experiment aimed at testing the effect of a simplified feeding program on growth and rumen development of dairy calves ("Technique Once a Day," Bonilait-Protéines, France). It was carried out on 16 male Holstein calves from birth (d1) to weaning (d63) moved to individual pens at birth. Two feeding programs were tested. Each one was based on a milk replacer (MR), with the same proportions of dairy proteins (from skim milk powder and/or whey protein concentrate) and the same chemical composition: 20% CP and 18% fat, on DM basis. Calves were divided into 2 groups at 4 d of age: (1) OAD (n = 8): calves received MR once a day (200 g/L of MR), (2) TAD (n = 8): calves received MR (125 g/L) twice a day; volume distributed per calf and per meal varied with age but did not differ between groups leading to a total of 34.1 and 40.9 kg/calf of MR over 63d for OAD and TAD, respectively. The week before weaning, all calves received MR once a day. All calves received water, wheat straw and a starter concentrate (16.6% CP) ad libitum. Four calves per group were harvested at weaning. Reticulo-rumen, omasum and abomasum were emptied, cleaned and weighted separately and carcass weight (CW) was recorded. Rumen epithelium was sampled at a fixed location (ventral sac) and fixed in a neutral 10% formaldehyde solution. Rumen papillae (RP) were counted and averaged on 3 1cm^2 areas by image analysis (Visilogue 6.5 Noesis, France). The mucosa was observed for histopathologic investigation. Body weight of calves averaged 45.9 ± 5.7 kg and 96.3 ± 11.4 kg at birth and weaning, respectively, without significant difference between treatments. Total stomachs weight (5.2% of CW, on average) and relative weights of reticulo-rumen (62.9%), omasum (16.8%) and abomasum (20.3%) did not differ with treatment. The RP count were higher ($P = 0.03$) for OAD calves (84.8 RP/cm^2) than TAD (64.7 RP/cm^2) and no pathologic abnormality was detected. Simplifying dairy farmer practices by giving MR once a day to dairy calves is possible without compromising calves' growth and reticulo-rumen development but effects on welfare remain not evaluated.

Key Words: calf, rumen, papillae

T274 Comparison of planes of nutrition on growth performance and rumen papillae development of dairy calves. J. A. Davidson*[1], B. L. Miller[1], H. C. Puch[1], T. J. Earleywine[2], K. M. O'Diam[3], and K. M. Daniels[3], *[1]Purina Animal Nutrition Center, Gray Summit, MO, [2]Land O'Lakes Animal Milk Products, Shoreview, MN, [3]Ohio Agricultural Research and Development Center, The Ohio State University, Wooster.*

The objective was to determine if the plane of nutrition combinations of specific protein:fat milk replacer and starter affect the growth performance of dairy calves from 0 to 84 d of age and subsequently altered the rumen papillae surface area. Holstein bull calves (n = 16) were assigned to 1 of 2 nutritional programs: conventional (C) or full potential (FP). Conventional program consisted of feeding 454 g DM/d of a 20:20 milk replacer and 18% CP starter. Full potential program consisted of 818 g DM/d of a 28:20 milk replacer followed by increased feeding rate to 1136 g DM/d at d 10 of age and 22% CP starter. Milk replacer was offered twice daily from 0 to 44 d of age, and calves were weaned (d 45) with 50% reduction in milk replacer DM for 6 d. Starter was offered ad libitum from 0 to 84 d of age. Body weight (BW, kg) and hip height (HH, cm) measurements were completed every 2 weeks. Calves were euthanized at 28, 56, or 84 d of age (2 per program at each age) to examine ruminal papillae characteristics. Four regions of the rumen were analyzed for muscle and sub-mucosal thickness, and length and area of the papillae. On d 42, 49, 56, and 84, calves fed FP had greater BW gains of 11.0, 8.9, 7.5, and 4.7 kg (SE = 2.77, $P = 0.05$) over gains of C fed calves. Average gains of frame were also greater for FP of (SE = 1.08, $P = 0.02$) relative to C fed calves. Sub-mucosal thickness and papillae area were different ($P < 0.05$) for age and region of rumen. Greatest increases of sub-mucosal thickness were observed in the caudal ventral region from d 28 to 84 of age, regardless of nutritional program. At d 28 of age, papillae area and length could not be measured digitally. At d 56, the ruminal papillae area were 4.8 and 6.5 mm^2 for FP and C fed calves, whereas at d 84 ruminal papillae area were 11.6 and 9.5 mm^2, regardless of region (SE = 1.55, ns). Growth performance was greater for calves fed a FP program, whereas rumen papillae area and sub-mucosal thickness increased similarly with age, regardless of the nutritional program.

Key Words: calf, papillae, growth

T275 Whole oats effects on digestive system development in neonatal dairy calves. F. X. Suarez-Mena*[1], A. J. Heinrichs[1], T. M. Hill[2], and C. M. Jones[1], [1]*The Pennsylvania State University, University Park,* [2]*Nurture Research Center, Provimi North America, Lewisburg, OH.*

The objective of this experiment was to study effects of whole oats in starter grain on digestive system development of pre-weaned calves. Male Holstein calves (n = 8, 42.5 ± 2.0 kg BW at birth) were fitted with a rumen cannula in wk 2 of life. Calves were housed in individual pens in a heated facility; bedding was covered with landscape fabric to avoid any consumption of bedding. Water was offered free choice, and milk replacer was fed to 12% of birth BW. A fixed amount of starter (containing 25% oats either ground and in the pellet or whole) was offered daily based on average intakes of calves on similar milk replacer diets; orts were fed through the cannula. Calves were randomly assigned to all pelleted starter (P, n = 4) or pellets plus whole oats (O, n = 4). Rumen contents were sampled at −8, −4, 0, 2, 4, 8, and 12 h after grain feeding for pH determination at wk 3, 4, and 5 of age. At 35 ± 1 d of age calves were euthanized, and organs were harvested, emptied, rinsed, and weighed to gauge digestive organ development. Total starter intake (3 wk; 4,596 P vs. 4,449 O ± 111 g) was not different ($P > 0.05$). Digestive organ mass was analyzed as a percentage of BW at harvest. Reticulorumen (0.81 P vs. 0.81 O ± 0.05%) and liver (2.21 P vs. 2.25 O ± 0.08%) were not different ($P > 0.05$). Omasum (0.16 P vs. 0.19 O ± 0.01%) was greater ($P < 0.05$), and abomasum (0.40 P vs. 0.46 ± 0.02%) had a tendency to be greater ($P < 0.10$) for O. Rumen papillae length (0.67 P vs. 0.59 ± 0.05 mm), width (0.48 P, 0.45 O ± 0.02 mm), and rumen wall thickness (0.96 O vs. 0.90 O ± 0.09 mm) were not different ($P > 0.05$). Average rumen digesta pH at 3 wk of age (6.32 P vs. 6.22 O ± 0.16) was higher ($P < 0.01$) than at 4 (5.93 P vs. 5.85 O ± 0.16) and 5 (5.86 P vs. 5.74 O ± 0.16) wk; pH was not different ($P > 0.05$) between treatments. Whole oats had no effect on reticulorumen weight or rumen papillae size but increased omasum and abomasum weight. Lack of treatment effect on papillae may be related to calves eating grain for only 3 wk. Rumen digesta pH decreased with age likely as a consequence of greater intake of starch and digestible nutrients.

Key Words: calf, rumen development, oats

T276 Puberty attainment is affected by growth performance before 4 mo of age in dairy heifers. V. Lollivier[1,2], F. Dessauge[1], M. Boutinaud*[1], and Y. Le Cozler[1,2], [1]*INRA UMR1348PEGASE, Saint Gilles, France,* [2]*Agrocampus Ouest, UMR1348 Pegase, Rennes, France.*

In seasonal calving systems where heifers first calved at a young age, age at 1st insemination may be delayed for those born at the end of the calving period. A possible alternative is to increase growth intensity during the 1st year of rearing, and then, to reduce age at 1st calving (21 mo of age or less). Puberty should then occur at an early age for optimal fertility. A long-term experiment aiming at studying the effect of controlled growth intensity throughout feeding procedure is being conducted since 2009 including 60 to 70 Holstein heifers / year. In 2012, the effect of rearing intensity on puberty attainment was closely studied on 65 heifers born between August 26 and December 27, 2011. Animals born before December 1 were either fed a standard (SD) or an intensive (ID) diet from 0 to 6 mo of age, to reach 190 to 200 kg or 220 to 230 kg at 6 mo of age, respectively. Animals born after received ID until artificial insemination (AI). From 5.5 mo of age, blood samples were obtained from jugular vein every 10 d to determine plasma progesterone concentration. The plasma progesterone analyses were performed with AIA 360 robot. The intra- and inter-assay variabilities were 12.3 and 7.5%, respectively. Blood samples were collected until synchronization or AI. Single Anova analyses were performed through R Software. Puberty was detected on 56 animals, at an average age of 10.2 (±2.0) mo and 296 (±37) kg body weight (BW). Age varied between 6.2 and 14.4 mo, whereas BW was comprised between 224 and 369 kg. Because of huge ADG variations within feeding regimen and limited number of observations, no effect of SD or ID was noted on puberty onset. Puberty occurred earlier when average daily gain (ADG) before weaning (77 to 80 d of age on average) increased (9.7 vs. 10.8 mo when ADG varied from less than 700 g/d to 700 g/d or more respectively; $P < 0.05$). To a lesser extent, ADG from weaning to 4 mo of age also affected puberty onset. In agreement with previous published studies, this study indicates that enhanced growth program during lactating phase and/or early stages of rearing may affect puberty attainment.

Key Words: heifer, puberty, onset

T277 The effect of various dilutions, milk replacer dry matter, and volume amounts on calf growth and performance. T. J. Earleywine, B. L. Miller, W. S. Bowen Yoho*, and T. E. Johnson, *Land O' Lakes, Inc., Webster City, IA.*

Feeding an established volume of milk replacer (MR) solution without regard for dry matter (DM) by lowering the percentage solids is being done by producers. The objective of this study was to examine the effects of delivering a more dilute solution at the same volume on calf growth and performance. One hundred thirty-three (133) 3–10 d old Holstein calves with an average initial BW of 47.6 kg (SD = 2.21 kg) were shipped from Wisconsin to the Land O' Lakes Research Facility. Calves were randomly assigned according to BW and blood gamma globulin to one of 4 27% all milk protein/10% fat MR diets varying in dilution, MR DM, and volume amount. Days 8–49, treatments were as follows: High Solids, High DM, Low volume (HS/HDM/LV; 17.6% solids, 1.13 kg DM, 6.62 L solution/d); Medium Solids, High DM, Medium volume (MS/HDM/MV; 15% solids, 1.13 kg DM, 7.8 L solution/d); Medium Solids, Low DM, Low volume (MS/LDM/LV; 15% solids, 0.97 kg DM, 6.62 L solution/d); Low Solids, High DM, High volume (LS/HDM/HV; 12.6% solids, 1.13 kg DM, 9.2 L solution/d). Days 1–7, calves were offered the same % solids and 72% of MR DM stated above, with volume amounts adjusted accordingly. Calves were fed MR twice per day. Offering of MR was reduced by half, and calves fed once per d, during the last wk. Calf starter (22% crude protein, as fed basis) was fed ad libitum throughout this 49 d trial. Data were analyzed by Mixed Procedures of SAS. While there were no statistical differences ($P > 0.05$) in total BW gain, starter feed intake, or feed:gain, calves fed the MS/LDM/LV diet were numerically lower in total BW gain and numerically higher in starter feed intake when compared with calves on all other treatments. When considering offering a more dilute MR solution, it is important to deliver the same amount of MR DM to calves by offering more MR solution to support adequate growth of calves.

Table 1.

	MR Diet				
Item[1]	HS/HDM/LV	MS/HDM/MV	MS/LDM/LV	LS/HDM/HV	SE
BW gain, kg	33.1	34.0	31.0	33.4	1.09
MR intake (DM), kg	46.3[a]	47.9[b]	40.8[c]	47.2[ab]	0.380
Starter intake (DM), kg	19.8	19.4	21.1	18.8	1.29
Feed:Gain	2.05	2.00	2.01	2.01	0.040

[a–c]Means in the same row not followed by a common letter differ ($P < 0.05$).

Key Words: calf, milk replacer, dilution

T278 The effect of varying fatty acid profile on growth and performance of calves fed milk replacer. B. L. Miller*, T. J. Earleywine, W. S. Bowen Yoho, and T. E. Johnson, *Land O' Lakes, Inc., Webster City, IA.*

In 2 separate trials, the growth and performance of calves fed milk replacer (MR) varying in protein level, fat level, and fatty acid profile were examined. Thirty-five (35) and 67 (67) 3- to 10-d-old Holstein bull calves with average initial weights of 46.6 kg (SD = 2.83 kg) and 47.9 kg (SD = 2.79 kg) were shipped from Wisconsin to the Land O' Lakes Research Facility for trials 1 and 2, respectively. Calves were randomly assigned according to body weight (BW) and blood gamma globulin to their respective MR diet offered in a 17.6% solids solution. Calves on trial 1 were assigned to 1 of 2 MR diets: 28% crude protein (CP), 20% fat with lard as the primary fat source; 27% CP, 10% fat with medium-chain triglycerides (MCT) as the primary fat source. Calves on trial 2 were assigned to 1 of 3 diets: 28% CP, 20% fat with lard as the primary fat source; 27% CP, 10% fat with MCT as the primary fat source; 26% CP, 10% fat with MCT as the primary fat source. Calves were fed to provide 816 g DM/d during d 1 – 7, and 1135 g DM/d during d 8 – 42, in 2 feedings at 0600 and 1515 h. Calves were offered 567.5 g in one feeding at 0600 h during the last week. Calf starter (22% CP, as fed basis) was fed ad libitum throughout these 49 d trials. Data were analyzed by Mixed Procedures of SAS. For trial 1, calves fed a 28:20 MR with lard as the primary fat source were inferior ($P < 0.05$) in starter feed intake, MR consumption ($P < 0.05$), and body volume gain ($P < 0.05$), and tended ($P = 0.14$) to be inferior in total weight gain, compared with calves fed a 27:10 MR with MCT as the primary fat source. For trial 2, total weight gain did not differ among treatments. Calves fed a 28:20 MR were inferior ($P < 0.05$) in starter feed intake to calves fed a MR with lower CP and fat (26:10 and 27:10). Calves fed a 28:20 MR were superior in feed:gain when compared with calves fed the 26:10 MR, but did not differ from calves fed the 27:10 MR. Milk replacers with a modified fatty acid profile may allow for a reduction in protein and fat levels without negatively affecting growth and performance.

Key Words: calf, milk replacer, fatty acid

T279 Efficiency of IgG absorption in fresh or pasteurized colostrum of various qualities. S. L. Gelsinger*, C. M. Jones, and A. J. Heinrichs, *The Pennsylvania State University, State College.*

Previous data show improved IgG absorption in calves when fed pasteurized colostrum. However, this has not been compared using colostrum of very low or very high quality. This study was conducted to investigate this phenomena using colostrum of various qualities. Colostrum was sorted based on colostrometer measurement. This process was completed in summers of 2011 and 2012, and sorted colostrum was pooled to create 6 unique batches. Half of each batch was rebottled to be fed without heat treatment. The second half of each batch was heated to 60°C for 30 min, then subsequently cooled and bottled. All colostrum was frozen until fed. Colostrum treatments were analyzed for standard plate count, coliforms, non-coliform gram-negative bacteria, IgG1, and IgG2. Plasma samples were collected from 145 calves 48 h after birth and analyzed for IgG1, IgG2, total protein, and hematocrit. All IgG analysis was done using a bovine IgG1 or IgG2 ELISA and values were combined to calculate total IgG and apparent efficiency of absorption (AEA). Heat-treatment significantly reduced all types of bacteria. Colostral total IgG concentrations were 83.5, 89.7; 66.1, 52.4; 45.2, and 32.0 in the high, mid-range, and low batches from 2011, 2012, respectively. Plasma IgG levels and AEA were analyzed using Mixed procedure in SAS. Sex of calf, colostrum batch, treatment and batch by treatment interaction were included as fixed effects and calf within treatment was included as a random effect. As expected, calves fed colostrum containing more IgG attained higher plasma IgG1 and IgG2 concentrations at 48 h ($P < 0.05$). Heat treatment of colostrum increased plasma IgG ($P < 0.05$) and tended to increase AEA. Female calves tended to have greater total IgG concentrations than male calves ($P = 0.05$). Results of this study suggest that heat-treatment of colostrum increases absorption of IgG in colostrum of various qualities including very high and very low quality.

Key Words: colostrum, heat-treatment, calf

T280 Performance of crossbred Holstein bull and heifer calves slaughtered 8-month old. M. Vestergaard*[1], P. Spleth[2], A. Mikkelsen[3], C. F. Børsting[3], and M. Kargo[1,2], *[1]Aarhus University, Foulum, Denmark, [2]Knowledge Centre Agriculture, Aarhus, Denmark, [3]Cattle Research Centre, Tjele, Denmark.*

Most newborn bull calves of the Holstein (HOL) dairy breed in Denmark are raised intensively at specialized units and harvested at either 10 or 12–13 mo of age as young bulls. To be sold as veal in EU, the calf needs to be harvested before 8 mo. The market for rosé veal in EU requests a higher carcass conformation score (>4.5) than HOL bull calves can match. Use of sexed semen to produce HOL heifer calves on the genetically best cows allows for crossbreeding with beef breeds. The objective was to investigate if use of crossbreeding will produce offspring that can match the market requirement for rosé veal. A total of 12 purebred HOL bull calves (HOL), 12 beef × HOL bull (BULX) and 12 beef x HOL heifer (HEIX) calves were purchased at 4 wk of age. Two sires were used; one Limousine and one Belgium Blue (6 calves per crossbreeding group). Calves were fed milk replacer (850 g/d), grass hay and concentrate until weaning at 8 wk of age, and then gradually changed to a high-energy TMR based on concentrate pellets, corn-cob silage (35% of DM in TMR), ground barley, sugar beet pulp, and soybean and canola meal fed ad libitum until slaughter at 8 mo. The concentrate pellets (1.4 kg/calf/d) were removed from the TMR at 200 kg BW. Individual feed intake was recorded from 4 to 8 mo. Energy intake was not different between trt groups. At 4 mo, HOL, BULX and HEIX weighed 142, 154 and 140 kg (n.s.), ADG from 4 to 8 mo was 1.50, 1.68 and 1.46 kg/d ($P < 0.001$), BW at slaughter was 330, 368 and 323 kg ($P < 0.001$), and FCE was 4.2, 4.0 and 4.4 Scandinavian Feeding Units (= 7.89 MJ NEg) per kg gain for HOL, BULX and HEIX, respectively ($P < 0.02$). Dressing percentage increased from 51.3 in HOL to 55.5 and 52.8 in BULX and HEIX, respectively, leading to carcass weights of 162, 196 and 164 kg with conformation scores of 3.5, 6.5 and 5.5, respectively (both $P < 0.001$). No HOL but all 12 BULX and 11 out of 12 HEIX passed the 4.5 conformation score criteria. It is concluded that both crossbred male and female offspring of HOL cows can be utilized for rosé veal production in EU.

Key Words: veal, crossbreeding, growth

T281 Comparison of two nutritional programs from birth to 84 d of age in Holstein steers: Body composition, body weight, and stature. K. M. Daniels*[1], K. M. O'Diam[1], C. J. O'Diam[1], T. J. Earleywine[2], H. C. Puch[3], B. L. Miller[3], and J. A. Davidson[3], *[1]Department of Animal Sciences, Ohio Agricultural Research and Development Center, The Ohio State University, Wooster, [2]Land O'Lakes Animal Milk Products Co., Shoreview, MN, [3]Purina Animal Nutrition Center, Gray Summit, MO.*

To compare effects of 2 nutritional programs on body composition, BW, and stature in dairy calves from 0 to 84 d of age, Holstein steers (n = 12) were assigned to either conventional (Con) or full potential

(FP) feeding and were slaughtered at 28, 56, or 84 d of age. Con were fed 454 g DM/d of a 20:20 milk replacer (MR) and 18% CP starter. FP were fed 818 g DM/d of a 28:20 MR followed by increased feeding rate to 1136 g DM/d at d 10 of age and 22% CP starter. MR was offered twice daily from 0 to 44 d of age; calves were weaned (d 45) with 50% reduction in MR DM for 6 d. Starter was offered ad libitum from 0 to 84 d of age. Hip height, BW, body length and heart girth measurements were obtained every 2 wk. At slaughter, animals were processed into: carcass; head, hide, feet, and tail (HHFT); blood; and total viscera. Body composition (water, protein, lipid) was estimated by analysis of 9–11th rib sections. All data were analyzed with a mixed model; weekly data were analyzed with repeated measures. Regardless of age, FP weighed more, were taller, longer, and had larger heart girths than Con. Estimated carcass composition averaged 72.3% water, 18.7% protein, and 6.7% lipid. Regardless of age, body protein content tended to be greater (0.5%) in FP ($P = 0.09$). At 28 d of age, lipid content was 1.0% greater in FP, whereas at 84 d of age Con had 2.5% more lipid than FP ($P = 0.04$). Water content was not affected by diet, but decreased with increasing age ($P = 0.01$). FP tended to have greater protein:fat than Con, which is indicative of better lean gain (3.2 vs. 2.2; $P = 0.07$). As calves aged, percentage of final BW occupied by the carcass decreased ($P = 0.03$), whereas percentage occupied by viscera increased ($P = 0.01$). Nutritional program did not affect percentage of final BW occupied by: carcass, HHFT, blood, or total viscera. These averaged 53.8, 15.1, 5.2, and 25.9%, respectively. FP resulted in heavier and larger framed calves with fairly similar body composition as Con.

Key Words: dairy calf, body composition, nutrition

T282 Survival of *Bifidobacterium animalis* ssp. *lactis* BB-12 in yogurt drink is influenced by timing of probiotic addition. Z. Ba*, E. J. Furumoto, and R. F. Roberts, *Department of Food Science, Pennsylvania State University, University Park.*

Probiotic containing yogurts and yogurt-based drinks have become increasingly popular for their potential health benefits. Viability of the probiotic throughout the shelf life of these products is a critical quality parameter. The effect of time of bacterial addition into the product on survival has not been well studied. As part of an ongoing study designed to compare the efficacy of *Bifidobacterium animalis* ssp. *lactis* BB-12 (BB-12) delivered by yogurt-based smoothie drink and tablets on immune status, fecal transit time, and fecal microbiota, the timing of addition of the probiotic on survival of BB-12 in the yogurt drinks over 4 weeks of storage at 4°C was evaluated. The 2 yogurt drink treatments, (A) BB-12 added after yogurt fermentation and (B) BB-12 added before fermentation were formulated to have 23% total solids and <1% fat. The target concentration of BB-12 per 240-gram serving was log 10 ± 0.5 cfu, commonly considered an effective daily dose. Three bottles of each yogurt drink from 6 batches were analyzed. Population of BB-12 was determined by pour plating method on selective medium MRS-NNLP followed by anaerobic incubation at 37°C after 0, 1, 2, 3, and 4 weeks of storage at 4°C. No statistical difference in the population of BB-12 between treatments A and B was detected immediately following manufacture (wk 0) (initial counts of log 10.52 ± 0.05 cfu/serving and log 10.49 ± 0.14 cfu/serving, respectively). As expected the population of BB-12 declined throughout the shelf life of the products. However, the population decreased faster in treatment A than in treatment B resulting in a significant difference after 2 weeks of storage. This trend continued and at the end of shelf life the BB-12 concentration had decreased significantly in both treatment A (log 9.64 ± 0.06 cfu/serving) and treatment B (log 10.18 ± 0.13 cfu/serving) after 4 weeks of storage. The BB-12 survived significantly better in B than that in A ($P = 0.000$) indicating that BB-12 survives better when added before fermentation, possibly as a result of adaptation to the acidic environment.

Key Words: BB-12, survival, yogurt drink

T283 Pectin-whey protein microparticles containing probiotics: Release and survival of *Lactobacillus acidophilus* La5 in simulated gastrointestinal conditions. C. Gebara, K. S. Chaves, M. C. E. Ribeiro, F. N. Souza, C. R. F. Grosso, and M. L. Gigante*, *University of Campinas, Campinas, SP/Brazil.*

Once microparticles produced by ionotropic gelation are porous, the coating of particles with different materials has been proposed to increase the protective effect for the delivery of probiotics. The aim of this study was to evaluate the release and survival of *Lactobacillus acidophilus* La5 microencapsulated by ionotropic gelation with Ca^{2+} using pectin as wall material, and covered by electrostatic interaction with whey protein heat treated (80°C/30 min) or without heat treatment when exposed to conditions simulating the passage through the gastrointestinal tract. The simulated conditions were assayed with artificial gastric juice, at pH 3.0 with addition of mucin and pepsin at 37°C for 120 min, followed by artificial intestinal juice at pH 7.0 with addition of pancreatin for 300 min. A randomized block with 3 replications was used. The effect of time of exposure to simulated gastric juice and simulated intestinal juice on the viability of free and microencapsulated *Lactobacillus acidophilus* was assessed by ANOVA and the significant differences were evaluated by Tukey's test at 5% significance level. Microencapsulation conferred greater protective effect to *Lactobacillus acidophilus* La5 as compared with the free cells. However, the coating of pectin microparticles with whey protein did not confer additional protection to probiotics when exposed to simulated gastrointestinal conditions. The pectin microparticles remained intact when exposed at pH 1.2, 3.0 and after 300 min at pH 7.0. On the other hand, both microparticles coated with whey protein heat treated or without heat treatment have remained intact for 120 min exposure to simulated gastric juice but have disintegrated after 300 min exposure to simulated intestinal juice (pH 7.0). This occurrence suggests that the probiotics would be released in a different part of the intestinal tract whether delivered by one microparticle or another. Acknowledgments: FAPESP.

Key Words: probiotics, microencapsulation, microcapsules

T284 Influence of some medicinal spices on the bile tolerance of *Streptococcus thermophilus* ST-M5. M. Sanchez-Vega*[1] and K. Aryana[1,2], [1]*School of Animal Sciences, Louisiana State University Agricultural Center, Baton Rouge,* [2]*Department of Food Science, Louisiana State University Agricultural Center, Baton Rouge.*

Spices such as onion, garlic, turmeric, and ginger are known for their medicinal properties such as being antimicrobial, and their potential for the treatment of cancer and cardiovascular diseases. *Streptococcus thermophilus* is a culture bacterium having health beneficial effects. Bile tolerance is an important probiotic characteristic. Although most studies use non water soluble spice extracts, the effect of pure spice juice on bacterial performance is not known. The objective was to elucidate the effect of spices on the bile tolerance of *Streptococcus thermophilus* ST-M5. Bile tolerance of *S. thermophilus* was analyzed using MRS broth supplemented with 0.3% (wt/vol) oxgall and 1% (vol/vol) of freshly extracted spice juice. Sample without spice juice acted as a control. Samples were incubated at 37°C for 5 h, in which they were removed hourly for plating for plating. Growth was determined by plating every hour for a period of 5 h. *S. thermophilus* was incubated aerobically at 37°C for 48 h. Data were analyzed using Proc Mixed model with a Tukey adjustment of Statistical Analysis System. Experiments were conducted in triplicate. Counts at 0 and 1 h of incubation were 10 and 9 log cfu/mL respectively. None of the 4 spices showed any significant ($P > 0.05$) difference in counts when compared with control up to 1 h. After 2 h of incubation, there were significantly lower counts for garlic, with a reduction of 1.3 log cfu/mL when compared with control. At 3 h of incubation, all spices showed significant lower counts when compared with control, with an average reduction of 1.8 log cfu/mL, except for onion whose reduction was 1.4 log cfu/mL. After incubating for 4 and 5 h, all spices showed significant lower counts when compared with control, with a maximum reduction of 3.1 log cfu/mL for garlic and a minimum of 2 log cfu/mL for onion. Although these spices showed significantly lower counts, *S. thermophilus* was still viable, showing that these spices can be used alongside with this probiotic bacterium allowing health benefits from both sources.

Key Words: spice, probiotic

T285 Effect of month on the composition and quality of milk from Holstein cows in a hot-arid environment. J. Méndez*[1], M. Mellado[1], F. G. Véliz[1], M. A. de Santiago[1], J. E. García[1], and A. Zúñiga[1], [1]*Autonomous Agrarian University Antonio Narro, Saltillo, Mexico,* [2]*Autonomous Agrarian University Antonio Narro, Torreon, Mexico.*

This study was designed to evaluate the month of the year on the variation of milk composition and microbial content of intensively-managed Holstein cows in northern Mexico (26°N). The milk samples were obtained from about 3,200 cows, which were sampled 4 times per month from January to December of 2011 and 2012. Bacteriological analyses were performed daily in the bulk tank milk. The MIXED procedure of SAS with the PDIFF option was used to detect differences among mean monthly milk components, somatic cell counts and bacteriological measurements. Non-linear analyses were also performed to describe the monthly trend of milk composition and quality. Only month was accounted for in the models with year included as covariable. A quadratic (U-shaped; $r^2 = 0.86$) model best described the relationship between month of the year and total solids, with the highest ($P < 0.05$) value in November (12.27%) and the lowest in July (12.03). Also, a U-shaped trend ($Y = 3.23 + 0.22/1 + 0.08x - 0.001 x^2$; $r^2 = 0.95$) showed the best fit to the relationship between month and milk protein content, with the highest level (3.22%; $P < 0.01$) in December and the lowest (3.12%) in April. A clear decrease during the warmer months ($Y = 8.73–0.52x/1–0.058x-0.0001x^2$; $r^2 = 0.93$) was observed for non-fat solids but no differences among month for this variable was detected. Differences in the milk content of urea nitrogen (range 12.28–13.39 mg/dL), lactose (range 4.75–4.82%), fat (range 3.36–3.44), coliform bacteria counts (range 18.3–68.33 cfu/ml), standard microbial count and somatic cell counts (range 236,149–295,335 cells/mL) were not detected among months. The thermoduric strain of bacteria count showed a v-shaped tendency ($Y = 0.14–0.06 \cos(-0.02x + 0.14)$; $r^2 = 0.83$) with the highest ($P < 0.05$) values in the coldest months and the lowest values in the summer. This results show that, except for lactose, coliform bacteria counts and urea nitrogen milk content, all other milk components and microbiological variables showed a noticeable depression during the hottest month of the year.

Key Words: coliform, somatic cell count, milk protein

T286 Development of a pilot test system for demonstration and evaluation of CIP cleaning. Y. Yu* and R. Roberts, *Department of Food Science, The Pennsylvania State University, University Park.*

Cleaning in place (CIP) is widely used in the dairy industry. Electrolyzed oxidizing (EO) water offers an attractive alternative to traditional chemicals for cleaning and sanitation. EO water is produced via electrolysis of a dilute sodium chloride solution, which results in a sodium hydroxide solution (pH ~11.0 and ORP ~ 1168 mV) and an acidic solution (pH ~2.5, ORP ~ −850 mV and >100 ppm of chlorine). Walker et al. (2005) evaluated EO water as a cleaning agent for on-farm milking systems and found it to be effective in a cleaning/sanitizing system. The use of EO water in CIP applications for heated dairy processing systems has not been evaluated. In this project, a pilot scale system was constructed to allow evaluation and optimization of EO water as CIP agent for dairy processing equipment. The test system was composed of a 4-gallon double jacked stainless steel vessel, whose temperature could be controlled by running cooling or heating media through the jacket, a probe and microprocessor based chart recorder for monitoring temperature during fouling and cleaning, a variable frequency drive pump, and a static spray ball for CIP cleaning. A range of pump speeds were evaluated and it was determined a flow rate of 8.3 L/min provided adequate coverage for CIP cleaning of the system using a riboflavin removal method. A 4-step CIP procedure for the test system was developed. The effectiveness of cleaning was assessed using ATP bioluminescence and residual protein detection, which is comparable to a standard manual cleaning procedure. Results indicated the system would serve as a suitable test bed for optimization of CIP procedure using EO water. Preliminary experiments using EO water in a 4-step manual cleaning procedure suggested that EO water can serve as a suitable cleanser for dairy processing equipment. With the test system validated experiments are underway to optimize temperature and time required for cleaning the system soiled with cold milk and when soiled during heating of milk. Use of this test system to demonstrate principals of cleaning in a senior level dairy products processing course will also be presented.

Key Words: CIP, EO water

T287 Development of a fresh cheese model to evaluate novel antilisterials. M. L. Van Tassell*[1], L. Vazquez-Portalatin[2], S. R. Takhar[1], and M. J. Miller[1], *[1]University of Illinois at Urbana-Champaign, Urbana, [2]University of Puerto Rico at Mayaguez, Mayaguez.*

Hispanic-style fresh cheeses such as queso fresco are difficult to preserve without compromising delicate organoleptic properties. Inherently low salt content, neutral pH, and high water activity predispose such cheeses to carriage and proliferation of *Listeria monocytogenes.* Incorporation of novel antimicrobials into cheese-making processes for investigating antilisterial activity is complicated by manufacturing constraints. Consequently, few studies have focused on in situ testing of antilisterials in fresh cheeses despite evidence of discrepancies between in vitro and in situ efficacy of many antimicrobial compounds in food matrices. To allow for high-throughput testing of novel antilisterials incorporated into fresh cheeses directly, we have developed a small-scale laboratory queso fresco model that can be completed in a biosafety cabinet. Milk of variably scaled batches can be blended with desired antimicrobials and mixed with rennet before being divided into microcentrifuge tubes for incubation. Cheese production is carried out in vitro, including centrifugation to replace conventional pressing techniques. *Listeria* can be incorporated at any step to replicate diverse contamination scenarios and recovery from the final cheeses can be carried out with common selective media. We have validated this model with nisin and commercial fermentate, clearly demonstrating detection of listerial inhibition over a multi-week shelf-life. This model allows for rapid and convenient production of small-scale fresh cheeses for screening antilisterials in an appropriate food matrix.

Key Words: cheese, *Listeria*, antimicrobial

T288 Antimicrobial susceptibility profile and toxigenic genes detection in *Staphylococcus* spp. samples isolated from Brazilian artisanal cheeses. D. L. S. Oliveira[1], L. S. Carmo[2], L. B. Acurcio[1], R. D. Castro[1], F. M. Sant'Anna[1], C. F. A. M. Penna[1], M. O. Leite[1], L. M. Fonseca[1], S. H. C. Sandes[3], A. M. Silva[4], M. M. O. P. Cerqueira*[1], and M. R. Souza[1], *[1]Departmento de Tecnologia e Inspecao de Produtos de Origem Animal, Escola de Veterinaria, Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil, [2]Fundacao Ezequiel Dias, Belo Horizonte, Minas Gerais, Brazil, [3]Departamento de Genetica, Instituto de Ciencias Biologicas, Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil, [4]Universidade Federal de Sao Joao Del Rey, Sete Lagoas, Brazil.*

The objective of this study was to detect the presence of enterotoxin coding genes and analyze the antimicrobial susceptibility profile of 15 *Staphylococcus* spp. samples isolated from Serra da Canastra artisanal cheeses produced in Brazil. The bacterial identification was made through molecular techniques based on the amplification of a fragment of rDNA 16S gene. The detection of *sea*, *sec*, *sed* and *see* was carried

out by PCR-Multiplex and *seb* and *tst* by individuals PCR-Uniplex. Antimicrobial susceptibility profile was determined according to the disc diffusion method. The 15 samples of *Staphylococcus* spp. were identified as *S. aureus* ssp. *aureus* (67%), *S. saprophyticus* ssp. *bovis* (20%) and *S. warneri* (13%). No gene for synthesis of classic staphylococci toxins was identified in none of the analyzed samples. Regarding the antibiogram, the 15 tested samples presented, in general lines, low resistance to the 20 tested antimicrobials. All samples presented resistance to sulfonamide. Resistance was also observed to penicillin (80% of the samples), ceftazidime (60%) and oxacillin (40%). Although, for the other 16 tested antimicrobials, resistance rates were below 30%. A total of 26.7% of the samples were resistant to ciprofloxacin, tetracycline, ampicillin and amoxicillin, and 13.3% to chloramphenicol, sulfatrim and nitrofurantoin. The other tested drugs (vancomycin, gentamicin, clindamycin, eritromicin, imipenem, cefoxitin, amikacin, ceftriaxone and cefaclor) were efficient against 100% of the tested samples. Although *Staphylococcus* spp. tested samples were not able of producing enterotoxins and TSST-1, they can represent public health risk due to phenotypic resistance to most common antimicrobials used in animal and human therapies.

Key Words: *Staphylococcus*, PCR-multiplex, antimicrobial susceptibility

T289 Analysis of a genetically distinct strain of the monomorphic subspecies *Bifidobacterium animalis* ssp. *lactis,* the complete genome of *Bifidobacterium animalis* ssp. *lactis* ATCC 27673. J. R. Loquasto*[1], R. Barrangou[1,2], E. G. Dudley[1], B. Stahl[2], and R. F. Roberts[1], [1]*Department of Food Science, Penn State University, University Park,* [2]*DuPont Danisco USA Inc., Madison, WI.*

Bifidobacterium animalis ssp. *lactis* (BAL) is a widely consumed probiotic microorganism, commonly added to a variety of foods, including fermented dairy foods such as yogurt. Characteristics making this subspecies desirable for use as a probiotic include its perceived health benefits as well as technological advantages over organisms in the same genus. The genomes of 9 strains of this subspecies have been sequenced and are publicly available. Analysis of these genomes reveals very little genetic diversity leading to the term "monomorphic" being used to describe subspecies. In previous work, Delétoile et al. (2010) used multilocus sequence typing (MLST) to characterize several bifidobacterial species and revealed BAL ATCC 27673 had a unique MLST type. As part of an effort to assess the genetic diversity in the *B. animalis* ssp. *lactis* group, this strain was chosen for full genome sequencing. Following DNA isolation, 454 shotgun pyrosequencing was conducted, contigs were aligned and assembled using the genome of BAL DSM 10140 as a reference scaffold and the genome was closed using a combination of PCR and Sanger sequencing. The full genome of ATCC 27673 was 1,963,012 bp long, contained 1,616 genes, 4 rRNA operons and had a G+C content of 61.55%. Further analysis revealed 5 distinct genomic islands differing from other strains of the same subspecies. In 4 islands, either mobile genetic elements or phage elements are present. In island 5, the largest island, a novel CRISPR locus was identified. This locus contains 81 novel spacers different from any spacers observed in other strains of BAL. In addition BAL ATCC 27673 was found to contain a type I-E CRISPR-cas system, whereas all other strains of this subspecies contain a type I-U system. This analysis revealed ATCC 27673 represents a novel strain of *B. animalis* ssp. *lactis*, differing substantially from other stains of the subspecies. This work suggests that the 9 commercial strains sequenced to date may represent only a limited portion of the genetic potential of this subspecies.

Key Words: *B. animalis* ssp. *lactis*, probiotic

T290 Microbiological quality of nonfat dry milk and skim milk powder produced in the United States A. K. A. Ali*, K. E. Smith, K. J. Burrington, and J. A. Lucey, *Wisconsin Center for Dairy Research, University of Wisconsin–Madison, Madison.*

Microbiological quality of nonfat dry milk powder/skim milk powder (NFDM)/(SMP) is important as it can affect the quality of food products in which the powder is used as an ingredient. The objectives of this study were to determine the microbiological quality of domestically produced NFDM/SMP. In this study, 23 samples of NFDM/SMP were obtained from 4 US processors for analysis. Samples were 25 kg or 50 pound bags of powder of low, medium and high heat NFDM/SMP that have not been agglomerated or instantized and were approximately 6 to 9 mo old. Total bacterial count, aerobic thermophiles, thermoresistant bacteria, coliforms, yeasts and molds, as well as, bacterial spores including mesophilic aerobic, mesophilic anaerobic, thermophilic aerobic, and thermophilic anaerobic were determined. Powders were <10 cfu/g for coliforms, thermoresistant bacteria, yeasts and molds. Total bacterial count for powders had a range of 2.0–2.9 $\log_{10}$ cfu/g with differences due to powder manufacturer. Samples had a large variation in thermophilic aerobic bacteria numbers with a range of 2.1–4.8 $\log_{10}$ cfu/g. While the numbers of mesophilic aerobic spores and thermophilic anaerobic spores did not show notable variations, the numbers of thermophilic aerobic spores varied greatly with a range of $1 < -4.1$ $\log_{10}$ cfu/g. The high numbers of thermophilic aerobic spores observed with samples from some producers may be explained by their presence on the surfaces of the equipment and/or the formation of biofilms on stainless steel surfaces. There was no significant variation among powders based on heat classifications or between NFDM and SMP. The results of this work indicate that the microbiological quality of powders was source dependent regardless of heat classifications or whether the product was NFDM or SMP. Based on the results, powders from some manufactures may be better suited to low-spore count applications than powders from other producers.

Key Words: NFDM/SMP, bacterial spore, microbiological quality

T291 Real-time PCR and TTGE for rapid and sensitive detection of *Staphylococcus aureus* in Ras and Domiati cheese during ripening. S. Awad*, *Department of Dairy Science and Technology, Faculty of Agriculture, Alexandria University, Alexandria, Egypt.*

Microbial diversity in cheese is considered essential to the sensory richness and variety of traditional Egyptian cheeses. However, some members of these complex communities may also be responsible for cheese flavor defects or may constitute a health risk. Being able to characterize the microbial communities in raw milk and follow the dynamics of the entire populations throughout the cheese-making and ripening processes is therefore critical. *Staphylococcus aureus* is a bacterial pathogen considered a principal etiological agent of food poisoning. The aim of this study was to apply real-time PCR-based method (TaqMan RT-PCR) comparing with temporal temperature gradient electrophoresis (TTGE) technique to detect *S. aureus* in Doimiati and Ras cheeses during their ripening periods. In parallel, all cheese samples were examined to conventional methods to ensure the detection limit of 10^0 cfu per gram. In this study, *S. aureus* was detected in all Ras and Domiati cheeses after 2 mo of ripening by using TTGE. The results of real time PCR showed that the *S. aureus* could not be detected in fresh cheese samples using TTGE method but it detected in fresh cheese sample using real time PCR. The real time PCR method could be used for *S. aureus* detection as a faster, highly specific, and more sensitive alternative to microbiological method with the potential for providing of improved food-processing hygiene control.

Key Words: real-time PCR, TTGE, *Staphylococcus aureus*

T292 Development of a rapid SNP-typing assay to differentiate *Bifidobacterium animalis* ssp. *lactis* strains used in probiotic-supplemented dairy products. S. Lomonaco*[2], E. J. Furumoto[1], J. R. Loquasto[1], P. Morra[2], and R. F. Roberts[1], *[1]Department of Food Science, Penn State University, University Park, [2]Dipartimento di Scienze Veterinarie Università degli Studi di Torino, Grugliasco TO, Italy.*

Identification at the genus, species, and strain level is required when a probiotic microorganism is added to foods. Strains of *Bifidobacterium animalis* ssp. *lactis* (BAL) have been commonly used worldwide in dairy products supplemented with probiotic. However, strain discrimination is difficult, given the high degree of genome identity (99.975%) between different genomes of this subspecies. Typing of monomorphic species can be efficiently carried out by targeting informative single nucleotide polymorphisms (SNPs). Findings from a previous study analyzing both reference and commercial strains of BAL detected SNPs that could be used to discriminate 14 groups/strains. This abstract describes the development of a primer extension reaction (PER) assay targeting multiple SNPs that can allow strain differentiation of *B. animalis* ssp. *lactis*. Based on previous data, 7 informative SNPs were selected for further testing and a multiplex preliminary PCR was optimized to amplify the 7 DNA regions comprising the selected SNPs. Extension primers (EPs), annealing immediately adjacent to the selected SNPs, were tested in simplex PER to evaluate their performance. Twenty strains belonging to 13 groups were selected and PERs were carried out on according to manufacturer's instructions (SNaPshot Multiplex System from Applied Biosystems), with minor modifications. Fragment analysis was subsequently carried out in duplicate at the Penn State University Genomics Core Facility. Simplex PER mostly gave rise to a peak of the expected color, specific to the targeted SNP and 8 specific profiles could be observed, separating the most commonly used commercial strains. Further tests will be necessary to fully assess the discriminating capacity of each EPs and to optimize a multiplex PER assay able to simultaneously interrogate the selected SNPs. Such a novel multiplex PER approach can represent a simple, rapid, flexible SNP-based subtyping method for proper characterization and identification of commercial probiotic strains of BAL from fermented dairy products.

Key Words: *Bifidobacterium animalis* ssp. *lactis*, strain identification, SNaPshot

T237 Studying the microbiological safety criteria and quality related problems of the traditional Kishk Sa'eedi. S. Awad*[1], M. El Soda[1], A. Ahmed[1], I. Nagady[1], C. Mestres[2], and D. Pallet[2], *[1]Department of Dairy Science and Technology, Faculty of Agriculture, Alexandria University, Alexandria, Egypt, [2]CIRAD (Agricultural Research for Development), Montpellier Cedex 5, France.*

Kishk Sa'eedi is an indigenous food that is part of the rich food heritage of Egypt. The name "Kishk" refers to a group of popular fermented dairy cereal mix products common to Egypt and the Middle East within the framework of the European funded "AFTER" Project (African Food Tradition rEvisited by Research). The natural microflora in Kishk Sa'eedi were studied and characterized. An inventory of both the technological flora (lactic acid bacteria) and pathogenic germs (*Salmonella* sp., *Listeria* sp., *Clostridium* sp., *Staphylococcus aureus* coagulase positive, *Brucella* spp., yeasts, and molds) were analyzed in the final product. During the microbiological analysis of raw materials and final product, lactic acid bacteria that could potentially act as starter cultures were isolated and identified. The isolates were identified using rep-PCR as *Lactobacillus acidophilus, Lb. helveticus, Lb. del. bulgaricus, Lb. del. lactis, Lb. casei, Lb. paracasei, Lb. plantarum, Lb. rhamnosus, Lb. brevis, Lb. fermentum.* The technological criteria (stability of lyophilized, acidification, activity flavor development, antagonistic activities, slimy production, peptidase activity, antibiotic resistance and amines production) were determined for all isolates. Mixing cultures were selected to produce the second generation Kishk Sa'eedi.

Key Words: Kishk Sa'eedi, lactic acid bacteria, pathogenic bacteria

Nonruminant Nutrition: Amino Acids and Energy

T293 The National Animal Nutrition Program. G. L. Cromwell*[1], T. J. Applegate[2], D. C. Beitz[3], M. L. Galyean[4], M. B. Hall[5], M. D. Hanigan[6], J. Odle[7], W. P. Weiss[8], and C. Kirk Baer[9], *[1]University of Kentucky, Lexington, [2]Purdue University, West Lafayette, IN, [3]Iowa State University, Ames, [4]Texas Tech University, Lubbock, [5]USDA/ARS, Madison, WI, [6]Virginia Tech University, Blacksburg, [7]North Carolina State University, Raleigh, [8]The Ohio State University, Columbus, [9]U.S. Department of Agriculture, Washington, DC.*

The National Animal Nutrition Program (NANP), initiated in 2010, is supported as a National Research Support Project (NRSP-9) with Hatch funds administered by the US Department of Agriculture. Funds for NRSPs are drawn from the total federal allocation before the formula distribution to state agricultural experiment stations. The NANP focuses on addressing challenges facing researchers in animal agriculture and filling voids in the research and academic communities. An integrated and systematic approach is used to share, collect, assemble, synthesize, and disseminate science-based information, educational tools, and enabling technologies for agricultural animal nutrition, with emphasis on beef, dairy, swine, and poultry. The NANP also facilitates high-priority research across domestic agricultural species. The purpose of the NANP is to identify the current state of coordination and networking within animal nutrition; explore animal nutrition over time, across geographic locations, by topic, and by networks of collaborators in animal nutrition research; define high-priority animal nutrition issues; and address existing collaborations to facilitate solutions to these issues. The committee will interact with the National Research Council on critical national priorities in animal nutrition and provide a forum to address research support needs. The NANP consists of a coordinating committee (listed as authors) appointed by NRSP-9's Administrative Advisors (N. M. Cox, KY; B. W. Hess, WY; D. A. Benfield, OH; C. Faustman, CN). The coordinating committee oversees 2 additional committees: (1) a modeling committee that will improve the use of predictive technologies and tools, enable use of common software platforms, and work with researchers to develop and share models and modeling information; and (2) a feed composition committee that will assemble data and research resources on feed composition, foster communication among those collecting feed composition information, and improve efficiency and consistency in data collection and maintenance. Ongoing details regarding the activities and accomplishments of the 3 committees are posted on the NANP website: http://www.ca.uky.edu/nrsp-9/index.htm.

Key Words: animal nutrition, NANP, NRSP

T294 The National Animal Nutrition Program: Feed composition committee. P. S. Miller*[1], R. N. Dilger[2], W. P. Dozier[3], M. B. Hall[4], A. N. Hristov[5], V. R. Moreira[6], M. L. Nelson[7], N. R. St-Pierre[8], and W. P. Weiss[9], *[1]University of Nebraska, Lincoln, [2]University of Illinois, Urbana-Champaign, [3]Auburn University, Auburn, AL, [4]USDA/ARS, Madison, WI, [5]Pennsylvania State University, University Park, [6]Louisiana State University, Baton Rouge, [7]Washington State University, Pullman, [8]The Ohio State University, Columbus, [9]The Ohio State University, Wooster.*

A feed composition committee has been developed in conjunction with the National Animal Nutrition Program (NANP). This committee is supported and funded as a National Research Support Project (NRSP-9). The NRSPs are initiated by the use of Hatch funds administered by US Department of Agriculture and are drawn from the total federal allocation before the formula distribution to state agricultural experiment stations. The committee is moving forward with the following objectives: (1) Collect information on feed composition from the published literature and other critically evaluated sources and maintain a current collection of that information as a resource to the research community; (2) Develop a forum to exchange and collate information on methods of analysis, with links to sources and critiques to provide a resource to the research community and identify gaps in our ability to analyze feeds to stimulate development of new techniques; (3) Identify assays or methods that have or proven to have potential benefits to diet formulation. Thus, the overall approach of the committee is to gather data and information critical to the development of feed ingredient composition repositories for the major livestock species (beef, dairy, poultry, and swine). A major focus of the committee is to work with current and future National Research Council (NRC) committees to facilitate development and revision of ingredient databases for NRC nutrient requirement reports and to bring consistency to the databases used for the reports. Also, the committee is working closely with the NRSP-9 committee on modeling to support needs regarding ingredient composition data as model inputs. Presently, the committees' activities are posted on the NANP website: http://www.ca.uky.edu/nrsp-9/index.htm. The feed composition committee has initiated its work with data sets used by previous NRC species committees. Design of an overall database structure is currently underway. Input templates for the database have been developed for beef, dairy, poultry, and swine. The committee will solicit data from the scientific literature and industry sources focusing primarily on information derived from North America.

Key Words: feed composition, database

T295 Accuracy of predicting digestible energy of corn for growing pigs from various data sources. R. Allen, A. Hassen*, B. Smith, M. Hinds, C. Iiams, D. Rice, D. Sevenich, F. Owens, D. Jones, and T. Sauber, *DuPont Pioneer, Johnston, IA.*

The objective of the current study was to evaluate accuracy of predicting swine digestible energy (DE) of corn based on Near-Infrared Transmittance Spectroscopy (NIT) scans and models, cross-species relationships, and literature equations. DE content of 83 corn grain samples was determined from total collection of feces using uniform sets of barrows (16 to 18 kg initial BW) of similar genetic background. Diets contained 89.5% ground corn supplemented with casein, minerals and vitamins. Nitrogen-corrected apparent metabolizable energy (AME_N) for these 83 corn grain samples was determined with 3-wk old broiler chicks. DE and AME_N data were initially analyzed using mixed models. The model for AME_N analysis included fixed effects of study, corn source within study and random effects of block and error; the DE model included the same fixed effects as AME_N and random effects of run within study, room within study and run, pig within study and room and error. Check means were used as a covariate in each model. Data from 66 corn samples were used for model development; the remaining 17 were used for cross-validation based on stratified random sampling procedure. NIT spectra data from each whole grain sample were used to develop NIT based predictions of swine DE (NIT-DE) and poultry AME_N (NIT-AME_N). Models were then developed to predict swine DE from AME_N and NIT-AME_N. Simple linear equations proved adequate to predict swine DE from either AME_N or NIT-AME_N (R^2 and root mean square error (RMSE) ranged from 0.71 to 0.73 and 53 to 54 kcal/kg, respectively). Validation test showed a similar prediction capability from either AME_N or NIT-AME_N with correlation (r) between observed and predicted values ranging from 0.88 to 0.92, and RMSE from 43 to 52 kcal/kg. Direct NIT prediction of DE from spectra data (NIT-DE) showed a comparable fit (r = 0.91 and RMSE = 48 kcal/kg). Published literature equations when combined with wet chemistry analyses showed

the weakest fit to measured DE (r = 0.51; RMSE of 112 kcal/kg). Relative DE of corn grain samples for growing pigs can be calculated reliably from measurements of poultry AME_N, NIT-AME_N or direct NIT scans.

Key Words: swine, poultry, corn

T296 Energy and amino acid digestibility of camelina meal fed to finishing pigs. R. K. Kahindi*[1], T. A. Woyengo[2], P. A. Thacker[3], and C. M. Nyachoti[1], *[1]University of Manitoba, Winnipeg, MB, Canada, [2]University of Alberta, Edmonton, AB, Canada, [3]University of Saskatchewan, Saskatoon, SK, Canada.*

This experiment was conducted to determine the apparent ileal (AID) and standardized ileal (SID) AA digestibility as well as the DE and ME content of camelina meal fed to finishing pigs. Six ileal cannulated barrows (80.2 ± 7.5 kg BW) were fed 2 diets in a 2-period cross over design to give 6 replicates per diet. The diets were a corn-soybean meal-based basal diet formulated to meet NRC (1998) nutrient requirements for 50 to 80 kg pig as well as the basal diet with a portion of the AA-yielding ingredients (corn and soybean meal) replaced with 20% camelina meal. The basal diet was fed to determine nutrient digestibility and retention by the difference method. The SID of N and AA was calculated using published values for ileal basal endogenous AA losses from our laboratory and NE was calculated using values from proximate analysis. Titanium dioxide (0.3%) was included in the diets as an indigestible marker. The GE, CP, Lys, Met, Thr, EE, NDF, ADF and glucosinolate content of camelina meal (on a DM basis) were 5,130 kcal/kg, 38.08, 1.80, 0.68, 1.68, 11.90, 31.46, 20.30% and 36.30 µmol/g, respectively. The AID and SID of N for camelina meal were 58.30 and 65.20%, respectively. The SID values of Lys, Met and Thr for camelina meal were 57.89, 53.39 and 52.48%, respectively whereas the corresponding standardized ileal digestible contents on a DM basis for the same AA were 1.04, 0.36 and 0.84%, respectively. The DE, ME, and NE values for camelina meal were 4185, 3,857, and 1,951 kcal/kg, respectively. In conclusion, camelina meal can be used as an energy and AA source in swine diets and the SID AA and DE and ME values of camelina meal from the current study could be used when formulating diets to minimize N excretion and feed costs.

Key Words: camelina meal, digestibility, pig

T297 Effect of levels of digestible lysine and ractopamine on the performace of castrated pigs from 70 to 97 kg. D. O. Fontes*[1], I. S. Fernandes[1], D. M. S. Junior[1], L. P. O. Souza[1], B. O. Rosa[1], I. J. Silva[1], A. P. L. Brustolini[1], V. S. Cantarelli[1,2], and G. M. Salum[1], *[1]Federal University of Minas Gerais, Belo Horizonte, Minas Gerais, Brazil, [2]Federal University of Lavras, Lavras, Minas Gerais, Brazil.*

A total of 180 hybrid barrows (initial and final body weight of 70.8 ± 3.78 and 97 ± 7.3 kg) were used to evaluate the effects of ractopamine (RAC) and digestible lysine (Lys) levels on late finishing pig performance. Pigs were blocked by weight and time and randomly allotted to one of 15 dietary treatments in a 27d experiment. There were 2 pigs per pen and 6 pens per treatment. Pigs were fed corn and soybean meal based diets formulated to meet the NRC (1998) requirements, with the exception of digestible lysine which were adjusted to satisfy the level of treatments. Treatments were arranged as a 3 × 5 factorial with main effects of RAC (0, 5 and 10ppm) and digestible lysine (0.50, 0.65, 0.80, 0.95, and 1.1%). The diets were isocaloric (3,23 Mcal/kg) and isoproteic (12,6%). The levels of lysine were obtained by the addition of L-lysine-HCl and to meet the ideal protein concept, where necessary, supplementing the diets were the other essential amino acids. The parameters evaluated were BW, ADG, ADFI and G:F. Significant effect of digestible Lys was evaluated by the regression of the observed variable on digestible Lys level of diet while means of ractopamine supplemented animals were compared by SNK test at 10% probability level. Interaction was observed between lysine and ractopamine for BW, ADG and G:F ($P < 0.05$). No interactions were observed ($P > 0.05$) for ADFI and digestible lysine intake. The recommended level of digestible Lys was 0.8, 0.91 and 1.1% for diets without and with 5 and 10 ppm RAC respectively for best values of final BW and ADG. For G:F the values were 0.53, 0.96 and 0.98% of digestible Lys, respectively. Thus, considering the values obtained and the best data adjustment, it can be concluded that for the better performance of finishing barrows the digestible lysine requirement was 0.8, 0.96 and 1.1%, which corresponds to an intake of digestible lysine of 23.51, 28.04 and 32.57 g/day for diets without and with 5 and 10 ppm RAC, respectively.

Key Words: swine, amino acid, requirement

T298 Determination of digestible and metabolizable energy concentrations in oilseed meals fed to growing pigs. A. R. Son* and B. G. Kim, *Konkuk University, Seoul, Republic of Korea.*

An experiment was conducted to determine digestible energy (DE) and metabolizable energy (ME) concentrations in feed ingredients including sesame meal (SM), 3 sources of soybean meal (SBM), high-protein distillers dried grains (HPDDG), perilla meal (PM), cannola meal (CNM), copra meal (CM), corn germ meal (CGM), palm kernel expeller (PKE), and tapioca distillers dried grains (TDDG). Twelve barrows with an initial BW of 31.8 ± 2.7 kg were individually housed in metabolism crates equipped with a feeder and a nipple drinker. A 12 × 10 Youden square design was employed with 12 dietary treatments, 10 periods, and 12 animals. A basal diet mainly consisted of corn and SBM was prepared to contain 15.6% CP, 0.68% standardized ileal digestible Lys, 0.47% Ca, and 0.21% available P. Eleven additional diets were formulated to contain 30% of each test ingredient. The quantitative feed and feces method using Cr2O3 as an indigestible marker was used for fecal collection with 4-d adaptation and 4-d collection periods. The statistical model for the mixed procedure of SAS included dietary treatment as fixed variable, and animal and period as random variable. Values for the DE and ME in the 3 sources of SBM were greater ($P < 0.05$) than other test ingredients except HPDDG (Table 1). Values for DE:GE in the 3 sources of SBM were greater ($P < 0.05$) than all other test ingredients. In conclusion, SBM has greater energy concentrations than most oilseed meals and has greater energy digestibility than other oilseed meals fed to growing pigs.

Table 1. Nutrient composition (%) and energy values (cal/g) of test ingredients fed to growing pigs, as-fed basis

Ingredient	DM	CP	GE	DE	ME
SM	97.0	50.0	4,688	2,592^{e}	2,269^{ef}
SBM 1, dehulled, Korea	90.2	47.1	4,299	3,925^{a}	3,782^{a}
SBM 2, India	90.1	39.6	4,221	3,610^{ab}	3,445^{ab}
SBM 3, Korea	90.2	47.4	4,332	3,725^{ab}	3,552^{ab}
HPDDG	91.5	38.0	4,924	3,544^{bc}	3,271^{bc}
PM	90.3	43.2	4,240	1,907^{f}	1,672^{g}
CNM	91.5	37.5	4,235	3,096^{d}	2,832^{cd}
CM	90.2	21.7	4,095	2,219^{f}	2,122^{f}
CGM	94.1	21.4	4,699	3,247^{cd}	3,071^{c}
PKE	89.6	15.3	4,407	2,586^{e}	2,506^{de}
TDDG	93.3	18.4	3,875	1,202^{g}	1,157^{h}
SEM				97	96
P-value				<0.001	<0.001

Key Words: energy concentration, protein supplement, swine

T299 Energy value of dried distillers grains with solubles and oilseed meals for pigs. C. Kong* and O. Adeola, *Purdue University, West Lafayette, IN.*

The energy values of 3 dried distillers grains with solubles (DDGS) derived from corn, triticale and sorghum, and 3 oil seed meals including canola meal (CM), cotton seed meal (CSM), and sunflower seed meal (SSM) were determined in 2 studies. Twenty-four crossbred barrows with average initial BW of 28.0 kg were grouped by weight into 6 blocks with 1 pig per metabolism crate in each study. There were 4 diets in each experiment consisting of a corn-soybean meal reference (RD) diet and 3 test diets (TD). The TD consisted of each of 3 DDGS (Exp. 1), or 3 oil seed meals (Exp. 2) that partly replaced the energy yielding sources in the RD at 300 g/kg (Exp.1) or 200 g/kg (Exp. 2) such that same ratios were maintained for all energy ingredients across all experimental diets. The DE, apparent metabolizable energy (AME), and nitrogen-corrected AME (AME_n) of the test ingredients were determined by the difference method in 2 studies each consisting of a 5-d adjustment and 5 d of total but separate collection of feces and urine. The respective DM or GE of corn DDGS, triticale DDGS, sorghum DDGS, CM, CSM, and SSM were 918, 927, 904, 912, 907, and 898 g/kg; or 4,985, 4,913, 4,785, 4,616, 4,829, and 4,122 kcal/kg of DM. Addition of DDGS to RD in Exp. 1 decreased dietary DE, AME and AME_n of the TD. In Exp. 2, the respective energy values of the TD were not affected by the addition of oil seed meals to RD with SSM, which decreased ($P < 0.01$) the energy values. In conclusion the DE, AME and AME_n were 3,751, 3,559, and 3,361 kcal/kg of DM, respectively, for corn DDGS; 3,720, 3,537, and 3,315 kcal/kg of DM, respectively, for triticale DDGS; and 3,520, 3,355, and 3,228 kcal/kg of DM, respectively, for sorghum DDGS. Furthermore, the DE, AME, AME_n of SSM for pigs were 2,449, 2,253, and 2,071 kcal/kg of DM, which were lower ($P < 0.01$) than the energy values evaluated for CM and CSM at 3,577, 3,428, and 3,087 kcal/kg of DM, respectively for CM; and 3,281, 3,139, and 2,892 kcal/kg of DM for CSM.

Key Words: dried distillers grains with solubles, energy, pigs

T300 Amino acid digestibility in copra expeller and palm kernel expeller by growing pigs. A. R. Son*[1], Y. Hyun[2], J. K. Htoo[3], and B. G. Kim[1], *[1]Konkuk University, Seoul, Republic of Korea, [2]Farm Story Dodram B&F, Seoul, Republic of Korea, [3]Evonik Industries AG, Hanau, Germany.*

An experiment was conducted to determine the apparent ileal digestibility (AID) and the standardized ileal digestibility (SID) of crude protein (CP) and amino acids (AA) in copra expeller (CE) and palm kernel expeller (PKE) by pigs. The CE contained 89.9% DM, 20.2% CP, 7.1% ether extract, 54.4% NDF, and 6.7% ash; and the PKE contained 91.9% DM, 17.2% CP, 7.1% ether extract, 66.7% NDF, and 4.0% ash on an as-fed basis. Six boars fitted with a T-cannula in the distal ileum with an initial BW of 65.2 kg (SD = 5.4) were individually housed in pens equipped with a feeder and a nipple drinker. A replicated 3 × 3 Latin square design was employed with 3 dietary treatments, 3 periods, and 6 animals. Two experimental diets were prepared to contain 40% of the CE or PKE as the sole source of nitrogen. A nitrogen-free diet was formulated mainly based on cornstarch and sucrose to estimate the basal endogenous losses of CP and AA. All diets contained 0.5% chromic oxide as an indigestible index. The statistical model for the mixed procedure of SAS included dietary treatment as fixed variable and replication, animal within replication, and period within replication as random variable. The values for the AID of all indispensable AA except His and Lys in the CE were greater ($P < 0.05$) than in the PKE. The values for the SID of CP (67.6 vs. 52.8%), Arg (90.0 vs. 80.4%), Leu (78.5 vs. 72.9%), Met (82.1 vs. 75.6%), Phe (81.4 vs. 76.4%), Thr (64.4 vs. 55.4%), Trp (66.3 vs. 54.9%), and Val (77.8 vs. 71.6%) in the CE were greater ($P < 0.05$) than in the PKE. The values for the SID of Lys in the CE and PKE (40.3 and 39.1%, respectively) were relatively less than those of other indispensable AA. In conclusion, the digestibility of CP and most AA in the CE was greater than in the PKE, and the values for the AID and SID of Lys were less than other indispensable AA in the CE and PKE.

Key Words: protein supplement, standardized ileal digestibility, swine

T301 Digestible tryptophan:lysine ratios and different protein sources in diets for barrows from 70 to 95 kg. C. Pereira[1], M. Hannas*[1], H. Rostagno[1], L. Albino[1], R. Rodrigueiro[2], J. Htoo[3], and J. Barrera[4], *[1]Federal University of Viçosa, Viçosa, Minas Gerais, Brazil, [2]Evonik Industries, Health & Nutrition, Animal Nutrition Services, São Paulo, São Paulo, Brazil, [3]Evonik Industries AG, Health & Nutrition, Animal Nutrition Services, Hanau-Wolfgang, Germany, [4]University of Tolima, Tolima, Peru.*

The objective of this trial was to evaluate the performance of barrows fed with 2 digestible tryptophan:lysine (Trp:Lys) ratios (18% or 21%) and 2 diets with different protein sources (soybean meal – SBM or soybean meal, meat and bone meal and feather meal – SBM-MBM-FM) during the finishing phase (70 to 95 kg). A total of 96 barrows (69.26 ± 4.97 kg) were distributed in a completely randomized block design. The treatments were arranged as 2 × 2 factorial (2 diets with different protein sources × 2 digestible Trp:Lys ratios) with 12 replicates and 2 animals per pen. The diets were formulated to meet or exceed the nutritional recommendations. The experimental period lasted 24 d and the parameters evaluated were final BW, ADFI, ADG and G:F. The results were analyzed using ANOVA procedure. The test used was F at the 5% significance level. No interaction ($P > 0.05$) was found between diets with different protein sources and Trp:Lys ratios on animal performance. The diets with different protein sources had no effect ($P > 0.05$) on final BW, ADFI, ADG and G:F. There was no significant ($P > 0.05$) effect of digestible Trp:Lys ratio on G:F, however, barrows fed diets with 21% digestible Trp:Lys ratio had better final BW ($P < 0.02$), ADFI ($P < 0.01$) and ADG ($P < 0.01$) than those fed with 18% digestible Trp:Lys ratio. The use of 21% of digestible Trp:Lys in diets resulted in better performance of pigs from 70 to 95 kg. For pigs from 70 to 95 kg the Trp:Lys requirement is greater than 18%. Also, barrows fed diets with SBM or SBM-MBM-FM, formulated on digestible amino basis, showed similar performance during the finishing phase.

Table 1. Growth performance of barrows from 70 to 95 kg

	Ingredient			Dig. Trp:Lys, %			
Item	SBM	SBM-MBM-FM	$P <$ [1]	18	21	$P <$ [1]	CV, %
Final BW, kg	92.62	93.24	NS	91.71	94.20	0.02	3.09
ADFI, g	2732	2724	NS	2650	2810	0.01	5.90
ADG, g	983	989	NS	946	1028	0.01	7.99
G:F, g/g	0.360	0.363	NS	0.357	0.366	NS	5.00

[1]ANOVA, F-test.

Key Words: digestible Trp:Lys ratio, barrow, protein source

T302 Digestible lysine and methionine + cystine levels on breast meat quality of broilers at 21 days old. C. H. F. Domingues*[1,3], K. F. Duarte[2,3], E. T. Santos[3], D. M. C. Castiblanco[3], T. C. O. Quadros[3], S. Sgavioli[3], J. C. R. Alva[3], T. G. Petrolli[3], O. M. Junqueira[4], and J. D. Messana[2,3], *[1]Fundacao de Amparo a Pesquisa do Estado de Sao Paulo FAPESP, Sao Paulo, SP, Brazil, [2]Coordenacao e Aperfeicoamento de Pessoal de Nivel Superior CAPES/PNPD, Brasilia, DF, Brazil, [3]Universidade Estadual Paulista Julio de Mesquita Filho, Jaboticabal, SP, Brazil, [4]Universidade Federal de Goias, Jatai, GO, Brazil.*

The aim of this study was evaluate different levels of digestible lysine and methionine + cystine on meat quality of pectoral muscle (Pectoralis major) of broilers at 21 d old. A total of 3,200 one-day-old male Cobb x Cobb 500 chicks were used, distributed in a completely randomized design in a factorial arrangement 2 × 5 (2 digestible lysine levels: 1.253 and 1.378% × 5 digestible methionine + cystine levels: 0.812, 0.860, 0.902, 0.947, and 0.992%) and 8 replicates of 40 birds each. At 21 d of age, 480 birds were culled to the achievement of sampling pectoral muscle, which were submitted to analysis of the following parameters of meat quality: Color (L* = lightness, a* = redness, and b* = yellowness), cook loss, shear force and pH values. There was no interaction ($P > 0.05$) of digestible lysine and methionine + cystine levels for any of the variables. There was an effect ($P < 0.05$) of digestible lysine levels on the meat color and shear force occurring highest rate of redness for birds that received the level of 1.253% digestible lysine when compared with those fed with diets containing 1.378% digestible lysine, while the opposite occurred with the shear force. The levels of digestible methionine + cystine did not influence ($P > 0.05$) the redness, yellowness, pH and cook loss of breast meat, however, there was a quadratic effect ($P < 0.05$) for lightness ($Y = 291.39 - 520.82x + 280.54x^2$, $R^2 = 0.94$), indicating 0.928% as the highest level of digestible methionine + cystine for this variable. It was observed a decreasing linear effect ($P < 0.05$) for shear force ($Y = 11.786 - 9.7403x$, $R^2 = 0.88$), with increased levels of digestible methionine + cystine feed. In conclusion, the results of this study suggest that diets with 1.253 and 1.378% digestible lysine levels improve redness and shear force respectively and 0.928% digestible methionine + cystine level improve the lightness.

Key Words: digestible amino acid, pectoral muscle, pH

T303 Determination of optimum amino acid to calorie ratio for grower and finisher pigs. A. Hassen*, B. Smith, C. Iiams, D. Rice, F. Owens, D. Jones, and T. Sauber, *DuPont Pioneer, Johnston, IA.*

Accurate diet formulation will minimize experimental error. This is critical for trials which require high sensitivity to experimental treatments. The objective of this study was to identify optimal corn-soy diet lysine:calorie ratios (LCR) for pigs reared in an environment that supports rapid growth (typically 0.9 to 1.25 kg/day from 25 to 120 kg BW). Individually-penned barrows (PIC Line 1055 females × Line 280 boars) were fed treatment diets in 3 growth phases: Grower (25 to 60 kg), Finisher1 (60 to 90 kg), and Finisher2 (90 to 120 kg). For each phase, diet ME was held constant and lysine concentration was increased in even increments of 0.11% across each of 6 treatments to achieve target ranges of 2.25 to 3.75 (grower), 1.75 to 3.25 (Finisher 1), and 1.25 to 2.75 (Finisher 2) for LCR (g lysine:Mcal ME). Twelve pigs were randomly assigned to each treatment in the Grower phase, and were fed to a constant BW before progressing to the next growth phase and dietary LCR treatment. Preceding phase dietary treatment was used as a blocking factor during re-randomization to the next set of 6 dietary treatments in each successive phase. Data within each phase were analyzed using linear and non-linear models to evaluate effects of treatment diets on gain-to-feed ratio (GF). Parameter estimates from linear models were used to estimate optimum GF and the corresponding LCR levels based on different approaches. For each phase, level of LCR produced a significant effect on GF and orthogonal contrasts of treatment effect suggested curvilinear relationships between GF and LCR. In all cases, the final prediction model included a concave-down quadratic curve; suggesting a unique maximum and a range of optimum animal performance values for the LCR used within each phase. Maximum GF (SE) for Grower, Finisher1, and Finisher2 were 0.57 (0.01), 0.44 (0.01), and 0.39 (0.01), respectively. The mean LCR at optimum performance ranged from 3.17 to 3.3, 2.41 to 2.80, and 2.11 to 2.45 for the respective phases. The estimates derived from the experiment will be used for formulation of diets for future trials in our facility.

Key Words: amino acid, energy, swine

T304 Digestible tryptophan:lysine ratios and different protein sources in diets for barrows from 30 to 65 kg. C. Pereira[1], M. Hannas*[1], H. Rostagno[1], L. Albino[1], R. Rodrigueiro[2], J. Htoo[3], and G. Viana[1], *[1]Federal University of Viçosa, Viçosa, Minas Gerais, Brazil, [2]Evonik Industries, Health & Nutrition, Animal Nutrition Services, São Paulo, São Paulo, Brazil, [3]Evonik Industries AG, Health & Nutrition, Animal Nutrition Services, Hanau-Wolfgang, Germany.*

A total of 96 barrows (30.14 ± 2.27 kg) were used to investigate the effects of 2 digestible tryptophan:lysine (Trp:Lys) ratios (18 or 21%) and 2 diets with different protein sources (soybean meal – SBM or soybean meal, meat and bone meal and feather meal – SBM-MBM-FM) on growth performance of barrows from 30 to 65 kg. Animals were distributed in a complete randomized block design and the treatments were arranged as 2 × 2 factorial (2 diets with different protein sources × 2 digestible Trp:Lys ratios) with 12 replicates and 2 animals per pen. The diets were formulated to meet or exceed the nutritional recommendations of Rostagno et al., 2011. The experimental period lasted 32 d and the parameters evaluated were final body weight (FBW), average daily feed intake (ADFI), average daily gain (ADG) and feed:gain ratio (F:G). There was no interaction ($P > 0.05$) between Trp:Lys ratios and the diets with different protein sources on pig performance. The SBM diet increased ADFI ($P < 0.03$), however, there was no effect ($P > 0.05$) of the experimental diets on FBW, ADG and F:G. Barrows fed 21% digestible Trp:Lys ratio had better ($P < 0.01$) FBW, ADG and F:G than those fed 18% Trp:Lys ratio. ADFI was not affected by Trp:Lys ratio ($P > 0.05$). Considering the performance of barrow from 30 to 65 kg, it is recommended the utilization 21% of digestible Trp:Lys ratio. Also, barrows fed diets with SBM or SBM-MBM-FM, formulated on digestible amino basis, showed similar performance during the growing phase.

Table 1. Growth performance of barrows from 30 to 65 kg

	Ingredient			Dig Trp:Lys, %			
Item	SBM	SBM-MBM-FM	$P <$ [1]	18	21	$P <$ [1]	CV
FBW, kg	64.13	63.55	NS	62.97	64.70	0.01	3.51
ADFI, g	2128	2045	0.03	2064	2109	NS	5.83
ADG, g	1064	1046	NS	1029	1081	0.01	6.56
F:G, g/g	2.002	1.957	NS	2.009	1.950	0.01	3.96

[1]ANOVA, F-test.

Key Words: digestible Trp:Lys ratio, barrow, protein source

T305 Oral administration of amino acids as energy sources for newborn piglets. N. E. Manzke[1], L. B. Scapini[2], W. Loyola[3], M. Kutschenko[4], J. M. Fontana[5], E. T. Nogueira[4], E. G. Xavier[1], A. Coldebella[3], and G. J. M. M. Lima*[3], *[1]Universidade Federal de Pelotas, Pelotas, RS, Brazil, [2]Universidade Federal do Parana, Palotina, PR, Brazil, [3]EMBRAPA, Concordia, SC, Brazil, [4]Ajinomoto, Sao Paulo, SP, Brazil, [5]Granja Fontana, Charrua, RS, Brazil.*

Amino acids have been supplemented in diets due to their beneficial effects on performance, health and immune status. Some of these occur because they may be readily available sources of energy, especially to young animals, which may face malnutrition after birth. This study was carried out to evaluate the effects of glutamine (Gln), glutamic acid (Glu) and AminoGut (Amg) supplementation on performance, immune response and blood parameters. Forty-seven litters, selected based on genotype and parity, were distributed according to a complete randomized block design. Within each litter, 4 piglets were chosen with body weights close to litter average. Treatments consisted of daily intragastric applications of 4-mL doses containing one of the following: Placebo: distilled water; Gln: 2 g L-glutamine; Glu: 2 g L-glutamic acid; Amg: 2 g of the commercial mixture of L-glutamine and L-glutamic acid. Animals were supplemented with treatments along the first 7 d of life with the first dose provided to piglets just after colostrum consumption. There were no treatment effects ($P > 0.10$) on individual weight and weight gain of piglets. Amino acid supplementation increased ($P = 0.06$) the diameter of the papule produced by *Phaseolus vulgaris* lectin skin test at 24 h after intradermal injection, compared with Placebo (6.12 mm). Amg (8.68 mm) and Glu (8.09 mm) showed the highest response for this variable ($P < 0.05$), at the same time as Amg promoted higher cell-mediated immunity than Gln (7.16 mm, $P < 0.05$) when compared with Placebo by *t*-test. There were no differences in plasmatic levels of glucose ($P = 0.40$) and creatinine ($P = 0.49$) among treatments. However, serum urea was significantly higher ($P < 0.0001$) in animals supplied with Gln, when compared with Glu, Amg and Placebo. Glu and Amg also increased blood urea compared with the Placebo group. Higher blood urea levels verified in amino acid supplemented piglets may suggest that the amounts supplied are above requirements. Despite there were no significant responses on piglet weight, amino acid supplementation provided better cell-mediated immunity, with a higher reaction shown by animals receiving Amg and Glu.

Key Words: glutamine, glutamic acid, AminoGut

T306 Effect of dietary lysine to energy ratio on growth performance and sensory characteristics of indigenous Venda chickens. O. J. Alabi*, J. W. Ng'ambi, and D. Norris, *University of Limpopo, Mankweng, Polokwane, South Africa.*

The study determined the effect of dietary lysine to energy ratio on optimal productivity, carcass and sensory characteristics of indigenous Venda chickens aged 8–13 weeks. A completely randomized design was used. One hundred and 60 female indigenous Venda chickens (BW 362 ± 10 g) were allocated to 4 dietary treatments. Each treatment was replicated 4 times and each replicate had 10 chickens. Four maize-soybeans based diets were formulated. Each treatment had similar dietary lysine (12 g/kg DM) but different energy levels (11, 12, 13 and 14 MJ ME/kg DM), thus, forming 4 dietary lysine to energy ratios (L:E) of 1.09, 1.00, 0.92 and 0.86, respectively. Data on chicken productivity, carcass characteristics (as percentages of live weights) and meat sensory attributes were measured. These data were analyzed using one way ANOVA. A quadratic curve estimate model was used to determine dietary lysine to energy ratio for optimum growth rate, feed intake, FCR, metabolizable energy, N-retention, relative carcass and sensory characteristic values. Results showed that dietary lysine to energy ratio of 0.88 supported optimum growth rate (17.89 g/bird/day), heart weight (0.76%) and meat flavor (4 points out of a 5-point hedonic scale). While a ratio of 0.99 g/MJ ME supported optimum feed intake (109.92 g/bird/day), FCR (6.05 g feed/g live weight gain), metabolizable energy value (11.33 MJ ME/kg), N- retention (1.63 g/bird/day), carcass (87.18%), breast meat (20.36%) and drumstick (12.00%). A higher ratio of 1.05 optimized liver (2.27%), wing (11.29%), gizzard (5.40%) and fat pad (2.84%). Meat tenderness and juiciness (3.25 points each out of a 5-point hedonic scale) were optimized at a ratio of 1.07. Thus, dietary L:E level for chicken production optimization depended on the particular parameter of interest. These findings have many implications on ration formulation for female indigenous Venda chickens.

Key Words: growth performance, lysine to energy ratio, optimization

T307 Evaluation of dietary glutamic acid plus glutamine levels on the growth performance of piglets. D. Lescano[1], L. Albino[1], M. Hannas[1], S. Salguero[1], M. Kutschenko[2], E. Nogueira[2], and H. Rostagno*[1], *[1]Federal University of Viçosa, Viçosa, MG, Brazil, [2]Ajinomoto of Brazil Ajinomoto Animal Nutrition, São Paulo, SP, Brazil.*

A study was conducted to evaluate the utilization of 4 dietary levels of a commercial product containing glutamic acid plus glutamine (min 95%) in diets for weanling pigs (18 d) to 46 d old. A total of 44 piglets were randomly assigned in a completely randomized block design into 4 treatments, 5 replicates and 2 or 3 pigs per experimental unit. The treatments were: T1 = 0.0%; T2 = 0.4%; T3 = 0.8% and T4 = 1.2% glutamic acid (Glu) plus glutamine (Gln). Diets were based on corn, soybean meal, pre-cooked corn, dairy products, blood plasma, L-lysine, L-threonine and DL-methionine. The experimental period lasted 28 d and the parameters evaluated were body weight, weight gain, feed intake and feed conversion ratio. The addition of Glu plus Gln improved linearly ($P < 0.05$) daily feed intake (DFI) and feed conversion ratio (F:G) of the piglets. There were also linear ($P < 0.01$) and quadratic effects ($P < 0.04$) of dietary Glu plus Gln level on final body weight (FBW), total weight gain (TWG) and daily weight gain (DWG) of the piglets (Table 1). It is concluded that the best dietary Glu plus Gln level is 0.8% for weanling piglets from 18 to 46 days of age.

Table 1. Growth performance of weanling piglets from 18 to 46 days of age

	Glu plus Gln (%)				Regression		
Parameter	0.0	0.4	0.8	1.2	Linear	Quadratic	CV (%)
BW initial, kg	5.24	5.24	5.22	5.06	NS	NS	3.22
FBW, kg	15.41	16.55	17.33	16.95	<0.002	0.03	4.24
DFI, kg	0.48	0.55	0.52	0.54	<0.04	NS	6.13
TWG, kg	10.16	11.30	12.11	11.88	<0.001	<0.04	6.13
DWG, kg	0.36	0.40	0.43	0.42	<0.001	<0.04	6.13
F:G ratio	1.34	1.33	1.17	1.23	<0.002	NS	5.12

NS = not significant ($P > 0.05$).

Key Words: piglet, growth performance, glutamic acid plus glutamine

T308 Effect of different space allocation and energy levels on growth performance and nutrient digestibility in growing-finishing pigs. J. Li, J. P. Lee, and I. H. Kim*, *Department of Animal Resource & Science, Dankook University, Cheonan, Choognam, South Korea.*

This study was conducted to investigate the effects of different space allocation (SA) and dietary ME levels on growth performance, apparent total tract nutrient digestibility (ATTD) in growing-finishing pigs. Data were collected from 4 growing, early (1 to 5 wk) and late (6 to 10 wk) finishing pigs experiments conducted from 2010 to 2012, and each experiment lasted for 5 wk. In each experiment, growing pigs (BW = 27.10 ± 1.60 kg) and finishing pigs (BW = 67.43 ± 1.97 kg) were fed 2 ME levels of corn/soybean-meal based diets (growing phase:3400 vs. 3550 kcal/kg; finishing phase:3300 vs. 3450 kcal/kg) by addition of 3% soybean oil. Pigs were given 0.80 and 0.60 m^2/pig for growing phase, and 1.08 and 0.81 m^2/pig for finishing phase. All statistical analysis was conducted as 2 × 2 factorial arrangement using the GLM procedure of SAS (1996) with pen as the experimental unit. The probability level of $P < 0.05$ was regarded as statistically significant. In growing pig experiments, the effect of low SA decreased ($P < 0.05$) ADG, ADFI, and G:F. The high ME level decreased ($P < 0.05$) ADFI, increase ($P < 0.05$) G:F and ATTD of energy. There was an interactive effect between SA and ME on ADFI, with the pigs fed high ME diet and in greater SA had lower ($P < 0.05$) ADFI than those fed control diet in low SA. In early finishing pig experiments, pigs given low SA consumed less feed, grew slower and had lower G:F ($P < 0.05$). Feed intake were reduced with high ME diet compared with control diet ($P < 0.05$). The ADFI was lowered ($P < 0.05$) by the interaction effect of greater SA and high ME diet compared with control diet and low SA. Late finishing pigs given low SA had lower ADG, ADFI, and G:F. No effect ($P > 0.05$) of ME level and their interaction was observed to influence growth performance and nutrient digestibility. In conclusion, results indicated reduction in ADFI, ADG, and G:F for pigs given low SA; the addition of high ME diet were found to improve feed efficiency in growing and early finishing pigs. Higher ME level was able to counteract the detrimental effect of SA to a certain extent.

Key Words: energy level, growing-finishing pig, space allocation

T309 Effect of vitamin E supplementation on its hepatic concentration in broiler chicken. M. A. Pompeu*[1], N. C. Baião[1], L. J. C. Lara[1], V. M. Barbosa[3], J. S. R. Rocha[1], P. C. Cardeal[1], R. C. Andrade[1], C. E. Cunha[1], C. W. R. Gondim[1], and L. F. L. Cavalcanti[1,2], *[1]Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil, [2]Texas A&M, College Station, [3]Universidade Federal da Bahia, Salvador, Bahia, Brazil.*

The main goal of vitamin E (VE) supplementation on poultry diets is to ensure good performance and welfare, rather than to attend the nutritional requirements. The liver is the main regulator of the body's VE levels and it appears to be the major site of VE metabolism and excretion, making it a good indicator of VE's body status. This study aimed to evaluate the VE liver concentration (VELC, mg/kg) in broilers with 21 or 39 d of age, fed with increasing levels of VE supplementation. The initial phase (IP) comprehended the birth to 21 d of age in which 15 animals were supplemented with 5 levels (3 animals/level) of VE, to achieve diets concentrations of 10, 30, 50, 75 or 100 mg/kg of DM. Additionally, another 15 animals (3 animals/level) were fed with the same supplementation levels from 21 to 39 d of age during the growth phase (GP). At the end of each phase, the animals were slaughtered and their livers were collected. The VELC was assessed by HPLC. A linear cubic regression was fitted to the IP ($VELC = a+b \times D+c \times D^2+d \times D^3$), whereas nonlinear logistic model was fitted to the GP phase [$VELC = A \times (1-B \times e^{-k \times D})^{-1}$]; where, A = asymptote (mg/kg), B = constant related to the intercept (mg/kg), k = growth rate (1/mg/kg), D = VE concentration in the diet (mg/kg). For both phases, was observed an increase on VELC when VE levels were increased from 10 to 30 mg/kg. However, for IP it readily tended to a plateau (61.99 ± 13.3 mg/kg) until the highest VE level, when it abruptly reached 135.3 ± 28.6 mg/kg, justifying the fitted cubic model ($a = -20.2 \pm 18.1$, $b = 4.3 \pm 1.5$, $c = -0.08 \pm 0.03$, $d = 0.0005 \pm 0.0001$, $r^2 = 0.89$). For the GP this plateau was only achieved when the diet VE levels reached 50 mg/kg, with a VELC close to the estimated A parameter of the logistic model ($A = 112.6 \pm 9.8$, $B = -151.53 \pm 429.4$, $k = 0.15 \pm 0.1$, Residual SE = 23.73). For the IP, the VE supplementation above 75mg/kg seems to overload the liver metabolism capacity, resulting in VE accumulation, what did not happen in the GP. The observed plateaus may be related to a balance between liver requirement and utilization, and the decision of the exact VE diet levels below those plateaus should be made based on additional performance results.

Key Words: diet, poultry, tocopherol

T313 Effects of a dietary antioxidant blend and vitamin E on growth performance and meat quality in broilers fed a high oxidants diet. T. Lu*[1], R. A. Dalloul[1], J. Zhao[2], and A. F. Harper[1], *[1]Virginia Tech, Blacksburg, [2]Novus International Inc., St. Charles, MO.*

The aim of this study was to determine the effects of a dietary antioxidant (AOX) (Agrado Plus, Novus Inc.) and vitamin E (VE) on performance and meat quality in broilers fed a diet high in oxidants. Cobb 500 male broilers (n = 1200, d 0) were randomly distributed into 60 floor pens across 6 treatments with 10 replicate pens of 20 chicks each. Treatments included (1) NC [negative control, VE at 10 IU/kg, 3% oxidized oil, 3% high PUFA source], (2) VE (NC + VE at 200 IU/kg), (3) AOX (NC + AOX at 135 mg/kg), (4) VE+AOX (NC + VE at 200 IU/kg + AOX at 135 mg/kg), (5) SC (standard control, VE at 10 IU/kg, 3% fresh oil, no high PUFA), and (6) PC (positive control, SC + AOX at 135 mg/kg). Performance parameters were measured on d 10, 21 and 42 and carcass quality assessed on d 42 by measuring drip loss, pH, and lactate levels. Data were analyzed using Glimmix of SAS with Tukey's multiple comparison. Compared with the SC birds, the NC, VE, AOX, VE+AOX groups had larger BW (855.4, 859.4, 901.3 and 889.5 vs. 785.2 g), ADG (38.6, 38.8, 40.8 and 40.2 vs. 35.3 g) and ADFI (58.2, 58.6, 60.9 and 60.1 vs. 53.1 g) from d 0 through d 21 ($P < 0.05$). However, the growth of birds fed the VE treatment fell behind that of other treatments (NC, AOX, AOX + VE, SC and PC, $P < 0.05$) during the 42 d trial. The AOX fed birds (AOX and VE+AOX) had heavier BW and ADG from d 10 forward, except that the SC treatment had the highest ADG from d 22–42 ($P < 0.05$). The AOX birds had the best G:F on d 10 and d 42, or throughout the experiment ($P < 0.05$). The high oxidants diet induced a higher drip loss (2.63 vs. 1.33, 1.24, 2.56, 1.46 and 2.08%) in NC fed birds, which was associated with a lower ultimate pH (5.91 vs. 5.95, 5.96, 6.06, 5.98 and 5.88) and the highest lactate concentration (76.48 vs. 68.48, 64.69, 58.44, 60.73 and 74.00 mmol/g) compared with VE, AOX, AOX + VE, SC and PC ($P < 0.05$). In conclusion, dietary addition of AOX or AOX plus VE was effective in improving growth. The addition of AOX alone and high VE reduced drip loss, but VE may exert a pro-oxidant property in the finisher phase as measured by growth.

Key Words: broiler, antioxidant, PUFA

T314 Pig bone trait responses to maternal vitamin D intake depend on nursery diet vitamin D and P concentrations. L. A. Rortvedt-Amundson* and T. D. Crenshaw, *University of Wisconsin-Madison, Madison.*

In earlier experiments, kyphosis was induced and bone mineral density (BMD) was reduced in pigs produced by sows fed no supplemental vitamin D_3 or minimum levels (325 IU/kg). This experiment was designed to evaluate carryover effects of maternal vitamin D_3 (D) intake on pig bone traits as implied by earlier results. In 2 trials, gilts were fed 1 of 3 diets (n = 6, 8, or 9 gilts/treatment, respectively) with 0, 325, or 1750 IU D/kg from breeding through lactation. Using a nested design, pigs within a litter at weaning (23 ± 2 d) were assigned to pens and fed an adjustment diet with no supplemental D for 1 wk. Then for 4 wk, pigs were fed 1 of 4 nursery diets (arranged as a 2 × 2 factorial) with 0 (-D) or 280 (+D) IU D/kg, each with 95% (95P) or 120% (120P) of the P requirement. Pigs were killed before colostrum consumption at birth (n = 23), weaning (n = 22), and a subsample at the end of the nursery (n = 185) for DXA (GE Lunar Prodigy) scans to determine whole body bone mineral content (BMC, g/pig) and BMD (g/cm^2). Individual femurs were scanned. Femur BMC and BMD responses were similar to pig DXA responses. Live births per litter (n = 14.3, 14.4, 14.1) were not different among maternal treatments. At birth and weaning, no differences due to maternal diet were detected in pig BMC and BMD. Pig BMC and BMD responses to nursery diets were dependent upon maternal diets (maternal × nursery diet interaction, $P < 0.05$). The interaction confirmed a carryover effect of maternal diets. BMD was reduced in pigs fed –D120P but increased in pigs fed +D120P nursery diets if produced by gilts fed 0 or 325 IU D/kg. However, BMD increased in pigs fed –D120P nursery diets if produced by gilts fed 1750 IU D/kg. Thus, maternal dietary D intake affects neonatal bone traits at 8 wk of age even though maternal dietary responses were not evident in pigs at birth and weaning.

Table 1.

Item	Maternal diet	Nursery diets				SEM[1]
		−D95P	−D120P	+D95P	+D120P	
BMD, g/cm^2	0	0.342	0.323	0.386	0.430	
	325	0.459	0.386	0.462	0.558	
	1750	0.473	0.580	0.515	0.514	0.028
BMC, g/pig	0	213	179	237	278	
	325	259	232	246	328	
	1750	276	310	270	312	12

[1]SEM pooled across 12 dietary treatments.

Key Words: phosphorus, maternal carryover, DXA

T315 True total-tract digestibility of P in monocalcium phosphate for 15- and 25-kg pigs. H. Zhai* and O. Adeola, *Purdue University, West Lafayette, IN.*

Two experiments were conducted to determine the true total-tract digestibility (TTTD) of P in monocalcium phosphate using the regression method. Forty-eight barrows (initial BW 15.7 ± 1.53 kg) in Exp. 1 and 24 barrows (initial BW 25.2 ± 1.04 kg) in Exp. 2 were used in a randomized complete block design with 6 replicate pigs per dietary treatment. Eight dietary treatments were established in Exp. 1 by incremental addition of 3.5 g/kg of monocalcium phosphate to a 3.3 g P/kg corn-soybean meal-based diet. In Exp. 2, 4 dietary treatments were constituted by incremental addition of 2.4 g/kg of monocalcium phosphate to a 2.96 g P/kg corn-soybean meal-based diet. In both experiments, limestone was added accordingly to maintain a constant Ca:P ratio of 1.25:1 across all diets. A 5-d adjustment period preceded a 5-d total collection of feces, and ferric oxide was used as a marker to time the initiation and termination of fecal collection. The results of Exp.1 showed that dietary P intake, fecal P output, and digested P increased linearly ($P < 0.001$) with the increasing supplementation of monocalcium phosphate. The regression of daily digested P against daily P intake gave a TTTD of 67.5% for P in monocalcium phosphate. The results of Exp. 2 showed that dietary P intake, fecal P output, and digested P increased linearly ($P < 0.05$) with the increasing supplementation of monocalcium phosphate. Regressing daily digested P against daily P intake gave the TTTD of 84.3% for P in monocalcium phosphate. In conclusion, the TTTD of P in monocalcium phosphate was determined to be 67.5 and 84.3% for, pigs with BW of 15 and 25 kg, respectively.

Key Words: monocalcium phosphate, pig, true total-tract digestibility

Physiology and Endocrinology I

T316 Effects of supplementation with different PUFA during the postpartum periods influence ovarian follicle size and number in lactating dairy cows. E. Dirandeh*[1], A. Towhidi[1], Z. Ansari Pirsaraei[2], M. Ganjkhanlou[1], S. Zeinoaldini[1], T. Saberifar[1], A. Rezaei Roodbari[1], M. A. Roodbari Shahmiri[3], and A. R. Zarenezhad[3], *[1]University of Tehran, Karaj, Alborz, Iran, [2]Sari Agricultural Sciences & Natural Resources University, Sari, Mazandaran, Iran, [3]Mahdasht Milk & Meat Company, Sari, Mazandaran, Iran.*

The objectives were to determine if a diet enriched in α-linolenic acid (n-3), or linolenic acid (n-6) would influence ovarian function in lactating dairy cows. Thirty high-yielding multiparous Holstein dairy cows without clinical illnesses were blocked according to calving date and parity. Cows were assigned randomly to be fed: (1) soybean whole roast (S, n = 10), or (2) linseed (L, n = 10), or 3) palm oil as a source of mostly saturated fatty acids (FA), (C, n = 10) from calving until d 60 postpartum (dpp). Supplementation of FA was at 1.5% of dietary dry matter, and there was no difference between groups (mean ± SEM) in parity (3.0 ± 1.90) or BCS at calving (3.2 ± 0.07). At 30 and 44 d postpartum cows received an injection of PGF2α for estrous synchronization Ultrasound measurements of follicle numbers were performed in 30 cows (n = 10 per group) on alternate days, from the day that second PGF2α inject until the d 10 of next estrous cycle (d 0 = day of estrus). The characteristics and fate of the first follicular wave was monitored using a real-time linear scanning ultrasound diagnostic system (B mode; Pie medical, Falco 100; 8 MHz transducer). Data were analyzed using the MIXED procedure of SAS. Results showed that the ovulatory follicle on the day preceding estrus synchronization (before the first AI, d 0) was larger in groups S (16.14 ± 0.91 mm) and L (15.24 ± 0.75 mm) compared with C (13.20 ± 0.86 mm; $P < 0.05$) but there were no significant differences between groups S and L. Mean number of small follicles (<5 mm), medium follicle (5-10 mm) and diameter of subordinate follicle were not affected by diets ($P < 0.05$). Cows offered diet S and L had a greater ($P = 0.037$) total number of follicles, number of large (>10 mm) follicles and tended to have a greater ($P = 0.064$) than cows offered diet C. In conclusion, these data demonstrate that n-3 and n-6 fatty acids increased follicle size and number but there was no difference among type of supplemental fatty acid.

Key Words: dairy cow, follicle, ultrasonography

T317 Feeding n-6 fatty acids during 40 dpp and shift to n-3 fatty acids from 40 to 120 dpp can improve fertility in lactating dairy cows. E. Dirandeh*[1], A. Towhidi[1], Z. Ansari pirsaraei[2], M. Ganjkhanlou[1], S. Zeinoaldini[1], A. Rezaei Roodbari[3], M. A. Roodbari Shahmiri[3], and A. R. Zarenezhad[3], *[1]University of Tehran, Karaj, Alborz, Iran, [2]Sari Agricultural Sciences & Natural Resources University, Sari, Mazandaran, Iran, [3]Mahdasht Milk & Meat Company, Sari, Mazandaran, Iran.*

The objectives were to determine if a diet enriched in α-linolenic acid (n-3), or linoleic acid (n-6) would influence reproductive performance in lactating dairy cows. Ninety high-yielding multiparous Holstein dairy cows with overtly clinical illnesses were blocked according to calving date and parity. Cows were assigned randomly to be fed: (1) soybean whole roast (S, n = 30), or (2) linseed (L, n = 30), or 3) palm oil as a source of saturated fatty acid (C, n = 30) from calving until first estrus after d 40 postpartum (dpp) and then half of the cows in each treatment group were switched to receive either L or C from first estrus after d 40 to 120 dpp. There was no difference between groups (mean ± SEM) in parity (3.0 ± 1.90) or BCS at calving (3.2 ± 0.07). Pregnancy was evaluated at 40 d after AI, and pregnant cows had their pregnancy reconfirmed at 60 and days after AI. All of the reproductive responses (binary responses) were analyzed by Glimmix. Result showed uterine involution in cows fed soybean whole roast occurred 1.2 earlier than the other groups ($P < 0.05$). Heat detection rate was not different between groups. For SL (% 44) and LL (% 45) groups compared with other groups pregnancy rate to first insemination was higher ($P = 0.001$); pregnancy rate to all inseminations was higher ($P = 0.019$) in SL (% 80) group and lower in LC (% 57) and CC (% 47) groups compared with other groups ($P = 00.1$). Conception rate tended to be higher ($P = 0.03$) in SL (% 84) group compared with other groups. There was a lower rate of early (d 0 to 24) embryo survival in SC (% 18) and CC (% 25) group compared with other groups ($P = 0.12$). In conclusion, feeding n-6 fatty acids during 40 dpp and shift to n-3 fatty acids from 40 to 120 dpp can improve fertility in lactating dairy cows.

Key Words: dairy cow, n-6 and n-3 fatty acids, pregnancy losses

T318 Presynchronization with PGF_{2a} and GnRH on the same day, 7 d prior to Ovsynch, allowed for similar pregnancies/AI compared with Presynch-10/Ovsynch. J. P. Martins*[1], M. J. T. Acevedo[1], T. O. Cunha[1], C. Piterini[1], M. R. Yousuf[1], K. Nobis[2], and J. R. Pursley[1], *[1]Department of Animal Science, Michigan State University, East Lansing, [2]Nobis Dairy Farm, St. Johns, MI.*

Fertility of dairy cows treated with Ovsynch is enhanced when the 1st GnRH of Ovsynch induces ovulation on d 6 or 7 of the estrous cycle, and PGF_{2a} (PG) 1 wk later, induces luteolysis. Current pre-synchrony programs that allow Ovsynch to be initiated on d 6 or 7 of the estrous cycle can be either logistically challenging for reproductive management personnel or can significantly lengthen duration of the entire program. The hypothesis of this experiment was that simplification of a Presynch program through the combination of PG (0.5 mg cloprostenol) and GnRH (0.1 mg gonadorelin diacetate tetrahydrate) on the same day, 7 d before Ovsynch, would allow for similar pregnancies/AI compared with Presynch-10. Lactating dairy cows (n = 444) 41 to 47 DIM were assigned in a random fashion to 2 treatments within 1st and 2nd+ parities for 1st service. Control cows received Presynch-10/Ovsynch consisting of the following: PG −14 d – PG −10 d – GnRH −7 d – PG −56 h – GnRH −16 h - AI. Treated cows received PG and GnRH - 7d – GnRH - 7 d – PG −56 h – GnRH −16 – AI. All cows received a 2nd injection of PG 24 h after the PG of Ovsynch to enhance complete luteolysis. All cows received AI between 75 and 81 DIM. Blood was collected to assess circulating concentrations of progesterone, and number of corpora lutea were recorded using ultrasonography, on d of PG of Ovsynch. Pregnancies/AI at 28 d post-AI were similar in controls compared with treated cows (45 vs. 45%). There was no effect of treatment on parity. There were no differences in pregnancy/AI between 1st and 2nd+ parities when treatments were combined (47 vs. 44%). Serum concentrations of progesterone were different in 1st parity, and similar in 2nd+ parity, control vs. treated cows (5.9 vs. 5.1 and 6.28 vs. 5.96 ng/mL). Percent of cows with >1 CL at time of PG was greater in 2nd+ parity treated vs. controls (89 vs. 75) and not different in 1st parity cows (65 vs. 70). In summary, administering both PG and GnRH on the same day, 7 d before the start of Ovsynch, appears to be a simple alternative that keeps pregnancies/AI to that of Presynch-10/Ovsynch.

Key Words: dairy, Ovsynch, fertility

T319 Effect of cloprostenol during early corpora lutea development on circulating concentrations of progesterone in breeding age dairy heifers. J. P. Martins*, M. J. T. Acevedo, C. Piterini, T. O. Cunha, and J. R. Pursley, *Department of Animal Science, Michigan State University, East Lansing.*

As part of an overarching objective to create a low progesterone environment during growth of the pre-ovulatory follicle in heifers to determine the effect of low progesterone on fertility parameters, we tested the effect of cloprostenol administration on early corpora lutea (CL) function. Dairy heifers between 12 and 13 mo of age were pre-synchronized to ensure all heifers were on d 6 of the estrous cycle at the start of the Ovsynch program. Only heifers that responded to the following strategy with CL regression and ovulation determined using ultrasound were utilized: 0.5 mg cloprostenol (PG)–2d - 0.1 mg GnRH – 6d - GnRH (G1; 1st GnRH of Ovsynch). Heifers (n = 164) that responded to the pre-synchrony injections were randomly assigned to 4 groups: high progesterone control (HPC), low progesterone control (LPC), and treatments P2 and P3. LPC, P2 and P3 received PG 1 d after G1 to regress all d 7 CL. Heifers from these groups had 1 new CL growing during the treatment period. Groups P2 and P3 received treatments of PG 2 and 3 d after G1, respectively. HPC did not receive PG on d 1 following G1, thus had a mature and a new CL growing during the treatment period. Blood samples were collected in all heifers on d 7 and in a subset of heifers on d 1, 2, 3, 4 (n = 88) after G1 to analyze circulating concentrations of progesterone. Pre-ovulatory follicle size (12.9 ± 0.1 mm; $P = 0.9$) at G1 and mean progesterone concentrations on d 1 (3.40 ± 0.15 ng/mL; $P = 0.9$) did not differ between randomized groups. Mean serum progesterone concentrations on d 7 were 8.23 (±0.43), 2.52 (±0.35), 1.53 (±0.20), and 1.24 (±0.15) ng/mL for HPC, LPC, P2, and P3, respectively. HPC had greater ($P < 0.001$) concentrations of progesterone compared with LPC, P2 and P3 on d 2, 3, 4 and 7 following G1. LPC had greater progesterone concentrations on d 7 than P3 ($P = 0.01$) and tended to be greater than P2 ($P = 0.08$). In summary, cloprostenol treatments during early corpus luteum development reduced circulating progesterone concentrations to sub-normal luteal levels compared with both high progesterone and low progesterone controls.

Key Words: dairy heifer, corpora lutea, progesterone

T320 Comparison of 200 µg of GnRH versus 1000 IU hCG in Beefmaster and Brahman Cattle using an Ovsynch protocol. C. E. Ferguson*[1], G. Richey[1], A. McDuff[1], and D. J. Kesler[2], *[1]McNeese State University, Lake Charles, LA, [2]University of Illinois, Champaign-Urbana.*

Previous research has reported 200 µg dose of GnRH at time of AI can improve pregnancy rates in *Bos indicus*-influenced cattle. This experiment was designed to compare the effect of 1000 IU of hCG versus the increased dose of GnRH on pregnancy rate in *Bos indicus*-influenced cattle. In the study, 4 groups of cattle were used; pure-bred Brahman (BR) heifers (n = 64) between 14 and 18 mo of age from Texas, Beefmaster (BM) lactating mature cows (n = 29) ~60 d postpartum from Louisiana, BM lactating mature cows (n = 50) from Florida, and BM heifers (n = 50) between 14 to 18 mo of age from Florida. All females were synchronized using an Ovsynch + CIDR protocol. At 48 h following $PGF_{2\alpha}$ females were randomly selected to receive either 200 µg GnRH or 1000 IU hCG and then artificially inseminated (AI) 15 to 20 h later for BR heifers or ~12 h following treatment for BM heifers or cows. The BR heifers were bred later than BM heifers because they were inseminated with sex-sorted semen while BM heifers received conventional semen. Each group was evaluated via ultrasonography at ~30 d post-AI to determine pregnancy. Statistical analysis was performed in SAS and a chi-squared test was used to determine differences between pregnancy rates. There was no difference ($P > 0.05$) in pregnancy rates between 200 µg GnRH versus 1000 IU hCG in *Bos indicus*-influenced cattle. The pregnancy rates for BR heifers was (GnRH, 3/18, 8% versus hCG 7/39, 18%), for lactating BM cows (from LA) was (GnRH 17/30, 57% versus hCG 9/15, 60%), for lactating BM cows (from FL) was (GnRH 17/30, 57% versus hCG 11/20, 55%) and for BM heifers was (GnRH 12/25, 48% versus 13/25, 52%). There was a significant effect ($P < 0.05$) of time from GnRH or hCG to AI in BR heifers bred with sexed semen on pregnancy rates with 60% of all pregnancies occurring with AI 17 to 18 h post GnRH or hCG. These results indicate that 1000 IU hCG is a cost effective alternative to replace the use of 200 µg GnRH in timed-AI protocols for *Bos indicus*-influenced cattle.

Key Words: GnRH, hCG, Ovsynch

T321 Effect of prostaglandin $F_{2\alpha}$ on growth of *Mycoplasma bovis* associated with bovine mastitis. A. Ahmadzadeh*[1], L. Fox[2], M. McGuire[1], and K. Carnahan[1], *[1]University of Idaho, Moscow, [2]Washington State University, Pullman.*

Mycoplasma bovis (*M. bovis*) is a major pathogen that is inherently refractory to antibiotics. Certain fatty acids have been shown to inhibit the growth of mastitis pathogens such as *Staphylococcus aureus*. In vitro experiments were conducted to determine the effects of prostaglandin $F_{2\alpha}$ ($PGF_{2\alpha}$) on growth of *M. bovis*. Five strains of *M. bovis* bovine origin were selected for the study. Two strains were reference strains (ATCC 25025 and 25523) and the other strains were isolated from diseased cattle. Isolates were cultured and suspended in saline to achieve an optical density of 0.2 at 520 nm, a suspension of approximately 10^7 to 2×10^8 cfu/mL. Subsequently, *M. bovis* suspensions were incubated in special culture media containing $PGF_{2\alpha}$ (dinoprost tromethamine) at final concentrations of 0 (control), 2, 4, and 8 mg/mL, for 8 h at 37°C in triplicate. A sample from each treatment group was obtained and cultured for 10 d and bacterial growth assessed as cfu. Data were analyzed by ANOVA and the model included the effect of treatment, strain, and their interaction. Treatment affected ($P < 0.01$) *M. bovis* growth and mean cfu decreased with concentrations of $PGF_{2\alpha}$ at 4 and 8 mg/mL (43.6, 42.1, 24.3, 7.8 [±1.1] for 0, 2, 4, 8 mg/mL, respectively). However, an effect of treatment × strain on mean cfu was detected ($P < 0.05$), indicating that the effect of $PGF_{2\alpha}$ on bacterial growth was not consistent across strains. Overall, the 2 mg/ml $PGF_{2\alpha}$ decreased ($P < 0.01$) cfu only in 2 strains compared with control whereas 4 and 8 mg/mL $PGF_{2\alpha}$ decreased ($P < 0.05$) cfu in all strains compared with control. These results provide evidence, for the first time, that $PGF_{2\alpha}$, in the form of dinoprost tromethamine, has inhibitory effects on growth of *M. bovis*, and this bacteriostatic effect appears to be strain and dose dependent.

Key Words: *Mycoplasma*, prostaglandin $F_{2\alpha}$, bacteriostatic

T322 Inclusion of bovine somatotropin in fixed-time AI protocols for *Bos indicus* beef cows. J. P. Albuquerque[1], R. F. Cooke[2], H. P. Dias[1], I. C. Bueno[1], A. D. P. Rodrigues[1], and J. L. M. Vasconcelos*[1], *[1]UNESP - Faculdade de Medicina Veterinária e Zootecnia, Botucatu, São Paulo, Brazil, [2]Oregon State University, Eastern Oregon Agricultural Research Center, Burns.*

Two experiments evaluated the effects of bovine somatotropin (ST) on pregnancy per AI of lactating Nelore (*Bos indicus*) cows assigned to the following estrus synchronization + fixed-time AI (FTAI) protocol: 2 mg injection of estradiol benzoate and insertion of intravaginal progesterone releasing device (CIDR) on d 0, 12.5 mg injection of $PGF2_{\alpha}$ on d

7, CIDR removal in addition to 0.6 mg of estradiol cypionate and 300 IU of eCG on d 9, and FTAI on d 11. Pregnancy status was verified via transrectal ultrasonography 30 d after FTAI. Data were analyzed with the PROC GLIMMIX of SAS. In Exp. 1, 896 cows (primiparous, n = 371; multiparous, n = 525) were randomly assigned to receive, concurrently with FTAI, 1 of 3 treatments: 1) 167 mg injection (s.c.) of sometribove zinc (bST167; n = 304), 2) 333 mg injection (s.c.) of sometribove zinc (bST333; n = 298), or 3) no injection (control; n = 294). Control cows had reduced pregnancy per AI compared with bST167 ($P = 0.08$) and bST333 ($P = 0.05$) cows (42.1, 49.0, and 49.8% of pregnant/inseminated cows, respectively; SEM = 4.0%), whereas no differences were detected ($P = 0.88$) between bST167 and bST333 cows. In Exp. 2, 290 cows (primiparous, n = 81; multiparous, n = 209) were randomly assigned to receive 333 mg of sometribove zinc (s.c.) at the beginning of the estrus synchronization protocol and at FTAI (bST, n = 111), or no injection (control; n = 179). Pregnancy per AI was similar ($P = 0.94$) between bST and control cows (37.6 and 38.1% of pregnant/inseminated cows, respectively; SEM = 4.8%). Hence, administration of bovine ST at FTAI enhanced pregnancy per AI in Nelore beef cows, independently of parity or dose evaluated. Conversely, 2 injections containing 333 mg of sometribove zinc and administered at the beginning and end of the estrus synchronization + FTAI protocol failed to improve pregnancy per AI in Nelore beef cows. The reason for this latter outcome is unknown, but may be attributed to increased milk production, as well as excessive circulating IGF-I and insulin concentrations that impaired, respectively, synchrony between embryonic/maternal tissues and oocyte quality in bST cows.

Key Words: bovine somatotropin, beef cows, artificial insemination

T325 Establishment of primary culture of omasal epithelial cells from newborn calves and detection of function for peptide absorption. Q. B. Xu*[1,2], H. Y. Liu[1,2], Y. M. Xie[1,2], Y. M. Wu[1,2], and J. X. Liu[1,2], *[1]Institute of Dairy Science, College of Animal Sciences, Hangzhou, China. [2]MoE Key Laboratory of Molecular Animal Nutrition, Zhejiang University, Hangzhou, China.*

It has been proved that small peptides can be absorbed in bovine forestomachs, especially omasum. However, little information is available on small peptide absorption by bovine omasal epithelial cells (OE cells). In this study, the bovine omasal tissues obtained from newborn Chinese Holstein calves were digested with 2.5% trypsin solution to obtain the OE cells. The isolated cells were then cultured in DMEM medium containing 5% fetal bovine serum, 5 μg/mL insulin, 10 ng/mL epidermal growth factor and 1% penicillin-streptomycin. Morphological observation revealed that the cultured cells displayed a homogeneous epithelial cell-like morphology as cobblestone with few fibroblasts visible. The OE cells possessed morphological features of desmosomes, tight junctions and microvilli. Immunocytochemistry assay showed that the cultured cells were cytokeratin 18 positive, indicating that they were omasal epithelial cells. These cells had normal growth properties with corresponding growth curve, and could be stably cultured for 10 passages. The transcriptional expression of peptide transporter 1 gene was detected in OE cells. To evaluate their function for absorption of small peptides, the OE cells were incubated with glycylsarcosine under different conditions. The glycylsarcosine could be absorbed intact into the OE cells in vitro and the absorption was dependent on concentration, time and temperature. From these results, it is inferred that peptide transporter 1 may play an important role in peptide absorption in the OE cells, and that the culture system of OE cells can be served as a useful in vitro model to study absorption of small peptides in bovine omasum.

Key Words: bovine omasal epithelial cells, primary culture, small peptide absorption

T326 Prepartum supplementation of beef cows: Hepatic and muscle gene expression of the offspring at weaning. M. Carriquiry*[1], J. Laporta[1], F. Pereyra[1], A. Astessiano[1], G. Quintans[2], and R. Perez-Clariget[1], *[1]Facultad de Agronomia, UDELAR, Montevideo, Uruguay, [2]Instituto Nacional de Investigaciones Agropecuarias, Treinta y Tres, Uruguay.*

The effect of supplementation during the last month of gestation on plasma IGF-I, muscle fiber characteristics and hepatic muscle gene expression was examined on multiparous beef cow offspring. Cows, ranked by body weight (BW) and body condition score, were blocked by calving day and assigned randomly to control (CON) or supplement (SUP) treatments. All cows were grazing native pastures (1200 kg DM/ha, 8% CP, 67% NDF) and supplemented cows were offered (1 kg/100 kg BW, 4.5 kg/d) whole rice-bran (15.2% CP, 31.7% NDF, 15.1%EE) during the last 40 d of gestation. Blood samples were obtained at 30, 90 and 180 (weaning) days and liver and muscle biopsies were collected at weaning in 10 crossbred (Angus/Hereford; n = 5/treatment) male calves. Gene expression was measured by SYBR-Green real time PCR using ACTB and HPRT as internal control genes. Data were analyzed in a mixed model with treatment as a fixed effect and block as a random effect. Data were considered to differ when $P < 0.05$ and are reported as lsmeans ± SEM. Prepartum supplementation did not affect calf BW at birth (40 ± 4 kg) or at weaning (183.3 ± 3 kg). Plasma IGF-I was greater in SUP than CON offspring (160.4 vs. 117.3 ± 10.4 ng/mL). At weaning, Semitendinous muscle fiber density was greater in SUP than CON offspring (2.9×10^{-4} vs. $2.4 \times 10^{-4} \pm 0.3 \times 10^{-4}$ fiber/μm^2) while muscle diameter did not differ among calves (69 vs. 72 ± 1.6 μm). Expression of IGFBP3 mRNA was greater in the liver (0.65 vs. 0.46 ± 0.06) and less in muscle (0.10 vs. 0.28 ± 0.04) in SUP than CON offspring. Neither liver nor muscle expression of GHR, IGF1 and INSR mRNA differed among treatments. Muscle expression of PPARγ mRNA was greater in SUP than CON offspring (0.11 vs. 0.04 ± 0.02) but SREBF1 mRNA did not differ among calves. Results of this experiment suggest that prepartum supplementation of beef cows in rangeland conditions would enhance growth and muscle adipogenesis potential in male calves.

Key Words: beef cattle, nutrition, fetal programming

T327 Morphometry of the tubular compartment in insulated boar testis. K. Yagoda*[1], F. Melo[2], and J. Parrish[1], *[1]University of Wisconsin-Madison, Madison, [2]Federal University of Goias Campus Jatai, Jatai, Goias, Brazil.*

Elevated ambient temperature is associated with summer infertility in boars. The aim of this study was to evaluate the effects on the testis of short-term scrotal insulation using morphometric analysis. One boar was used as a control and the other boar's scrotum was insulated in a sack for 48 h. The insulation procedure has been shown to increase scrotal temperature by 1.8°C. Testes sections were collected, fixed in Karnovsky solution, dehydrated, and embedded in Epon. Two-micrometer-thick sections from each sample were stained with 1% toluidine blue/sodium borate. All statistical methods were done using an ANOVA test and all values are presented as the mean ± standard deviation. We measured in the control and insulated boar, respectively, the volume density by counting 2880 points on a grid and found the percentages of interstitium (28.8 ± 0.1 vs. 33.7 ± 0.1, $P = 0.0705$), and seminiferous tubules (71.2 ± 0.2 vs. 66.3 ± 0.2, $P = 0.63$) did not differ. We measured the seminiferous tubule diameters (in microns) in 30 cross sections in each boar (214.9 ± 17.5 vs. 216.3 ± 16.2, $P = 0.747$) and found no difference. In contrast, the heights of epithelium in 30 cross sections (59.3 ± 6.2 vs. 53.5 ± 8.1, $P = 0.0029$) was different. We counted cell populations in 9 stage 1 cross sections and only found a difference in the preleptotene/

leptotene primary spermatocytes (13.1 ± 2.5 vs. 8.7 ± 1.6, $P = 0.0004$). In the insulated boar we observed a high density of cells in the lumen and small round vacuoles in the basal compartment. The lowered height of epithelium could be associated with greater cell loss during the thermal injury in the insulated boar. The preleptotene/leptotene primary spermatocytes appear to be the first cells affected by the heat, and had we allowed more time to pass after the insulation this effect would have been seen in the later cell stages. Morphometric analyses realized in this study showed that the scrotal insulation impaired the testicular function and affect the spermatic production.

Key Words: scrotal insulation, reproduction, spermatogenesis

T328 Impact of increased oxidative stress through excessive accumulation of adipose tissue on circulating adiponectin concentrations in dairy cows. S. Häussler*[1], S. P. Singh[1], L. Laubenthal[1], L. Locher[3], J. Winkler[2], U. Meyer[2], S. Dänicke[2], and H. Sauerwein[1], *[1]Institute of Animal Science, Physiology and Hygiene Group, University of Bonn, Bonn, Germany, [2]Institute of Animal Nutrition, Friedrich-Loeffler-Institute (FLI), Braunschweig, Germany, [3]University of Veterinary Medicine, Foundation, Hannover, Germany.*

Adipokines play an important role in regulating energy metabolism and glucose homeostasis. Fat accumulation (FA) correlates with systemic oxidative stress that may dysregulate the production of adipokines. We are interested in the insulin-sensitizing adipokine Adiponectin (Aq); the objective of our present study was to investigate the effect of excessive FA on oxidative stress and on circulating Aq concentrations in cows. Non-pregnant, nonlactating, pluriparous German Holstein cows (n = 8) were gradually adapted to a high-energy ration (corn-grass-silage with increasing the proportion of corn silage), including a successive increase of the proportion of the concentrate feed (within 6 wk from 0% up to 60% of the dry matter of the daily ration). Within 20 wk, the mean body weight (BW) increased from 540 ± 56.8 kg to 792 ± 81.7 kg; body condition score (BCS, 5-point scale) rose from 2.31 ± 0.35 to 4.53 ± 0.39. Subcutaneous fat from the tail head region was biopsied every 8 wk. Cryosections (14 µm) were prepared, fixed in acetone and stained with hematoxylin. Adipocyte sizes (μm^2) were determined in 100 randomly selected adipocytes. Blood samples were collected monthly; serum Aq concentrations were measured by ELISA (Mielenz et al. 2013). Derivatives of reactive oxygen metabolites (dROM) were photometrically quantified in serum using *N*,*N*,diethyl-1,4-phenylendiamine as chromogen. Data (means ± SEM) were analyzed using ANOVA and Pearson correlations. Serum Aq concentrations (µg/mL) decreased gradually throughout the FA period (41.3 ± 1.76 to 31.1 ± 0.72; $P = 0.006$). Serum Aq concentrations were negatively correlated with BCS ($r = -0.724$, $P < 0.001$), BW ($r = -0.573$, $P = 0.004$), and adipocyte size ($r = -0.475$, $P = 0.022$) and tended to be related with dROM ($r = -0.372$, $P = 0.073$). Increased dROM concentrations (from 49.9 ± 9.24 up to 113 ± 14.5 µg H_2O_2 equivalents/mL) indicating mitochondrial dysfunction as a result of excessive FA, were accompanied by decreased concentrations of the insulin-sensitizing adipokine Aq.

Key Words: adiponectin, reactive oxygen species, dairy cows

T329 The effect of heat stress on lipolytic response of bovine primary adipocytes. M. P. Faylon*[1], L. H. Baumgard[1], R. P. Rhoads[2], and D. M. Spurlock[1], *[1]Iowa State University of Science and Technology, Ames, [2]Virginia Polytechnic Institute and State University, Blacksburg.*

Heat stress (HS) has an enormous economic impact on the global dairy industry, and recent research indicates lipid metabolism is altered in lactating cows experiencing HS. In particular, basal and stimulated lipolytic responses are severely blunted in multiple species during HS. Thus, we hypothesized that HS directly affects adipose tissue by diminishing its response to lipolytic signals. Bovine primary adipocytes were isolated from 5 multiparous Holstein cows in late lactation and cultured at either 42C (HS) or 37C (thermal neutral, TN). Isoproterenol (ISO) was administered at varying concentrations and glycerol release was measured as an indicator of lipolytic response. A dose response curve to ISO was determined under HS and TN conditions for adipocytes isolated from each cow, and differences in the curve-fitting parameters between HS and TN treatments were compared using paired-samples *t*-test. Likewise, the abundance of several lipolytic proteins in relation to HS was evaluated. Adipocytes exposed to HS had an elevated maximal response to ISO (106.9% increase, $P = 0.024$), and were more sensitive to lipolytic stimulation by ISO ($P = 0.02$) compared with cells cultured at TN. Basal lipolytic response was not different between HS and TN cells ($P > 0.05$). At a high ISO concentration, a significant decrease in lipolytic response was observed for HS but not TN cells, suggesting potential downregulation of β-adrenergic receptors in HS but not TN cells. Thermal treatment also increased phosphorylation of hormone sensitive lipase (HSL) at Ser^{563}, confirming increased activation of the PKA pathway under HS conditions. The increased sensitivity of HS cells to lipolytic stimuli was unexpected, as in vivo data previously reported a diminished response to lipolytic signals. Further investigation is warranted to understand the relationship between the in vitro results and the effect of HS on lipid metabolism in vivo.

Key Words: heat stress, adipose tissue, lipolysis

T330 Once-daily milking during a feed restriction does not alter transcription of key lipid metabolism genes in adipose tissue of grazing dairy cows. T. M. Grala[1], J. R. Roche[1], C. V. C. Phyn[1], A. G. Rius[1], R. H. Boyle[1], R. G. Snell[2], and J. K. Kay*[1], *[1]DairyNZ, New Zealand, [2]University of Auckland, New Zealand.*

Study objectives were to investigate the effect of once-daily (1×) milking, at 2 feeding levels, on transcription of key lipid metabolism genes in adipose tissue of grazing dairy cows. Multiparous cows (n = 120) were grazed on pasture and milked twice daily (2×) from calving until 34 ± 6 d in milk (mean ± SD). Cows were then allocated to one of 4 treatments in a 2 × 2 factorial arrangement. Treatments were imposed for 3 wk and consisted of 2 feeding levels (adequately fed; AF, consuming 14.3 kg DMI/cow per d, or underfed: UF, consuming 8.3 kg DMI /cow per d) and 2 milking frequencies (2× or 1×). After the 3-wk treatment period, all cows were AF and milked 2×. Adipose tissue was collected from 12 cows per treatment at wk −1, 3, and 5 relative to treatment start, RNA extracted and transcript abundance of genes involved in lipid metabolism quantified. At the end of the 3-wk treatment period, transcript abundance of genes involved in glyceroneogenesis, glycerolipid synthesis and fatty acid (FA) transport, synthesis, and oxidation were greater ($P < 0.05$) in AF cows milked 1× compared with all other treatments. There was no effect of feeding level on the expression of genes involved in FA oxidation. Additionally, there was no effect of milking frequency on the expression of genes involved in lipid metabolism in UF cows. At wk 5, when all cows had returned to AF and 2× milking for 2 wk, there were no consistent differences in transcript abundance of lipid metabolism genes between treatments. In conclusion, milking cows 1× during a 3-wk nutrient deficit did not alter lipid metabolism compared with 2× milking; however, 1× milking in AF cows upregulated genes associated with FA synthesis, storage and oxidation. These data indicate that by wk 3 of

a feed deficit, lipostatic mechanisms, such as reduced milk production and limited lipolysis, prevented excess body tissue mobilization in UF cows. Furthermore, lipostatic mechanisms, such as greater FA oxidation, prevented excessive adipose deposition in AF cows milked 1× that were in an improved energy state.

Key Words: once-daily milking, nutrition, lipid metabolism

T331 GPR109A mRNA abundance in two different fat depots of dairy cattle considering nicotinic acid and transition period related changes. P. Friedrichs[1], L. Locher[2], K. Huber[2], S. Dänicke[3], H. Sauerwein*[1], and M. Mielenz[1,4], *[1]Institute of Animal Science, Physiology & Hygiene Unit, University of Bonn, Bonn, Germany, [2]Department of Physiology, University of Veterinary Medicine, Hannover, Germany, [3]Institute of Animal Nutrition, Friedrich-Loeffler-Institute (FLI), Federal Research Institute for Animal Health, Braunschweig, Germany, [4]Leibniz Institute for Farm Animal Biology (FBN), Department of Nutritional Physiology, Dummerstorf, Germany.*

The G-protein coupled receptor (GPR) 109A is predominantly expressed in adipocytes and mediates anti-lipolytic effects. We aimed to determine if nicotinic acid (NA), a known agonist of GPR109A influences the expression of this receptor in subcutaneous (SC) and retroperitoneal (RP) adipose tissue (AT) of dairy cattle. Likewise we studied time-dependent changes and differences of GPR109A mRNA abundance between both AT. For this, 20 pluriparous German Holstein cows were divided into a NA (n = 10) and a control group (n = 10). The animals from the NA group received a NA supplement (Lonza, Basel, Switzerland; 24 g/d) from d 1 until d 21 postpartum. The SCAT from tail head and RPAT were biopsied at d −21, 1 and 21 relative to calving. GPR109A mRNA abundance was quantified by qPCR. The statistical analyses were performed with SPSS 20.0 (SPSS Inc., Chicago, IL, USA) using ANOVA for analysis of the single tissues and Mann-Whitney U test for comparison of both AT. The mRNA abundance was not different between the NA versus control group neither in SCAT nor in RPAT. Thus, groups were pooled for further analyses. In both tissues GPR109A expression was independent of time. Comparing the mRNA abundance from pooled data of all sampling dates between both tissues yielded 1.51-fold higher values in RPAT than in SCAT ($P = 0.001$). When comparing both fat depots within the individual sampling times, RPAT showed 1.46-fold higher expression of GPR109A than SCAT on d −21 ($P = 0.014$) and 1.75-fold higher on d 21 ($P = 0.015$), but we detected no significant difference between both tissues at d 1. In conclusion, neither NA treatment nor time affected the mRNA expression of GPR109A in SCAT and in RPAT, respectively. The different GPR109A mRNA abundances between SCAT and RPAT confirmed our earlier works and indicate different importance for lipolysis and energy mobilization in both fat depots.

Key Words: adipose tissue, nicotinic acid, GPR109A

T332 Evaluation of the Idexx pregnancy detection assay for milk samples. B. Lawson*[1], D. Ray[1], K. Velek[2], E. Martel[2], R. Linscott[2], P. McCoy[1], M. Tate[1], J. Lawrence[2], and W. Silvia[1], *[1]University of Kentucky, Lexington, [2]Idexx Laboratories Inc., Westbrook, .*

The objective of this experiment was to assess the accuracy of the Idexx pregnancy detection assay for milk samples. Lactating Holstein cows (n = 17) were bred by timed artificial insemination. Pregnancy was evaluated by ultrasonography at 37, 65 and 93 d after breeding. Milk samples were collected on d 2 after insemination and at weekly intervals either 1) through d 58 post insemination if the cow was not pregnant on d 37 or 2) through d 93 if the cow was found pregnant. Plasma and milk samples were shipped to Idexx Laboratories Inc. to measure pregnancy associated glycoproteins (PAGs) using an ELISA. This ELISA classifies samples as (1) nonpregnant (NP; PAG concentration below a low critical threshold), (2) pregnant (P; PAG concentration above a high critical threshold) or (3) requiring recheck (RR; PAG concentration between the low and high thresholds). The Idexx staff was not informed of pregnancy status. Seven cows were pregnant by ultrasound on d 37, 65 and 93. All of these cows were classified as P using the milk PAG ELISA on d 30 and 37. Ten cows were found to be open by ultrasound on d 37. All 10 were classified as NP on d 30 and 37. A total of 70 samples were collected from the 7 pregnant cows from d 30 to 93 postinsemination. Using the milk PAG ELISA, 65 (93%) of these samples were classified as P, 5 as RR and 0 as NP. A total of 50 samples were collected from the 10 cows found not pregnant by ultrasound on d 37. In the milk PAG ELISA, 48 (96%) were classified as NP, 2 as RR and 0 as P. A total of 120 milk samples were collected on d 30 or after from these 17 cows. Sixty-five samples were classified P. All of these were from the 7 pregnant cows (positive predictive value: 100%). Forty-eight samples were classified as NP, all from nonpregnant cows (negative predictive value: 100%). Seven samples were classified as RR, 5 from pregnant cows and 2 from nonpregnant cows. We conclude that the milk PAG ELISA identifies pregnant and nonpregnant cows with a high degree of accuracy as early as 30 d after insemination.

Key Words: bovine, milk, pregnancy

T333 Gestational form of supplemental selenium (Se) affects gene expression in the newborn calf testis. II. Spermatogenesis. C. R. Skees*, P. J. Bridges, J. D. Patterson, and J. C. Matthews, *Department of Animal and Food Sciences, University of Kentucky, Lexington.*

In states with Selenium (Se)-deficient soils it is necessary for cattle producers to supplement Se in livestock feed rations. The objective of this study was to determine how inorganic versus organic forms of maternal dietary Se supplementation affect the expression of genes known to affect spermatogenesis in the newborn bull calf testis. Twenty-four Angus-cross cows managed under a standard forage-based cow calf production setting were randomly assigned (n = 8) to 1 of 3 treatment groups: sodium selenite (inorganic, ISe; Prince Se), Sel-Plex (organic, OSe; Alltech) or a 50/50 mix of ISe/OSe (mix). Cows were given ad libitum access to a commercial mineral mix that contained 35 ppm of Se beginning 4 mo before breeding through to calving. Thirteen bull calves were born (ISe n = 5, OSe n = 4, Mix n = 4) and castrated within 48 h of birth. Total RNA was extracted from small pieces of whole testis collected at castration. A microarray analysis was performed using bovine 1.0 ST arrays (Affymetrix) and the data set analyzed by one way ANOVA followed by a post hoc pairwise comparison (*t*-test). Overall, 1112 genes were affected ($P < 0.05$) by Se treatment, including 13 known to be involved with spermatogenesis: Ift52, Acvr1, Tlr3, Mapk14, Egf, Npr1, Raf1, Lep, Ldha, Meis1, Cdk5r1, Ccnd2 and Nphp1. When compared ($P < 0.05$) to ISe (the standard supplementation regimen) the expression of mRNA for Npr1, Lep, Nphp1 and Ccnd2 was increased, and Raf1 decreased, in testis of calves born to OSe supplemented cows, whereas mRNA for Egf and Ldha increased, and Tlr3, Mapk14 and Meis1 decreased, in testis from calves born to Mix supplemented cows. The relative ($P < 0.05$) content of mRNA for Ift52, Acvr1, Tlr3, Mapk14, Npr1, Lep, Meis1, Ccnd2 and Nphp1 was greater, whereas Raf1, Ldha and Cdk5r1 mRNA was lesser, in testis of calves born to OSe vs Mix supplemented cows. Our results provide evidence that the gestational source of dietary Se

affects development of the neonatal calf testis. Whether dam gestational form of supplemental dietary Se affects spermatogenesis and fertility of mature bulls requires investigation.

Key Words: selenium, spermatogenesis, testis

T334 Effect of implants on steroidogenic capacity of bovine granulosa cells. A. D. Stapp*[1], C. A. Gifford[1], K. B. Parker[1], B. I. Gómez[1], D. M. Hallford[2], and J. A. Hernandez Gifford[1], *[1]Oklahoma State University, Stillwater, [2]New Mexico State Universty, Las Cruces.*

Feedlot heifers are often implanted with steroids to increase growth efficiency thereby altering hormone profiles and changing the milieu in which ovarian follicles develop. Because granulosa cell (GC) culture is commonly used and often bovine ovaries are collected from abattoirs with no record of implant status, the objective of this study was to determine if the presence of anabolic and estrogenic steroids during bovine GC development affects FSH-regulated steroidogenesis. Sixteen feedlot heifers were assigned to 1 of 3 treatments: non-implanted (n = 5), and Revalor 200 for 30 d (30 d; n = 5) or 90 d (90 d; n = 6). At slaughter, paired ovaries were collected and small follicle (1 to 5 mm) GC were isolated from each pair and incubated with PBS (n = 16) or 100 ng/mL FSH (n = 16) for 24 h. Effects of FSH treatment on real-time PCR analysis of gene expression and hormone concentrations were analyzed using GLM procedure of SAS. Efficacy of treatment was confirmed by increased ($P < 0.01$) concentrations of medium estradiol in FSH-treated cells (62.31 ± 9.16 pg/mL) compared with PBS-treated controls (14.81 ± 9.16 pg/mL). Treatment with FSH tended to increase steroidogenic acute regulatory protein ($P = 0.09$) mRNA expression in GC of implanted heifers (−0.84 ± 0.56 and −1.79 ± 0.52) compared with non-implanted females (−0.21 ± 0.56). Similarly, P450 side chain cleavage ($P = 0.07$) tended to increase in response to FSH in GC of heifers implanted (2.89 ± 0.29 and 3.04 ± 0.27) compared with non-implanted heifers (1.99 ± 0.33). However, no difference in mRNA expression of 3-β-hydroxysteroid dehydrogenase ($P = 0.57$) and aromatase ($P = 0.23$) were demonstrated in implanted or non-implanted heifers. Medium estradiol concentrations of GC treated with FSH were similar ($P = 0.11$) between implanted (88.8 and 80 ± 21 pg/mL) and non-implanted heifers (80 ± 19.24 pg/mL). Similarly, FSH-mediated progesterone did not differ among treatment groups ($P = 0.22$). Results indicate follicles developing in the presence of high androgenic and estrogenic steroids tend to have an impaired ability to respond to FSH stimulation of the steroidogenic enzymes but not subsequent steroid production.

Key Words: granulosa cells, implant, steroidogenesis

T335 Effects of heat stress and plane of nutrition on liver insulin responsiveness in lactating cows. G. Xie*[3], M. V. Skrzypek[1], S. R. Sanders[1], L. H. Baumgard[2], and R. P. Rhoads[3], *[1]University of Arizona, Tucson, [2]Iowa State University, Ames, [3]Virginia Tech University, Blacksburg.*

Multiparous cows (n = 12; parity = 2; 136 ± 8 DIM, 560 ± 32 kg BW) housed in climate chambers were fed a TMR consisting primarily of alfalfa hay and steam-flaked corn. Cows were subjected to 2 experimental periods (P): (1) thermoneutral conditions (18°C, 20% humidity) with ad libitum intake (TN for group 1, WF for group 2) for 9d and (2) either heat-stress (HS) conditions (cyclical temperature 31.1–38.9°C, 20% humidity: min THI = 73, max THI = 80.5) fed for ad libitum intake (n = 6), or TN conditions, pair-fed (PF) with a HS animal (n = 6) for 9d. Rectal temperature (Tre) and respiration rate (RR) were measured thrice daily at 0430, 1200 and 1630h. Study objectives were to evaluate hepatic insulin responsiveness during HS and PF. Liver biopsies were obtained immediately before and after an insulin tolerance test (ITT) on the last day of each period. Insulin receptor β (IRβ), insulin receptor substrate 1 (IRS-1), Akt/protein kinase B (AKT) and phosphorylated AKT (P-AKT) were measured by Western blot analyses. During P2, HS increased Tre and RR by 1.48°C and 2.4-fold, respectively ($P < 0.01$). HS reduced ($P < 0.01$) DMI by 8 kg/d and by design PF cows had similar intake reductions. Milk yield was decreased similarly (30%) in HS and PF cows and both groups entered into a similar (−4.5 Mcal/d) calculated negative energy balance during P2. Compared with P1 ($P < 0.05$), basal glucose levels increased (5%) in PF cows, but decreased (5%) in HS cows during P2. The ITT caused a more rapid glucose disposal in P1 compared with P2 ($P < 0.05$), but glucose clearance did not differ between environments in P2. Protein abundance of IRβ remained constant during each period. The protein level of IRS-1 was lowered ($P < 0.05$) by insulin in WF only. Insulin increased P-AKT protein content in each period ($P < 0.05$) except PF. Abundance of AKT tended to decrease ($P = 0.057$) only in PF. Phosphorylation ratio of AKT increased 120% in each period ($P < 0.05$) after insulin infusion. These results indicate that liver insulin responsiveness remains unchanged despite mild systemic insulin resistance during HS and reduced nutrient intake.

Key Words: heat stress, insulin, liver

T336 Progesterone, TNF-α, IGF-1, and $PGF_{2\alpha}$ concentrations in blood plasma of beef cows within 14 days after transfer of embryos. J. Copeland*[1], J. Batton[1], E. J. Cuadra[1], T. H. Elsasser[2], B. Johnson[3], J. E. Larson[4], M. C. Mason[1], and J. Yoonsung[5], *[1]Alcorn State University, Alcorn State, MS, [2]USDA ARS, Bovine Functional Genomics Laboratory, Beltsville, MD, [3]Coastal Plain Branch Experiment Station, Newton, MS, [4]Mississippi State University, Mississippi, [5]Prairie View A&M University, Prairie View, TX.*

Lactating beef recipient cows previously synchronized for estrus were randomly assigned to one of 4 treatments to assess the magnitude in progesterone (P_4) rise and its effects on TNF-α, IGF-1 and $PGF_{2\alpha}$ after transfer of embryos. Cows exhibiting estrus received an embryo in the uterine horn ipsilateral to CL 7 d post-estrus. Cows received either no treatment (Control, n = 16), a CIDR (Controlled Internal Drug Release) (CIDR, n = 16), an injection of 1000 IU of hCG (hCG, n = 15) or an injection of 100 µg of GnRH (GnRH, n = 15) at the time of embryo transfer. Blood samples were taken from all cows immediately on d 0 (day of transfer), 7, and 14 for analysis of P_4, TNF-α, and IGF-1. Blood samples for determination of 13,14-dihydro-15-keto $PGF_{2\alpha}$ (PGFM) were collected from half the animals in each treatment group on d 7 and the remaining half on d 14; samples were collected every 15 min for 2 h on both days. Data was analyzed using the SAS MIXED procedure. Pregnancy 60 d after embryo transfer was 56.2, 62.5, 46.7 and 6.7% for the control, CIDR, hCG and GnRH respectively. P_4 was higher ($P < 0.05$) in cows receiving hCG compared with other groups on d 7. Cows, whether pregnant or not at diagnosis, had an increase in P_4 from d 0 to 7 and a decline ($P < 0.05$) in P_4 from d 7 to 14. Non-pregnant cows had an overall decline in P_4 and TNF-α from d 0 to 14 ($P < 0.05$). Treatments did not affect TNF-α. No significant differences ($P > 0.05$) in IGF-1 were observed among treatment groups and between pregnant and non-pregnant cows. While PGFM increased ($P < 0.05$) from d 7 to 14 in cows receiving the CIDR and hCG, concentrations in the hCG group were only higher than those observed in the GnRH ($P < 0.05$) on d 14. Contrary to the non-pregnant cows, no significant differences were observed in concentrations of PGFM between samples collected

every 15 min in the pregnant cows on d 14 ($P < 0.05$). Regardless of pregnancy status, cows had a significant decline in P_4 during the second week after the transfer of an embryo; additionally, $PGF_{2\alpha}$ seems to be steadier in pregnant cows than in non-pregnant cows during that same period.

Key Words: embryo, P4, $PGF_{2\alpha}$

T337 Effect of an essential fatty acid (EFA)-deficient diet on luteal and uterine function in pseudopregnant (PSP) rats and prostaglandins (PG) E1, E2, and F2a (PGF2a, PGE1; PGE2) in nonpregnant (NP) and pregnant (P) ewes. C. W. Weems*[1], Y. S. Weems[1], and R. R. Magness[2], *[1]Dept. of Human Nutrition, Food, and Animal Sciences, University of Hawaii, Honolulu, [2]Dept. of Obstetrics and Gynecology, University of Wisconsin, Madison.*

PGF2a is the uterine luteolysin, but PGE1 or PGE2 are antiluteolysins and prevent luteolysis. PGE1 or PGE2 prevent a natural or induced luteolysis. The precursor for PGF2a and PGE2 is arachidonic acid (AA) and di-homo-gamma linolenic acid (DHGLA) for PGE1. The objective of EXPT 1 was to assess length of PSP and fatty acid (FA) profile by GLC in control 7 EFA deficient PSP rats. A control or EFA-free diet was fed to rats from weaning on d 21. EXP 2 objective was to measure uterine weight on d 9 in control and EFA-deficient PSP rats treated with Vehicle, PGE1, PGE2, or PGE1+PGE2 intrauterine at deciduomata (DCR) induction. PSP length was analyzed by a one-way ANOVA and data in Expt. 2 by a 2 × 2 × 4 CRD for ANOVA. EXPT 3 objective was to measure PGF2a, PGE1 and PGE2 in caruncles and uterine blood by HPLC and RIA on d 13 in NP and P ewes (n = 10 each). EXPT 3 data were analyzed by a one-way ANOVA. An EFA-deficient diet increased ($P < 0.05$) PSP length (12.1 ± 0.5 vs. 17.1 ± 0.6 d), decreased AA 78% ($P < 0.05$), and increased ($P < 0.05$) DHGLA (133%). Uterine weight of DCR rats was lower ($P < 0.05$) in EFA deficient PSP rats (3.2 ± 0.2 vs. 5.9+0.6 g). PGF2a in uterine blood was lower ($P < 0.05$) in EFA-deficient rats (1.9 ± 0.6 vs. controls 11.2 ± 0.21). Uterine weight in PGE1, PGE2, or PGE1+PGE2 at induction of DCR increased ($P < 0.05$) more in PGE2 than PGE1 in EFA-deficient PSP rats (78% vs. 1%). PGF2a in uterine blood was lower in EFA-deficient rats (1.9 ± 0.6 vs. controls 11.2 ± 0.21). PGE1 and PGE2 in caruncles increased ($P < 0.05$) in P ewes on d 13 NP PGE1 (4.7 ± 0.5 ng/g); NP PGE2 (11.7 ± 1.4 ng/g); P PGE1 (12.5 ± 2.3 ng/g), and P PGE2 (24.3 ± 5.1 ng/g). PGF2a, PGE1, and PGE2 in uterine blood of NP ewes averaged 7.3 ± 0.2, 1.2 ± 0.4, and 2.6 ± 0.5 and PGF2a, PGE1, and PGE2 in P ewes averaged 9.9 ± 1.2, 11.6 ± 1.6 and 16.5 ± 2.1. In summary, an EFA deficiency increased PSP and decreased the DCR response in PSP rats. Both PGE1 and PGE2 increases in P ewes support PGE1 and PGE2 as antiluteolysins. Deceased contributors: Hal Behrman and Dorothy Cope.

Key Words: EFA, PSP rats, ewe

T338 Effects of FSH stimulation on β-catenin accumulation in bovine granulosa cells. K. B. Parker*[1], C. A. Gifford[1], A. D. Stapp[1], B. I. Gomez[1], D. M. Hallford[2], and J. A. Hernandez Gifford[1], *[1]Department of Animal Science, Oklahoma State University, Stillwater, OK, USA, [2]Department of Animal and Range Sciences, New Mexico State University, Las Cruces, NM, USA.*

Regulation of estradiol (E_2) biosynthesis by FSH requires the transcriptional co-factor β-catenin (CTNNB1). Increased abundance of CTNNB1 is demonstrated in large antral follicles with greatest concentrations of intra-follicular E_2. In bovine granulosa cells (GC), FSH increases CTNNB1 and protein kinase B (AKT) protein, and WNT2 mRNA expression. These data indicate FSH regulates CTNNB1 through the canonical WNT or AKT signaling pathways. The objective of this study was to elucidate AKT's role in CTNNB1 accumulation. Bovine GC were pre-incubated with AKT inhibitor (LY294002; LY) for 30 min, then cultured with or without FSH for 24 h (n = 4). Total protein was collected for analysis by Western blot. Relative abundance of protein was analyzed using one-way ANOVA procedure of SAS. Expectedly, LY reduced total AKT abundance ($P = 0.05$) and ablated phosphorylated AKT protein. Inhibition of AKT signaling with LY alone ($P = 0.13$) or in combination with FSH ($P = 0.16$) tended to reduce CTNNB1 protein compared with control and FSH-treated GC. Progesterone (P_4) media concentrations did not differ among treatment groups ($P = 0.52$); however, numerical reduction in P_4 was demonstrated in LY compared with FSH-treated GC. Inhibition of AKT reduced ($P < 0.01$) production of FSH-mediated E_2 production. A subsequent study was conducted to investigate whether a known AKT stimulator, IGF-I, could also mediate CTNNB1 accumulation (n = 4). Bovine GC treated with FSH had greater CTNNB1 compared with control and IGF-I groups ($P = 0.01$). Though, FSH did not increase P_4 ($P = 0.42$), IGF-I alone and in combination with FSH increased ($P < 0.01$) P_4 to 161.8 and 185.9 (±13) ng/mL, respectively. Estradiol concentrations were 93 pg/mL for control, and addition of IGF-I alone or in combination with FSH increased E_2 to 280 and 343 (±65) pg/mL, respectively. Data demonstrate that AKT is required for FSH-induced accumulation of CTNNB1 and steroid synthesis. However, IGF-I stimulation of AKT increased steroid production but not CTNNB1 accumulation indicating AKT is necessary for FSH-induced accumulation of CTNNB1, and CTNNB1 is not required for IGF-I induction of steroidogenesis.

Key Words: FSH, granulosa cells, β-catenin

T339 Combined effect of cytological endometritis and cyclicity on fertility of dairy cows. A. Vieira-Neto*[2], W. R. Butler[3], R. O. Gilbert[3], and K. N. Galvão[1], *[1]University of Florida, Gainesville, [2]Universidade do Estado de Santa Catarina, Lages, SC, Brazil, [3]Cornell University, Ithaca, NY.*

Anovulation is associated with cytological endometritis (CTE); therefore, the negative association of either condition with fertility could be confounded by the other. The objective was to evaluate if both cyclicity and CTE would be negatively associated with fertility. Holstein cows (n = 403) from 5 dairies in upstate New York were used. Cyclicity was characterized by serum progesterone concentration ≥1.0 ng/mL at 21, 35, or 49 DIM. CTE was characterized by the presence of ≥4% neutrophils on the uterine cytology performed at 49 DIM. Time to pregnancy up to 300 DIM was analyzed using the PHREG and LIFETEST procedure of SAS. The PHREG model included the effects of cyclicity, CTE, interaction between cyclicity and CTE, parity, body condition score, calving season, PGF treatment, and herd. An interaction between cyclicity and CTE was observed ($P = 0.02$), and 4 dummy variables were created based on the permutation of cyclicity and CTE: Cyclic with CTE (CycCTE; n = 118), cyclic without CTE (CycHealthy; n = 205), anovular with CTE (AnovCTE; n = 34), and anovular without CTE (AnovHealthy; n = 46). Compared with CycHealthy cows, AnovCTE [hazard ratio (HR) = 0.54; CI = 0.34–0.88; $P = 0.01$] and AnovHealthy (HR = 0.69; CI = 0.47–1.00; $P = 0.05$) cows had decreased hazard of pregnancy, and CycCTE tended (HR = 0.79; CI = 0.60–0.1.02; $P = 0.07$) to have decreased hazard of pregnancy. CycHealthy cows were the most fertile as evidenced by the fact that they had the shortest median time to pregnancy (122 d). On the other hand, AnovCTE had the longest median time to pregnancy

(180 d), while CycCTE and AnovHealthy were intermediate (159 and 171 d, respectively). In summary, cyclicity and uterine health statuses are both important for fertility in dairy cows. Both, anovulation and presence of CTE were negatively associated with fertility, and when combined, they had an additive negative effect.

Key Words: cyclicity, cytological endometritis, fertility of dairy cows

T340 Effect of propionate, palmitate and insulin on chemerin gene expression in monolayer cultures of bovine hepatocytes. S. G. Roh*[1], S. Kitayama[1], Y. Suzuki[1], K. H. So[1], K. J. Yi[1], E. Yamauchi[1], S. Haga[2], and K. Katoh[1], *[1]Lab of Animal Physiology, Graduate School of Agriculture Science, Tohoku University, Sendai, Miyagi-ken, Japan, [2]NARO Institute of Livestock and Grassland Science, Japan.*

Chemerin, an adipokine, gene was highly expressed in adipose and liver tissues of Japanese Black cattle, and TNF-α increased the expression of chemerin and chemerin receptor in cultured bovine adipocytes. However, it is not known about the regulatory factors on gene expression of chemerin in cultured bovine hepatocytes. The objective was to investigate the effect of propionate, palmitate and insulin on chemerin mRNA expression in in vitro cultured bovine hepatocytes prepared from preweaning and postweaning cattle. The caudate lobes of liver tissues were sampled from Japanese Black cattle (3-week, 3- and 5-mo-old). The collagenase solution was recirculated through the caudate lobe to collect cells in the medium. The cells were seeded and cultured for 48 h. The cells were washed 3 times with fresh medium and cultured for an additional 6 h in serum-free medium. Then the medium was exchanged with fresh serum-free medium in the presence or absence of propionate (0.1, 1 m*M*), palmitate (50, 100, 250 μ*M*) and insulin (1, 10, 100 n*M*) for 24 h and total RNA was extracted from the cells for analysis of chemerin mRNA. Data were analyzed by 2-way ANOVA using PROC GLM (SAS Inst. Inc.). Values are representative of at least 2 separate series of cultures (5 to 6 replicates per each treatment). Propionate treatment (1 m*M*) reduced ($P < 0.05$) the expression levels of chemerin gene in cultured hepatocytes of 3-wk-old cattle by 40%, while it increased ($P < 0.05$) the expression in 5-mo-old cattle by 1.3-fold. Palmitate (100 μ*M*) did not change the expression level of chemerin mRNA in hepatocytes of 3-week-old cattle ($P > 0.1$), while it increased ($P < 0.05$) the expression in 3-mo-old cattle by 1.4-fold. Insulin (100 n*M*) decreased ($P < 0.05$) the levels of chemerin gene expression in 3-wk- and 3-mo-old cattle by 65% and 20%, but not in 5-mo-old cattle. The expression of chemerin gene was differently controlled by propionate, palmitate and insulin treatments in hepatocytes, and between preweaning and postweaning animals, indicating that chemerin may play a role on nutrient metabolism associated with development.

Key Words: bovine, hepatocyte, weaning

T341 Gene expression in Holstein bull testicular testis after scrotal insulation. J. R. Schindler* and J. J. Parrish, *University of Wisconsin, Madison.*

Holstein bulls (n = 9, approximately 5 years old) were used to study the effects of heat stress on testis gene expression. Bulls were split into a control, insulated, and insulated and recovered groups. Tissue from the control group was harvested without insulation and from the insulated group immediately following insulation for 48 h. Semen was collected from the recovered group for 2 weeks prior, and for 45 d after insulation (3 d per week). Semen was analyzed for nuclear shape (Fourier Harmonic Analysis) to confirm that a heat stress event occurred. The mean harmonic amplitude 1 increased on d 19 post insulation compared with pre-insulation (mean ± SEM, 0.196 ± 0.017 vs. 0.171 ± 0.003; $P < 0.05$). The mean harmonic amplitude 3 increased on d 19, 21, 23, 26, and 28 post insulation compared with pre-insulation (mean ± SEM, 0.173 ± 0.012, 0.170 ± 0.012, 0.179 ± 0.016, 0.185 ± 0.017, and 0.167 ± 0.013 vs. 0.145 ± 0.003; $P < 0.05$). The mean harmonic amplitude 5 increased on d 19 post insulation compared with pre-insulation (mean ± SEM, 0.153 ± 0.012 vs. 0.132 ± 0.003; $P < 0.05$). A mixed effects model was used to compare the control days to each day, post-insulation. Changes in harmonic amplitudes are consistent with previous results. Total RNA from the testis of the control and insulated groups was extracted and microarray analysis was done using a Nimblegen 385K custom bovine expression array. Using a targeted approach, a subset of 200 genes in the array was investigated. The subset was constructed using a National Center for Biotechnology Information search of genes involved in heat stress, apoptosis, DNA repair, and hypoxia. Six genes in the insulated group were statistically different from the control: Cytochrome C-testis, BCL2L13, Dynein, RPS6KB1, OBFC2A, and TIMP-2. These 6 genes were subjected to a validation experiment using qRTPCR. Only TIMP-2 showed a trend for a difference with a 122% decrease in expression from the control ($P = 0.06$) using a mixed effects model. Decreased TIMP-2 expression in the testis would lead to an increase in remodeling of the extracellular matrix in interstitial space and/or the seminiferous epithelium.

Key Words: bull, heat stress, gene expression

T342 Effect of induction of ovulation, early in lactation, on uterine health and fertility in dairy cows. J. H. Bittar*[1], P. Pinedo[3], K. E. Hencken[1], C. C. Barbosa[1], M. Gobikrushanth[1], S. Croyle[1], C. A. Risco[1], A. Vieira-Neto[2], J. E. Santos[1], and K. N. Galvão[1], *[1]University of Florida, Gainesville, [2]Universidade do Estado de Santa Catarina, Lages, SC, Brazil, [3]Texas A&M University, Amarillo.*

Objective was to evaluate the effect of GnRH early postpartum on induction of ovulation, uterine health and fertility in dairy cows. Holstein cows without a CL at 17 ± 3 DIM (n = 255) were randomly assigned to receive an injection of GnRH (n = 128) at 17 ± 3 DIM and at 20 ± 3 DIM or to remain as controls (n = 127). Cows had their ovaries scanned by ultrasonography (US) twice a week for a total of 4 US. Ovulation was characterized by the appearance of a corpus luteum (CL) ≥ 20mm in any US or when a CL < 20mm appeared in 2 consecutive US. Clinical (CE) and cytological endometritis (CTE) were diagnosed at 35 ± 3 DIM. Data was analyzed using the LOGISTIC and PHREG procedure of SAS adjusting for the effect of parity, calving related problems, metabolic problems, or metritis. Cows receiving GnRH had increased ovulation (71.1 vs. 43.3%; $P < 0.001$). GnRH treatment (GTRT) did not affect the prevalence of CE (26.2 vs. 20.8; $P = 0.41$) or CTE (30.9 vs. 32.8; $P = 0.29$). Cows having calving problems (39.7 vs. 17.5%; $P = 0.004$) and metritis (39.7 vs. 16.2%; $P < 0.001$) had increased prevalence of CE. Metritis (39.7 vs. 16.2%; $P < 0.001$) also increased the prevalence of CTE (50.7 vs. 23.5%; $P < 0.001$). An interaction between GTRT and ovulation after GTRT (GTRT × Ov) showed that treated cows that ovulated had decreased CTE compared with cows that did not ovulate (25.6 vs. 43.2%; $P = 0.05$), but ovulation did not affected ($P = 0.88$) CTE in control cows. GTRT did not affect conception rate (CR) at 32 (42.2 vs. 43.3%; $P = 0.74$) or 74 d after AI (37.5 vs. 35.4%; $P = 0.26$), or pregnancy loss (11.1 vs. 18.2%; $P = 0.30$). The interaction GTRT × Ov showed that treated cows that ovulated had increased CR at 74 d compared with cows that did not ovulate (42.9 vs. 24.3%; $P = 0.05$), while there was no difference ($P = 0.57$) in control cows. The interaction GTRT × Ov showed that treated cows that did not ovulate had decreased hazard of pregnancy up to 300 DIM compared with cows that ovulated (HR = 1.9; $P = 0.01$), or control

cows that did (HR = 1.8; $P = 0.03$) or did not ovulate (HR = 1.9; $P = 0.01$). GnRH treatment early postpartum increased ovulation; however, it failed to improve uterine health or fertility.

Key Words: ovulation, uterine health and fertility, dairy cow

T343 Temporal gene expression profiling of liver from peripartal dairy cows during spring and summer. H. Akbar[1], U. Bernabucci[2], L. Basiricò[2], P. Morera[2], and J. J. Loor*[1], *[1]University of Illinois, Urbana, [2]Università degli Studi della Tuscia, Viterbo, Italy.*

Thermal stress during hot seasons renders dairy cattle more susceptible to metabolic disease, including liver lipidosis. Hepatic transcriptome-wide changes during heat stress remain unknown. We examined temporal gene expression profiles during the dry period and early lactation in liver of 12 Holstein cows that calved in the spring (SP, March to April) or summer (SU, June to July) using a whole-transcriptome bovine microarray (Agilent) and quantitative RT-PCR (qPCR). Liver tissue was harvested at −30, 3, and 35 d relative to parturition. The 23 target genes selected for qPCR were associated with heat shock response (HSP70A1A, HSTF1), fatty acid oxidation (CPT1A, PPARA, ACOX1), hepatokines (FGF21, ANGPTL4), esterification and VLDL assembly (MTTP, APOB100, DGAT1, SREBF2), glucose metabolism (PC, PCK1, PDK4), and inflammation and stress (TNF, GPX1, SOD1, SOD2, SAA3, HP, HAMP). The ANOVA model included day, season, and day × season as fixed effects, and cow within season as the random effect. Statistical difference for interaction and main effects was declared significant at $P < 0.05$. Results from qPCR revealed a 2-fold increase in expression of HSP70A1A in SU between −30 and 3 d. In contrast, expression of HSTF1 between −30 and 3 d increased 20-fold in SP and 7-fold in SU. Despite the 6- to 11-fold increase in CPT1A between −30 to 3 d in SU and SP, SU was associated with lower overall expression (~2-fold) of CPT1A and also PPARA and ACOX1. Except for MTTP, expression of APOB, DGAT1, and SREBF2 was 2- to 6-fold greater overall in SP than SU. The gluconeogenic enzyme PCK1 increased 14-fold from −30 and 3 d in SP but decreased 2-fold in SU. Expression of acute-phase proteins increased > 60-fold between −30 and 3 d regardless of season, but there was greater overall expression (~40-fold) in SU. Overall, results revealed that during hot seasons the liver transcriptome in peripartal cows is markedly altered and likely contributes to the susceptibility of those cows to develop disease.

Key Words: heat stress, transition cow, transcriptomics

T344 Chronic uterine infusion of melatonin or melatonin receptor antagonist during mid-gestation alters ovine placental nitrites and superoxide dismutase activity. K. E. Brockus*[1], L. E. Camacho[2], K. A. Vonnahme[2], and C. O. Lemley[1], *[1]Mississippi State University, Mississippi State, [2]North Dakota State University, Fargo.*

Previous data from our laboratory showed an increase in umbilical artery blood flow in ewes infused with melatonin (MEL), while in contrast MEL receptor antagonist (luzindole, LUZ) infusion decreased blood flow. The objectives of the current experiment were to determine maternal and fetal concentrations of total nitrites (an index of nitric oxide production) and placental superoxide dismutase (SOD) activity following a 4 week uterine infusion of MEL (n = 5), LUZ (n = 5), or vehicle control (CON; n = 4). Singleton pregnant ewes were implanted with Alzet osmotic pumps (Durect Co; 2.5 μL/h infusion of 1 mg/mL MEL or LUZ) under the perimetrium of the gravid uterine vascular network on d 62 of gestation. This infusion model resulted in local delivery of MEL to the fetus as evident by a 25% increase in maternal MEL concentrations vs. a 125% increase in fetal MEL concentrations. On d 90 of gestation maternal blood samples were collected, ewes were euthanized, umbilical cord blood samples were collected (combination of umbilical artery and vein), and placentomes were separated and frozen for later determination of tissue levels of nitrites or SOD activity. Total nitrites in maternal serum were not different ($P > 0.50$) across all treatments; however, total nitrites in umbilical cord serum were increased ($P < 0.03$) in both LUZ and MEL vs. CON dams. Placental concentrations of nitrites in the caruncle were increased in LUZ and MEL vs. CON dams, while cotyledon nitrites were not different ($P > 0.10$) across all treatments. Caruncle SOD activity was increased ($P < 0.05$) in MEL dams vs. CON and LUZ; however, cotyledon SOD activity was not different ($P > 0.30$) across all treatments. The results from the current study show an increase in placental antioxidant enzyme activity following chronic uterine MEL infusion, which may be mediating the previously observed increase in umbilical artery blood flow. Moreover, placental nitric oxide production may be increased in both LUZ and MEL infused dams irrespective of the previously observed differences in umbilical artery blood flow.

Key Words: melatonin, nitrites, superoxide dismutase

T345 Follicular dynamics in Holstein heifers subjected to 5-d protocols to synchronize ovulation. H. Ayres*[1,3], L. M. Vieira[1], R. M. Ferreira[1], E. O. S. Batista[1], R. V. Sala[1], J. P. Barbuio[3], F. P. Rennó[1], J. E. P. Santos[2], and P. S. Baruselli[1], *[1]Department of Animal Reproduction, University of São Paulo, São Paulo, Brazil, [2]Department of Animal Sciences, University of Florida, Gainesville, [3]MSD Animal Health, São Paulo, Brazil.*

Three experiments (Exp) were designed to evaluate follicular dynamics in Holstein heifers treated with 5-d protocols to synchronize ovulation. Protocols differed in the source of progesterone (P4), the use or not of GnRH on d 1 of the protocol and type of ovulatory stimulus. In Exp1, heifers received a P4-releasing intravaginal device on D0 and were assigned to receive (n = 12) or not (n = 12) 0.1mg gonadorelin (GnRH; Fertagyl, Merck). On D5, the P4 device was removed and 0.53 mg cloprostenol (PGF; Ciosin, Merck) were administered followed by 0.1 mg GnRH 48 h later. In Exp2, heifers received a protocol similar to Exp1, except that on D0 they were assigned to receive a P4 device and no GnRH (n = 13), a Norgestomet implant (Crestar, Merck) and no GnRH (n = 11), or a norgestomet implant combined with GnRH (n = 12). In Exp3, heifers received a norgestomet implant on D0, which was removed on D5. PGF was administered on D5 and heifers were assigned to receive either 1mg estradiol benzoate (EB, Gonadiol, Merck AH; n = 11) 48 h or GnRH (n = 12) 72 h later. Ultrasonographic evaluations of the ovaries were performed using a 5-MHz linear transducer. Continuous data were analyzed by ANOVA and for binary data by logistic regression (GLIMMIX, SAS). In Exp1, the use of GnRH on D0 did not affect follicular growth and synchronization of ovulation. In Exp2, the use of norgestomet implant without GnRH on D0 anticipated ovulation (76.4 ± 4.3) compared with P4 device (98.5 ± 4.1; $P = 0.003$) and norgestomet implant with GnRH was similar a both. Regardless the use of GnRH on D0, norgestomet implant-treated heifers had larger diameter of the ovulatory follicle (OF) (13.6 ± 0.4) than P4 device-treated heifers (12.3 ± 0.4; $P = 0.01$). As for the ovulatory stimuli, both GnRH and EB had similar ovulation rates (100 and 91.7%, respectively; $P = 0.90$). When P4 was administered via intravaginal insert use of GnRH at the beginning of the protocol did not improve synchronization of follicle growth. However, when norgestomet was the source of P4, administration of GnRH increased the diameter of the OF and synchronized ovulation compatible with insemination at 72 h after implant removal.

Key Words: follicle dynamic, Holstein heifer, progesterone

T346 Associations between plasma anti-Müllerian hormone (AMH) and fertility responses of seasonally calving grazing dairy cows. E. S. Ribeiro*[1], R. L. A. Cerri[2], R. S. Bisinotto[1], F. S. Lima[1], L. F. Greco[1], A. Morrison[3], A. Kumar[3], W. W. Thatcher[1], and J. E. P. Santos[1], *[1]Department of Animal Sciences, University of Florida, Gainesville,, [2]Department of Land and Food Systems, University of British Columbia, Vancouver, BC, Canada, [3]Ansh Labs Inc., Webster, TX.*

The objective was to investigate associations between plasma AMH and fertility of grazing dairy cows subjected to synchronized AI on the first day of a 100-d breeding season. Lactating cows (n = 1,237) in 2 farms had estrous cycles presynchronized and were enrolled in a timed AI (TAI) protocol (GnRH on d −8, $PGF_{2\alpha}$ on d −3 and −2, and GnRH + AI on d 0). All cows received the first AI on the same day (study d 0). Blood was sampled on d −8 and analyzed for AMH using a chemiluminescence immune assay (AnshLite Bovine AMH CLIA). From d 19 to 34, detection of estrus was performed daily and cows were re-inseminated. On d 35, bulls were placed with cows for 65 d of breeding. Concentrations of AMH were affected ($P < 0.01$) by breed and lactation number. Concentrations were higher for Jersey cows, followed by crossbreds and then Holsteins (337 vs. 298 vs. 264 pg/mL). Cows on lactations 2 and 3 had higher ($P < 0.05$) AMH than those on lactations 1 and > 3 (342 and 328 vs. 257 and 273 pg/mL). Plasma AMH was related negatively (AOR = 0.93; $P = 0.01$) with estrous expression at TAI. The odds of detecting a cow in estrus at timed AI reduced 7% per every 100 pg/mL increase in plasma AMH. Nevertheless, AMH was not associated with detection of estrus and re-insemination after first AI. Plasma AMH was not associated with pregnancy per AI (P/AI) for the TAI, but tended ($P = 0.10$) to be positively related to P/AI for the second AI performed after estrous detection (AOR = 1.07) and pregnancy for natural service (AOR = 1.07). Non-pregnant cows at the end of 100-d breeding period had lower ($P = 0.05$) plasma AMH than those that became pregnant (252 vs. 310 pg/mL). In conclusion, concentrations of AMH in plasma were associated with reduced expression of estrus at TAI but not later in the breeding period. Plasma AMH was not associated with fertility of cows subjected to synchronized ovulation, but was associated with fertility of cows that failed to become pregnant to TAI and were subsequently bred on estrus (AI on estrus + natural service). Synchronization of ovulation might override associations of AMH and fertility of lactating grazing cows.

Key Words: AMH, dairy cow, reproduction

T347 Comparison of four methods to determine pregnancy success in beef cattle. G. A. Perry*[1], M. F. Smith[2], and K. G. Pohler[2], *[1]Department of Animal Science, South Dakota State University, Brookings, [2]Division of Animal Science, University of Missouri, Columbia.*

Transrectal ultrasonography has been available for several years, but accuracy is dependent upon a well-trained technician. More recently, blood tests to determine pregnancy have become commercially available. Therefore the objective of this study was to compare the accuracy of determining pregnancy status on d 30 after fixed-time AI among: transrectal ultrasonography, visual observation for return to estrus, and 3 different blood tests. Beef heifers (n = 42 and 69 at location 1 and 2, respectively) and cows (n = 102 at location 1) were synchronized using the PG 6-d CIDR protocol with FTAI at 66 to 72 h after CIDR removal concurrent with an injection of GnRH. EstroTect estrus detection patches were placed on animals (6 or 19 d after AI at location 1 and 2, respectively) and estrus was monitored twice daily until d 30. On d 30, pregnancy status was determined by transrectal ultrasonography and blood samples were collected. Blood samples were sent to Genex, University of Missouri (UM), and BioTracking for determination of pregnancy status. Data were analyzed using the GLIMMIX procedures of SAS with herd as a random effect. When compared with transrectal ultrasonography there was no difference ($P = 0.14$) for assay sensitivity (ability to correctly identify pregnant animals; 99, 98, 94, and 95% for estrous detection, Genex, UM, and Biotracking). There was a tendency ($P = 0.09$) for decreased specificity (ability to correctly identify non-pregnant animals; 82, 67, 82, and 87% for estrous detection, Genex, UM, and Biotracking). There was no difference in the positive predictive value ($P = 0.20$; likelihood a pregnant animal was called pregnant) or negative predictive value ($P = 0.29$; likelihood a non-pregnant animal was called not pregnant) among tests (90 and 99%, 83 and 97%, 89 and 89%, and 92 and 91% for estrous detection, Genex, UM, and Biotracking). Furthermore, there was no difference ($P = 0.25$) in the overall accuracy of the test (percent of time correctly identified; 92, 86, 89, and 92%, for estrous detection, Genex, UM, and Biotracking, respectively). Therefore, several options are available to determine pregnancy status in cattle.

Key Words: fixed-time AI, pregnancy status, blood test

T348 The relation of two apoptosis-related proteins (bax and bcl-2) to adipocyte cell size in bovine adipose tissue. D. Germeroth[1], M. Steyer[2], T. Ettle[3], M. Rodehutscord[2], H. Sauerwein[1], and S. Häussler*[1], *[1]Institute of Animal Science, Physiology and Hygiene Group, University of Bonn, Bonn, Germany, [2]Institute of Animal Nutrition, University of Hohenheim, Hohenheim, Germany, [3]Bavarian State Research Center for Agriculture, Institute of Animal Nutrition and Feed Management, Grub, Germany.*

Programmed cell death (apoptosis) in adipose tissue (AT) is related to adipocyte size. The initiation and regulation of apoptosis can be mediated by the intrinsic pathway through mitochondria. Members of the Bcl-2 protein family, e.g., bcl-2 (anti-apoptotic) and bax (pro-apoptotic) are key regulators involved in this mitochondrial pathway. Our objective was to evaluate whether adipocyte size and the mitochondrial pathway are related in bovine AT. Therefore, Simmental heifers (n = 39) from 2 feeding trials with a mean BCS of 4.0 ± 0.13 (scale 1–5) were examined and AT from the tail head region was biopsied. Cryosections were cut (12–14 µm) and stained with Mayer's hematoxylin, adipocyte area (μm^2) of 100 randomly selected cells per section was evaluated. For immunohistochemistry, sections were fixed in ice-cold acetone at room temperature (RT). Endogenous peroxidase activity and unspecific binding sides were blocked with 0.3% H_2O_2 (15 min, RT) and normal goat serum (1:10, 20 min, RT), respectively. Sections were incubated with monoclonal mouse antibodies against human bax (1:30, RT) and human bcl-2 (1:30, 4°C) over night. Afterward, sections were incubated with biotinylated polyclonal goat antibodies against mouse IgG (1:200) and peroxidase-labeled streptavidin (1:1000) both for 30 min at RT. Staining was achieved by 3-amino-9-ethylcarbazol, counterstaining was done by Mayer's hematoxylin. Bovine placenta (6 µm) served as control. Data (means ± SEM) were evaluated using Spearman correlations. The mean adipocyte size was 6,833 ± 295 μm^2. The mean portions of bax and bcl-2 positive cells were 6.45 ± 0.67% and 12.74 ± 1.31%, respectively. Adipocyte size was positively correlated with bax ($r = 0.571$, $P < 0.001$) and bcl-2 ($r = 0.654$, $P < 0.001$) as well as the portion of bax to bcl-2 ($r = 0.632$, $P < 0.001$). The presence of both apoptosis-related proteins indicates that the mitochondrial pathway of apoptosis functions in bovine AT. Both bax and bcl-2 were related to adipocyte size. The amount of anti- and pro-apoptotic parameters was similar. Therefore, we assume that the mitochondrial pathway leading to apoptosis is not initiated.

Key Words: adipocyte size, dairy cows, Bcl-2 family

T349 Niacin increases adiponectin secretion in differentiated bovine preadipocytes in vitro via G-protein coupled receptor 109A. C. Kopp[1], S. P. Singh[1], H. Sauerwein*[1], and M. Mielenz[2], *[1]Institute of Animal Science, Physiology & Hygiene Unit, University of Bonn, Bonn, Germany, [2]Leibniz Institute for Farm Animal Biology (FBN), Department of Nutritional Physiology, Dummerstorf, Germany.*

Adiponectin (AdipoQ), an insulin-sensitizing adipokine, is involved in regulating energy homeostasis and lipid metabolism by increasing fatty acid oxidation in liver and glucose uptake in adipocytes of monogastrics. The G-protein coupled receptor 109A (GPR109A) is involved in downregulating lipolysis not only by its endogenous ligand β-hydroxybutyrate but also by pharmacological doses of Niacin (NA). In rat adipocytes, increased AdipoQ secretion in response to stimulation with NA was attributed to GPR109A signaling. In cattle, corresponding data are missing. Our objective was thus to examine the effect of NA on AdipoQ secretion and the involvement of GPR109A in bovine adipocytes. A primary cell culture system using differentiated preadipocytes was established. Subcutaneous adipose tissue was collected from 5 Holstein-Friesian dairy cows. Stromal-vascular cells were isolated, pooled and seeded at 2500 cells/cm^2. Preadipocytes after 12 d of differentiation were used. After starvation, cells were incubated either with 100 ng/mL pertussis toxin (PTX), a nonselective G-protein uncoupling agent, or PBS for 16 h to characterize the NA mediating pathway. Afterward cells were treated with NA (10 or 15 μ*M*) for 12 or 24 h or with PBS as controls, respectively. The AdipoQ concentrations in the cell culture supernatants were quantified by ELISA (Mielenz et al., 2013, doi:10.1016/j.domaniend.2012.10.004). Statistical analyses were performed using ANOVA with Bonferroni post hoc tests. Data are given as means ± SEM. The concentrations of AdipoQ for both NA doses and durations of NA treatment were increased ($P \leq 0.001$) to maximal 306 ± 11 ng/mL compared with controls (48 ± 2 ng/mL). Pre-incubation with PTX reduced ($P \leq 0.001$) the response to NA to maximally 2.2 fold higher concentrations than in the controls. Our results of NA stimulated AdipoQ secretion from differentiated bovine adipocytes together with the dampened increase after PTX treatment point to GPR109A as mediating at least partially the NA stimulated increase of AdipoQ secretion in cattle.

Key Words: bovine adiponectin, niacin, G-protein coupled receptor 109A

T350 Effect of storage time on the viability of cryopreserved bovine spermatozoa. A. I. Gallegos*[1], S. A. Ericsson[1], H. D. Blackburn[2], S. F. Spiller[2], B. J. Warnock[1], M. K. Meador[1], M. W. Smith[1], and P. H. Purdy[2], *[1]Sul Ross State University, Alpine, TX, [2]USDA-ARS-National Animal Germplasm Program, Fort Collins, CO.*

Long-term cryopreserved semen viability can affect the National Animal Germplasm Program's (NAGP) sampling strategy and ability to reconstitute livestock populations. Therefore, the purpose of this project was to determine if prolonged storage of cryopreserved sperm affects cell viability. Cryopreserved sperm samples from 12 Hereford bulls were utilized from the NAGP repository. These samples were separated into groups based on storage time of 40–50, 30–39, 20–29 or 10–19 yr. The percentage of progressively (PMS) and total motile sperm (TMS), curvilinear velocity (VCL), and beat cross frequency (BCF) was obtained using computer assisted sperm analysis. Flow cytometric analysis and specific fluorescent stains were utilized for the following viability assessments: FITC PNA – percent live non-acrosome reacted sperm (LNARS); propidium iodide – percent membrane intact sperm (MIS); Yo-Pro-1 - cell membrane integrity/ non-apoptotic sperm (NAS); merocyanine 540 (M540) - percent of sperm with relatively ordered membranes (ROM); and the combination of Yo-Pro-1 with M540 for assessment of membrane phospholipid order (MPO). Differences in measures of sperm viability were assessed using ANOVA with a fixed effect model that included the effects of storage time, type of cryopreservation diluent (milk or egg yolk), and their interaction. Significant differences were not observed for the main effects or for the interaction term (Table 1). These results demonstrate that bovine sperm viability was not affected as a result of the storage time in liquid nitrogen. These results suggest sample deterioration is not occurring and need not be a factor for consideration in collection development and sample utilization.

Table 1. Mean values of stored sperm viability

	Storage (yr)				
Measure	40+	30–39	20–29	10–19	SEM
PMS (%)	6	15	12	11	1.7
TMS (%)	26	45	48	39	3.3
VCL (μm/s)	134	167	164	148	7.9
BCF (Hz)	36	35	32	31	1.3
LNAR (%)	62	81	47	35	3.5
MIS (%)	63	63	57	57	5.1
NAS (%)	66	57	55	47	5.3
ROM (%)	84	77	57	83	5.2
MPO (median)	92	9	22	8	14.7

Key Words: sperm, viability, cryopreservation

T351 Effect of exogenous eCG during the first or second service during the Ovsynch protocol upon the pregnancy per insemination of lactating Holstein cows. K. G. Gonzalez-Garcia*[1], C. Leyva[1], C. A. Cancino[1], J. L. Morales[1], M. Mellado[2], F. G. Veliz[2], and C. A. Meza-Herrera[3], *[1]Universidad Autonoma Agraria Antonio Narro Unidad Laguna, Torreon, Coahuila, Mexico, [2]Universidad Autonoma Agraria Antonio Narro, Saltillo, Coahuila, Mexico, [3]Universidad Autonoma Chapingo, URUZA, Bermejillo, Durango, Mexico.*

The aim of this study was to evaluate the effect of eCG during Ovsynch protocol upon the pregnancy per insemination in dairy cattle. Lactating Holstein cows (n = 200) from a dairy herd in northern Mexico, were divided into 2 groups (n = 100 each). Females from both groups were treated according to the Ovsynch protocol (d0 GnRh, d7 PgF2α, d9 GnRh, d10 AI). However, while one group received 400 IU of eCG on d 7 of the protocol, the other group was defined as the control group; all animals in both groups were inseminated at first service. In the second part of experiment, those cows diagnosed as non-pregnant (n = 48), were used to evaluate the effect of a second Ovsynch protocol with (n = 21) and without (n = 27) application of eCG. Those cows injected with eCG but diagnosed as non-pregnant, served as control to the non-pregnant, non-eCG-injected in the first part of treatment. All cows were inseminated at fixed time. Pregnancy diagnosis was performed by rectal palpation at d-39. The pregnancy per insemination of both groups was compared using a chi-squared test (SYSTAT 10 (Evenston, ILL, USA, 2000). The results of the pregnancy per insemination of cows subjected to Ovsynch with and without eCG are included in Table 1. Results suggest that injection of eCG in the first or second service does not improve the pregnancy per insemination in lactating Holstein cows in northern Mexico.

Table 1. Effect of eCG injection at first or second service during Ovsynch protocol on the pregnancy per insemination in Holstein cows

Group	First service (no.)	Pregnancy per AI (%)	Second service (no.)	Pregnancy per AI (%)
eCG	100	21[a]	21	23.8[a]
Control	100	17[a]	27	40.7[a]

[a]Means with different superscripts in each column differ significantly ($P > 0.05$).

Key Words: eCG, Ovsynch protocol, pregnancy

T352 Visual analytics of bovine nutriphysiogenomics datasets. M. J. Khan*[1], M. Welge[1,2], C. Bushell[1,2], M. Berry[1,2], L. Gatzke[1,2], and J. J. Loor[1], *[1]University of Illinois, Urbana, [2]National Center for Supercomputing Applications, Urbana, IL.*

High-throughput microarray technology has provided a wealth of information on the dynamism of the transcriptome in key tissues of dairy cattle during key life stages such as the transition from pregnancy to lactation. With the advent of next-generation sequencing technology and its application in bovine bioscience, high-dimensional data are becoming more prevalent. The research of transcriptome data mining has relied on the use of software which places strict limits of the feature dimensionality, utility, and comprehensibility of analysis. The objective of this study is to develop new, innovative visual and interactive techniques for effectively studying, exploring and experimenting with the data to help form and confirm hypothesis. Technique development is focused on the use of statistical and machine learning tools and approaches in support of data driven biology that are required to underpin and enable modern nutriphysiogenomics research. Five different data sets including cow performance and transcriptomics of mammary gland, adipose tissue and liver were used. Mammary data encompass d −30, −15, 1, 15, 30, 60, 120, 240 and 300 relative to parturition. Adipose data encompass −65, −42, −14, 1, and 14 d in cows fed control or a moderate-energy diet prepartum. Liver data encompass −65, −30, −14, 1, 14, 30, and 49 d in cows fed control, moderate-energy, or underfed energy prepartum. Specifically we are applying approaches in the following areas 1) analyzing and interrogating microarray and next-generation sequencing data sets; 2) extracting quantitative features from large and complex data sets; 3) capturing variation and linking biological processes to phenotypic traits; 4) supporting knowledge-discovery in biological data using visualization approaches. These approaches will allow the researcher to extract relevant features to explain phenotypic behavior. These include the use of "small-multiples" each visually representing the distribution of the data, the display of gene expression amplification for comparison over time and tissues, and techniques that support the exploration of "what if scenarios" to produce alternative phenotypic outcomes.

Key Words: bioinformatics, nutrition, transcriptomics

T353 Effect of vitamin E and R-carnitine on beef cattle finishing performance and profitability. E. Ponce-Cruz[1], J. R. Garduño-Juárez[1], G. Aranda-Osorio*[1], O. Hernandez-Mendo[2], J. C. Garcia-Ortiz[1], M. Cordoba-Alvarez[1], and J. M. Monzon Armenta[1], *[1]Universidad Autonoma Chapingo, Texcoco, Mexico, [2]Colegio de Postgraduados, Montecillo, Mexico.*

The aim of this study was to evaluate the effect of vitamin E and R-carnitine supplementation on feedlot performance of beef cattle and profitability. Twenty-four commercial crossbred (*Bos taurus* × *Bos indicus*) young bulls initially weighing 425.3 ± 31.3 kg were used, which were homogenously divided into 4 groups and randomly assigned to the following treatments: (T1) Control (no supplement added), (T2) vitamin E (3,000 IU/animal/d) for 71 d, (T3) R-carnitine (5 ppm) for 45 d, and (T4) combination of T2 and T3. Cattle received a reception management (identified, vaccinated, dewormed, vitamined and implanted). They were housed in individual pens. The chemical composition of the basal diets was: 13.13% CP; 1.79 and 1.16 Mcal/kg of NEm and NEg, respectively, 11.16% CF, and Ca:P of 1.94. A completely randomized design with the GLM procedure of SAS was used, and when statistical differences were observed, a Tukey test was carried out. The response variables were: dry matter intake (DMI), average daily gain (ADG), feed conversion (FC), feed efficiency (FE) and benefit/cost ratio (BC). There were found not differences ($P > 0.05$) among treatments in any of the variables evaluated, with mean of 12.25 kg/animal/d, 1.65 kg, 7.85 kg, 0.134 g/kg, for DMI, ADG, FC, and FE, respectively. The BC was slightly better for the vitamin E and R-carnitine treatments (1.07) than for the control treatment (1.05). The inclusion of vitamin E at 3,000 IU/hd/d showed not to have negative effect on feedlot performance, thus, it could be used as an antioxidant for beef. R-Carnitine at 5 ppm does not improved animal performance, thus the concentration probably must be increased to find a positive response.

Key Words: bullock, additive, feedlot performance

T354 Influence of prepartum dietary energy on cow and progeny performance. T. B. Wilson*, D. B. Faulkner, and D. W. Shike, *University of Illinois, Urbana-Champaign.*

The objectives of this study were to evaluate the effects of prepartum dietary energy on cow performance, lactation, and reproduction, as well as progeny performance and carcass traits. Spring-calving, mature cows (n = 106; BW = 690 ± 76 kg) were blocked by BW and allotted to 2 dietary treatments: 1) 93% ground hay and 7% dried distillers grains plus solubles (REQ), or 2) 50% corn bran and 50% ground cornstalks (HE). Treatment diets were formulated to be isonitrogenous with REQ and HE providing 100% and 125% of TDN requirements, respectively, and were fed from 90d prepartum to calving. All cows were fed a common diet postpartum. Cow BW and BCS were recorded at 90d prepartum, 24h post-calving, and breeding. Milk production was estimated by the weigh-suckle-weigh technique at 65 ± 9 and 120 ± 9d of age. Calf BW was measured at birth and at weaning (120 ± 9d of age). Calves (n = 86) were fed a common feedlot diet 28d after weaning and individual feed intake was monitored using GrowSafe. Progeny were harvested in 3 groups to target a 12th rib fat thickness of 1.3 cm, determined via ultrasound. From 90d prepartum to breeding, change in BW was greater ($P < 0.01$) for cows fed HE and BCS change tended ($P = 0.07$) to be greater. Birth BW tended ($P = 0.10$) to be heavier for calves born to cows fed HE with no increase ($P \geq 0.18$) in dystocia. There was no effect ($P \geq 0.43$) of dietary treatment on milk production or conception rates. Marbling score, measured via ultrasound, was greater ($P = 0.03$) at weaning for calves born to cows fed HE. Calf weaning BW, initial feedlot BW, final BW, and days on feed were not affected ($P \geq 0.12$) by cow treatment. Feedlot DMI and ADG were not different ($P \geq 0.20$); however, calves born to cows fed REQ tended ($P = 0.06$) to be more efficient. There was no effect ($P \geq 0.29$) of cow treatment on calf mortality or morbidity. Although marbling score was different at weaning, there was no effect ($P \geq 0.20$) of cow treatment on final marbling score or other progeny carcass traits. Feeding cows 125% of TDN requirement from 90d prepartum to calving increased cow BW change with no effect on conception rates, or progeny health, growth and DMI.

Key Words: prepartum, energy, progeny

T355 Effect of ration composition on income over feed cost and milk yield. M. H. Buza*, L. A. Holden, R. A. White, and V. A. Ishler, *The Pennsylvania State University, University Park.*

Feed is the greatest expense in the cost of milk production. With volatility in feed and milk markets, income over feed cost (IOFC) may be a more advantageous measure of profit than feed cost per cow. The objective of this study was to evaluate the effects of ration cost and ingredient composition on IOFC and milk yield. The Pennsylvania State Extension Dairy Team IOFC tool was used to collect data from 91 Pennsylvania farms from 2009 to 2011 and determine IOFC per cow per day. The data collected included average milk yield, milk income, purchased feed cost, ration ingredients, ingredient cost per ton, and amount fed. Feed costs were based on market values rather than on-farm cost. Actual costs were used for purchased feed. Mean lactating herd size was 169.4 ± 10.55, and milk yield was 31.7 kg ± 0.19. Mean IOFC was $7.71 ± 1.006 ranging from -$0.33 in March, 2009 to $16.60 in September, 2011. Data was analyzed using a one-way ANOVA in SPSS. Values were grouped by quartiles and analyzed by individual year and all years combined. Purchased feed cost per cow per day averaged $3.16 ± 1.07 from 2009 to 2011. Milk yield and IOFC did not significantly differ with purchased feed cost, suggesting that purchased feed cost per cow was not a key factor in high milk yield or IOFC. Intermediate levels of forage cost between $1.45 and $1.97 per cow per day resulted in the highest ($P < 0.01$) average IOFC of $8.19 and the highest ($P < 0.05$) average milk yield of 32.3 kg. This suggests that optimal ration formulation was key to increasing milk yield and IOFC. Total feed costs in the top quartile ($6.27 or more per cow per day) resulted in the highest ($P < 0.01$) IOFC showing that minimizing feed cost per cow per day did not result in the highest IOFC. In 2010, the IOFC was highest ($P < 0.01$) at $8.09 for dairies that fed one or more by-products. Intermediate levels of forage cost and higher levels of total feed cost per cow per day resulted in both higher milk yield and higher IOFC suggesting that profit margin was affected by more than just feed cost per cow.

Key Words: income over feed cost, profitability, dairy management

T356 Evaluation of Kemtrace brand chromium propionate on milk production by Holstein cows under heat stress conditions in Pennsylvania. J. Ferguson*, *University of Pennsylvania, Kennett Square.*

A field trial was conducted from June through October 2012 on an 800-cow Holstein dairy in Pennsylvania to evaluate the effect of Chromium Propionate (CrPr, KemTRACE Chromium Propionate 0.4%, Kemin

Industries Inc., Des Moines, IA) on milk production by second lactation and greater cows between 14 and 150 DIM. Two parallel treatment groups, Control (no CrPr) and CrPr (supplemented to provide 8 mg Cr/h/d), were populated by random assignment one wk before trial start. Subsequently, cows leaving the post-fresh group entered treatment groups on an alternating basis while cows with the greatest DIM were removed to maintain pen size at 104 to 116 cows. At the trial start, pre-fresh (−21 d to calving) and post-fresh (≤14 d postpartum) groups received CrPr, supplemented to provide 8 mg Cr/h/d. Data for milk yield, milk components, and DIM were analyzed using PROC MIXED in SAS. The model included fixed effects for treatment, time, DIM, and the interaction of treatment by time, and the random effect of cow within treatment group. Milk yield, kg/h/d, was greater (48.8 vs. 46.2, $P < 0.0001$) for CrPr cows compared with control cows. Milk fat % was lower (3.63% vs. 3.75%, $P < 0.001$) for CrPr cows compared with control cows, but milk fat yield, kg/h/d, was not different (1.76 vs. 1.71, $P > 0.10$). Milk protein % was not different (2.90% vs. 2.91%, $P > 0.10$) between treatment groups, but milk protein yield, kg/h/d, was greater (1.41 vs. 1.33, $P < 0.02$) for CrPr cows compared with control cows. For cows randomized to treatment at the trial start, CrPr supplementation supported 3.6 kg more milk/h/d ($P < 0.05$) than cows receiving no CrPr during heat stress. A treatment by time interaction existed where cows supplemented for <4 wk with CrPr before entering treatment groups were not different ($P > 0.05$) in milk yield between treatments, and cows supplemented for >4 wk with CrPr before entering treatment groups produced 4.8 kg/h/d more milk ($P < 0.05$) from wk 3 to 11 postpartum. These results suggest CrPr supplementation from −21 d pre-fresh through 150 DIM may help maintain milk yield during periods of heat stress.

Key Words: heat stress, chromium, milk yield

T357 Evaluation of KemTRACE brand chromium propionate on reproductive performance of Holstein cows in Pennsylvania. J. Ferguson*, *University of Pennsylvania, Kennett Square.*

A field trial on an 800-cow Holstein farm in Pennsylvania evaluated the effect of Chromium Propionate (CrPr, KemTRACE Chromium Propionate 0.4%, Kemin Industries Inc., Des Moines, IA) on reproductive performance. The trial was conducted from January to October 2012; the dairy was naïve to supplemental Cr. Lactating cows received 8 mg Cr/h/d as CrPr in a base corn mix. Reproductive performance over the previous 6 years served as a baseline for treatment comparisons, and binomial trend analysis with Chi-Square values was used to compare changes in conception rate (CR). Body condition score (BCS) was assessed on post-fresh and high group cows before and during CrPr supplementation and compared by Chi-Square test. Pregnancy rate (PR), determined by life-test method using 21-d intervals post-calving, had increased from 17% in October 2006 to a plateau of 27% from January 2010 through December 2011. This improvement corresponded to an increase in first service CR (FSTCR) from 30% to 45%, which plateaued with the PR. Second, 3rd and 4th service CR were typically below 30% over this period. Following initiation of CrPr supplementation in January, PR began to increase in March, and continued to increase to 31.5% by July and remained over 30% through October. The FSTCR remained at 45%, but 2nd, 3rd, and 4th insemination CR increased from 25, 28, and 33% to 32, 37, and 45%, respectively. The binomial trend for CR from 1st to 4th service was significantly reduced ($P < 0.05$) from a chi-squared value of 11.9 in January to 6.8 in October. Changes in CR for repeat services were not associated with transition cow health, parity or milk yield. Mean BCS for post-fresh cows was similar ($P = 0.22$) from January to May (3.5 vs. 3.5, ± 0.02 SEM), but mean BCS in high group cows significantly increased ($P = 0.023$) over the same period (2.5 vs. 2.8, ± 0.03 SEM). In conclusion, based on the improvement in BCS and the increase in CR for repeated services, the results would suggest that CrPr supplementation ameliorated negative energy balance in cows possibly associated with failure to conceive at FSTCR and with lower CR for subsequent services.

Key Words: reproduction, chromium, dairy

T358 Supplementation with soybean oil increases milk fat and improves milk fatty acid profile in heat-stressed dairy goat. S. Hamzaoui*[1], A. A. K. Salama[1,2], G. Caja[1], E. Albanell[1], and X. Such[1], *[1]Group of Ruminant Research (G2R), Universitat Autonoma de Barcelona, Bellaterra, Spain, [2]Animal Production Research Institute, Dokki, Giza, Egypt.*

In a previous work we observed that heat-stressed goats suffered reductions in milk yield, milk fat, and milk protein. Supplementation with soybean oil may be a useful way to enhance milk quality. Eight multiparous Murciano-Granadina dairy goats (42.8 ± 1.3 kg BW; 99 ± 1 DIM) kept in metabolic cages were used in a replicated 4 × 4 Latin square design with 4 periods; 21 d each (14 d adaptation, 5 d for measurements, and 2 d transition between periods). Goats were allocated to one of 4 treatments in a 2 × 2 factorial arrangement. Factors were no oil (C) or 4% of soybean oil (S), and thermal neutral (TN; 15 to 20°C) or heat stress (HS; 12 h/d at 37°C and 12 h/d at 30°C) conditions. This resulted in 4 treatment combinations: TN-C, TN-S, HS-C, and HS-S. The humidity was maintained at 40 ± 5%. Feed intake, milk yield, milk composition, milk fatty acids, and digestibility were measured. Compared with TN, HS goats had lower ($P < 0.05$) feed intake, milk yield, and milk protein. Soybean oil increased ($P < 0.01$) milk fat by more than 30% and conjugated linoleic acid (CLA) by more than 360%. The Soybean oil supplementation increased milk fat with the same magnitude regardless the ambient temperature. Goats under HS had 5 to 9 points greater ($P < 0.05$) digestibility coefficients than TN goats. In conclusion, feeding soybean oil to heat-stressed dairy goats was a useful way to increase milk fat, CLA, without any effects on intake, milk yield, or milk protein content.

Table 1.

	Treatment				
Item	TN-C	TN-S	HS-C	HS-S	SEM
DMI, kg/d	2.26[a]	2.26[a]	1.47[b]	1.34[b]	0.09
Milk, L/d	1.88[ab]	1.99[a]	1.79[b]	1.75[b]	0.11
Fat, %	3.98[b]	5.07[a]	3.64[b]	4.85[a]	0.14
Protein, %	3.40[a]	3.40[a]	2.85[b]	2.96[b]	0.07
Fatty acids[1]					
<C16	37.4[a]	29.7[b]	34.0[c]	23.4[d]	0.82
C16 + C16:1	39.2[a]	26.3[c]	31.2[b]	22.6[d]	1.36
>C16	22.9[d]	43.6[b]	34.0[c]	53.6[a]	1.40
CLA[2]	0.47[b]	2.17[a]	0.37[b]	1.95[a]	0.38
Digestibility, %					
DM	67.8[b]	68.5[b]	74.0[a]	72.6[a]	1.35
CP	73.4[b]	74.7[b]	78.8[a]	78.6[a]	1.26
NDF	50.5[b]	50.2[b]	58.1[a]	56.6[a]	2.39
ADF	43.5[b]	43.6[b]	52.5[a]	52.8[a]	2.90

[a–d]Different superscripts indicate significant differences between treatments.
[1]<C16 de novo synthesis, >C16 taken up by the gland, C16 + C16:1 de novo and preformed.
[2]Conjugated linoleic acid.

Key Words: heat stress, soybean oil, milk fatty acid

T359 Effects of dietary sea urchin shell powder supplementation on growth performance and ammonia emissions in broilers. C. M. Kim[1], S. C. Kim[2], S. M. Amanullah[2], D. H. Kim[3], H. J. Lee[3], J. H. Choi[4], and I. H. Choi*[5], *[1]Division of Science Education, Chemistry Education Major, Daegu University, Gyeongsan, South Korea, [2]Department of Animal Science (Inst. Agric. & Life Sci.), Gyeongsang National University, Jinju, South Korea, [3]Division of Applied Life Science (BK 21), Gyeongsang National University, Jinju, South Korea, [4]Department of Chemistry, Hanyang University, Seoul, South Korea, [5]Department of Companion Animal & Animal Resources Science, Joongbu University, Geumsan, South Korea.*

A 4-wk trial was conducted to evaluate the effect of diet supplementation with sea urchin shell powder and vitamin D on growth performance and ammonia fluxes in broilers. A total of 240 broiler chickens (Arbor Acres) were allocated in 4 treatments with 3 replicates of 20 birds and fed diets supplemented with 0 (control), 0.1% (T1) and 1.0% (T2) sea urchin shell powder or 1% (T4) vitamin D. The feeding program consisted of a starter diet until 3 wk of age and a finisher diet until 4 wk of age. All broilers and feed were recorded for calculation of growth performance at 1 and 28 d. A 100 g litter sample was collected weekly from 4 random locations within each pen to measure pH. Ammonia fluxes of 4 different sampling locations sampling location were analyzed using a multi-gas analyzer. During the experimental period, there were significantly differences ($P < 0.05$) among all treatments with and no sea urchin shell powder (0.1% and 1%) or vitamin D (1%) in body weight, feed intake, and feed conversion (feed:gain ratio), except for initial body weight. Litter pH values in treatments with 0.1% and 1% sea urchin shell powder and 1% vitamin D (pH 5.87 to 6.77) were significantly lower ($P < 0.05$) than the control treatment (pH 7.60 to 7.73) at 2 through 4 wk. Ammonia fluxes were reduced by 0.1% and 1% sea urchin shell powder and 1% vitamin D treatment ($P < 0.05$) at 2 and 4 wk. When compared with the controls at 4 weeks (25.11 ppm), 0.1%, and 1% sea urchin shell powder (17.78 ppm and 15.67 ppm) and 1% vitamin D (18.11 ppm) resulted in reduction ammonia fluxes form litter by as much as 29.2%, 37.6%, and 27.9%, respectively. Based on the results of this experiment, adding 0.1% and 1% sea urchin shell powder to poultry diets holds great promise for feed additive in broilers or for reduction in environmental impacts, suggesting that a decrease in ammonia fluxes was chiefly related to the lower litter pH.

Key Words: sea urchin shell powder, growth performance, ammonia

T360 Effect of oral supplementation with colostrum and cross-fostering on gilt's litter performance focused on low birth weight piglets. R. Muns*[1], C. Silva[2], X. Manteca[1], and J. Gasa[1], *[1]Servei de Nutrició i Benestar Animal (SNiBA), Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Barcelona, Catalonia, Spain, [2]Departamento de Zootecnia, Universidade Estadual de Londrina, Londrina, Paraná, Brazil.*

The experiment studied the effect of oral supplementation of small piglets, born weighing less than 1.35kg (CON: control group; COL: 15 mL of sow colostrum fed within 4 h after birth), and the effect of cross-fostering 24 h after farrowing on litter performance (litters fixed at 11 piglets, with 3 piglets being born weighing less than 1.35 kg, HL; or with all the piglets being born weighing less than 1.35 kg, LL). Fourteen litters from primiparous sows with 154 piglets (81 small piglets) were used. Litters were allocated to 1 of the 4 treatments: CON-HL, CON-LL, COL-HL, COL-LL. Piglets were weighed on d 1 and 19 postpartum. Mortality was recorded. Data was analyzed using GLIMMIX procedure of SAS with litter as experimental unit and treatment effects and their interaction introduced in the model. At d1, gilts did not differ for litter average piglet BW or CV of litter BW, although HL gilts had quantitatively higher litter average piglet BW than LL gilts (1.52 vs. 1.23 ± 0.028 kg; $P = 0.214$). As expected, HL gilts had higher litter average piglet BW than LL gilts at d 19 (5.43 vs. 4.38 ± 0.267 kg; $P < 0.001$), in addition, LL gilts increased litter average piglet BW when combined with COL rather than with CON (4.81 vs. 3.96 ± 0.153kg; $P = 0.035$). Compared with CON, COL supplementation reduced CV of litter BW at d19 ($P = 0.076$), especially when combined with LL (18.9 vs. 10.1 ± 1.37%; for CON-LL and COL-LL respectively; $P = 0.025$). No small piglets died in HL litters during lactation, and CON-LL nearly doubled COL-LL small piglet mortality rate (8.0 vs. 4.6 ± 0.67%) although such differences were not significant. Allocating small piglets in the same litter through cross-fostering reduced litter growth with numerical negative effect on mortality. Nevertheless, colostrum supplementation of small piglets to improve growth and survival is especially recommended in litters fixed with all of the piglets being small.

Key Words: pig, colostrum, cross-fostering

T361 Forage intake by grazing lactating cows kept in creep-feeding system. V. R. M. Couto*[1], M. F. Paulino[2], N. F. De Paula[2], E. Detmann[2], S. C. Valadares Filho[2], I. M. De Oliveira[2], I. F. S. Maciel[2], C. H. A. Cabral[2], E. Arnhold[1], and J. J. R. Fernandes[1], *[1]Universidade Federal de Goias, Goiania, Goias, Brazil, [2]Universidade Federal de Vicosa, Vicosa, Minas Gerais, Brazil.*

The objective was to evaluate the milk production, the change in body weight (BW) and body condition score (BCS), forage intake, and digestibility of dietary components by lactating Nellore or crossbred cows, with zebu blood predominance, kept under creep-feeding system from 4 to 8 mo of lactation. Forty-one cows and their respectively calves were used. Each set (dam and calf) was randomly assigned to one of 5 supplementation strategies of energy-protein supplement, as follows: control (without energy and protein source, mineral mixture only fed ad libitum), T250 (0.250 kg/animal), T500 (0.500 kg/animal), T750 (0.750 kg/animal), and T1000 (1.000 kg/animal). The forage DM intake, as well as other dietary components were not ($P > 0.10$) affected by treatments and was on average 10.171 kg/day or 22.734 g/kg of BW. No differences were observed ($P > 0.10$) for total digestible nutrients (TDN) intake by the cows with increasing levels of supplementation of the offspring. The digestibility of organic matter, crude protein and neutral detergent fiber did not differ ($P > 0.10$) among treatments. A quadratic effect was observed ($P < 0.10$) for variation of BW gain with a maximum gain of cows when the calves are supplemented with 0.598 kg of concentrate. There was an increase in BW ($P < 0.10$), on average 13.8 kg in cows which calves were supplemented, to the control treatment, this variation was only 1.9 kg throughout the experimental period. There was a linear decrease in milk intake as it provided the concentrate to calves ($P < 0.02$) for each kg of supplement provided to offspring, 2.088 kg of milk was no longer consumed by these calves. The supplementation of suckling calves with protein-energy sources results in lower milk production by the dams and consequently allows an increase in BW of the cows.

Key Words: *Brachiaria decumbens*, energy supplementation, protein supplementation

T362 Heart rate and energy expenditure in pure and crossbred beef cows grazing two allowances of native pastures in Uruguay. A. Espasandin*[1], P. Batista[1], P. Soca[1], M. do Carmo[2], and M. Carriquiry[1], *[1]School of Agronomy, Udelar, Paysandu, Uruguay, [2]INIA-Tacuarembo, Tacuarembo, Uruguay.*

There is information that have demonstrated that heart rate (HR) is an appropriated estimator of energy Expenditure (EE, or heat production) in dairy and beef cows. The objective of this work was to estimate the EE from HR in multiparous beef cows of 2 genotypes: purebred Angus and Hereford (PB), and crossbred F1 (AH and HA; CB) grazing high (HI) or low (LO) forage allowances (6 and 10 kg DM/100 kg LW/day, respectively) of native grasslands in Uruguay. The HR (beats/min) was measured in 24 beef cows (4/treatment) during 5 consecutive days in the summer (lactation period) and registered with individual radio transmitters each 15 s. The EE was estimated using predefined equations relating O_2 pulse and HR and assuming a constant value of O2 uptake-bit between and within cows (HR/day × 0.343 mL O_2/(beat × kg $LW^{0.75}$) × (21.47 J/mL O_2) × (1440 min/day)/1000 J/kJ). The effects of cow genotype, forage allowance and their interaction were analyzed by ANOVA and adjusted Tukey LSmeans were obtained. The HR and EE were affected ($P < 0.05$) by cow genotype, forage allowance and their interaction. CB and LO cows had greater ($P < 0.05$) EE than PB and HI (1174 ± 85 and 1160 ± 72 for CB and LO, vs. 920 ± 59 and 933 ± 74 kJ/day/kg$LW^{0.75}$ for PB and HI, respectively). Those values result as consequence of greater ($P < 0.05$) HR (109 ± 8 and 107.7 ± 7 vs. 86 ± 6 and 87 ± 7 bits/minute). However, the HR was greater ($P < 0.05$) for CB-LO than PB-HI, PB-LO and CB-HA (133 ± 12, 85 ± 8, 83 ± 8 and 86 ± 11 kJ/day/kg$LW^{0.75}$, respectively). The greater EE probably were related to the longer daily grazing time, and consequently dry matter intake, in these cows.

Key Words: beef cow, energy expenditure, forage allowance

T363 Effect of forage allowance on individual and per area production of primiparous beef cows grazing Campos native pastures. M. Claramunt[1], M. Carriquiry[3], and P. Soca*[2], *[1]Facultad de Veterinaria, Universidad de la Republica, Paysandu, Uruguay, [2]Facultad de Agronomia, Universidad de la Republica, Paysandu, Uruguay, [3]Facultad de Agronomia, Montevideo, Uruguay.*

The objective of this study was to evaluate 2 levels of forage allowance (FA) on forage mass (FM) and productivity of primiparous beef cows grazing Campos native pasture. The study took place in Facultad de Agronomía, Uruguay (31°S 57°W). Eighty primiparous cows were assigned to a completely randomized experiment of 2 FA in spatial replication on 2 blocks during 2 years. The experiment started in autumn −150 d postpartum (dpp) and finished 190 dpp. Annual FA averaged 6 and 10 kg DM/100kg liveweight (LW)/d for low (L) and high (H) FA, respectively. The grazing system was continuous. Cow BW and FM were measured monthly and used to adjust FA using the "put and take" method. At 82 ± 12 dpp, cows were exposed to bulls for 80 d. Calf suckling was restricted with a nose plate for 12 d and cows were offered 2 kg/d during 20 d of whole rice middling at 76 ± 12 dpp. Pregnancy diagnosis (PRE) was performed at 205 ± 12 dpp. To use PRE in individual production a reduction of 10% was applied to include calf losses from pregnancy to weaning. Calf weaning weight was adjusted to 205 d (CW). Individual production (kgLW/cow) was calculated as PRE × CW. SR (kgLW/ha) was calculated with testers plus grazers cows × testers weight/plot area. Production/ha was calculated as SR in animal units (380 kg/cow) × individual production. The experimental unit was the plots and group of cows for FM and animal measurements, respectively. Effect of FA on PRE was analyzed by generalized linear mixed model using the logit link function for a binomial distribution. CW and SR were analyzed using a generalized linear model and repeated measurements respectively. Greater FA improved FM (L = 1212 vs. H = 1474 ± 33 kg/ha, $P < 0.004$), PRE (L = 0.6 vs. H = 0.9 ± 0.04; $P = 0.07$) and CW (L = 175 vs. H = 194 ± 16 g, $P < 0.05$). FA did not affect SR but values were quite different (L = 437 vs. H = 339, $P < 0.12$). However H FA increased production/ha (L = 100 and H = 138 kg/ha). In conclusion, greater FA increased production and reproduction of primiparous cows grazing Campos native pastures.

Key Words: forage allowance, stocking rate, beef cow

T364 Natural occurrence of mycotoxins and toxigenic fungi on corn and sorghum silage in Sao Paulo State, Brazil. C. A. R. Rosa*[1,2], L. A. K. Keller[1,2], M. Aronovich[3], and L. R. Cavaglieri[4], *[1]University Federal Rural of Rio de Janeiro (UFRRJ), Seropédica, RJ, Brazil, [2]Conselho Nacional de Pesquisas Científicas (CNPq), Belo Horizonte, MG, Brazil, [3]Agricultural Development Company of the Rio de Janeiro State (PESAGRO), Niteroi, RJ, Brazil, [4]Universidad Nacional de Río Cuarto (UNRC), Rio Cuarto, Cordoba, Argentina.*

Silage is a common widespread practice to preserve forages in Brazil. Poor storage conditions can lead to mold contamination and mycotoxin production. The aim of this study was to establish the occurrence of toxigenic fungal species and to determine aflatoxins (AFs), ochratoxin A (OTA), fumonisin B_1 (FB_1) and deoxinivalenol (DON) in corn and sorghum silages intended for bovines before and after fermentation in farms located São Paulo State in Brazil during period of 2009 to 2012. Fungal counts were done by surface-spread method and toxigenic ability of isolates strains was evaluated with in vitro conditions. AFs and OTA natural contamination was determined by TLC and HPLC. DON and FB_1 was determinate by ELISA. Total fungal counts were generally high (molds that exceeded 1×10^4 cfu/g). *Aspergillus flavus*, *Penicillium citrinum*, and *Fusarium verticillioides* were the prevalent toxigenic strains were isolated. Aflatoxin levels differed ($P < 0.0001$) from 2 to 45 µg/kg and from 2 to 100 µg $kg^{-1\ in}$ pre and post-fermentation samples, respectively (Table 1). OTA, FB_1 and DON levels found in pre-fermentation samples were higher than in post-fermentation (Table 1). Mycotoxins and toxigenic fungi are present before and after fermentation in silages. Aflatoxin B_1 (AFB_1) increased during storage whereas OTA, FB_1 and DON had a little decrease. Determination of mycotoxin levels and their frequency of occurrence in corn and sorghum silage (the main substrates used in Brazil) are important to provide information so that the assessments of risk for animal feed and livestock environment can be made.

Table 1. Mycotoxin levels found in silages samples before and after fermentation (pre- and postfermentation)

Sample	Mycotoxin	Contamination frequency (%)	Level range (µg/g)	Samples exceeding regulation limits[1] (%)
	AFB_1	31	0.002 – 0.045	0
	OTA	9.5	2.00 – 30.00	100
	FB_1	20	0.31 – 2.00	0
Prefermentation	DON	26	0.50 – 2.00	0
	AFB_1	40	2.00 – 100.00	84
	OTA	7	4.47 – 20.39	100
	FB_1	30	0.32.- 2.00	0
Postfermentation	DON	20	0.30 – 1.00	0

[1]Limits: 0.02 µg/g AFB_1 (GMP, 2008), 0.25 µg/g OTA, 50 µg/g FB_1, 12 µg/g DON (EU, 2006).

Key Words: aflatoxin, feedstuffs, mycotoxin

Teaching/Undergraduate and Graduate Education: Teaching and Learning Tools for Animal Sciences

T377 A learner-centered approach to teaching animal reproduction. J. Moro-Mendez*, *EARTH University, Guacimo, Limon, Costa Rica.*

The objective of this study was to develop a method to assess the learning of animal reproduction and artificial insemination (AI) by students enrolled in EARTH University. The student population comes from 25 countries (Africa, Caribbean, Latin America, and the United States). Within the curriculum there are animal science courses, one being Animal Reproduction and Lactation. This second-year course is based on a student-centered approach and combines hands-on practices and theory aimed at facilitating the understanding of reproductive physiology as well as the acquisition of skills, such as AI, body condition scoring, animal welfare assessment, and heat detection. The course is given to 2 groups (approximately 27 students each) from January to May and 2 other groups from September to December. From January 2011 to December 2012, a total of 213 students were evaluated with a questionnaire at the beginning and end of each session to obtain an objective evaluation of their knowledge and skills related to animal reproduction. Grades were analyzed by a one-way ANOVA to determine the effectiveness of the course. The mean grades of the first and second questionnaires were different ($P < 0.05$), 2.7 and 8.1, respectively (in a scale from 1 to 10). At the beginning of each session, 9.5% of the students reported to have some knowledge and/or limited practice of semen thawing and AI; in contrast, the written evaluation showed that 98% of the students did not know how to properly handle frozen semen, or how to perform AI. At the end of the sessions 82% of the students were able to correctly execute each step of the AI process. A group of 23 cycling Brahman cows was synchronized, and students randomly selected from 2 groups (September–December 2012) were assigned to inseminate them in November 2012. After a period of 35 d, 8 cows (34.8%) did not return to heat and were deemed pregnant. It was concluded that the course allowed students the acquisition of a working knowledge of animal reproduction and AI. Additionally, the evaluation tool provided for an objective assessment of the student learning outcome.

Key Words: student-centered, reproduction physiology, artificial insemination.

T378 Targeting global competencies in animal sciences: Reproduction cases on Mexico. J. J. Parrish* and R. L. Monson, *University of Wisconsin, Madison.*

A global perspective is essential to success of the modern animal scientist. Students are unlikely to take specific courses in global competencies or do not have the flexibility. It is essential that a global perspective be incorporated into the required courses in animal sciences. In the fall of 2011 we initiated case study work in a required Reproductive Physiology course dealing with Mexico. Products were a website that presented background and solutions to the case, and a public service announcement related to the case but targeted at a Mexican audience. Results were from evaluations of the project in the fall 2012 semester. The global learning outcomes we sought to address were (1) critical thinking skills and application to solving problems related to a foreign country, (2) communication skills and in particular, strategies to communicate in a language other than English, and (3) appreciation of ethical issues in global agriculture as they relate to reproduction manipulation. The overall impacts we expected to have on students were (1) understanding how theory applies to application in the novel environment of a new culture and ethical system, (2) empathize with individual that have differences based on culture and ethnicity, and (3) development of human capacity for competitiveness in global agriculture. Survey questions were scored on a 1 – 5 scale with 1 being not successful, 3 being somewhat important and 5 being very successful (n = 84). The mean ± SEM scores indicate that the project increased global awareness/competency (3.71 ± 0.11); use of electronic communication tools (3.26 ± 0.13); appreciation of ethical issues in a global agriculture (3.94 ± 0.10); critical thinking ability (4.06 ± 0.11); empathy for individuals whose differences are based on culture, social-economic status, and/or ethnicity (3.92 ± 0.11); and preparedness for understanding global issues in agriculture (3.96 ± 0.11). The approach encouraged students to investigate Mexico, utilize both verbal and written communication skills and appreciate challenges faced in the management of reproduction in Mexico.

Key Words: case studies, international, reproduction

T379 Evaluation of relationships between questions on the IDEA survey for university and animal science courses. M. J. Anderson, K. J. Stutts, M. M. Beverly*, and S. F. Kelley, *Sam Houston State University, Huntsville, TX.*

The Individual Development and Educational Assessment (IDEA) survey is a mechanism that uses student feedback to assess and improve teaching, learning, and the higher education process. The IDEA survey contains questions pertaining to course objectives, teaching methods and styles, and a description of the course with the goal of determining the quality of the instructor and overall course. The objective of this study was to determine relationships among questions on the survey and to determine if differences existed between animal science courses and all other courses offered at the university. Data from 27,430 courses (238 animal science courses) taught over a 6-year period at Sam Houston State University were used in this study. Correlations were calculated between all questions on the survey to determine if relationships existed between each of the individual questions for both university (Univ) and animal science (AnSc) courses. Questions which pertained to the amount of work, assignments, and overall course difficulty (questions 33–35), were not strongly correlated ($r < 0.70$; $P < 0.01$) to any other survey questions for Univ or AnSc courses. Additionally, for AnSc courses, questions concerning the desire to take the course regardless of the instructor and students' workload compared with other courses (questions 37 and 39) were not strongly correlated ($r < 0.70$; $P < 0.01$) to any other survey questions. For Univ courses, questions pertaining to instructor abilities and progress toward specific objectives (questions 1–32) were consistently strongly linked ($r > 0.70$; $P < 0.01$) to each other. However, for AnSc courses, this association between questions 1–32 was weaker than the association observed for Univ courses. These correlations indicate that students in animal science have a different perception of courses than the university student body as a whole. As instructors in animal science, it is our obligation to identify how our students differ from the rest of the university and adjust our teaching styles to accommodate those differences.

Key Words: undergraduate teaching, IDEA, animal science

T380 Implementation of a hybrid-flexible instructional model in the animal sciences—Technical considerations to optimize student educational experience. M. C. Chakerian*, T. A. Evans, B. A. Wenner, R. W. Flood, M. R. Hendrick, H. N. Zerby, and J. M. Osborne, *The Ohio State University, Columbus.*

Instructors of the animal sciences writing course Animals in Society redesigned it to utilize technology to enhance the student learning experience (funded by the OSU Office of Distance Education and eLearning). The priority was to provide students flexibility for how and where they attended lectures, while considering student preferences for in-person engagement with the instructor and/or lack of confidence in technology skills. Increased class size, limited access to large lecture halls, and issues with student movement on the Columbus campus due to conversion to a semester system contributed to the need for course attendance options. The Hybrid-Flexible (Hy-Flex) Instructional Model is a course framework that allows students to choose daily to attend lecture in-person or synchronously online. Elements of the delivery system were selected for compatibility with classroom infrastructure and the OSU course management system, cost to students, and ease of use by instructors and students. Based on these criteria, Adobe Connect and Poll Everywhere were selected; an activity was designed for students to test the technologies before course implementation. In autumn 2012, 94 students consented to participate in a research study. At the start of the term, 8% of students noted they would always/almost always attend class online, while 79% indicated they planned to attend mostly/always in person. At the conclusion of the course, 72% reported attending always/almost always online, while 21% reported attending almost always/always in person. Attendance data support student perception. For the term, 19% of students attended online less than 20% of the time and 64% attended online greater than 60% of the time. The problem most frequently reported by students attending online was wireless access in their location. Student perception of satisfaction and comfort with technology utilized both exceeded 85%. Results suggest that the technologies employed satisfied the criteria to support student engagement with the course and provided a highly acceptable alternative for students.

Key Words: technology, online, anytime/anywhere learning

T381 Student perception of horsemanship skills after completion of a horse judging course. M. Nicodemus*, T. Bova, and B. Tisdale, *Mississippi State University, Mississippi State.*

Through thorough consideration horse judging officials form an opinion concerning the ranking of horse show classes they are judging and this is done using their past horse experience. Through collegiate horse judging courses students develop the experience needed to judge. This experience is often based on observations of horse show classes, but it usually does not include the students performing the activities associated with the class they are judging; and thus, study objective was to determine if through the observational activities during a collegiate horse judging course students gain a perceived ability to be able to perform the classes they are judging. A 19 question survey was given to students (n = 20) at the start and end of a collegiate horse judging course with questions focused on the students' perceived ability of their horsemanship skills using a Likert scale of 1–5 with higher scores indicating a higher perceived ability to perform the horsemanship activity. Average scores were determined for each question and analyzed by a one-way ANOVA to determine the influence of the course on perceived horsemanship abilities. All questions showed score improvement with 3 questions resulting in significant increase of scores ($P < 0.05$) in which these questions focused on more advanced pattern work on the ground and under saddle, which were all topics covered in the course. None of the questions resulted in an average score of 5 as the highest score was 4.5 given for 2 questions for the final course survey focused on basic ground handling and health care activities. By the end of the course, the lowest score was 3.1 with the question focusing on advanced riding activities specific to society-type breeds in which these breeds and their associated classes such as native costume, liberty, and saddle seat were not covered in this course. In conclusion, while the learning objectives of a collegiate horse judging course are not focused on developing horsemanship skills, the students' perception of their horsemanship abilities may be improved by the development of their abilities to judge the classes associated with these horsemanship activities.

Key Words: horse judging, horsemanship

T382 Reorganization of experiential learning activities into a single multi-section course. A. C. Dilger*, L. Redman, and W. L. Hurley, *University of Illinois, Urbana.*

Encouraging students to engage in out-of-the-classroom learning experiences is a long-standing priority in the Department of Animal Sciences at the University of Illinois. Recently, experiential learning opportunities fulfilling this curriculum requirement were organized under one multi-section course. Students are required to complete a memorandum-of-agreement with a faculty supervisor outlining their proposed activity, learning objectives, and work product to demonstrate their learning. Considerable flexibility was maintained within this organization so that students can pursue a wide range of experiences. This reorganization provides the opportunity to evaluate the breadth of the students' experiential learning activities. From the summer 2012 through spring 2013, 185 students (39% of the animal sciences majors) completed 238 experiences supervised by 38 different faculty supervisors. Students engaging in multiple experiences accounted for 17.7% of the total, with 14.3% engaging in 2 experiences and 3.4% engaging in 3 to 5 experiences. Students earned 1 (49.2%), 2 (29.8%), 3 (13.0%), or 4 h (8.0%) of credit for experiences across an array of activities. The majority of experiences involved undergraduate research (33.2%). A substantial number of experiences reflected a companion or exotic animal interest including internships at a local county humane society (18.9%), companion animal spring break trip (13.4%), working with a veterinarian (8.0%) and interning at zoos, sanctuaries or rescue organizations (3.0%). Other experiences included teaching assistance in the required animal handling course (8.0%), on-campus special projects (4.2%) and internships with agriculture groups (1.7%) or companies (1.7%). Study abroad accounted for 3.8% of the experiences. Organization of diverse experiential learning opportunities under one course number with multiple sections provides important information about the range and nature of opportunities in which students engage. This allows the department to further enhance the value of experiential learning to its students.

Key Words: experiential learning, course organization, undergraduate

T383 Effect of correcting missed exam questions (regrading) as a learning tool in physiology courses. J. Winkler*, A. Sexten, A. Rhodes, and T. Rozell, *Kansas State University, Manhattan.*

Teaching large lecture courses presents many challenges for enhancing and monitoring student learning using exams. One technique that may improve student learning and provide more individualized opportunities for instructor feedback is the use of an exam "regrading" exercise. Students in ASI 533, Anatomy and Physiology, at KSU have the opportunity to correct exam questions and receive up to half credit for

points originally missed. This assignment allows students an opportunity to correct misconceptions soon after the exam, with an incentive of receiving credit to improve their overall score. The objective of this study was to determine whether performance on the regrade assignment is predictive of the comprehensive final exam and overall grades in the course. To meet this objective, original exam scores, regrade scores, final exam scores, and overall course scores were analyzed by ANOVA (n = 999). Data have been compiled over the past 7 years, beginning in the fall of 2005. Students doing at least one exam regrade had significantly greater mean final exam scores and overall course grades ($P < 0.05$). The results varied from year to year, but in most years students that did regrades for at least 3 exams had greater final exam and overall course grades ($P < 0.05$) than those doing no regrades. From our results it appears that the exercise of going through exam questions missed soon after the test and explaining the correct answer is valuable for student comprehension and likely retention of basic concepts, as assessed by the comprehensive final exam and overall course grades.

Key Words: student learning, exam regrades, comprehension

Graduate Student Competition: ADSA Dairy Foods Division Oral Competition

14 Tracking heat-resistant, spore-forming bacteria in the milk chain: A farm-to-table approach. M. Estrada*, J. Stratton, and A. Bianchini, *University of Nebraska-Lincoln, Lincoln.*

Thermoduric spore-forming bacteria *Bacillus* and *Paenibacillus* spp. can survive processing and refrigerated conditions causing spoilage of fluid milk, limiting the shelf life of the product beyond 14 d. The objective of this study was to evaluate the fluid milk chain for *Bacillus* and related genera to identify their potential sources. Raw milk, pasteurized milk and environmental samples representing the farm-to-table continuum were collected in the spring of 2012 from a dairy farm and a medium-size processing plant in the Midwest, supplied exclusively by that farm. Environmental samples from the dairy farm included feed, drinking water, bedding material, manure, milking parlor wash water, teat cloths and sponges (milking clusters and teats). Environmental samples from the processing plant included rinse water (tanks and mixer), and swabs (filler's surface and nozzles). Environmental and raw milk samples were heat-treated at 80°C for 12 min to eliminate vegetative cells. Pasteurized milk samples were evaluated for quality and, along with heat treated samples, stored at 6°C for 21 d. Samples were enumerated for microbial load and the plates used for bacterial isolation throughout storage. Colonies with the distinct morphology of *Bacillus* spp. were isolated and characterized using a subtyping method based on the DNA sequence of their rpoB gene. A total of 34 different rpoB allelic types representing *Bacillus* (99% of isolates) and *Paenibacillus* spp. (1%) were identified among 72 bacterial isolates. The *Bacillus* spp. clade was represented mainly by *B. licheniformis* (40% of isolates), *B. pumilus* (33%) and *B. subtilis* (14%). Two allelic types were identified in both raw and pasteurized milk, indicating the raw milk supply as a possible source of these bacteria. Six allelic types were found in milk and environmental samples (farm and processing plant), suggesting that these bacteria can enter the fluid milk chain from different sources. This data will help in the development of intervention strategies for controlling spoilage by spore-formers and extending the shelf life of pasteurized milk.

Key Words: HTST milk, spore-formers, subtyping

15 Pulse electric fields treatment maintains the antiproliferative activity of the milk fat globule membrane on colon carcinoma cells. S. Xu*[1], M. Walkling-Ribeiro[2,1], M. W. Griffiths[2,1], and M. Corredig[1], *[1]University of Guelph, Guelph, ON, Canada, [2]Canadian Research Institute for Food Safety (CRIFS), Guelph, ON, Canada.*

The milk fat globule membrane (MFGM) components have antiproliferative activities against colon cancer cells. The present work investigated the effect of processing of the cream on the antiproliferative activity of MFGM. Unheated cream and commercially pasteurized cream were collected from a local dairy immediately after separation. Pulsed electric fields (PEF) with 37 kV/cm field strengths for 1705 μs was applied to unheated cream, at 50°C and 65°C. The electrode gap was 0.21 cm and the flow rate of cream was 25 mL/min. PEF control treatments were carried out at 50°C and 65°C for 3min, the passage time in PEF chamber to mimic the effect of heating. For comparison, the unheated cream was also heat treated at 5 different temperature/time combinations: 50°C/10 min, 60°C/2 min, 60°C/10 min, 70°C/30 s and 70°C/2 min. After processing, all cream was processed to butter, and MFGM isolates were obtained from buttermilk using centrifugation at 70,000 × *g* for 45min at 15°C. The antiproliferative activity of extracts was tested on human adenocarcinoma HT-29 cells, incubated for 24 h then stimulated with 0.4, 0.2, or 0.1 mg/mL various MFGM isolates for another 24 h. Cell proliferation was tested using a colorimetric method (BrdU). All samples heated below 70°C showed significant cell reduction ($P < 0.05$, using ANOVA) from control at the highest 2 concentrations, with 70°C/30 s sample only at the highest concentration. The 70°C/2 min sample even helped cell growth, comparable to the commercially pasteurized sample. There was a reduction up to 52% in cell proliferation in PEF samples, with no significant difference compared with PEF controls, suggesting electrical field itself did not affect the anticarcinogenic activity of MFGM. Commercially pasteurized samples and heat treated samples showed a decrease in bioactivity. PEF did not change the phospholipids composition compared with PEF controls, while heating showed protein-protein interactions and a decrease in phospholipids as measured by ^{31}P NMR. PEF may be a promising process to maintain valuable bioactivity in the MFGM.

Key Words: milk fat globule membrane (MFGM), anticarcinogenic activity, pulsed electric field (PEF)

16 Effect of the heating of whey proteins in the presence of milk fat globule membrane extract or phospholipids from buttermilk. M. Saffon*[1], R. Jiménez-Flores[2], M. Britten[3], and Y. Pouliot[1], *[1]STELA Dairy Research Center, Institute of Nutrition and Functional Food (INAF), Laval University, Quebec City, QC, Canada, [2]Dairy Products Technology Center, California Polytechnic State University, San Luis Obispo, [3]Food Research and Development Center (FRDC), Agriculture and Agri-Food Canada, St-Hyacinthe, QC, Canada.*

Previous work suggests that phospholipids from buttermilk were involved during the heat-induced formation of protein aggregates from whey and buttermilk proteins. It was hypothesized that "free" phospholipids from buttermilk initiates the formation of whey proteins aggregates. Whey protein isolate (WPI) was dispersed in water to a concentration of 5% protein (w/v), and the pH was adjusted to both 4.6 and at 6.8. Solutions were heated to 65°C or 80°C for 15 min under constant stirring. Milk fat globule membrane (MFGM) extract isolated from whey buttermilk or commercial phospholipids (PL) powders were dispersed in the WPI solutions at 1.0% (w/v) before heating. The aggregate composition was characterized with Ellman's reagent (free thiols), SDS-PAGE electrophoresis, thin layer chromatography (TLC), and 3-dimensional confocal laser-scanning microscopy (CLSM). All experiments were performed in triplicate and the concentration of free thiol groups were tested according to a factorial design. Addition of phospholipids or MFGM extract did not significantly affect the liberation of free thiol groups of whey proteins but delayed the loss of the native form of major whey proteins by 5 min at pH 6.8. TLC profiles showed no trace of phospholipids after 20 min of heating WPI-PL mixtures at 80°C at pH 4.6. CLSM images confirmed that only a few interactions occurred between whey proteins and MFGM proteins/phospholipids in the whey solution, while the interactions were frequent in the presence of MFGM extract or phospholipids. Overall, our results show evidence that phospholipids from buttermilk are involved in the formation of protein aggregates through the MFGM fragments at 65°C, whereas they can directly interact with the proteins at 80°C. Results allow the consideration of

new potential applications for the use of dairy products that are rich in phospholipids such as regular or whey buttermilks.

Key Words: buttermilk, phospholipid, aggregation

17 Effect of ultra-high pressure homogenization on physicochemical properties of pasteurized skim milk. M. S. Mohan*, R. Ye, and F. Harte, *Department of Food Science and Technology, University of Tennessee, Knoxville.*

Recent developments in material science and engineering enabled us to study the effect of ultra-high pressure homogenization (HPH; up to 500 MPa) on the physicochemical properties of milk. We report the effect of HPH of pasteurized skim milk (0 to 500 MPa followed by immediate chilling) on pH, apparent casein micelle size (dynamic light scattering; pH 2 to 10), turbidity (absorbance at 550 nm; pH 2 to 10), heat stability (120°C; pH 6.3 to 6.7), viscosity (flow curve), and viscoelasticity after rennet addition (G′; 90 min, 1Hz, 0.1% strain). All HPH milks were stable for more than 10 d without visible coagulation. The pH of all except 500 MPa milk were slightly higher (up to 0.13 pH units) than 0 MPa milk (pH 6.81). Maximum casein micelle size was observed after HPH of milk at 500 MPa (ca. 500 nm) compared with 0 MPa milk (ca. 250 nm) at pH 5. However, 500 MPa milk remained stable above this pH and coagulated together with the other milks below pH 5. From pH 6 to 8 the casein micelle size of 500 MPa milk decreased until it was same as 0 MPa milk at pH 9 and 10. Although the absorbance of 0 MPa was higher than 500 MPa milk at pH 8 to 10, indicating differences in particle size and absorbance observations, the trend was similar for both measurements at pH 6 and 7. At normal milk pH (6.6 and 6.7) all the HPH milks remained stable for 24 min at 120°C. With increase in pressure the casein micelles were first partially broken down (at 100 MPa), re-aggregated (until 400 MPa) and then re-dispersed (at 500 MPa), confirmed by microscopic image and particle size analysis. The rennet coagulation of 500 MPa milk did not occur even after 90 min. Overall, 500 MPa pressure did not significantly affect the pH, heat and shelf stability of milk, but altered the viscosity and renneting properties. Further understanding these changes will enable the novel use of HPH milk proteins as ingredient in products including cheeses.

Key Words: high pressure homogenization, pasteurized skim milk, casein micelle

18 Performance of modified milk protein concentrates in model high-protein nutrition bars. J. Banach*, S. Clark, and B. Lamsal, *Iowa State University, Ames.*

The nutritional value and flavor of milk protein concentrates (MPC) are desirable for high-protein nutrition (HPN) bar applications. However, rapid hardening and crumbly texture upon incorporation limit its use. Extrusion and toasting were used to modify MPC at 80% protein (MPC80) and performance was evaluated in model HPN bars. MPC80 was extruded in a twin-screw co-rotating extruder at 2 ramped temperature profiles with die temperatures of 65 or 120°C. Extrudates were dried and finely ground (<250 mm). Toasting of MPC80 was done in a convection oven at 75 or 110°C for 4 h. Model bars contained 30% protein, 22% glycerol, 19% palm kernel stearin, 12% maltitol syrup, 10% high-fructose corn syrup, and water. Dough was sealed into cylindrical molds and in water activity sample cups, and stored at 22, 32, or 42°C. Bar texture (hardness, fracturability, and shear), water activity, and color change were measured over 42 d. Disulfide bond formation in bars was studied with sodium dodecyl sulfate PAGE (SDS-PAGE). Sample means were compared with Tukey's adjusted *P*-value ($P < 0.05$). Toasted MPC80 in bars had texture similar to unmodified MPC80 (control). Bars prepared with MPC80 extruded at 65°C were significantly softer than bars made with control MPC80. Significant difference in hardness and fracturability between bars formulated with MPC80 extruded at 120°C and those prepared with control MPC80 was intermittent. Water activity of the bars increased slightly during storage, but remained less than 0.65, which assured shelf stability. Total color change was limited at 22°C storage, but increased significantly at 32°C and 42°C. Non-reduced SDS-PAGE showed that the whey protein in bars prepared with extruded MPC80 was not soluble on Day 0; its solubility under reduced conditions indicated that disulfide bonds were formed before bar manufacture. Internal protein aggregation did not occur because free sulfhydryls were previously reacted, and thus low temperature (65°C) extrusion of MPC80 may improve performance in HPN bars.

Key Words: milk protein concentrate, high-protein nutrition bar, texture

19 Concentration of milk by ultrafiltration modifies the acid-induced gelation properties of casein micelles. Y. Li* and M. Corredig, *University of Guelph, Guelph, ON, Canada.*

Membrane filtration is a widespread unit operation in dairy technology, and little is understood on how concentration by ultrafiltration (UF) and diafiltration (DF) may change the processing functionality of the casein micelles. This study investigated the acid (gluconoδ-lactone, 1.3% wt/wt for control; 1.8% wt/wt for 2×; 3.0% wt/wt for 4×, at 40°C) induced gelation behavior of milk concentrated by UF and DF with and without heat treatment at 80 ± 1°C for 15 min. Measurements of soluble and insoluble calcium by ion chromatography suggested that there was a lower amount of colloidal calcium phosphate in the casein micelles concentrated (4 ×) by UF compared with those in single strength milk. In addition, the amount of colloidal calcium in the heated concentrated milk was significantly lower than for unheated concentrated milk. Size exclusion chromatography on the soluble fraction demonstrated that DF caused compositional changes in the serum fraction compared with UF. The processing history (DF, UF and heating) strongly affected the gelation behavior of the concentrated milk: The gelation pH, measured by rheology and diffusing wave spectroscopy, significantly increased with the extent of concentration ($P < 0.05$, as measured by ANOVA), due to a reduction in the interparticle distance and because of the changes occurring to the soluble fraction. Concentrated samples formed significantly ($P < 0.05$) stiffer gels than control milk because of an increased amount of linkages in the network. DF milk showed a significantly higher gelation pH compared with the UF milk at the same volume fraction. In addition, compared with UF milk, heated DF milk had even higher pH of gelation, but no significant difference in the gel stiffness (pH = 4.6) between the 2 treatments. This work clearly demonstrated for the first time that UF and DF changes the composition of the soluble fraction, and affects the acid induced behavior of concentrated milk.

Key Words: concentrated milk, unheat and heat treatment, gelation behavior

20 The effects of sodium reduction, with and without KCl, on blue cheese. A. Pataky*[1], S. Rankin[2], Z. Vickers[1], and T. Schoenfuss[1], *[1]University of Minnesota, Saint Paul, [2]University of Wisconsin, Madison.*

Blue cheese contains approximately 400 mg sodium per 28-g serving, twice the amount found in Cheddar. Salt is essential to blue cheese ripening and microbial safety. Because blue cheese is often surface-salted, the effects of sodium reduction may be more noticeable in the center of the cheese wheel. The purpose of this study was to evaluate the effects of sodium reduction (25%) on blue cheese composition, flavor, sensory, and proteolytic properties with and without the use of potassium chloride (KCl) at 2 locations in the cheese wheel. Three-kg wheels of pasteurized milk blue cheese were produced from 2,100 kg of milk (in duplicate), and 3 salting treatments were applied to randomly selected wheels. Salt was applied by % weight of the wheel in the following treatments: Control (C; 3.5 wt% NaCl), reduced sodium (R; 2.63 wt% NaCl), and reduced sodium with KCl (RK; 2.63 wt% NaCl, 1.17 wt% KCl). Wheels were evaluated monthly during 5 mo of aging, sampling both inner and outer portions of the cheese wheel. Sodium and potassium concentrations, fat, moisture, pH, a_w, volatile free fatty acids, and extent of proteolysis (as measured by free amino acids) were measured. Sensory attributes (aroma, taste, aftertaste) and volatile flavor chemicals were measured at mo 3 and 5. Salt reductions of 24% and 21% in RK and R, respectively, were achieved. The water activity of C and RK treatments was 0.935 at 5 mo of age. R was higher (0.945). A greater extent of proteolysis was observed in R compared with C. A descriptive sensory panel found higher overall flavor intensity and "waxy" aroma in the inner portion of the cheese compared with outer portions ($P = 0.013$), and in RK when compared with C ($P = 0.036$). Concentrations of medium chain fatty acids were higher in RK than C. Flavor volatiles associated with blue cheese were found in higher concentrations in RK treatment, specifically 2-octanone, 2-nonanone, butanoic acid, and 2-hexanone. A consumer panel (n = 95) ranked overall liking for all treatments similarly, and higher texture liking for RK. Reduction in sodium with and without KCl produced consumer-acceptable blue cheese despite sensory and compositional differences.

Key Words: sodium reduction, blue cheese, KCl

21 Improving the quality of low sodium Cheddar cheese. M. Ozturk*[1], S. Govindasamy-Lucey[2], J. J. Jaeggi[2], M. E. Johnson[2], and J. A. Lucey[1,2], *[1]University of Wisconsin, Madison, [2]Wisconsin Center for Dairy Research, Madison.*

Low Na cheeses often exhibit acidic and bitter flavor and pasty texture. We proposed that starter-induced acidity could be prevented by decreasing microbial activity by the application of high hydrostatic pressure (HHP), and by increasing curd buffering with use of ultrafiltration (UF) retentates. Camel chymosin was used as a coagulant to reduce proteolysis and thus bitterness. Three types of low Na (0.8% NaCl) cheeses were manufactured: non-UF fortified, no HHP applied; UF fortified (17.2 ± 0.6% TS), no HHP applied; and UF fortified, HHP (500 MPa for 3 min applied at 1 d). Regular salt (2% NaCl) non-UF fortified, no HHP applied cheese was also manufactured. Average composition of all cheeses was 36.3 ± 1.4% moisture, 33.8 ± 0.8% fat, and 25.4 ± 0.8% protein. Analysis was performed at 4 d, 2 wk, 1, 3 and 6 mo after cheese manufacture. Cheese functionality during ripening was assessed using texture profile analysis (TPA) and dynamic low-amplitude oscillatory rheology. Quantitative descriptive analysis was conducted with 9 trained panelists to evaluate texture and flavor attributes using a 15 point scale. Pressure treated low Na cheese had ~1.5, and ~3 log lower starter culture numbers than all samples at 4 d and 2 wk, respectively. Cheese milk retentate fortification and HHP treatment resulted in low Na cheeses with significantly ($P < 0.05$) higher acid/base buffering capacity and pH values. For low Na cheeses, retentate fortification significantly ($P < 0.05$) increased cheese firmness measured at 4 d of ripening; however, by 1 mo all low Na cheeses exhibited similar hardness values, which were lower than regular salt cheese. Pressure treatment significantly ($P < 0.05$) increased maximum loss tangent (meltability) and decreased melt temperature. Sensory results indicated only very slight bitterness (<2 out of 15 point scale) development for all cheeses during 3 mo of ripening. Pressure treated and UF-fortified cheese was rated significantly ($P < 0.05$) lower in acidity during ripening. Pressures of 500 MPa and milk retentate fortification could be used to improve the quality of low Na cheese.

Key Words: high pressure processing, low sodium cheese, milk retentate

22 Influence of depletion flocculation and continuous phase viscosity on the stability of sodium-caseinate-stabilized emulsions. Y. C. Liang*[1,2], H. Patel[3], L. Matia-Merino[2], A. Q. Ye[4], G. Gillies[1], and M. Golding[2,4], *[1]Fonterra Research and Development Centre, Palmerston North, New Zealand, [2]Institute of Food, Nutrition and Human Health, Massey University, Palmerston North, New Zealand, [3]Dairy Science Department, South Dakota State University, Brookings, [4]Riddet Institute, Massey University, Palmerston North, New Zealand.*

Creaming has a detrimental effect on the quality of a protein-rich oil-in-water emulsion because the emulsion tends to separate into a droplet-rich phase and a droplet-poor phase during aging, which reduces its visual appearance and mouthfeel. We explored the stability and rheological properties of sodium-caseinate-stabilized emulsion. The formation of the transient gel network was studied by microstructure, and by large and small deformation rheology. Sodium caseinate was reconstituted to a 3% (wt/wt) solution. Corn oil (60% wt/wt) was mixed with the protein solution. The mixture was homogenized to yield a stock emulsion, which was then mixed with stock caseinate (20% wt/wt), xanthan gum (2% wt/wt), and maltodextrin (40% wt/wt) solutions to produce final 30% oil-in-water emulsions containing 2 to 10% caseinate, 0.01 to 0.2% xanthan gum, and 5 to 20% maltodextrin, respectively. The pH was adjusted to 6.8 ± 0.04 for all model emulsions. All the samples were prepared separately in duplicates. The emulsions displayed 2 types of behavior. At 1.5 to 4% caseinate, the emulsion separated rapidly, whereas a droplet network with stronger attractions formed slowly at high concentrations (5 to 10%), arresting the phase separation transiently. Small deformation rheology showed that the development of the transient droplet network depended markedly on the unadsorbed caseinate concentration. Droplet rearrangements were possibly influenced by both the strength of the depletion force and the continuous phase viscosity at high caseinate concentrations. Interestingly, droplet network was weakened with the addition of maltodextrin, with a stabilizing mechanism that differed from the prediction that the low shear viscosity will prevent phase separation of the emulsion. The understanding of the development of caseinate-induced droplet network provides a mechanism capable of controlling the creaming behavior of emulsion. We find a good correlation between visual observation and small deformation rheology. More stable samples exhibit a longer droplet network formation time than the less-stable ones.

Key Words: caseinate, depletion flocculation, stability

Graduate Student Competition: ADSA Production Division Oral Competition, PhD Division

23 High feed efficiency for milk is associated with high feed nitrogen efficiency in dairy cows. C. Arndt*[1], M. A. Wattiaux[1], J. M. Powell[2], and M. J. Aguerre[1], *[1]Department of Dairy Science, University of Wisconsin, Madison, [2]USDA-Agricultural Research Service, US Dairy Forage Research Center, USDA-ARS, Madison, WI.*

Greater feed N efficiency for milk N could enhance dairy farm profits and reduce manure N excretion and environmental risks. The objective was to evaluate relationships between feed efficiency for milk (FEmk, kg milk/kg DMI) and measures of feed N efficiency in dairy cows. Eight pairs of mid-lactating cows (primiparous or multiparous <16 DIM apart within each pair) with high and low FEmk of 1.78 and 0.98 kg/kg, respectively, were fed a TMR (47% DM) consisting of 28% corn silage, 27% alfalfa silage and 45% concentrate, containing 16% CP and 28% NDF (DM basis) for at least 4 weeks. During a 3-d period TMR, feed refusals, milk, total feces and total urine were measured, sampled daily and analyzed for N concentrations. Data were analyzed as a randomized complete block with cow pairs as blocks and FEmk as treatment. High FEmk cows had 15% greater N intake (NI), 32% greater fecal N (FN) excretion and 5% lower apparent N digestibility than low FEmk cows (see Table 1). Despite similar digested N high FEmk cows secreted 1.9 times more N in milk than low FEmk cows, yet urine N (UN) and manure N (FN + UN) excretion were similar. High FEmk cows had greater feed N efficiencies (30% of NI secreted as milk N) than low FEmk cows (19%). Also, high FEmk cows excreted 45% less manure N/milk N and manure UN to FN ratio was 30% lower than in low FEmk cows. High FEmk cows were more feed N efficient due to metabolic rather than digestive processes. Selection for high FE cows may increase feed energy utilization as well as feed N utilization and decrease risk of manure ammonia and nitrous oxide emissions due to reduced manure UN to FN ratio.

Table 1.

Item	FEmk1		SEM	*P*-value
	High	Low		
N intake, g/d	641	559	22.9	0.01
N digestibility, %	63.8	67.1	1.01	0.06
Digested N, g/d	409	376	17.0	0.12
Milk N, g/d	193	102	10.2	<0.01
Fecal N, g/d	210	159	8.6	<0.01
Urine N, g/d	210	226	15.4	0.40
(Fecal N + Urine N), g/d	420	384	21.8	0.18
Milk N/N intake, %	30.3	18.5	1.97	<0.01
Milk N/digested N, %	47.5	27.6	2.98	<0.01
Manure N/milk N, g/g	2.17	3.97	NA	<0.01
Urine N/Fecal N, g/g	1.00	1.42	0.07	<0.01

[1]FEmk = feed efficiency for milk (kg milk/kg DMI).

Key Words: feed efficiency, nitrogen efficiency, dairy cattle

24 Tumor necrosis factor-α injection promotes liver inflammation and decreases gluconeogenesis in early lactation dairy cows. K. Yuan*[1], J. K. Farney[1], L. K. Mamedova[1], L. M. Sordillo[2], and B. J. Bradford[1], *[1]Kansas State University, Manhattan, [2]Michigan State University, East Lansing.*

The first week of lactation in dairy cows is characterized by substantial metabolic stress and high rates of metabolic disorders. We hypothesized that inflammation may contribute to these problems. Therefore, we tested whether administering an inflammatory cytokine, recombinant bovine tumor necrosis factor-α (TNFα), affects liver inflammation, gluconeogenesis, and metabolism during this period. Thirty-three Holstein cows (9 primiparous and 24 multiparous) were randomly assigned to 1 of 3 treatments at parturition. Treatments were 0, 1.5, or 3.0 μg/kg BW TNFα, and were administered once daily by subcutaneous injection for the first 7 d of lactation. Plasma samples were collected daily for analysis of metabolites and hormones, and liver samples were collected on d 7 for triglyceride and qPCR analyses. Glucose turnover rate was determined by a U-^{13}C-glucose dilution technique on d 7 to estimate gluconeogenic rate. Data were analyzed using mixed models with repeated measures over time and significance was declared at $P < 0.05$ and tendencies at $P < 0.10$. Preplanned contrasts evaluating control vs. TNFα treatments and low vs. high doses were evaluated. The TNFα treatments increased ($P < 0.01$) concentrations of plasma haptoglobin, but did not affect plasma insulin, nonesterified fatty acids, glucose, β-hydroxybutyrate, triglyceride, 3-methylhistidine, or liver triglyceride. Plasma TNFα concentrations tended to be increased when quantified 16 h after daily TNFα administration. Few plasma eicosanoids were affected by treatment, but surprisingly, TNFα administration decreased prostaglandin D_2 and leukotriene D_4 concentrations. Hepatic carnitine palmitoyltransferase 1a transcript abundance increased in a TNFα dose-dependent manner. Plasma glucose turnover rate tended to be decreased 18% by TNFα administration, suggesting impaired glucose production. Taken together, these results indicate that administration of TNFα daily for the first 7 d of lactation increased hepatic inflammation, tended to decrease gluconeogenesis, but did not affect liver triglyceride accumulation or lipid metabolism in dairy cows.

Key Words: gluconeogenesis, metabolism, tumor necrosis factor-α

25 Efficacy of on-farm use of ultraviolet light for inactivation of bacteria in milk for calves. S. L. Gelsinger*, A. J. Heinrichs, C. M. Jones, R. J. Van Saun, C. M. Burns, and H. R. Lysczek, *The Pennsylvania State University, State College.*

UV light has been suggested as an alternative method to heat for bacterial inactivation in milk for calves. However, limited data are available to show the efficacy of this method. Thus, the objective of this study was to investigate the efficacy of on-farm UV (UV) light treatment in reducing bacteria levels in waste milk used for feeding calves. Samples were collected from 9 Pennsylvania herds, twice daily for 15 d, both before and after UV light treatment (n = 60 samples per farm). All samples were analyzed for standard plate count (SPC), coliforms (C), non-coliform gram-negative bacteria (NC), environmental and contagious streptococci (ES and CS, respectively), coagulase-negative staphylococci (CNS), *Streptococcus agalactiae* (SAG), and *Staphylococcus aureus* (SA) count. Log reduction and percentage log reduction were calculated. Data were analyzed using the proc mixed procedure in SAS. UV light treatment significantly reduced all types of bacteria ($P < 0.001$). Weighted least squares means for log reductions (percentage log reduction) were 0.78 (23%), 1.06 (61%), 1.12 (42%), 1.38 (56%), 1.86 (93%), 1.09 (38%), and 1.24 (21%) for SPC, C, NC, ES, CS, CNS, and SA, respectively. Prior to UV light treatment 30% of samples had SPC <10,000 cfu/mL and 17%

of samples had C <10 cfu/mL. These percentages increased to 74% and 47% for SPC and C, respectively following treatment with UV light. A percentage log reduction of 50% has been suggested as a goal for calf milk pasteurization and has been shown to be achievable with heat pasteurization. Others have suggested maximum bacterial counts of 10,000 cfu/mL for SPC, 5,000 cfu/mL for ES, CS, and NC, and <10 cfu/mL for C. A percentage log reduction of 50% was achieved in 3 of 7 bacteria types, and 116 samples (43%) contained bacterial levels within the suggested limits after UV light treatment. Overall results of this study suggest that UV light treatment is not an acceptable alternative to heat pasteurization systems for bacterial inactivation in milk for use in calf feeding.

Key Words: ultraviolet light, milk, calf health

26 Fatty acid profile differs between organic and conventionally produced milk independently of sampling time. B. H. Schwendel*[1], P. C. H. Morel[2], T. J. Wester[2], M. H. Tavendale[1], C. Deadman[3], B. Fong[3], N. M. Shadbolt[2], A. Thatcher[2], and D. E. Otter[1], *[1]Food Nutrition & Health Team, Food & Bio-based Products Group, AgResearch Grasslands, Palmerston North, New Zealand, [2]Animal Nutrition Group, Institute of Veterinary, Animal and Biomedical Sciences, Massey University, Palmerston North, New Zealand, [3]Fonterra Research Centre, Palmerston North, New Zealand.*

Many differences reported in fatty acid (FA) composition between organic and conventionally produced cow's milk can be explained by the differing amounts of fresh forage and concentrates fed in the 2 systems. Comparisons in most previous studies were made between grazed organic cows and housed conventional cows. Our study investigated differences between organic and conventional milk produced using year-round pasture grazing utilized in New Zealand for both systems. FA composition was measured in milk sampled on 4 occasions during morning and evening milking in spring and autumn. Samples were taken from 24 cows selected randomly from the Massey University organic herd and compared with 26 cows from the corresponding conventional herd grazed and managed similarly at the same location. Thirteen out of 25 analyzed FA were influenced by season ($P < 0.001$), while one-third of the FA were different due to time of milking ($P < 0.001$). In addition, one-third were also different between production systems ($P < 0.001$). Variation observed in FA is illustrated using selected polyunsaturated FA. For example, linoleic acid (LA) and α-linolenic acid (ALA) were greater in organic milk while conjugated linoleic acid (CLA) and docosahexaenoic acid (DHA) were greater in conventional milk ($P < 0.001$; Table 1). Also, an interaction between system and milking time was observed for docosapentaenoic acid (DPA) and LA, where levels were greatest in conventional milk in the evening and were lowest in organic milk in the morning ($P < 0.005$). Our results confirm widely described reports that FA profile is affected by sampling time, however, we also showed an effect due to production system, even when cows are kept on pasture continuously.

Table 1. Effect of system, stage of lactation, and time on selected fatty acids

Fatty acid	System		Season		Time				
(g/100g)	Conventional	Organic	Spring	Autumn	am	pm	System	Season	Time
LA	0.81	0.92	0.72	1.01	0.87	0.86	***	***	NS
ALA	0.94	1.11	0.91	1.13	1.02	1.02	***	***	NS
CLA	1.55	0.93	1.01	1.47	1.18	1.30	***	***	*
DPA	0.14	0.14	0.12	0.16	0.13	0.14	NS	***	**
DHA	0.31	0.24	0.25	0.29	0.27	0.28	***	*	***

***$P < 0.001$, **$P < 0.01$, *$P < 0.05$, NS $P > 0.05$.

Key Words: milk, organic, fatty acid

27 An in vitro assessment of the antibacterial effects of plant essential oils. K. A. E. Mullen*, A. R. Lee, R. L. Lyman, S. P. Washburn, and K. L. Anderson, *North Carolina State University, Raleigh.*

In the growing organic dairy industry, there is need for non-antibiotic treatments for mastitis. Plant essential oils have anecdotal efficacy for treatment of mastitis in dairy cattle. The potential mechanism of action of essential oils in mastitis therapy has not been well studied. The objective of the current study was to evaluate the antibacterial activity of the essential oil components of Phyto-Mast, an herbal intramammary mastitis treatment, against 3 mastitis-causing pathogens (*Staphylococcus aureus*, *Streptococcus uberis*, and *Staphylococcus chromogenes*). The essential oils evaluated were *Thymus vulgaris*, *Gaultheria procumbens*, *Glycyrrhiza uralensis*, *Angelica sinensis*, and *Angelica dahuricae*. Broth dilution testing according to CLSI standard protocol was performed using ultra-pasteurized whole milk. Controls included milk only (negative control), milk + bacteria, and milk + penicillin-streptomycin (positive control, at 1 and 5% dilutions). Essential oil of *T. vulgaris* was tested by itself and not in combination with other oils because of its known antibacterial activity. The other essential oils were tested alone and in combination for a total of 15 treatments, each replicated 3 times and tested at 4, 2, 1, and 0.5% to simulate concentrations achievable in the pre-dry off udder quarter. Of all the individual essential oils tested, only *T. vulgaris* oil had consistent antibacterial activity against all 3 pathogens tested, and activity was seen at or above 2%. *T. vulgaris* essential oil completely inhibited bacterial growth in all replications of 2% or greater concentration. Though the combinations of oils did not show typical dose-response effects, some concentration levels were consistently antibacterial across all 3 replications. Our results indicate that only *T. vulgaris* essential oil has consistent antibacterial activity. Further evaluation of the physiological effects of essential oils on mammary tissue is recommended.

Key Words: essential oil, mastitis, antibacterial

28 Low doses of recombinant bovine somatotropin (rbST) enhance fertility of dairy cows. E. S. Ribeiro*[1], R. G. S. Bruno[2], A. M. Farias[2], J. A. Hernandez-Rivera[2], G. C. Gomes[1], R. Surjus[1], G. Sasser[3], D. H. Keisler[4], W. W. Thatcher[1], T. R. Bilby[2], and J. E. P. Santos[1], *[1]Department of Animal Sciences, University of Florida, Gainesville, [2]Texas A&M AgriLife Research and Extension, Stephenville, [3]BioTracking LLC, Moscow, ID, [4]Department of Animal Sciences, University of Missouri, Columbia.*

Objectives were to evaluate the effects of a single or 2 low doses of rbST on plasma hormone concentrations and fertility in dairy cows. Lactating Jersey and crossbred cows (n = 1,493) from 2 farms were inseminated for first AI postpartum on estrus. On the day of AI (study d 0), cows were blocked by parity and assigned randomly to receive a single placebo injection at AI (control), a single treatment injection with 325 mg of rbST at AI (S-bST), or 2 treatment injections with 325 mg of rbST administered at AI and 14 d later (T-bST). Blood was collected twice weekly and plasma analyzed for concentrations of GH, IGF-1, insulin, progesterone, and pregnancy-specific protein B (PSPB). Pregnancy was diagnosed on d 31 and 66. Ultrasonographic morphometry of conceptuses were performed on d 34 and 48. Data were analyzed using PROC GLIMMIX of SAS according to data distribution. Treatment with bST increased plasma concentrations of GH (control: 3.5 vs. S-bST: 6.4 vs. T-bST: 7.6 ng/mL; $P < 0.01$) and IGF-1 (control: 64.1 vs. S-bST: 77.4 vs. T-bST: 98.5 ng/mL; $P < 0.01$) from d 3 to 31, and increments were extended in T-bST. Treatments did not affect concentrations of insulin, progesterone and PSPB. However, a distinction in plasma PSPB between pregnant and non-pregnant cows ($P < 0.01$) occurred earlier for bST-treated cows (on d 21) than for controls

(on d 24). Pregnancy per AI, amniotic vesicle and embryo/fetus sizes were all increased by T-bST compared with control and S-bST (Table). In conclusion, administration of 325 mg of bST on d 0 and 14 relative to AI increased concentrations of GH and IGF-1, enhanced conceptus size, and improved fertility of dairy cows.

Table 1. Effect of bST treatments on fertility and conceptus morphometry

Item	Treatment			*P*-value
	Control	S-bST	T-bST	
Pregnant, %				
d 31	35.6^{b}	37.5^{ab}	43.1^{a}	0.08
d 66	29.9^{b}	29.2^{b}	38.0^{a}	0.01
Pregnancy loss, %	12.6^{ab}	19.1^{a}	8.6^{b}	0.04
Amniotic vesicle length, mm				<0.01
d 34	12.5±0.6^{B}	12.5±0.6^{B}	13.9±0.6^{A}	
d 48	29.3±0.8^{b}	28.5±0.8^{b}	31.8±0.8^{a}	
Embryo/fetus crown-rump length, mm				<0.01
d 34	10.6±0.5^{B}	10.5±0.6^{B}	12.0±0.6^{A}	
d 48	23.6±0.8^{b}	22.5±0.8^{b}	26.1±0.8^{a}	

Different superscripts within row: $^{a,b}P < 0.05$, $^{A,B}P < 0.10$.

Key Words: bST, dairy cow, fertility

29 Individual cow risk factors for development of ketosis in lactating dairy cattle. J. L. Gordon*[1], T. F. Duffield[1], T. H. Herdt[2], D. F. Kelton[1], and S. J. LeBlanc[1], *[1]University of Guelph, Guelph, ON, Canada, [2]Michigan State University, East Lansing.*

The purpose of this study was to determine risk factors at the cow level that lead to ketosis. Records from cows in 5 herds enrolled in 3 field trials on subclinical ketosis treatment were collected for evaluation. In all trials, study herds were visited once a week and cows between 3 and 16 DIM that had not been previously diagnosed with ketosis or a displaced abomasum or enrolled in the study were tested for blood β-hydroxybutyrate (BHBA) concentration using an electronic hand-held meter (Precision Xtra; Abbott). Electronic records were also collected at each visit. Information on previous lactation days carried calf (DCC), days dry (DDRY), days open (DOPN) and milk yield, as well as current parity was available for 1414 multiparous cows. DDRY was categorized into normal (30–60 d) long (>60 d) and short (<30 d) and parity as 2 or ≥3. Ketosis was defined as ≥ 1.2 mmol/L BHBA in whole blood using the Precision Xtra. Ketosis incidence was 35% overall, with incidence in Herd A at 15%, Herd B 30%, Herd C 32%, Herd D 38%, and Herd E 39%. Previous lactation total milk and 305ME had no effect on ketosis risk (P = 0.7–0.9), whether expressed as an absolute value or deviation from herd average. DDRY category also had no effect on ketosis risk (P = 0.3–0.8). DCC and DOPN were significantly associated with ketosis risk, controlling for herd and parity. An increase of 21 DOPN and a decrease of 10 DCC increased the odds of ketosis 1.3 (1.1–1.6, P = 0.003) and 1.2 (1.1–1.4, P = 0.01) times respectively. Controlling for parity, DOPN, and DCC, there were differences between herds in ketosis risk. In 1 herd, the trial was performed 2 years in a row and 334 cows were tested both years. Being diagnosed with ketosis the first year increased the odds of ketosis the second year by 2.2 times (1.4–3.4, P = 0.001) in this herd. There were no interactions between the risk factors. Herd, and ketosis and time to pregnancy in the previous lactation are associated with ketosis risk in lactating dairy cattle.

Key Words: ketosis, risk factor

30 Postnatal changes in gut bacteria and mucosal immune system development in dairy calves. N. Malmuthuge*[1], G. Liang[1], T. B. McFadden[3], P. J. Griebel[2], and L. L. Guan[1], *[1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, [2]Vaccine and Infectious Disease Organization, Univ. of Saskatchewan, Saskatoon, SK, Canada, [3]Divison of Animal Sciences, University of Missouri, Columbia.*

Gut microbial establishment plays a vital role in development of the host mucosal immune system. However, there is limited knowledge on how postnatal establishment of the gut microbiome influences development of mucosal immune responses in dairy calves. This study investigated the relationship between the gut bacteria and mucosal immune responses over time. Small intestinal (mid jejunum, distal jejunum, ileum) tissue and digesta samples were collected from d 0 (n = 3), 1 (n = 6), 3 (n = 6) and 6 (n = 6) week old calves and quantified total bacteria, *Lactobacillus* and *Bifidobacterium* sp. as well as mucosal expression of bovine toll-like receptors (TLR), and immune-regulatory genes. Multivariate ANOVA of bacterial population and gene expression data revealed that calf age exerts a joint effect on bacterial density and mucosal immune responses. Total bacterial density in the small intestine of 6-wk-old calves (4.0 ± 2.0 × 10^{10} copies of 16S rRNA gene) was significantly higher than that of d 0 calves (7.3 ± 2.0 × 10^{8} copies/g). The prevalence of *Lactobacillus* sp. was lower in d 0 and 6-wk-old calves (>1%) compared with 1-wk (7.1%) and 3-wk (5.7%) old calves. In contrast, *Bifidobacterium* were prevalent than *Lactobacillus* at all ages with peak prevalence (21.2%) observed in 3-wk-old calves. Expression of TLR 1 to 10, except TLR9, was age dependent and expression of most TLRs was lowest in d 0 calves. Strong correlations were observed between total bacterial density and TLR expression levels but these associations varied with age. Mucosal expression of IL8 and IL10 was significantly higher in 1 and 3-week-old calves compared with d 0 and 6-week-old calves and cytokines expression was positively correlated with *Lactobacillus* and *Bifidobacterium* populations but not with total bacteria, signifying these specific bacterial species may associate with postnatal mucosal immune regulation. The present study revealed that gut bacterial density and mucosal immune system change significantly within the first weeks of life and changes in gut bacteria may influence the immune development during the early life of dairy calves.

Key Words: gastrointestinal tract, bacteria, mucosal immunity

31 Management of dairy goats during the transition between lactations. G. Zobel*[1], K. Leslie[2], D. M. Weary[1], and M. A. G. von Keyserlingk[1], *[1]Animal Welfare Program, University of British Columbia, Vancouver, BC, Canada, [2]Population Medicine, University of Guelph, Guelph, ON, Canada.*

Dry-off and the onset of the new lactation are key periods of risk for intramammary infections, but little work to date has examined how management of this transition affects dairy goat health and welfare. To guide such research, it is helpful to describe management practices currently employed. The aim of this study was to determine the practices of dairy goat milk producers in Ontario, Canada. The survey was sent by mail to all 229 licensed farms of which 67 responded (i.e., response rate of 29%). Analyses are descriptive and all results are presented as means ± SD. On average, farms milked 203 ± 125 goats, with an average lactation length of 330 ± 99 d (1st lactation) and 386 ± 168 d (2+ lactations). The most common breeds were Saanen (66 ± 25%) and Alpine (28 ± 21%). The majority of producers (79%) ranked days until kidding and milk production as their top deciding factors when choosing to drying-off their goats; interestingly, 83% had no ability to record individual milk production. Furthermore, although the average

dry period cited was 53 ± 11 d, nearly 20% of the farms noted that does are occasionally milked for over 600 d, regardless of pregnancy status. They cited the top reasons for skipping a dry period as persistent milk production, even when pregnant (71%) and continuing to milk because the doe had not been bred in the current year (17%). Two respondents indicated that they did not dry-off their goats at all. To induce dry-off, 40% of producers reported restricting access to feed, while water restriction was used on 4 of the farms. Interestingly, not all producers felt diet had a major effect on dry-off, with 26% reporting no change in feeding practices. Intramammary antibiotic and teat sealer use was minimal (17% and 2%, respectively) despite producers expressing that they were "moderately or extremely concerned" about subclinical and clinical mastitis (28% and 35%, respectively). These results suggest the need for research to determine the effects of the large variety of dry-off methods being used by producers, including extended lactations and skipped dry periods in dairy goats.

Key Words: does, dry-off, udder health

32 Comparison of NRC and industry dietary trace mineral standards for yearling feedlot steers. C. J. Berrett*, J.J. Wagner, K. L. Neuhold, E. Caldera, and T. E. Engle, *Colorado State University, Fort Collins.*

Effect of trace mineral (TM) concentration and source on yearling feedlot steer performance, carcass characteristics, and liver TM status, were determined utilizing 360 crossbred steers (initial BW = 350 ± 4.0 kg). Steers were blocked by initial BW and randomly assigned to one of 4 treatments (10pens/treatment; 9 hd/pen). Treatments consisted of (1) negative control (NC), no supplemental TM (basal diet contained 7.65 mg Cu/kg DM, 50.5 mg Zn/kg DM, 27.7 mg Mn/kg DM, and 0.12 mg Co/kg DM); (2) basal diet supplemented with 10 mg Cu/kg DM from $CuSO_4$, 30 mg Zn/kg DM from $ZnSO_4$, 20 mg Mn/kg DM from $MnSO_4$, 0.50 mg I/kg DM from EDDI, 0.10 mg Se/kg DM from Na_2O_3Se, and 0.10 mg Co/kg DM from $CoCO_3$ (NRC); (3) basal diet supplemented with inorganic forms of Cu, Zn, Mn, EDDI, Se and Co at consulting nutritionist recommendations (CNI, 20, 100, 50, 0.50, 0.20, and 0.20 mg of mineral/kg DM, respectively); and (4) basal diet supplemented with 66.6% inorganic and 33.4% organic Cu, Zn, Mn and Co, and inorganic forms of I and Se at iso-concentration to consulting nutritionist recommendations of treatment 3 (CNO). All steers were fed a high concentrate steam-flaked corn-based diet for 154 d. Steers were individually weighed on d −1, 0, 35, 121, 153, and 154. Continuous data were analyzed on a pen mean basis using a mixed model appropriate for a randomized block design (fixed effects = treatment and time; random effect = replicate). Categorical data were analyzed utilizing GLIMMIX (fixed effect = treatment; random effect = replicate). Initial and final BW, ADG, DMI, F:G and G:F ratios and calculated net energy recoveries were similar ($P > 0.23$) across treatments. Subcutaneous adipose tissue depth, HCW, KPH, yield grade, marbling score, and quality grade were similar across treatments ($P > 0.17$). Final liver Zn, Mn, Se, and Co concentrations were similar across treatments ($P > 0.37$). Under the conditions of this experiment, it appears that basal dietary concentrations of Cu, Zn, Mn, and Co were adequate for growth and performance of finishing yearling feedlot steers.

Key Words: beef cattle, feedlot, trace mineral

33 Effects of BovaZyme WP enzyme supplementation on frothy bloat and performance in stocker cattle grazing winter wheat. W. E. Pinchak*[1], D. W. Pitta[1,2], J. Miller[1], G. M. Shipp[3], and J. D. Fulford[1], *[1]Texas A&M AgriLife Research, Vernon, [2]School of Veterinary Medicine University of Pennsylvania, Kennett Square, [3]Texas A&M AgriLife Research, Amarillo.*

Frothy bloat is the major non-pathogenic cause of mortality and depressed performance in cattle grazing hard red winter wheat in the southern Great Plains. Value-added bloat intervention strategies mitigate direct bloat effects, while enhancing performance in non-bloated animals as well. Frothy bloat occurs when rumen bacteria produce extra-cellular, low gas permeable, polysaccharide biofilms. These biofilms interconnect with fluid and particle phase rumen contents to entrap fermentative gases and disrupt eructation. Supplementation with exogenous enzymes could decrease the rate and extent of polysaccharide formation, thereby decreasing bloat severity and duration. An in vitro experiment utilizing rumen fluid from bloated and non-bloated rumen cannulated steers and 4 levels of BovaZyme WP (York Ag Products Inc., York, PA) was conducted. BovaZyme supplementation to rumen fluid reduced ($P < 0.001$) foam strength, time of foam collapse, biofilm and viscosity. Subsequently, a grazing experiment was conducted utilizing 65 cross-bred heifers (avg. initial wt. = 191 kg) with 3 replicate groups of mineral Control and mineral + BovaZyme supplemented herds (10 to 12 hd) stocked at 1 ha/hd. During the study period, 58 of 65 head (89%) experienced at least one bloat event. The number of head that experienced bloat more than 4 d was greater ($P < 0.10$) in Control than in BovaZyme herds (7.0 d and 4.7 d respectively). Conversely, the percentage of head observed with bloat score 1 (minor bloat) was greater ($P < 0.10$) in BovaZyme than in Control herds (34.7% and 19.3% respectively). Collectively, BovaZyme supplementation decreased the severity and duration of bloat under the conditions of this experiment. Total gain and ADG for the grazing period was greater ($P = 0.1003$) for the BovaZyme supplemented mineral group than for the mineral only Control group at 6.71kg and 0.07 kg/hd/d, respectively. Results from these preliminary experiments support the use of BovaZyme in a complete mineral supplement as a value-added bloat mitigation chemistry. Further research is warranted across multiple years to validate the results of this research.

Key Words: biofilm

34 Individual ad libitum intake of mineral mix by beef cows is less than NRC recommendations and form of selenium (Se) in mineral mix affects Se levels of cows and suckling calves. J. D. Patterson*, W. R. Burris, J. A. Boling, and J. C. Matthews, *University of Kentucky, Lexington.*

This project was conducted to determine (1) individual ad libitum intake of mineral mix by beef cows managed under a year-long, fall-calving, forage-based production regimen and (2) if form of Se in mineral mix affected blood Se levels of cows and suckling calves. In August 2011, 24 late-gestation (6 to 8 mo) Angus-cross cows (2.7 ± 0.8 yr; BW = 585 ± 58 kg) were blocked by BW and randomly assigned (n = 8) to a mineral supplement treatment (TRT) containing 35 ppm Se as either inorganic (ISe; sodium selenite), organic (OSe; SEL-PLEX), or a 1:1 combination of ISe:OSe (Mix). Cows commonly grazed a 10.1 ha Kentucky-31 tall fescue pasture and had individual ad libitum access to TRT using an in-pasture Calan gate system. Cows calved from September to November and calves had common ad libitum access to creep feed and a mineral supplement that lacked Se. Cow jugular blood was taken at 28-d intervals (13 periods) and calf blood taken with cows' from birth through weaning. Data were analyzed using mixed models with main effects of experimental period, TRT, and their interaction evaluated. Main effect means were separated using the pdiff option. Pearson's partial correlation coefficient was calculated to assess linear associations between cow and calf blood Se levels. Cow mineral intake (g/d) was affected ($P < 0.0001$) by period, with Periods 1–3 (92.2 ± 6.7) > Periods 4, 9, 12 (56.3 ± 7.0) > Periods 5–8, 10, 11 and 13 (36.2 ± 6.9); but not ($P = 0.24$) by cow Se TRT. Cow blood Se (0.115 to 0.229 ± 0.01 μg/mL) was affected by Period ($P < 0.0001$), Se form ($P = 0.001$), and their interaction ($P = 0.03$), with ISe = Mix < OSe for Periods 3, 7, 8, 10, 12; ISe < Mix < OSe for Periods 9 and 11; and ISe = Mix = OSe for Periods 1, 2, 4–6. Calf blood Se (μg Se/mL) was correlated (r = 0.63, $P = 0.0001$) with cow blood Se and was affected by ($P < 0.0001$) cow Se TRT, with ISe (0.07 to 0.11) < Mix (0.10 to 0.15) = OSe (0.16 to 0.19). In conclusion, ad libitum cow mineral intake (54.7 g/d) was 36% less than NRC recommendations (85 g/d) and cow Se TRT affected cow and calf blood Se levels.

Key Words: cow, mineral intake, selenium

35 Effects of dietary ferric ammonium citrate on performance and carcass quality of beef cattle fed 20, 40, or 60% distillers grains with solubles. M. E. Drewnoski[2], S. J. Morine*[1], and S. L. Hansen[1], *[1]Iowa State University, Ames, [2]University of Idaho, Moscow.*

Previously, the addition of ferric ammonium citrate (FAC) to high S diets was found to decrease hydrogen sulfide (H_2S) concentrations. The objective of this experiment was to determine the effects of feeding FAC to steers fed varying concentrations of dried distillers grains plus solubles (DDGS) on steer performance, mineral status, and carcass quality. Angus-cross steers (n = 128) were assigned to one of 6 treatments, composed of 3 concentrations of DDGS in the diet (20, 40, or 60% of diet DM; 0.28, 0.41, 0.54% dietary S respectively) and one of 2 levels of FAC (0 or 300 ppm of added Fe). Treatments were replicated in 5 pens (20, 40% DDGS) or 6 pens (60% DDGS). During the 98 d study H_2S concentrations were measured on d 0, 7, 14, 21, and 95 at 6 h post feeding. Steer DMI was linearly and quadratically affected ($P \leq 0.02$) by increasing inclusion of DDGS, with no differences between 20 and 40% DDGS-fed steers, and lesser DMI by 60% DDGS-fed steers. Steer ADG was linearly decreased ($P < 0.01$) as DDGS inclusion increased, primarily due to the lesser ADG of steers consuming 60% DDGS. Increasing DDGS linearly increased ($P < 0.01$) ruminal concentrations of H_2S. Inclusion of FAC did not affect ($P \geq 0.21$) ADG, DMI, G:F (study means: 1.67 kg/d, 11.05 kg/d, and 0.15, respectively) or ruminal H_2S concentrations. Inclusion of FAC or increasing DDGS did not affect ($P \geq 0.32$) ribeye area, backfat, or KPH. Inclusion of FAC tended to increase HCW ($P = 0.10$), while increasing DDGS linearly decreased HCW ($P = 0.03$). Increased inclusion of DDGS had a quadratic effect ($P = 0.03$; 423, 443, and 413 for 20, 40, and 60% DDGS, respectively) on marbling score, and the inclusion of FAC increased ($P = 0.05$) marbling score. Liver Cu averaged 233 ppm and tended ($P = 0.06$) to be decreased by increasing DDGS, and was decreased ($P < 0.01$) by FAC addition, but was not decreased to the point of deficiency. Results of this study suggest 40% DDGS is the optimal inclusion in finishing cattle diets and including FAC in diets does not affect steer gains, but may increase HCW and marbling scores of cattle fed high S diets.

Key Words: cattle, dried distillers grain, iron

36 Feeding ferric citrate to decrease risk of sulfur toxicity: effects on trace mineral absorption and trace mineral status of steers. M. E. Drewnoski*[2] and S. L. Hansen[1], *[1]Iowa State University, Ames, [2]University of Idaho, Moscow.*

We have previously shown that adding ferric Fe to diets in the form of ferric ammonium citrate will decrease ruminal hydrogen sulfide concentrations and thus may reduce risk of S toxicity when feeding elevated levels of S. However, Fe can have negative effects on absorption of other trace minerals such as Cu, Mn and Zn. Therefore, this study was designed to determine the effect of supplementing 300 mg/kg DM of ferric Fe in high S diets on trace mineral absorption and trace mineral status of cattle. Eighteen Angus cross steers (370 ± 9.5 kg) were individually fed 1 of 3 high concentrate diets: (1) a moderate sulfur diet (MS; 0.3% S), (2) a high sulfur diet (HS; 0.5% S), or (3) HS plus 300 mg/kg of ferric Fe from ferric ammonium citrate (HS+Fe). Steers were adapted to diets for 7 d in individual pens and then moved into metabolism crates for a 5 d crate adaptation followed by a 5-d period of total fecal collection to determine apparent absorption of Cu, Fe, Mn and Zn. Steers were then moved back to individual pens and fed diets for an additional 56 d to determine effects on performance. Liver biopsies were conducted before the start of the trial and again at the end of the trial to determine trace mineral status. During the collection period DMI was greater ($P < 0.02$) for MS than HS and HS+Fe, which did not differ ($P = 0.87$). However, the apparent absorption of Cu, Fe, Mn and Zn were not affected ($P \geq 0.14$) by treatment. Additionally, after 73 d of consuming diets there were no effects of treatment ($P \geq 0.28$) on liver concentrations of Zn, Mn or Fe. However, steers fed the MS had greater ($P < 0.01$) liver Cu (273 mg/kg DM) than did those fed HS or HS+Fe. Liver Cu of steers fed HS (156 mg/kg) did not differ ($P = 0.44$) from those fed HS+ Fe (136 mg/kg), suggesting that the reduced liver Cu was due to the increased dietary S. The 56 d ADG of steers did not differ ($P = 0.45$) among treatments and were 2.33, 2.15, 2.11 kg/d (SEM ± 0.125) for MS, HS and HS+Fe, respectively. In this study, feeding 300 mg/kg ferric Fe in a high S diet did not appear to affect trace mineral absorption or status of steers.

Key Words: copper, iron, sulfur

37 Phytonutrients or calcified marine algae as natural alternatives to monensin in beef feedlot diets. F. M. Hagg*[1,2], L. J. Erasmus[2], R. H. Van der Veen[1], E. Haasbroek[2], S. Taylor[3], and C. Oguey[4], *[1]Allied Nutrition, Pretoria, South Africa, [2]University of Pretoria, Pretoria, South Africa, [3]Celtic Sea Minerals, Cork, Ireland, [4]Pancosma, Geneva, Switzerland.*

Public concern regarding possible antibiotic resistance led to the evaluation of a mixture of phytonutrients (XT) containing capsicum oleoresin, cinnamaldehyde and eugenol, and a commercial buffer (AB), containing *Lithothamnium calcareum* (calcified marine algae), as natural alternatives to monensin (MON) in beef cattle. The objective of the study was to determine if XT or AB can successfully replace MON in commercial beef feedlot diets. In Trial 1 (Experimental trial) 180 recently weaned male beef cattle (±225 kg) were randomly allocated to one of 3 treatments: 1) Monensin (21 – 33 mg/kg DM); 2) XT (XTRACT 7065, Pancosma) at 1.0 – 1.2 g/head/day; 3) AB (Acid Buf; Celtic Sea Minerals) at 0.6% of DM. Same basal diets (ME = 10.6 – 11.7 MJ/kg DM) were used during 4 different feeding periods, with only MON, XT or AB inclusion differing between diets. Six pens, with 10 animals each, were randomly allocated to each treatment for a period of 119 d. In Trial 2 (Commercial trial), 1170 recently weaned male beef cattle (±225 kg) were used in a similar design, but for each treatment 3 pens, with 130 cattle per pen, were randomly allocated, with a trial period of 115 d. Growth, feed intake and health parameters were measured. Statistical analyses were done with one-way ANOVA (ANOVA). In Trial 1 there were no differences ($P > 0.05$) in DMI, FCR or ADG between treatments. In Trial 2, ADG was increased (1.77 vs. 1.70 kg/d) when XT replaced MON ($P < 0.05$) and there was a tendency ($P = 0.09$) toward improvement of ADG when AB replaced MON. DMI tended to be increased ($P = 0.09$) by XT (10.05 kg/d) compared with MON (8.96 kg/d). Overall performance expressed as FCR was not affected when either AB or XT replaced MON ($P > 0.2$). Percentage of healthy animals was reduced ($P < 0.05$) when AB replaced MON, however growth performance was not impaired. Percentage of healthy rumens was improved ($P < 0.01$) when either XT (76.3%) or AB (49.2%) replaced MON (27.1%). Results suggest that both XT and AB could be used to replace MON in commercial beef feedlot diets without impairing animal performance.

Key Words: calcified marine algae, monensin, phytonutrients

38 Interaction between supplemental zinc and zilpaterol in feedlot steers. C. L. Van Bibber-Krueger*, K. A. Miller, C. C. Aperce, C. A. Alvarado-Gilis, J. M. Gonzalez, and J. S. Drouillard, *Kansas State University, Manhattan.*

Interactive effects of supplemental zinc (Zn) and zilpaterol hydrochloride (Zil) were evaluated in feedlot steers (n = 40; initial BW 653 kg ± 14) to determine the effect on feedlot performance, blood constituents, and carcass traits. The study was conducted as a randomized complete block with a 2 × 2 factorial treatment arrangement. Steers were blocked by BW and randomly assigned to treatments. Factors consisted of supplemental Zn (60 or 300 mg/kg), and Zil (0 or 8.3 mg/kg) concentrations in the diet. Zil was fed for 21 d followed by a 3-d withdrawal. Cattle were housed in partially-covered individual feeding pens equipped with automatic waterers, fence-line feed bunks and supplied an ad libitum diet once daily. Plasma samples were collected d 0 and 21 to assess changes in zinc, urea nitrogen (PUN), glucose, and lactate concentrations, and serum samples were collected d 21 to assess IGF-1 concentration. On d 24 cattle were weighed, transported 450 km to a commercial abattoir for harvest, and HCW and incidence of liver abscesses were recorded. Carcass data were collected after 24 h of chilling. Data were analyzed as a mixed model with Zn, Zil, and Zn × Zil as fixed effects, block as a random effect, and steer as the experimental unit. No interaction or effects of Zn or Zil ($P > 0.05$) were observed for IGF-1 concentration. Interactions between Zn and Zil were observed for changes in plasma glucose and lactate ($P < 0.05$). No interaction between Zn and Zil was observed for PUN concentration, but PUN decreased over time with Zil ($P < 0.05$). There were no effects of Zil or Zn on ADG, DMI, final BW, feed efficiency, HCW, LM area, backfat, KPH, quality grade, or incidence of liver abscesses ($P > 0.05$), though Zn numerically improved marbling and tended ($P = 0.08$) to improve proportion of carcasses grading USDA Choice. Feeding Zil decreased yield grade ($P < 0.05$) without compromising marbling score ($P > 0.05$) and tended to increase LM area ($P = 0.07$). In conclusion, increasing dietary concentrations of zinc does not affect response to zilpaterol, but feeding zilpaterol alters circulating concentrations of blood constituents associated with muscle accretion.

Key Words: IGF-1, lactate, plasma urea nitrogen

39 Influence of supplementing vitamin C to cattle fed a high sulfur diet late in the finishing period on meat color and tenderness. D. J. Pogge*, S. M. Lonergan, and S. L. Hansen, *Iowa State University, Ames.*

The objective of this study was to determine the effects of supplementing a rumen-protected vitamin C (VC) for approximately 102 d before harvest on meat color, tenderness, and nutrient content of longissimus dorsi (LD) collected from cattle receiving a 0.55% S diet. Angus-cross steers (n = 140) were blocked by initial BW (432 ± 0.4 kg), stratified within blocks by ultrasonographic initial intramuscular fat (3.6% ± 0.06), and assigned to treatments (5 steers per pen, 7 pens per treatment), including: 1) no VC control (CON), 2) 5 g VC·h^{-1}·d^{-1} (5VC), 3) 10 g VC·h^{-1}·d^{-1} (10VC), and 4) 20 g VC·h^{-1}·d^{-1} (20VC). Cattle were harvested by block on d 91 (n = 40), d 105 (n = 40), and d 112 (n = 60). Three, 1.27 cm steaks (n = 136) were removed from each carcass after a 24 h chill. One steak was displayed under retail-simulated lighting at 2°C and color analysis was conducted on d 1, 2, 3, and 7; and after 7-d of display Warner-Bratzler shear force (WBSF) was determined. Separate steaks were analyzed for hydroxyproline, VC, vitamin E (VE), and cholesterol. For all analyses pen (n = 7 per treatment) was the experimental unit. The supplemental VC intake (g·h^{-1}·d^{-1}) averaged 5.1 (5VC), 10.1 (10VC), and 20.2 (20VC). Inclusion of VC resulted in a lesser ($P < 0.01$) L* than CON, and VC supplemented treatments did not differ from one another ($P \geq 0.46$). No differences among treatments ($P \geq 0.30$) in WBSF values, a* and b*, or hydroxyproline content of LD muscle were noted. However, WBSF values tended to be negatively correlated with a* ($R = -0.33$; $P < 0.08$). The VC content of the LD was not different ($P \geq 0.48$), but the inclusion of VC increased ($P < 0.01$) VE content of LD compared with CON (1.24, 1.71, 1.45, and 1.53 µg/g tissue ± 0.07, for CON, 5VC, 10VC, and 20VC, respectively). Cholesterol content of LD demonstrated a quadratic response ($P < 0.01$), CON (54.4), 5VC (57.4), 10VC (59.8), and 20VC (54.9 mg/100 g ± 1.4). Under the conditions of our study, supplementation of VC to steers fed a high S diet late in the finishing period did not influence color stability or WBSF, but increased VE content of LD.

Key Words: cattle, sulfur, vitamin C

40 Effect of a supplemental zinc complex on beef cattle performance and plasma and liver trace mineral concentrations. O. N. Genther* and S. L. Hansen, *Iowa State University, Ames.*

The objective of this experiment was to determine the effect of a supplemental zinc (Zn) complex (ZnC) on steer performance and plasma and liver trace mineral concentrations. Forty-one steers (380 ± 5.3 kg) were fed a finishing diet of 61% ground corn, 23% dried distillers, 14% corn silage, 2% micronutrients, and 60 mg supplemental Zn/kg diet DM (as Zn sulfate). Steers were assigned to 1 of 4 treatments for 86 d: Zn0: no supplemental ZnC (n = 6), Zn30: 30 mg Zn/kg from ZnC (n = 12), Zn60: 60 mg Zn/kg from ZnC (n = 12), and Zn90: 90 mg Zn/kg from ZnC (n = 11). Individual DMI was recorded daily, body weights were taken on d 0, 1, 28, 56, and 86, and ultrasound measurements were taken on d 0 and 86. Steer was the experimental unit and DMI, ADG and G:F were analyzed as repeated measures. Steer DMI (11.3, 11.4, 11.0 and 11.0 ± 0.17 kg for Zn0, Zn30, Zn60 and Zn90, respectively) was not affected ($P > 0.20$) by treatment. However, Zn60 ADG was greater (2.2 kg/d) than Zn90 (1.9 kg/d; $P < 0.05$), tended to be greater than Zn30 (1.98 kg/d; $P < 0.10$) and was not different from Zn0 (2.05 ± 0.07 kg/d; $P > 0.10$). The Zn60 steers had greater G:F and final BW than Zn30 and Zn90 (G:F: 0.197, 0.174 and 0.168 ± 0.007, respectively; $P < 0.05$; final BW: 571, 547, 543 ± 5.6 kg, respectively; $P < 0.05$), and were not different from Zn0 (G:F: 0.180 ± 0.008; $P > 0.10$; final BW: 554 ± 7.8kg; $P > 0.10$). Day 86 ultrasound-determined ribeye area and intramuscular fat were not affected by treatment ($P > 0.20$). Steers receiving the Zn60 diet had greater d 86 back fat than Zn90 (1.47 and 1.17 cm, respectively; $P < 0.05$) but were not different from Zn0 and Zn30 (1.32 and 1.32 ± 0.07 cm, respectively; $P > 0.10$). Plasma Cu and Fe, and liver Zn and Cu concentrations were not affected by treatment ($P > 0.20$). Plasma Zn tended ($P < 0.10$) to be higher in Zn90 than Zn0 and Zn60 (1.48, 1.30, 1.35 ± 0.04 mg/L, respectively) and no treatments were different from Zn30 (1.44 mg/L). During the 86 d finishing period Zn60 steers performed better than Zn30 or Zn90, and were similar to Zn0 steers.

Key Words: cattle, growth, zinc

41 Influence of lipid-extracted algae on intake and digestibility of a concentrate diet. M. K. Beckman*, L. N. Tracey, C. L. Shelley, K. L. Norman, K. H. Marchetti, E. J. Scholljegerdes, C. A. Löest, S. A. Soto-Navarro, and S. L. Ivey, *New Mexico State University, Las Cruces.*

The co-product resulting from the oil extraction of microalgae, intended for biofuel production, may be of interest to ruminant producers as a proteinaceous feedstuff. The objective of this study was to determine the influence of lipid extracted algae (LEA) on feed intake and digestibility of a concentrate diet. We hypothesized that an isonitrogenous addition of LEA in a concentrate diet fed to sheep would yield results similar to that of dried distillers grains with solubles (DDGS). Fifteen crossbred wether lambs (46 ± 7.1 kg BW), fitted with ruminal and duodenal can-

nulas, were used in a completely randomized design. Lambs were fed twice daily at 110% of previous 3 d DMI. Treatments included: 1) lipid extracted algae diet (CP 16.3%; NDF 23.4%, DM basis; ALGAE) and 2) dried distillers grains with solubles diet (CP 15.7%; NDF 22.3%, DM basis; DGS). Animals were adapted to treatments for 10 d followed by a 6 d sample collection period. Treatment did not influence OM, NDF, or CP intake ($P \geq 0.21$). Ruminal and total tract OM digestibility was lower in animals consuming ALGAE compared with DGS (78.6 vs 83.6 ± 1.77%, $P = 0.05$ and 81.0 vs 86.8 ± 1.38%, $P < 0.01$, respectively). There was no treatment influence on lower tract OM digestibility ($P = 0.93$). Ruminal N digestibility was unaffected by treatment ($P > 0.10$), however N digestion in the total tract was lower for sheep fed ALGAE versus DGS (76.0 vs 86.1 ± 1.49%; $P < 0.01$). Additionally, total tract NDF digestion was greater for DDGS treated lambs, than for those consuming LEA (76.6 vs 70.5 ± 2.19%; $P = 0.05$). There was a tendency ($P = 0.09$) for ALGAE fed animals to show increased microbial efficiency over those fed DGS. Ruminal pH, NH_3, and VFA concentrations did not differ by treatment ($P \geq 0.34$). These data may indicate that LEA is palatable in ruminant diets. However, reduction in digestibility of OM, N and NDF when LEA is added compared with DDGS is concerning and warrants further investigation.

Key Words: biofuel, digestibility, sheep

42 The effect of *Aspergillus oryzae* extract on feedlot performance and carcass merit in yearling steers fed steam-flaked corn based finishing diets. K. A. White*[1], J. J. Wagner[1], T. E. Engle[1], D. R. Woerner[1], R. K. Peel[1], T. C. Bryant[2], J. S. Jennings[3], and K. M. Brennan[3], *[1]Animal Sciences Department, Colorado State University, Fort Collins, [2]JBS Five Rivers Cattle Feeding, Greeley, CO, [3]Alltech Inc., Nicholasville, KY.*

Crossbred yearling steers (n = 270) averaging 319 ± 7.11 kg initial BW were utilized in a randomized block design experiment to evaluate the effects of supplementing a steam-flaked corn based finishing diet with *Aspergillus oryzae* extract containing α-amylase activity on feedlot performance and carcass characteristics. Steers were ranked by weight and allocated into 15 weight block replicates. Within each weight block replicate, steers were randomly assigned to 1 of 2 treatments resulting in 9 steers per pen. Treatments consisted of: 1. Amaize (AMZ; 5 g/head daily providing 750 fungal α-amylase units/g, Alltech Inc. Nicholasville, KY) and 2. Control (CON; providing 5 g/head daily of a corn meal placebo). All cattle were fed for 149 d and 2 individual and 1 pen weight were collected on d 32, 69, and 105, respectively. Final BW and ADG were similar ($P > 0.10$) across treatments. Dry matter intake and gain to feed (G/F) ratios were similar ($P > 0.10$) across treatments throughout the entire study. From d 106 through slaughter, there was a tendency ($P > 0.11$) for G/F ratio to be greater for AMZ supplemented cattle as compared with CON. Hot carcass weight was similar ($P > 0.60$) across treatments. The distribution of HCW among light, average, and heavy weight categories ($P > 0.75$) and longissimus muscle area ($P = 0.17$) did not vary by treatment. Fat depth over the 12th rib ($P = 0.06$, 1.24 vs. 1.35 cm) and Yield grade calculated from carcass measurements ($P = 0.12$, 2.81 vs. 2.98 units) tended to be lower while dressing percentage tended ($P = 0.06$, 63.0 vs. 62.6%) to be greater for the AMZ vs. CON supplemented cattle. Liver abscess rates were lower ($P < 0.01$) for CON (3.8%) vs. AMZ (15.8%) supplemented cattle. Under the conditions of this experiment, results indicate that AMZ supplementation has minimal effects on live cattle performance but may improve dressing percentage.

Key Words: amylase, beef feedlot, carcass merit

43 Effect of supplementing gestating and lactating beef cows with supranutritional concentrations of vitamin D on cow production and pre-weaning growth of the calf. J. P. Schoonmaker*[1], M. Engstrom[2], K. N. Condron[1], C. N. Shee[1], and R. P. Lemenager[1], *[1]Purdue University, West Lafayette, IN, [2]DSM Nutritionals, Parsippany, NJ.*

Angus × Simmental cows (n = 156, age = 4.7 yr, BW = 639 ± 12.4 kg, BCS = 5.2 ± 0.07) were allotted by BW, BCS, and breed to 4 treatments to determine the effect of supranutritional vitamin D during gestation and/or lactation on milk production and composition, reproductive efficiency, and pre-weaning progeny growth. At 173 d in gestation, cows were allotted to 2 pastures and fed a molasses based vitamin/mineral block formulated to provide 6300 IU D daily (LD) or 100,000 IU D daily (HD). At the mid-point of calving season cows were placed on lactation treatments and fed LD or HD in drylot. Treatments were arranged as a 2 × 2 factorial: LD in gestation, followed by LD (LDLD) or HD (LDHD) in lactation, or HD in gestation followed by LD (HDLD) or HD (HDHD) in lactation. Treatments concluded at breeding (79 d postpartum; DPP) and cattle were commingled and managed as a group until weaning which occurred at 188 DPP. At 69 and 79 DPP milk production and composition was assessed on 10 cows per treatment. Categorical and continuous data were analyzed with the GLIMMIX and MIXED procedures of SAS, respectively. Cows fed HD during gestation were 29.6 kg heavier at the end of the gestation period ($P = 0.02$), whereas cows fed HD during lactation were 26.0 kg lighter at study termination ($P = 0.04$). Cow weight at weaning ($P > 0.69$) and BCS ($P > 0.29$) did not differ. Conception rates were lowest for LDHD cows (interaction, $P = 0.04$) and overall pregnancy rates tended ($P = 0.06$) to be greater for cows fed HD during gestation. Milk production was lower ($P = 0.03$) for cows fed HD during gestation but did not differ due to D during lactation ($P = 0.79$). Milk protein was lowest for LDHD cows (interaction; $P = 0.01$). Milk fat tended ($P = 0.10$) to be lower for cows fed HD during lactation. Calf birth weight did not differ among treatments, however, HD during gestation tended to decrease calving difficulty ($P = 0.07$) and to produce heavier calves at weaning ($P = 0.08$). In conclusion, feeding supranutritional D during gestation improves cow weight and reproductive efficiency and may benefit the offspring.

Key Words: beef, developmental programming, vitamin D

Bioethics Symposium I: The Hunger Games: Should "Big Ag" Be Left Standing?

44 "Valuing" alternative agricultural systems: What do consumers perceive about different labels and where do they get their information? N. J. O. Widmar*, C. Croney, and M. G. S. McKendree, *Purdue University, W. Lafayette, IN.*

Consumers today are interested in not only what they buy, but how it was made and who/what was affected. What are consumer's preferences surrounding attributes such as organic, animal-friendly and all-natural? Who do consumers trust for information on socially-relevant agriculture debates, such as animal welfare? Consumer's tastes, preferences, and values are highly variable and heterogeneous. Determining which agricultural system is ethically superior to another is complicated, especially without consensus on what makes a production method or system "good." Even consumers' interpretations of simple labels such as all-natural vary widely; survey respondents report that they associate such labels with improved animal welfare practices, no antibiotics, no hormones, no preservatives added, improved taste and improved food safety. As labels such as "all-natural" appear, it is important for producers to understand what they are perceived to mean, and how and to what extent purchasing them aligns with a consumer's values. For example, does such a label suggest improved welfare or a food safety enhancement? Along with perceptions, the consumer's knowledge base, information sources, and past experiences may also influence their demand for alternative practices. Consumers asked where they seek animal welfare information relied on HSUS and PETA, and to a lesser extent, federal government agencies and "other." More recently, when asked this question with the option to select not having any source for animal welfare information, the majority (55%) selected no source. As debates continue about what animal agriculture should look like, it is important to recognize that deficits of trusted sources of objective information, combined with underlying value notions may explain why consumers' purchasing behavior may or may not reflect their stated preferences. Understanding the value that consumers place on various systems and their attributes and the basis for forming their opinions enables constructive discussion surrounding how agricultural industries can meet consumers' demands, and do so profitably.

Key Words: consumer demand, preference

45 Farm size and animal welfare. D. M. Weary* and M. A. G. von Keyserlingk, *Animal Welfare Program, Faculty of Land and Food Systems, University of British Columbia, Vancouver, BC, Canada.*

Concerns about the welfare of farm animals often revolve around the issue of farm size. Many critics suggest that animals on larger farms are less likely to receive individual attention and instead are treated only as units of production, and that the shift to larger farms results in a decline in standards of care and ultimately in the quality of life for animals. In this talk we outline the historical background of this criticism, drawing parallels with the earlier debate over the shift from an agrarian to an industrial society. We also argue that farm size influences different aspects of animal welfare in different ways. For example, larger farms may permit more specialized and professional management of animal health, but make it difficult to provide access to pasture for dairy cows. We also review the limited empirical literature linking farm size and welfare and conclude that available research provides little support for any simple relationship. In conclusion, increases in farm size provide opportunities to improve the welfare of farm animals but also create welfare risks. Policy and advocacy efforts, instead of trying to reverse the increase in farm size, would be better directed toward generalizing the welfare benefits and minimizing the risks.

Key Words: natural living, professionalism, industrial agriculture

46 Can the fox guard the hen house? Can big corporations be socially responsible? T. Grandin*, *Colorado State University, Fort Collins.*

Three factors make big food corporations socially responsible. They are the (1) top leader's ethical principles, (2) a health emergency, and (3) activists that expose serious problems. During a 40-year career working with big corporations, I have observed animal welfare switching from an abstract nuisance that is delegated to the legal or public relations department to a real issue. This occurred when top executives went on tours of farms and slaughter plants. They saw reality; many things were acceptable but there were bad practices that needed changing. Since 1999, there have been huge improvements in animal handling in large slaughter plants. The improvement started when big restaurant chains started auditing animal welfare. Activist pressure was an initial stimulus, but the long-term motivator was top executives getting their "eyes opened." Industry organizations responded by developing guidelines and I have served on many committees. Sometimes the worst producers get on the committees to weaken standards. Large corporations can be socially responsible but many of them will need some outside pressure to prevent the worst abuses. On the other hand, big corporations are not the evil empire depicted by activists. Reality is always somewhere in the middle.

Key Words: animal welfare, social responsibility, welfare standard

47 Bioethical implications of retailer decisions and agreements with activists: HSUS-UEP Agreement. J. C. Swanson*, *Michigan State University, East Lansing*

The objective of this talk is to examine the ethical challenges that have occurred through activist pressure on food retailers, use of state initiatives, and industry-led change that have led to the HSUS-UEP historic agreement. During the last 15 years, social and political activism has instigated change to standard food animal production practices, including transport and slaughter. In the 1990s, animal activist organizations directly engaged the food retail sector to promote social responsibility for the welfare of animals used in the supply chain. Major food retailers responded by forming advisory committees, developing policies, and setting standards for their supply chain using market access as leverage for change. In the mid-2000s, the game changed. Social pressure on food retailers was coupled with the citizen referendum and successfully codified housing standards in several states. The targets were housing systems utilizing battery cages, sow gestation stalls, and stalls for veal calf production. A patchwork of legislation emerged. Each state-negotiated law left affected animal industries with serious production and market access issues. Most affected by the differences in state laws was the US egg industry. In 2011, the United Egg Producers (UEP) and the Humane Society of the United States (HSUS) mutually agreed to pursue federal legislation to set a common baseline for egg production within the United States.

Key Words: bioethics, animal welfare, agreements

48 Population structure and identification of lineages in a Brazilian Guzerat metapopulation. J. C. C. Panetto*[1], M. G. C. D. Peixoto[1], G. G. Santos[1], F. A. T. Bruneli[1], R. S. Verneque[1], M. A. Machado[1], A. L. S. Azevedo[1], D. R. L. Reis[1], L. A. Silva[1], A. A. Egito[2], and M. R. S. Carvalho[3], *[1]Embrapa Gado de Leite, Juiz de Fora, MG, Brazil, [2]Embrapa Gado de Corte, Campo Grande, MS, Brazil, [3]Universidade Federal de Minas Gerais, Belo Horizonte, MG, Brazil.*

Guzerat (*Bos primigenius indicus*) cattle was included in the FAO list of breeds to be conserved by means of management due to its beef and dairy potentials under various, especially harsh, environmental conditions. This study aimed to ascertain the population structure and the identification of distinct lineages in a metapopulation of the Guzerat breed in Brazil. Blood samples were collected from 664 animals in 15 seedstock herds in the country, including 5 herds with selection focused on beef, 9 herds in dual purpose systems and one closed herd with selection exclusively for dairy purposes. Genomic DNA was extracted from these samples and a panel of 21 microsatellites was selected for the Guzerat breed, according to their polymorphism information content (PIC). F-Statistics were used to estimate differentiation among subpopulations (F_{ST}) and the degree of reduction in heterozygosis due to non-random mating within subpopulations (F_{IS}). Lineages were determined by cluster analysis with a Bayesian approach with increasing numbers of inferred populations, assuming an admixture model based on the correlations between allelic frequencies. PICs ranged from 0.57 to 0.88, with a mean of 0.75. There was a large variation among herds on F_{IS} (values ranged between −0.109 and 0.061) indicating that some herds were more inbred than others. Average F_{ST} for this metapopulation was 0.034 ± 0.002. The closed dairy herd was the most differentiated among all (average pairwise F_{ST} = 0.052). The pairwise F_{ST} matrix demonstrated that, in general, the dual purpose herds were less differentiated within the entire metapopulation, when compared with the studied beef herds. Cluster analysis resulted in the identification of 6 lineages. Among them, 3 lineages included mostly animals from dual purpose herds, 2 lineages included mainly animals from beef herds, and one lineage included animals from dairy or dual purpose herds. One practical consideration is that the existence of herds with different purposes has contributed to the genetic structure of this breed. This project was supported by FAPEMIG.

Key Words: cluster analysis, genomic DNA, population structure

49 Genetic relationships among milk production and teat and udder scores in cows sired by seven prominent beef cattle breeds. L. A. Kuehn* and H. C. Freetly, *USDA-ARS, US Meat Animal Research Center, Clay Center, NE.*

Milk production and teat and udder quality are key components to lifetime cow productivity in commercial beef cattle. Our objective was to determine genetic relationships and breed differences for milk production and teat and udder quality in young and mature cows. Cows (n = 602) were crosses of F_1 cows and bulls (F_1^2) ; the F_1 parents resulted from matings of industry Angus, Hereford, Red Angus, Charolais, Gelbvieh, Limousin, and Simmental bulls with base Hereford, Angus, and MARC III composite cows. These F_1^2 cows were produced in 3 seasons and evaluated as 2 yr olds after their first calf and again as 5 yr olds. Milk production was measured approximately 100 d after parturition using the weigh-suckle-weigh method. Teat size and udder suspension were scored on a 9-point subjective scale in which 5 was considered an optimum. Genetic correlations and breed effects were derived from MTDFREML using a mixed model with fixed season, calf sex (for milk production), and breed and heterosis covariates and random effects of animal and error. Heritability estimates for 2 and 5 yr teat score, 2 and 5 yr udder score, and 2 and 5 yr milk production were 0.27, 0.31, 0.14, 0.32, 0.32 and 0.49. Genetic correlations among the same trait measured in different years were high (0.79 to 0.84). Similar to heritability estimates, correlations with udder score at 2 yr were lower than for other score traits likely indicating greater error in phenotyping udder suspension at 2 yr. Correlations between score traits and milk production were low and not significantly different than zero. Teat size was smallest in Charolais and largest in Simmental across years. Udder suspension was most optimal in Charolais. No breed effects were detected for milk production. This result is counter to breed effects generally observed on maternal effects for weaning weight in national cattle evaluation. Selection for these traits may lead to increased lifecycle productivity in beef cattle due to decreased culling on udder conformation.

Key Words: cow productivity, beef cattle, milk production

50 Genetic parameters for udder quality in Hereford cattle. H. L. Bradford*, D. W. Moser, J. M. Bormann, and R. L. Weaber, *Kansas State University, Manhattan.*

Udder quality is an important trait for beef producers because udders affect cow longevity and calf performance. The objective of this study was to estimate the genetic parameters for udder quality in Hereford cattle. The Beef Improvement Federation recommends collecting subjective scores on udder suspension and teat size. Prior to these guidelines, the American Hereford Association (AHA) recorded an overall score, which combines all udder characteristics into a single score. In all cases, scores ranged from 1 to 9 with a score of 9 considered ideal. Records on 78,556 animals and a 3-generation pedigree with 196,540 animals were obtained from the AHA, Kansas City, MO. These records contained repeated observations for overall score (n = 126,753), suspension (n = 61,758), and teat size (n = 61,765). Data were modeled using a multiple trait animal mixed model with random effects of additive genetic and permanent environment and with fixed effects of age and contemporary group (herd-year-season). Variances were estimated with ASREML 3.0. Heritability estimates (standard errors) of overall score, suspension, and teat size were 0.32 (0.01), 0.31 (0.01), and 0.28 (0.01), respectively. These results showed udder quality was moderately heritable, agreeing with previous research. The phenotypic correlations (standard errors) between teat size and suspension, overall score and teat size, and overall score and suspension were 0.64 (0.003), 0.31 (0.01), and 0.31 (0.01), respectively. Of the records for suspension and teat size, 57% had the same score for both traits. The genetic correlations (standard errors) between teat size and suspension, overall score and teat size, and overall score and suspension were 0.83 (0.01), 0.72 (0.02), and 0.70 (0.02), respectively. The genetic correlations between traits were extremely strong, indicating that these records were different measures of the same trait. In addition, differentiating between suspension and teat size might be difficult for producers.

Key Words: beef cattle, genetic parameter, udder score

51 Phenotypic relationships between docility and reproduction in Angus heifers. K. L. Otteman*[1], J. M. Bormann[1], K. C. Olson[1], J. R. Jaeger[1], S. Johnson[1], B. Downey[2], D. M. Grieger[1], J. W. Waggoner[1], D. W. Moser[1], and R. L. Weaber[1], *[1]Kansas State University, Manhattan, [2]Cowney Ranch Inc., Wamego, KS.*

Reproductive success is economically relevant in beef cattle operations, and may be influenced by temperament. The objective of this study was to elucidate the phenotypic relationships between docility and first service AI conception rate in heifers. Data (n = 337) collected from 3 cooperator herds in Kansas at the start of the synchronization protocol and included exit velocity (EV), chute score (CS), fecal cortisol (FC), and blood serum cortisol (BC). Statistical analysis was done using logistic regression with 30 d pregnancy rate as the dependent variable. The model included the fixed effect of contemporary group, and the covariates FC, BC, EV, CS, weight, and age. Correlation coefficients were also calculated between all continuous traits. Pregnancy rate ranged from 34% to 58% between herds. Blood cortisol positively correlated with EV (r = 0.22, $P < 0.01$), negatively correlated with age (r = −0.12, $P < 0.03$), and tended to be negatively correlated with weight (r = −0.10, $P = 0.09$). Exit velocity was positively correlated with CS (r = 0.24, $P < 0.01$) and negatively correlated with weight (r = −0.15, $P < 0.01$) and age (r = −0.12, $P < 0.03$). Chute score negatively correlated with age (r = −0.14, $P < 0.01$), and as expected, age and weight were moderately positively correlated (r = 0.42, $P < 0.01$). In general, older, heavier animals had better temperament, as indicated by lower BC, EB, and CS. The power of our test could not detect any significant predictors of 30 d pregnancy for the combined data from all ranches. When the data was divided by ranch, however, chute score ($P < 0.03$) and weight ($P < 0.01$) were both found to be significant predictors for 30 d pregnancy for ranch 1. Fertility is a complex trait that is dependent on many factors; our data suggest that docility is one factor that warrants further investigation.

Key Words: beef cattle, fertility, docility

52 Docility and heifer pregnancy heritability estimates in Angus heifers. K. L. Otteman*, J. M. Bormann, D. W. Moser, and R. L. Weaber, *Kansas State University, Manhattan.*

The objective of this study was to determine the genetic control of docility and reproduction in heifers as measured by pregnancy rate. Data included weaning contemporary group information, yearling contemporary group information, sex, docility score, yearling weigh date, age of dam, breeding contemporary group, age at first breeding, pregnancy check results, and first service sire. A subjective chute scoring system was used as the basis of their genetic evaluation for docility. Pedigree information included 508,015 animals over 30 generations. Contemporary groups were formed by the concatenation of weaning contemporary group, yearling contemporary group, and breeding contemporary group. Heritabilities were computed from estimates of genetic and residual variance components computed using ASReml 3.0 (VSN International, Hemel Hempstead, UK). Heifer pregnancy variance components were estimated from a univariate threshold model, with pregnancy outcome as the dependent variable, animal and contemporary group as random effects, and age at first breeding as a covariate. The heritability of heifer pregnancy was estimated to be 0.16 ± 0.02. Docility was fit as a univariate, linear animal model with docility score as the dependent variable, and animal and contemporary group modeled as random effects. The heritability for docility score was estimated to be 0.22 ± 0.03. Low to moderate heritability on these traits indicates that slow but definite genetic improvement can be made by selection on heifer pregnancy and docility.

Key Words: genetics, docility, reproduction

53 The effect of sire breed on birth weight, preweaning ADG, and adjusted 205-d weight of calves from commercial Angus dams mated to Angus, Braunvieh, and Hereford sires. C. L. Ferring*, G. A. Hansen, and J. P. Cassady, *North Carolina State University, Raleigh.*

The objective of this study was to assess the effects of breed of sire on birth weight, preweaning ADG, and adjusted 205-d weight. Angus (n = 58), Hereford (n = 37), and Braunvieh (n = 41) sires were randomly mated to commercial Angus cows (n = 184, 75% or greater Angus). Hereford and Braunvieh sired calves should express 100% heterosis. Data were available for 389 calves born from 2003 to 2011 at the Tidewater Research Station in Plymouth, NC. Male calves were castrated by 5 mo of age. Calves were not creep fed and never implanted. The GLM Procedure of SAS was used. The model included fixed effects of sire breed, age of dam, sex of calf, and calf birth year. Gestation length, calculated based on the day a cow was bred by AI and the day she calved, was included as a covariate. Age of dam and sex of calf affected birth weight, pre-weaning ADG, and adjusted 205-d weight ($P < 0.01$). Calf birth year affected preweaning ADG and adjusted 205-d weight ($P < 0.01$). A 1-d increase in gestation length increased birth weight by 0.19 kg ($P < 0.01$), increased preweaning ADG by 0.12 kg ($P < 0.05$), and decreased adjusted 205-d weight by 0.42 kg ($P < 0.06$). Sire breed affected birth weight ($P < 0.01$). Angus, Hereford, and Braunvieh sired calves had average birth weights of 34.6, 36.9, and 37.4 kg, respectively. Effects of sire breed on preweaning ADG and adjusted 205-d weight were not statistically significant. Birth weight, preweaning ADG, and adjusted 205-d weight increased as age of dam increased up to 5 years of age. In summary, breed of sire influenced birth weight but did not affect preweaning ADG and adjusted 205 d weight. These results are surprising in that heterosis did not result in significantly heavier calves at weaning.

Key Words: beef cattle, crossbreeding, growth

54 Breed × sex effects on birth weight in Brahman-Simmental embryo transfer calves. J. A. Dillon*[1], R. M. Thallman[2], J. O. Sanders[1], and D. G. Riley[1], *[1]Texas A&M AgriLife Research, College Station, [2]US Meat Animal Research Center, Clay Center, NE.*

Brahman cross calves exhibit unusual inheritance of birth weight: Brahman-sired crossbreds out of *Bos taurus* females are heavier with greater difference between sexes than calves of the reciprocal cross. The objective of this work was to compare birth weight in various crosses of Brahman, Simmental, and Simbrah. Embryo transfer (ET) calves (n = 2,486) were born in central Texas from 1984 – 1990 and were 1/4, 3/8, 1/2, 5/8, or 3/4 Brahman produced by multiple types of matings, dependent upon the breed group. Data were analyzed with an animal model, with 6,061 animals in the pedigree. Fixed effects investigated included contemporary group (n = 36; combinations of year, birth season, and location), sex of calf, breed group (n = 5), and linear covariates of direct expected breed heterozygosity (HET) and proportion of Brahman in the sire (BIS). Random effects included additive genetic and maternal permanent environmental (of the recipient dam); maternal genetic did not improve likelihood values and was not included in the final model. The regression coefficient for HET was 11.2 ± 3.52 kg ($P = 0.02$). The regression coefficient for BIS was 7.7 ± 1.04 kg ($P < 0.001$). There was a breed group by sex interaction detected ($P < 0.001$). Males were heavier ($P < 0.05$) than females in 1/4, 3/8, and 3/4 Brahman groups. Among females, 3/4 Brahman calves had lower ($P < 0.05$) birth weights than all other breed groups. In male calves, 1/2 and 3/4 Brahman calves had lower ($P < 0.05$) birth weights than all other groups. The estimate of heritability for birth weight from these data was 0.34 ± 0.05. Maternal permanent environmental variance as a proportion of phenotypic variance was 0.34 ± 0.09.

Proportion Brahman in the sire relative to proportion Brahman in calf significantly influences birth weight in Brahman-Simmental crosses produced by ET. This effect is not consistent with standard models used in genetic evaluation, but is consistent with the mechanisms of genomic imprinting, early (before ET) embryonic maternal effects, and/or X chromosome effects.

Key Words: birth weight, Brahman, non-Mendelian inheritance

55 Phenotypic and genetic correlations as well as linear relationships of performance, carcass, feed efficiency, and economic characteristics of beef feedlot steers. K. M. Retallick*[1], D. B. Faulkner[2], S. L. Rodriguez-Zas[1], J. D. Nkrumah[3], and D. W. Shike[1], *[1]University of Illinois, Urbana, [2]University of Arizona, Tucson, [3]Pfizer Animal Genetics, Kalamazoo, MI.*

Several feed efficiency measures are being investigated including: feed conversion ratio in terms of feed:gain (FCR), residual feed intake (RFI), residual BW gain (RG), and residual intake and BW gain (RIG). These traits have production efficiency potential since they include feed intake inputs and production outputs. The objective of this study was to investigate 1) how these measures of efficiency affect one another and their heritability estimates and 2) relate measures of efficiency both genetically and phenotypically to feedlot cattle performance, carcass, and economic characteristics. All feed efficiency traits were favorably correlated genetically and phenotypically to each another. Heritability estimates were moderate ranging from 0.22 to 0.38 ± 0.10. Feed conversion ratio was genetically correlated to RG and RIG at −0.97 and −0.95, respectively. Feed conversion ratio was also highly correlated with growth traits therefore an increase in weight led to a more desirable FCR. A genetic increase in carcass value was associated with a more desirable FCR due to an increase in HCW. As expected due to genetic correlation to FCR, similar affects were shown for RG. A unit reduction in DMI yielded a 0.42 improvement in RFI and genetic results were similar. As designed, RIG reduced DMI similar to RFI and increased ADG similar to RG. Marbling was correlated phenotypically to RG and RIG at −0.08 and −0.09, respectively and correlated genetically to RFI and RIG at 0.59 and −0.59, respectively. This indicated that marbling decreased as measures of feed efficiency improved; however, the linear regression slope was small which indicated only a small decrease in marbling. As a result, carcass value was still favorably correlated with RG (r = 0.15) and RIG (r = 0.10) and not correlated to RFI. As profitability increased for steers, all feed efficiency measures improved.

Key Words: feedlot feed efficiency, genetic relationship, phenotypic relationship

56 Genotype by environment interaction effects on crossbred lambs at finishing. G. C. Márquez*[1], W. Haresign[2], M. H. Davies[3], R. Roehe[4], L. Bünger[4], G. Simm[4], and R. M. Lewis[1,4], *[1]Virginia Tech, Blacksburg, [2]Aberystwyth University, Aberystwyth, UK, [3]ADAS Rosemaund, Preston Wynne, UK, [4]Scottish Agricultural College, Edinburgh, UK.*

Accounting for genotype by environment interactions (GE) in genetic evaluations is important because animals may not perform predictably across environments. The purpose of this study was to investigate GE on full body weight (FWT), ultrasonic muscle (UMD) and fat (UFD) depth at finishing in crossbred lambs. Data on 6,325 lambs sired by Charollais, Suffolk, and Texel rams were obtained. The experiment was done between 1999 and 2002 on 3 farms in the UK. In total 89 sires (selected from the top or bottom 10% on a selection index that increased carcass lean weight while keeping fat constant) were mated to 1,984 ewes of 2 types (Bluefaced Leicester × 2 hill breeds). Most rams were used for 2 successive mating seasons, with some rotated among farms to create genetic links. Lambs were reared on pasture and assessed for fat cover until they reached a target of 11% subcutaneous fat, and then were weighed and ultrasonically scanned for fat and muscle depth. The UFD data were log-transformed to approach normality. All models included the fixed effects of sire index category, lamb sex and birth year, age of dam, and birth-rearing category. Subcutaneous fat at finishing was a covariate for FWT and UMD, and age at finishing for UFD. An additive genetic effect was fitted with a pedigree-based relationship matrix among lambs. Six genetic groups were fitted (3 sire breeds, 2 dam breed types, 1 maternal grandsire breed). For FWT a random rearing dam effect was fitted, which was unimportant for UFD or UMD ($P > 0.2$). The GE in the data was first investigated by fitting a random sire by farm interaction term. Likelihood ratio tests indicated that GE defined variation ($P < 0.001$). The ratio of interaction variance to total variance for FWT, UMD, and UFD was 0.07 ± 0.02, 0.11 ± 0.02, and 0.22 ± 0.03, respectively. Additionally, data from the 3 farms were fitted as separate but correlated traits. Heritabilities differed in the 3 farms ($P < 0.01$). Genetic correlations among farms were generally high, as were rank correlations of sire EBV (0.7–0.9). This indicates that, especially for scanning traits, GE should be considered in robust genetic evaluation programs.

Key Words: genetics by environment interaction, sheep

57 Tolerance of the maternal immune system to the fetal semi-allograft. M. G. Petroff*, S. M. Alam Khorshed, C. Linscheid, and S. Jasti, *Department of Anatomy and Cell Biology, University of Kansas Medical Center, Kansas City, KS.*

Pregnancy has often been likened to an allograft due to the genetic differences between the mother and her baby. Upon the discovery of the major histocompatibility complex antigens in the 1950s it was reasoned that in order for the mother to tolerate the fetus, the 2 must somehow prevent or suppress an immune response that could result because of their immunogenetic differences. Initial hypotheses of how the mother could tolerate the semiallogeneic fetus included maternal immune suppression, immunological immaturity of the fetus, and physical separation of the mother and fetus. The last 60 years of research have enlightened us greatly in the mechanisms by which this paradoxical situation flourishes; to varying degrees, all of Sir Peter Medawar's hypotheses regarding the fetal "allograft" are true. The trophectoderm-derived placental trophoblast provides the physical interface between mother and baby, and although this tissue restricts expression of major histocompatibility complex molecules, there is no shortage of paternally-inherited minor histocompatibility antigens. These minor antigens, when mismatched between organ donor and recipient, cause chronic allograft rejection in transplantation; in pregnancy, minor antigens are expressed by the trohpoblast, and are detected and robustly tolerated by the maternal immune system. We have hypothesized that paternally-inherited as well as placenta-specific antigens are detected by the maternal immune system as a result of trophoblast expression, and moreover, by virtue of shedding of copious amounts of trophoblast microvesicles and exosomes into the maternal blood. The detection of feto-placental antigens by maternal CD4+ and CD8+ T lymphocytes occurs as a muted immune response that is controlled by placental factors co-expressed with the antigens. Despite this highly controlled lymphocyte response to the fetus, maternal memory T cells develop and can persist in women for decades. Although the physiological ramifications of these persistent T cells are not understood, they may include effects on long-term health of mothers. Supported by NIH R01HD045611 and P01HD049480.

Key Words: pregnancy, placenta, trophoblast

58 The immune system in CL formation/angiogenesis/lymphangiogenesis and its role in establishment of pregnancy. A. Miyamoto*[1], K. Shirasuna[2], S. Haneda[1], T. Shimizu[1], and M. Matsui[1], *[1]Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Japan, [2]Jichi Medical University, Tochigi, Japan.*

The establishment of pregnancy needs a well-balanced regulation in endocrine and immune systems and involves interactions among conceptus, oviduct/uterus and CL. In particular, the optimal rate of increase in plasma P4 during the first 1wk after ovulation is critical for the conceptus growth, leading to successful in pregnancy in cattle. Events involved in maternal recognition of pregnancy (MRP) may commence before 1wk from AI, as interferon-stimulated genes (ISGs) and IL10 mRNA expressions in circulating immune cells increase in pregnant cows. To regulate optimal endocrine condition in this narrow time window, CL should develop rapidly with active angiogenesis/lymphangiogenesis. Major angiogenic factors VEGF and FGF2 work in developing CL, but may also act as chemoattractant to PMN. Indeed, PMNs were observed at highest number in new CL with highest IL8 expression, and PMN secrete IL8 to induce active angiogenesis/lymphangiogenesis in CL. The findings led us to hypothesize functional polarization of neutrophils (proinflammatory N1 vs. anti-inflammatory N2). It is interesting that on d 5 after AI circulating PMN exhibit upregulated expression of ISGs, and that PMN in CL are stimulating luteal angiogenesis, both of which are physiological prerequisites for occurrence of pregnancy. During later phase of MRP, the conceptus secretes a large amount of interferon-tau (IFNT), thereby preventing CL regression. Likely IFNT reaches CL and acts on acquisition of PG-resistance. New lymphangiogenesis stimulated by IFNT may occur at MRP without any new angiogenesis in cows. Taken into account that PGE2 is also upregulated in CL at MRP, some shifting of local immunity toward immune tolerance may occur in CL of early pregnancy. Interestingly, persistent CL (non-pregnant) and CL of early pregnancy showed similar mRNA expression, but differed in higher expression of Foxp3 mRNA in CL of pregnancy. Elucidating the immune system for earlier MRP together with local regulation of CL development utilizing immune system may help in understanding physiology and pathophysiology of early pregnancy in cows.

Key Words: corpus luteum, angiogenesis/lymphangiogenesis, early pregnancy

59 Effects of maternal obesity on placental and gut inflammation and immune function. M. Zhu*[1], H. Wang[2], M. Du[3], and S. P. Ford[2], *[1]School of Food Science, Washington State University, Pullman, [2]Department of Animal Science, University of Wyoming, Laramie, [3]Department of Animal Science, Washington State University, Pullman.*

Obesity in pregnant women is a growing public health concern, which negatively affects fetal development and has long-term effects on offspring health. The placenta mediates nutrient transport to fetuses and is a source of inflammatory cytokines. Maternal obesity in sheep induces placental inflammation as indicated by enhanced expression of inflammatory cytokines including tumor necrosis factor (TNF)-a, interleukin (IL)-6, IL-8 and IL-18, and exaggerated c-Jun N-terminal kinase (JNK)/c-Jun and nuclear factor kappa-light-chain-enhancer of activated B cells (NF-kB) inflammatory signaling pathways. Accompanying placental inflammation, maternal obesity induces an inflammatory response in the late gestation fetal large intestine of sheep, manifested by elevated expression of TNF-a, IL-1β, IL-6, IL-8, and monocyte/macrophage chemotactic protein-1 (MCP-1), as well as macrophage markers, CD11b, CD14, and CD68 in the fetal gut. In addition, we observed that inflammation persisted in offspring gut of obese mothers. Using non-obese diabetic (NOD) mice, we further demonstrated that offspring born to obese mothers had higher gut epithelial permeability, called "leaky gut," which is one of the main etiological factors for several common diseases including inflammatory bowel diseases, Type I diabetes and related autoimmune diseases. In agreement with increased gut permeability, we showed that maternal obesity resulted in an increased incidence of Type I diabetes, as evidenced by a severe lymphocyte infiltration and destruction of pancreas islets in the offspring of obese NOD mice. In summary, maternal obesity induces inflammation in the placenta and fetal gut, which has long-term effects on offspring gut immunity, likely pre-disposing offspring to inflammatory bowel diseases, type 1 diabetes and other autoimmune diseases. (Supported by NIH 7R15HD073864–02; USDA 2008–35203–19084; 2009–65203–05716).

Key Words: maternal obesity, offspring, placenta

George C. Fahey Companion Animal Nutrition Symposium I: Effect of Dietary Format on Nutrition, Food Management, and Food Safety

60 Introduction—Defining natural pet foods. K. R. Kerr*, *Department of Animal Sciences and Division of Nutritional Sciences, University of Illinois, Urbana.*

Many pet owners are choosing alternative diets for their dogs and cats. Therefore, it is not surprising that more and more pet food packaging contains words like "holistic," "natural," "organic," "real meat," "no preservatives," and a multitude of other claims. In 2009, it was estimated that 249 new natural products were available in the pet market, up from 154 new natural products in 2007. While the pet food market is benefiting from the current natural and organic trends, the definitions of these terms are either vague or misunderstood by consumers, allowing a multitude of products to be categorized and purchased under these terms. We have invited some of the field's most reputable speakers, who have first-hand experience with researching, marketing, formulating, and managing the safety of natural pet foods.

Key Words: companion animal, nutrition

61 From wild to captive diets: Metabolic flexibility of cats. A. Verbrugghe*, *Ontario Veterinary College, University of Guelph, Guelph, ON, Canada.*

The domestic cats' wild ancestors (*Felis silvestris*) are known to be obligate carnivores, consuming prey which are high in protein, moderate in fat, and contain only minimal amounts of carbohydrates. Evolutionary events adapted the cat's metabolism and physiology to this diet strictly composed of animal tissues, which led to unique digestive and metabolic peculiarities of protein, carbohydrate, fatty acid, and vitamin metabolism. Cats have a high protein requirement and are unable to adapt hepatic catabolic enzyme activity to a low protein diet. Cats also have a higher requirement for essential amino acids such as arginine, methionine, cysteine and taurine. Carbohydrate digestion is characterized by a very low salivary amylase activity, a rather low intestinal amylase activity and a non-adaptive sugar transport system across the intestinal brush border. Moreover, hepatic glucokinase and glycogen synthase activity are limited, while hepatic gluconeogenic enzymes are upregulated. The modern domestic cat (*Felis catus*) still closely resembles its wild ancestor. Although the carnivore connection of domestic cats is well recognized, little is known on the precise nutrient profile to which the digestive physiology and metabolism of the cat has adapted throughout evolution. Data from dietary habits of feral cats combined with compositional data of the consumed prey species revealed a typical diet containing a crude protein, crude fat and nitrogen-free extract content on dry matter basis of 63.1, 20.1 and 8.9%, respectively. Still a distinct difference must be made between the optimal diet composition and nutrient requirements. Also this diet composition did not discriminate between reproduction and maintenance nor accounted for disease or other physiological states. It can be argued that the shift from an obligatory meat based diet to a pet food with higher carbohydrates levels places the cats' metabolism under stress and might have unwanted negative health effects in the long-term, especially when accompanied by a shift from an outdoor environment to an indoor lifestyle and a decreased physical activity.

Key Words: feline nutrition, metabolism

62 What is natural? Marketing versus science of natural pet diets. P. R. Buff*, R. A. Carter, and J. H. Kersey, *The Nutro Company, Franklin, TN.*

In recent years, the natural segment of pet foods has grown steadily from $2.0 billion in 2008 to $3.9 billion in 2012. This growing trend may be attributed to anthropomorphism of dogs and cats as 63% of pet owners consider their pets to be family members. The term natural when used to describe pet foods or pet food ingredients has been defined by the Association of American Feed Control Officials (AAFCO). The regulation requires at a minimum the pet food is preserved with natural preservatives. However, pet owners consider natural as something different than the AAFCO definition. Pet owner perception of natural pet food is variable and includes the following; organic, less additives, no by-products, no added preservatives and high protein. Much of the trend in natural pet food focuses on ingredients with a rise in grain free, human grade and organic claims. However, the research behind the benefit of these natural ingredients may be lacking. Where evidence exists, some natural pet foods focus on structure-function claims to provide nutritional benefits linked to natural ingredients. New food formats have emerged in recent years, evolving from only extruded and canned diets to formats such as frozen, freeze-dried and baked. The processing of pet food can affect digestibility, nutrient bioavailability and safety. Some trends have focused on evolutionary diet formulation based on wild species. Domestic cats have been shown to prefer a macronutrient profile similar to wild cats. However, dogs prefer a diet different than wolves, with a macronutrient profile of approximately 30% of their caloric intake from protein. This may be attributed to recent data showing dogs have evolved much different than wolves in their ability to metabolize carbohydrates as dogs are scavengers rather than hunters. Future opportunities include the integration of sustainability with natural pet foods. The challenge is to match the consumer demand and provide natural nutrition to pets while reducing the impact on the environment. The market for natural pet food continues to grow as pet owners are becoming closer to their pets than previous generations and more aware of their pets' diet.

Key Words: nutrition, natural, pet food

63 Potential health benefits of phytochemicals in pets. P. Nguyen*[1], B. Paragon[2], H. Hazewinkel[3], V. Leray[1], G. Blanchard[4], S. Serisier[5], and A. André[1], *[1]National College of Veterinary Medicine, Food Science and Engineering Nantes-Atlantique (Oniris), Nantes, France, [2]National Veterinary School of Alfort, Maisons-Alfort, France, [3]Utrecht University, Utrecht, the Netherlands, [4]Animal Nutrition Expertise, Antony, France, [5]Royal Canin R & D, Aimargues, France.*

In addition to the chemicals used as "usual" nutrients, plants contain secondary metabolites that are involved in adaptation to environment, defense against 'predators' and pathogens, and regulation of symbiosis and seed germination. These phytochemicals include phenolics, alkaloids, carotenoids, and organosulfur compounds. Although some are toxic when consumed, others may be associated with health benefits, including anti-mutation, anti-carcinogenesis, anti-oxidation and anti-angiogenesis properties. For the most part, their bioactive potency is low, but they may induce significant

effects when consumed daily over the long-term. Higher doses of phytochemicals can be provided in the form of nutraceuticals that are often phytochemical-enriched extracts or phytochemicals-like compounds synthetized and/or modified so that to increase their bioavailability and efficacy. The health effects of phytochemicals particularly concern age-related diseases, such as cardiovascular and neurodegenerative diseases, diabetes, osteoporosis, and several types of cancer. They have also been shown to improve obesity-related metabolic disturbances, especially low insulin sensitivity, and low-grade inflammation, as well as dyslipidemia. As phytochemicals are very numerous, several mechanisms of action can be involved, including the increase of the total antioxidant power, or modifications of gene transcription through activation of nuclear receptors or epigenetic modifications. For companion animals, less evidence is available as regards phytochemical efficacy than for humans and rodents from in vivo clinical and experimental trials, and in vitro studies. In pets, phytochemicals would improve insulin resistance, aging cognition impairment, osteoarthritis, carcinomas, urolithiasis, atopic dermatitis, and 'antioxidants' would improve immunological status. Some studies have concerned the bioavailability and tissue distribution of some phytochemicals but most often clinical studies are missing. It is known, however, that more is not always better. Moreover, we raise the question of how phytochemicals act, and that of the metabolic basis for 'dietary' supplementation of diets supposed to be balanced and meeting dietary 'requirements'.

Key Words: phenolic compound, carotenoids, plant secondary metabolite

64 Ramifications of the food safety modernization act on the pet food industry, along with new technologies to control salmonella in pet food. C. Knueven*[1] and G. Aldrich[2], *[1]Research and Development, Jones-Hamilton Co., Walbridge, OH, [2]Grain Science & Industry, Kansas State University, Manhattan.*

In 2007 there were 2 very significant food safety events in the pet food industry; one a chemical economic adulterant (melamine-cyanuric acid) and one a microbial pathogen (*Salmonella schwarzengurnd*). They each carried over into the human food chain and subsequently garnered enough attention of Congress to sweep pet food safety into the legislation crafted for the Food Safety Modernization Act of 2011. Since that time pet food manufacturers, equipment suppliers, laboratories, and ingredient suppliers have been gearing up for what they expect to be new rules regarding safety and traceability in the production of foods for companion animals. The new rules should be published by mid-summer 2013 and are expected to mirror the recently published cGMP rules for human foods. Diligence regarding testing has been expanding since 2007 with more than 99 recall events identified for various pet foods and treats during the period from 2008 to the present. While many of these events were due to mixing or labeling errors, the one large element generating great concern is the zero tolerance for pathogens such as Salmonella. For this there are several strategies being developed to bring contamination under control. This discussion will further discuss the requirements for facilities to conduct a hazard analysis, implement risk-based preventive controls, monitoring procedures, corrective actions, verification and recordkeeping steps to remain in compliance with the act. It will also provide an insight into new technologies and results from research on mitigation strategies for pathogen reduction and control and their influence on companion nutrition and food management.

65 The effect of feeding rumen-bypass protein on milk yield and composition in Irish dairy cows. M. R. Sheehy*[1,2], F. J. Mulligan[1], P. A. McLaughlin[2], O. Brennan[2], S. Taylor[2], and A. G. Fahey[3], *[1]School of Veterinary Medicine, University College Dublin, Dublin, Ireland, [2]Devenish Nutrition Ltd., Belfast, UK, [3]School of Agriculture and Food Science, Dublin, Ireland.*

Inclusion of rumen-bypass proteins in dairy cow diets is a standard management practice in many areas around the world. However, supplementing diets with rumen-bypass protein is not standard practice with a typical perennial ryegrass based Irish diet. Therefore the objective of this study was to determine if supplementing rumen-bypass protein would alter milk yield and composition for cows fed this diet type. Holstein-Friesian dairy cows (n = 112) were balanced for DIM, pre-experimental milk yield, and milk composition and assigned to either a control (n = 58) or a rumen-bypass protein (n = 54) treatment. Cows were put into 2 large pens and after each milking the cows rotated into a new pen to account for environmental effects in the shed. Cows were fed rumen-bypass protein in individual stanchions. Therefore cow is considered the experimental unit. The trial was carried out over a 10 wk period and on weekly intervals yield was recorded and milk composition was determined (fat yield and %, protein yield and %, lactose yield and %). All data were analyzed in SAS with a repeated measures mixed model. The fixed effects included treatment, parity (1 to ≥5), week (1 to 10), and the interactions between treatment and parity, and treatment and week. Days in milk, genetic potential for milk production, and the covariates of production for milk yield and composition −2, −1, and +1 week of the trial were included in the model. Cow within treatment was included in the model as a random effect. Cows fed the bypass protein had significantly greater milk yield ($P < 0.01$), protein yield ($P < 0.05$), protein % ($P < 0.01$), and a tendency to have an increase in lactose yield ($P < 0.10$). There were significant differences between the rumen-bypass protein and control treatments for fat yield, fat percentage, or lactose percentage. In conclusion bypass protein supplementation in the diet resulted in increased milk yield, and protein yield and composition for cows fed typical Irish forages. Therefore supplementation of rumen-bypass protein in Irish dairy systems may improve milk yield and protein production.

Key Words: milk composition, milk yield, rumen-bypass protein

66 Rescue from diet-induced milk fat depression in monensin-supplemented dairy cows. D. E. Rico*[1], A. W. Holloway[2], and K. J. Harvatine[1], *[1]The Pennsylvania State University, University Park, [2]Elanco Animal Health, Greenfield, IN.*

Sixteen Holstein cows were used in a crossover design to investigate the effect of monensin (MN) on the recovery from milk fat depression (MFD). MFD was induced at the start of each period by feeding a low fiber, high oil diet with monensin (Rumensin 90, Elanco Animal Health) for 10 d. A recovery phase of 18 d followed where cows were fed a high forage, low oil diet (31.2% NDF and no oil). Treatments during recovery were (1) control (no MN supplementation) or (2) monensin administered as a topdress at a rate of 450 mg/cow/d. Dry matter intake was observed daily and milk yield and composition and milk fatty acid (FA) profile were measured every 3 d during recovery. Data were analyzed as repeated measures and tested control vs MN at each time point. There was no effect of monensin on DMI or yield of milk, protein, and lactose ($P > 0.05$). Milk fat concentration and yield increased progressively during recovery in both treatments. However, there was no treatment by time interaction for milk fat yield ($P > 0.10$). Monensin decreased milk fat yield from d 6 to 15 (12% on average; $P < 0.05$), but was the same as control on d 18. There was a treatment by time interaction for milk fat concentration ($P < 0.10$), which was decreased by MN only on d 3 and 6. The yield of milk de novo synthesized FA increased progressively in both treatments and was not affected by treatment. Similarly, yield of 16C FA increased progressively, but was decreased by MN on d 6 and 9. Preformed FA yield was lower in the MN group from d 6 to 15 (13.9%; $P < 0.05$), but was not different from control on d 18. Importantly, milk FA concentration of trans-10 C18:1 and trans-10, cis-12 CLA rapidly decreased in both groups, however, MN slightly increased trans-10 C18:1 concentration on d 15 and 18 (21% of FA; $P < 0.01$). Monensin feeding reduced the rate of recovery from MFD predominantly through a delayed recovery of preformed FA, although a similar level of recovery was achieved by d 18. Monensin supplementation has minimal effect on recovery of normal rumen biohydrogenation and de novo fatty acid synthesis during recovery from MFD by correction of dietary NDF and PUFA concentration.

Key Words: dairy cows, milk fat depression, monensin

67 Behavior of dairy cattle housed on differing freestall bed types compared with cattle kept at pasture. J. Lau[1], J. K. Margerison*[1], M. Hedley[1], D. Horne[1], J. Hanley[1], N. Powell[2], and A. Shilton[2], *[1]Institue of Agriculture and Environment, Massey University, Palmerston North, New Zealand, [2]School of Engineering & Advanced Technology, College of Sciences, Massey University, Palmerston North, New Zealand.*

This research aimed to compare differing types of free stall beds on the lying time of dairy cattle and compare this with animals grazed at pasture. Three groups of 12 adult dairy cattle, of similar age, live weight and condition score were offered access overnight to; pasture (P) or were housed in free stalls that were fitted with sand beds (S) or dual chamber water beds (W). All housed cows were offered each bed type in a changeover design, with a 5 d house acclimatization period, followed by a 3 d behavior measurement and a 5 d rest period on pasture. Each day cows were grazed for 4 h, waited to be milked for 2 × 2 h and were either housed or grazed for 16 h overnight. During the training period all cows adapted quickly to lying in deep litter sand beds (0.61 (±0.05) days). During the 3 d of 24 h behavior measurement, cows lay in water beds for significantly less time, and stood fully in and half in beds for significantly longer compared with sand beds, while there was no significant difference between sand beds and cows at pasture (Lying: 11.1; S: 11.1; W: 9.9 (0.71) h/d). More cows housed on water beds lay in the alley (3) compared with cows housed on sand beds (0). Cows quickly adapted to lying in sand beds, despite not having used freestall housing previously. Cows housed on sand beds lay down for similar amount of time as cows kept at pasture. Cows housed on water beds lay down for significantly less time than cows on sand beds and more lay in the ally, and stood for longer and often stood half in the beds.

Key Words: housing, pasture, dairy

68 Effects of amount of palmitic and stearic fed to mid-lactation dairy cows on intake, milk yield, and diet digestibility. D. N. Lobão da Silva*[1], R. S. Younker[2], and N. B. Litherland[1], *[1]University of Minnesota, Saint Paul, [2]Milk Specialties, Eden Prairie, MN.*

Dietary supplementation with stearic and palmitic acid can increase energy available for dairy cows when energy intake constrains milk yield. Questions still remain regarding the impact of carbon chain length (pure stearic or palmitic acid) of saturated fatty on DMI, milk production, and milk fat yield. The objectives of this study were to determine if pure stearic or palmitic acid fed at 2.5% and 5% of total diet DM would affect DMI, milk yield, milk components and DM digestibility. Forty (n = 8) multiparous cows at 219 ± 10 DIM, producing 33 ± 1.8 kg of milk/d were randomly assigned to 1 of 5 treatments for 6 wk with a 5-d adaptation period. Data were analyzed by PROC MIXED with model containing effect of treatment and random effect of cow within treatment. Treatments were: TMR with 0% fat of diet DM Control (C); 2.5% stearic (S2.5); 5% stearic (S5); 2.5% palmitic (P2.5); 5% palmitic (P5). Diets were 17% CP, 28% NDF, 22% starch, and varied only in ether extract (4.1, 6.5, 8.8, 6.5, 8.8 %) for C, S2.5, S5, P2.5 and P5, respectively. There were no treatment effects on DMI, energy intake, or milk yield. Due to high summer temperatures (35°C) during this study, cows were heat stressed (93 THI) with low DMI. Higher energy diets from fat source did not alleviate the effects of heat stress on production.

Table 1.

	Treatment						
Variable	C	S2.5	S5	P2.5	P5	SEM	*P*-value
Calculated supplemental FA intake, g/d	0.0	452.4	932.7	466.1	847.5	32.1	<0.001
DMI, kg/d	18.8	18.1	18.7	18.6	16.9	0.9	0.57
Energy intake, Mcal/d	29.3	30.3	33.5	30.9	30.7	1.5	0.50
3.5% FCM, kg/d	23.5	25.1	27.6	27.1	25.2	1.6	0.35
Fat yield, g/d	0.8	0.9	1.0	1.0	0.9	0.1	0.28
Apparent total-tract DM digestibility, %	64.3	67.8	64.8	69.3	68.6	1.6	0.10

Key Words: milk production, palmitic acid, stearic acid

69 Effects of dietary starch content and corn particle size on intake, digestion and milk production by dairy cows. S. M. Fredin*, S. J. Bertics, and R. D. Shaver, *University of Wisconsin, Madison.*

An experiment was conducted to evaluate the effects of dietary starch concentration and corn particle size on intake, ruminal fermentation, digestibility, and milk yield, composition and component yields. Eight ruminally-cannulated multiparous Holstein cows (96 ± 8 d in milk at trial initiation) were randomly assigned to a 2 × 2 factorial arrangement of treatments in a replicated 4 × 4 Latin square design with 21-d periods. Treatments were finely (F; mean particle size = 552 µm) and coarsely (C; 1270 µm) ground dry shelled corn in normal (NS) and reduced (RS) starch rations fed as TMR. The NS and RS rations contained 27 and 18% starch (DM basis), respectively, by partially replacing corn with soy hulls. Milk samples were collected at both milkings on d 16 and 17 and rumen fluid 4 times daily at 2-h intervals on d 18–20 such that the samples represented a 24-h feeding cycle. Fecal samples were collected 2 times daily on d 18–20. Apparent total tract DM digestibility (DMD) was estimated using indigestible NDF as a marker. Data were analyzed using the MIXED procedure of SAS. Mean DMI (23.2 kg/d) was unaffected by treatment. Cows fed NS produced 1.9 kg/d more milk (41.0 vs. 39.1 kg/d; $P = 0.03$) and 0.06 kg/d of milk protein (1.18 vs. 1.12 kg/d; $P < 0.01$) than cows fed RS. There tended ($P = 0.06$) to be an interaction for milk fat yield with greater yield for NSF and RSC. The DMD, ruminal VFA (mM) and ammonia (mg/dL) were unaffected by treatment. Cows fed F had greater ruminal propionate (20.0 vs. 18.9 mol/100 mol; $P < 0.001$) and lower acetate: propionate ratio (3.45 vs. 3.68; $P < 0.001$) and pH (6.27 vs. 6.33; $P = 0.04$). Average rumen pH was above 5.8 for all treatments. Feeding normal starch diets increased milk and protein yields and finely ground corn increased ruminal propionate concentration.

Key Words: digestion, particle size, starch

70 Effect of time of storage on ammonia nitrogen concentration and ruminal in vitro starch digestibility of high moisture corn—A field survey. L. F. Ferraretto*, R. D. Shaver, and P. C. Hoffman, *University of Wisconsin-Madison, Madison.*

The objectives of the study were to (1) determine relationships between HMC ammonia-N, DM, pH and soluble CP concentrations and 7-h ruminal in vitro starch digestibility (IVStarchD), and (2) evaluate the effects of storage time on HMC pH, ammonia-N, soluble CP and IVStarchD measurements. Month of submittal was assumed to be associated to length of time in storage. To achieve these objectives a data set comprised of 2,685 HMC samples, within 50 to 80% DM, from Dairyland Laboratories Inc. (Arcadia, WI) and Cumberland Valley Analytical Services Inc. (CVAS, Maugansville, MD). Ammonia-N and soluble CP were reported as % of CP. Data evaluating the effects of month of submittal were analyzed using Proc Mixed in SAS with month as a fixed effect and laboratory as a random effect. Regressions to determine linear relationships between IVStarchD and ammonia-N, soluble CP, pH and DM content were performed using Proc Reg in SAS. Statistical significance and trends were declared at $P \leq 0.05$ and $P > 0.05$ to $P < 0.10$, respectively. IVStarchD increased from October to September of the following year, with October/November values 6%-units lower than May through September values. Similar results were observed for ammonia-N and soluble CP with an increase from 3.5% or 30% in October to 6.6% or 48% in August, respectively. The pH of HMC decreased from 4.6 in October to 4.3 in August of the following year. Ammonia-N was positively related to soluble CP ($R^2 = 0.92$) and StarchD ($R^2 = 0.53$). The DM content of HMC was negatively related ($R^2 = 0.58$) to IVStarchD with a decrease of 0.4%-units in IVStarchD per 1%-unit increase in DM. Combined, ammonia-N and DM provided good predictions of IVStarchD (Adj. $R^2 = 0.66$). The pH of HMC was negatively related to ammonia-N ($R^2 = 0.61$), soluble CP ($R^2 = 0.56$) and IVStarchD ($R^2 = 0.43$). Increasing ammonia-N, soluble CP and IVStarchD values suggest that HMC may need up to 8 mo to achieve maximum starch digestibility. Furthermore, ammonia-N and DM content are good indicators of starch digestibility in high moisture corn.

Key Words: high moisture corn, ammonia, starch digestibility

71 Using a systems model approach to assess the potential effect of changes in gene expression in adipose tissue of dairy cattle on production and reproductive efficiency. S. Shields and J. McNamara*, *Washington State University, Pullman.*

Variation in efficiency is a function of genetic, physiological and nutritional control in several organs and systems, including adipose tissue. To identify key physiological control points of metabolic flux and reproductive functions in dairy cattle, an existing metabolic model was used and expanded to include reproductive cycling, follicular growth, and steroid clearance. Our objective was to relate transcription of mRNA in adipose and liver which control metabolism, and potentially, reproductive processes and efficiency. The model describes substrate sensitivity

and maximum velocity for lipogenesis, esterification and lipolysis in adipose and gluconeogenesis and protein synthesis in the liver. Data from late gestation through 56 DIM on nutrient intake, milk output, adipose lipid, visceral and body protein and lipid, adipose metabolism and gene transcription in adipose and liver were collected. Genes coding for lipogenic pathways, as well as rates of lipogenesis decreased, but rates of lipolysis increased without increased mRNA abundance. In the liver, several genes of glucose, fatty acid and amino acid metabolism increased. In the simulation study, we altered the Vmax and Ks for lipogenesis, lipolysis, gluconeogenesis and protein synthesis, and milk production and intake were allowed to vary in response. Milk production ranged from 38.3 to 38.9 kg/d, body fat change from −0.07 to 0.4 kg/d, maintenance energy 22.0 to 25.4 Mcal/d and efficiency of milk energy as a percent of ME from 44.3 to 49% (at 56 DIM). Changing rates of lipogenesis, lipolysis, gluconeogenesis and protein synthesis did not affect milk production or feed intake, but altered milk fat percentage and maintenance costs and varied postpartum interval to first ovulation approximately 3 d. Increases in metabolic rate increased rates of estrogen and progesterone degradation. This model may be used to help interpret genomic and transcriptomic data to pinpoint the most effective ways to select and manage for changes in productive and reproductive efficiency.

Key Words: efficiency, systems model, adipose tissue

72 Effects of feeding millet silage cultivars on performance of lactating dairy cows. T. Brunette*[1], B. Baurhoo[2], and A. Mustafa[1], *[1]McGill University, Ste-Anne-De-Bellevue, QC, Canada, [2]Belisle Solution Nutrition, St-Mathias, QC, Canada.*

Fifteen lactating Holstein cows were used in a replicated 3x3 Latin square experiment to determine the effects of feeding regular and high water soluble carbohydrate (WSC) millet silages on the performance of dairy cows. Dietary treatments (68:32 forage:concentrate ratio) were a corn silage diet (control, CS), a regular millet silage diet (RM), and a high WSC millet silage diet (SM). Experimental silages constituted 37% of each diet DM. Three ruminal-fistulated cows were used to determine the effect of dietary treatments on ruminal fermentation and total-tract nutrient utilization. Relative to corn silage, regular and high WSC millet silages contained 37% more CP, 66% more NDF, and 67% more ADL. Cows fed CS consumed more ($P < 0.05$) DM (24.4 kg/d) and starch (5.7 kg/d), and less ($P < 0.05$) NDF (7.9 kg/d) than cows fed RM or SM. Millet silage type had no effect on DM (22.8 kg/d), starch (3.7 kg/d) and NDF (8.7 kg/d) intakes. Feeding RM relative to CS reduced ($P < 0.05$) milk yield (32.7 vs. 35.2 kg/d), ECM (35.8 vs. 38.0 kg/d) and SCM (32.7 vs. 35.3 kg/d). However, cows fed SM had similar milk yield, ECM, and SCM relative to cows fed CS or RM. Milk efficiency was not affected by dietary treatments. Milk protein concentration was greatest for cows fed CS, intermediate for cows fed SM, and lowest for cows fed RM ($P < 0.05$). Milk concentration of SNF was reduced ($P < 0.05$) while MUN was greater ($P < 0.05$) for cows fed RM than for those fed CS. However, millet silage type had no effect on SNF and MUN concentrations. Furthermore, concentration of milk fat, lactose and TS were not affected by silage type. Ruminal pH was greatest for cows fed SM, intermediate for cows fed RM, and lowest for cows fed CS ($P < 0.05$), while ruminal NH_3-N was lower ($P < 0.05$) for cows fed CS than for those fed RM or SM. Total-tract digestibility of DM (67.9%), NDF (53.9%), CP (63.3%) and GE (67.9%) were not influenced by dietary treatments. It was concluded that cows fed CS performed better than those fed RM or SM likely due to the higher starch and lower NDF intakes. However, no major differences were noted between the 2 millet silages.

Key Words: millet silage, milk production, ruminal fermentation

73 Variability in the concentrations of free and esterified fatty acids in corn silage and byproduct feeds. C. M. Klein[1], J. C. Ploetz[1], T. C. Jenkins[2], and A. L. Lock*[1], *[1]Michigan State University, East Lansing, [2]Clemson University, Clemson, SC.*

This study examined the concentration of fatty acids (FA) as either free FA (FFA) or esterified FA from corn silages and byproduct feeds. Total lipids were extracted and lipid classes separated with solid-phase extraction cartridges. Esterified fractions were combined following separation, which resulted in a single esterified FA fraction and a FFA fraction. For corn silage samples (n = 75), DM (%), NDF, starch, and CP (all % DM) ranged from 35.3 ± 4.2, 36.5 ± 3.9, 36.4 ± 3.9, and 7.1 ± 0.7 (mean ± SD), respectively. Total FA ranged from 1.6 to 3.6% DM (mean 2.5 ± 0.3% DM). Esterified FA ranged from 1.2 to 2.8% DM (mean 2.0 ± 0.3% DM) and FFA ranged from 0.3 to 0.8% DM (mean 0.5 ± 0.1% DM). Esterified FA accounted for 69 to 86% (mean 80 ± 4%) and FFA 13 to 31% (mean 20 ± 4%) of total FA. Esterified FA (% DM) were positively correlated with starch concentration (r = 0.35, $P = 0.001$), whereas FFA (% DM) were positively correlated with lactic acid concentration and corn silage processing score (CSPS), and negatively correlated with in vitro starch digestibility. Multiple regression analysis identified 4 factors (CSPS, lactic acid, starch concentration, and in vitro starch digestibility; all $P < 0.05$) that explained 41% of the variation in the proportion of total FA as FFA. Concentration of esterified FA in distillers grains (n = 27), canola meal (n = 21), and cottonseed (n = 12) was 11.0 ± 1.7, 6.1 ± 5.1, and 18.4 ± 3.5% DM, respectively. Concentration of FFA was 1.2 ± 0.2, 0.9 ± 1.7, and 1.2 ± 1.7% DM, respectively. Ether extract (% DM) values for byproducts agreed with esterified FA plus FFA concentrations ($R^2 = 0.95$). Furthermore, in a dual-flow continuous fermenter study, soy FFA increased the accumulation of total *trans* 18:1 and *trans*-10 18:1 by 28 and 48% (both $P < 0.05$), respectively, when compared with soy oil (both at 1.5% DM). In conclusion, there is considerable variation in total FA concentration of corn silages and byproduct feeds and a variable proportion of these FA are present as FFA. Results suggest that FFA may negatively affect rumen biohydrogenation to a greater extent when compared with esterified FA.

Key Words: byproduct feed, corn silage, dietary fatty acid

76 Effects of milking frequency on integrin signaling in mammary glands of dairy cows. R. Murney*[1], K. Stelwagen[2], T. T. Wheeler[1], J. K. Margerison[3], and K. Singh[1], *[1]AgReserach Limited, Ruakura Research Centre, Hamilton, New Zealand, [2]SciLactis Limited, Waikato Innovation Park, Hamilton, New Zealand, [3]Massey University, Palmerston North, New Zealand.*

In dairy cows, short-term changes of milking frequency (MF) in early lactation can have an immediate and a long-term effect on milk yield. The effect is controlled locally within mammary glands and is thought to be a function of secretory mammary epithelial cell (MEC) number and/or activity. Attachment to the extracellular matrix (ECM) via β_1-integrin is required for both MEC survival and function. Focal adhesion kinase (FAK) mediates the intracellular signaling of integrins. In this study we investigated if ECM/β_1-integrin signaling in MEC is affected by changes in MF. Ten multiparous cows (5 ± 2 DIM) were unilaterally milked for 14 d; udder halves were either milked once a day (1×) or 4 times a day (4×). On d 14, biopsy samples were collected from both rear quarters and mRNA and protein were analyzed by real time RT-PCR and Western blot, respectively. The cows were then milked twice daily (2×) for the remainder of lactation. By the end of the treatment period the 4×-milked udder halves were producing 2-fold ($P < 0.001$) more milk than the 1×-milked udder halves and continued to produce 15% ($P < 0.01$) more milk than 1×-udder halves once returned to 2× milking. Relative secretory activity was estimated by determining mRNA levels of the major milk proteins, αS_1-casein, β-casein and α-lactalbumin, which were increased in the 4×-samples, 8-, 9-, and 12-fold, respectively ($P < 0.01$). Signal transducer and activator of transcription 5 (STAT5) phosphorylation was dramatically ($P < 0.001$) higher in the 4×-tissues, while protein levels for β_1-integrin and FAK were 5- ($P < 0.001$) and 40-fold ($P < 0.001$) higher in 4×-tissues, respectively. Furthermore, STAT5-phosphorylation correlated strongly with the protein abundance of both β_1-integrin ($r = 0.78$, $P < 0.001$) and FAK ($r = 0.86$, $P < 0.001$). The data indicate that β_1-integrin and FAK proteins may be involved in the regulation of milk production in differentially milked bovine mammary glands.

Key Words: milking frequency, cell signaling, β_1-integrin

77 Prolactin-inhibitor cabergoline enhanced the mammary remodeling during drying-off in dairy cows. M. Boutinaud*[1], N. Isaka[4], A. Deflandre[4], E. Gandemer[1,2], P.-G. Marnet[2,3], F. Dessauge[1,2], and V. Lollivier[2,3], *[1]INRA, UMR 1348 PEGASE, Saint Gilles, France, [2]AGROCAMPUS UMR 1348 PEGASE, Rennes, France, [3]Université Européenne de Bretagne, Rennes, France, [4]CEVA Santé Animale, Libourne, France.*

In ruminants, the early phase of drying-off is a period of intense mammary gland remodeling that has great consequences on the next lactation and that is marked by the cessation of prolactin (PRL) release. To assess the effect of PRL inhibition on mammary remodeling, 14 Holstein dairy cows were injected with a single i.m administration of 5.6 mg cabergoline (n = 7) or placebo (n = 7) just after the last milking before drying-off. Mammary biopsy samples were collected one week before drying-off (D-6), at D1 and D8 and used for zymography analyses. Mammary secretion samples (290 mL) were collected using a teat-cannula once during lactation (D-6) and at D1, D2, D3, D4, D8 and D14 after the drying-off. The mammary secretion samples were used for SCC, Na^+, K^+ and BSA determinations and zymography analyses. Mammary epithelial cells (MEC) were purified from mammary secretions after centrifugation and immunocytochemical binding. Blood samples were collected before and after the morning mammary secretion collection for PRL determination. Cabergoline treatment decreased the blood PRL level from D1 to D8 compared with control treatment ($P < 0.001$). SCC was 2.4 fold higher in cabergoline treated cows than in control cows ($P < 0.01$). In addition, cabergoline induced an increase in MEC count ($P = 0.04$) with a reduction of their viability on D3 and D4. No significant cabergoline effect was observed on Na^+ and BSA except a tendency for a higher K^+ content in the mammary secretions of cabergoline treated cows ($P = 0.06$ at D1), suggesting a small increase in the tight junction opening in the mammary gland. In mammary tissue, cabergoline increased the activity of MMP-2 (matrix metalloproteinases) after drying-off (1.4 fold, $P \leq 0.01$). In mammary secretion, cabergoline increased the activity of MMP9 (1.7 fold, $P < 0.05$). Cabergoline treatment was efficient to enhance the extracellular matrix mammary remodeling, the MEC exfoliation and the migration of somatic cells responsible for the mammary gland remodeling. The mammary gland remodeling induced by the lower plasmatic PRL concentration may only be in part explained by a higher tight junction opening.

Key Words: cow, drying-off, prolactin

78 Efficacy of cabergoline to reduce udder pressure and milk leakage after dry-off in dairy cows. S. Bertulat*[1], N. Isaka[2], A. Deflandre[2], A. Lopez[2], T. Hetreau[3], and W. Heuwieser[1], *[1]Clinic for Animal Reproduction, Freie Universität Berlin, Berlin, Germany, [2]CEVA Santé Animale, Libourne, France, [3]Centre d'élevage Lucien Biset, Poisy, France.*

A recent study demonstrated a relationship between high milk yield, high udder pressures (PRE) and elevated stress levels after dry-off and revealed an animal welfare concern regarding current dry-off strategies. Cabergoline inhibits prolactin release and is approved to treat false pregnancies in bitches. The objective of this study was to evaluate the efficacy of cabergoline to reduce PRE and milk leakage after dry-off. Two hundred sixty-three high-yielding (≥16 kg milk/d) dairy cows were enrolled 7 d before (d −7) and followed up until 14 d (d 14) after dry-off. Cows were milked twice daily until dry-off (d 0) and treated with a single i.m. injection of 5.6 mg cabergoline (CAB; n = 130) or placebo (PLA; n = 133) after last milking (controlled, randomized and blinded study design). PRE was measured 4 d before (i.e., before and after milking) and 1, 2, 3, 7, 10 and 14 d after dry-off using a hand-held dynamometer (Penefel DFT 14; Bertulat et al., 2012). Udder firmness was assessed manually using a 4-point firmness score (0 = flabby, 3 = very hard; Gleeson et al., 2007). Milk leakage was recorded on d −4, d 1, d 2, d 3 and d 7, respectively. Data were analyzed using Chi^2 or Fisher exact test to compare qualitative variables and two-sample *t*-test for quantitative variables. After dry-off PRE increased in both groups, but was lower ($P < 0.05$) on d 1 and d 2 in CAB (d 1 = 0.79 ± 0.35 kg; d 2 = 0.93 ± 0.45 kg) than PLA cows (d 1 = 1.16 ± 0.6 kg; d 2 = 1.07 ± 0.49 kg). PRE on d 1 exceeded values measured on d -−4 before milking in 53.2% of PLA, but only 26.2% of CAB cows ($P < 0.001$). Moreover, cows in PLA group were more likely ($P < 0.05$) to have an udder firmness score of 3 than CAB cows on d 1 (27.9% vs. 67.2%), d 2 (41.5% vs. 54.9%) and d 3 (27.1% vs. 42.1%), respectively. The percentage of cows with milk leakage during the 1st wk after dry-off was also lower in CAB (10.2%) compared to PLA (19.8%) cows (P = 0.03). Our data provide evidence that a single injection of cabergoline

reduced PRE and firmness after dry-off and decreased the prevalence of milk leakage. Further research is warranted to evaluate, if cabergoline is able to reduce stress and alleviate pain after dry-off.

Key Words: cabergoline, dry-off, udder pressure

79 The effects of continuous light on milk yield, milk composition, IGF-1 and prolactin in dairy cows. S. Ferneborg*[1], E. Ternman[1], A. A. K. Salama[2], G. Caja[2], and S. Agenäs[1], *[1]Department of Animal Nutrition and Management, Swedish University of Agricultural Sciences, Uppsala, Sweden, [2]Group of Ruminant Research (G2R), Universitat Autonoma de Barcelona, Bellaterra, Spain.*

Light improves the lactational performance (feed intake and milk yield) of dairy cows. When long (16h) and short (8h) photoperiods are compared the higher milk yield in the 16h photoperiod seems to be mediated by higher secretion of IGF-1 and prolactin (PRL). Continuous lighting, on the other hand, is not recommended since no positive effect is seen on milk yield. However, it is often used as an on-farm management tool to keep cow activity high in intensive production systems with automatic milking. In calves, decreased levels of PRL have been seen in 24h light compared with 16h light, but the effect of 24h light on IGF-1 is unknown. In this pilot study, the short-term effects of 2 different light treatments on milk yield, milk composition, IGF-1 and PRL secretion were examined. Five lactating Swedish Red dairy cows were daily subjected to 24–0 (continuous light) or 4–20 (light 0930 to 1330) light-dark treatments in a changeover design. Cows were adapted to the treatments for 60h before recording and sampling started. Milking was performed at 12h intervals, and milk samples were collected at each milking for milk composition analysis. Blood samples were taken through a permanent jugular cannula hourly over a 36h sampling period, frozen and analyzed for IGF-1 (IMMULITE immunoassay) and PRL (ELISA). Neither milk yield (26.8 ± 5.2 L/d) nor milk composition differed between treatments, but plasmatic IGF-1 concentrations were greater ($P < 0.05$) in the 4–20 vs. 24–0 cows (133 ± 2 vs. 124 ± 2 ng/mL). Moreover, IGF-1 levels were greater ($P < 0.05$) during the circadian night than during the circadian day in the 4–20 cows and tended to be greater ($P < 0.10$) in the 24–0 cows. The secretory pattern of PRL differed between treatments, with an increase in secretion 1 min after the start of milking for 4–20 vs. 24–0 cows (124 ± 13 vs. 78 ± 8 ng/mL; $P < 0.05$), while basal concentrations did not differ between treatments. In conclusion, short-term continuous light did not change basal PRL, but decreased IGF-1 levels in plasma without changing milk yield or milk composition. Further research will explore the effects of continuous light on milk production and welfare of dairy cows.

Key Words: photoperiod

80 Timing of first milking and colostrum feeding affect serotonin (5-HT) concentrations in cows and calves. J. J. Gross[2], J. Laporta[1], R. M. Bruckmaier[2], and L. L. Hernandez*[1], *[1]University of Wisconsin, Madison, [2]University of Bern, Bern, Switzerland.*

Hormonal signals differentially regulate the timing of parturition, as well lactogenesis and potentially colostrum formation in the mammary gland. Serotonin (5-HT) has been determined to be a homeostatic regulator of lactation. To this end, we performed an experiment in which we manipulated the timing of first milking to investigate the effects on 5-HT concentrations in the maternal and calf circulation, as well as colostrum composition. Twenty cows were randomly assigned to 2 groups: control (CON) milked for the first time 4 h post-calving, and a treatment (TRT) group that were milked for the first time approximately 1 d before calving, and were milked 4 h post-calving. Maternal blood samples were collected for 4 d pre-partum, 3 times daily, and one blood sample was taken 4 h after parturition. Calves were fed 2 L of colostrum from their respective dam that was collected at their first milking, either 1 d before parturition (TRT) or 4 h post-calving (CON) 4 h after birth. Calf blood samples were collected 4 h after birth (before colostrum feeding), 12 h after birth, and at 3 wk of age. Colostrum samples were collected from the entire udder. 5-HT was analyzed in serum and colostrum samples. Circulating 5-HT concentrations were significantly higher in CON cows when compared with TRT cows ($P < 0.0001$). Colostrum 5-HT concentrations were increased in TRT cows compared with the CON ($P = 0.0165$). Finally, calves born to TRT cows had increased circulating 5-HT concentrations compared with the CON on all dates evaluated, with the greatest increase being at 3 wk of age. These data suggest that 5-HT plays a role in regulating colostrum composition, and may be of importance to the calf. Further research should be conducted in an attempt to separate the roles of circulating 5-HT from that produced within the mammary gland.

Key Words: serotonin, lactation, colostrum

81 Essential amino acid deficiencies and imbalances regulate milk protein synthesis through mTOR signaling in lactating bovine mammary glands. J. Doelman*[1], R. V. Curtis[2], M. Carson[1], J. J. M. Kim[2], J. P. Cant[2], and J. A. Metcalf[1], *[1]Nutreco Canada Agresearch, Guelph, ON, Canada, [2]Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada.*

Part of the mechanism by which essential amino acids (EAA) stimulate milk protein synthesis may be through effects on mammalian target of rapamycin (mTOR) signaling in the mammary gland. To determine the effect of imbalance and deficiencies of EAA on mammary mTOR signaling, 6 early-lactation, rumen-fistulated dairy cows (102 ± 4 DIM) were abomasally infused for 5 d with either saline, EAA, EAA less methionine, EAA less phenylalanine, EAA less histidine, or EAA less tryptophan in a 6 × 6 Latin square design. The EAA infusion rates were based on the EAA content of 1000 g/d casein. Cows were fed a TMR with a forage to concentrate ratio of 65:35 to provide 100% of the NE_L requirement and 65% of the metabolizable protein requirement. Mammary tissue was collected by biopsy on the final day of each experimental period for quantification of signaling protein activity. Milk protein yield increased 22% during the EAA infusion, compared with saline ($P < 0.001$), while methionine, phenylalanine and histidine deficiencies decreased milk yield by 15.7, 23.6, and 22.6%, respectively, compared with EAA ($P < 0.001$). Additionally, milk protein concentration was 0.36, 0.37 and 0.25 percentage points lower during methionine, phenylalanine and histidine deficiencies, respectively ($P < 0.001$). Immunoblot analysis showed increased phosphorylation of ribosomal protein S6 kinase (S6K1) in response to methionine deficiency ($P < 0.04$), while the phosphorylation state of eukaryotic initiation factor 2B (eIF2B) was decreased in all treatments relative to saline ($P < 0.04$). These results indicate that milk protein synthesis is sensitive to the supply of methionine, histidine, and phenylalanine, specifically. S6K1 and eIF2B appear to be sensitive to the supply of total EAA, yet their activation during EAA deficiency did not stimulate milk protein yields.

Key Words: milk protein, essential AA, mTOR signaling

82 Effects of arginine concentration on the in vitro expression of casein and mTOR pathway related genes in mammary epithelial cells from dairy cattle. M. Z. Wang*[1,2], B. L. Xu[1], H. R. Wang[1], D. P. Bu[2], J. Q. Wang[2], and J. J. Loor[3], *[1]College of Animal Science and*

Technology, Yangzhou University, Yangzhou, Jiangsu, China, [2]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [3]Department of Animal Sciences and Division of Nutritional Sciences, University of Illinois, Urbana.

Arginine is a conditionally-essential amino acid that is taken up by bovine mammary gland in excess of its output in milk. In this study we evaluated the effects of arginine level on the expression of casein and signaling pathway-related genes in mammary epithelial cells. The treatments (applied for 24 h) were designed to be devoid of Arg 0X (control; 0.00 mg/L), resemble the profile of Arg in casein (Arg 1X; 278.00 mg/L), be deficient, Arg 0.25X (69.50 mg/L) and Arg 0.5X (139.00 mg/L), or be in excess of the amount in casein, Arg 2X (556.00 mg/L), Arg 4X (1,112 mg/L), and Arg 8X (2,224 mg/L). The expression of CSN1S, CSN3 and mTOR in the experimental groups was higher than those of the control group ($P < 0.05$). Except for Arg 0.25X and Arg 8X ($P > 0.05$), the expression of CSN1S2, CSN2 and JAK2 in other experimental groups was higher ($P < 0.05$) than those in the control group. Except for Arg 8X ($P > 0.05$), the expression of STAT5 in the other experimental groups was higher than those of the control group ($P < 0.05$). It was also observed that, except for Arg 0.5X, S6K expression was higher in other experimental groups than the control group ($P < 0.05$). In contrast, except for Arg 0.25X, the other experimental groups resulted in lower 4EBP1 expression than the control group ($P < 0.05$). Among groups, the expression of CSN1S1, CSN1S2, CSN2, CSN3, JAK2, STAT5, mTOR and S6K gene was highest with Arg 2X ($P < 0.05$); the reverse was true for 4EBP1 gene, with the lowest expression in this group ($P < 0.05$). Taken together, arginine appears to play an important role in the transcriptional regulation of casein genes and mTOR related genes in bovine mammary epithelial cells.

Key Words: arginine, casein expression, mammary epithelial cell

83 Enhancing mammary involution during early stages of the dry period by infusing mammary serum amyloid A3. A. Domenech[1], S. Parés*[1], A. Bach[1,2], and A. Arís[1], *[1]Department of Ruminant Production, Institut de Recerca i Tecnologia Agroalimentàries (IRTA), Torre Marimon, Caldes de Montbui, Barcelona, Spain, [2]Institució Catalana de Recerca i Estudis Avançats (ICREA), Barcelona, Barcelona, Spain.*

The aim of this study was to evaluate the potential of recombinant mammary serum amyloid A3 (M-SAA3) in the improvement of the dry period in dairy cows by stimulating the immune system and epithelial regeneration. At dryoff, immediately after the last milking, the 4 quarters of 9 cows were treated as follows: 1 quarter infused after drying with 1 mg of M-SAA3 (MS3), another quarter infused with 80 ng of LPS (LP) to reproduce the possible effect of LPS traces in purified recombinant fraction, and the other 2 contralateral quarters were infused with saline solution as a negative control (CTRL). Mammary secretions (MS) were obtained just before treatment and at 0800 h during the 3 consecutive days. MS was analyzed for somatic cell count (SCC), fat, protein, and the activity of involution promoters such as metalloproteinases (MMP). Also, in vitro experiments were performed to test the effect of M-SAA3 on primary mammary cells challenged with *S. aureus* and on bovine dendritic cells. Cytokine concentrations were evaluated by qPCR. Data were analyzed using a mixed-effects linear model in the in vivo experiment and by ANOVA in the in vitro study. The activity of MMP-9 during the 3 d of the in vivo experiment was greater ($P < 0.0001$) in MS3 than in the other treatments, and there was a numerical increase in SCC at d 2 compared with LP and CTRL. MS fat and protein were increased ($P < 0.01$ and $P < 0.1$, respectively) in the MS3 treatment compared with LP and CTRL. Results for qPCR of the in vitro experiment showed activation and maturation of the dendritic cells and an increase ($P < 0.05$) in the expression of IL-8 ($6 \times 10^{-3} \pm 0.3 \times 10^{-3}$ vs. $3.9 \times 10^{-4} \pm 3.8 \times 10^{-4}$) in primary mammary cells. Moreover, M-SAA3 decreased by 25% the infection of mammary cultures with *S. aureus*. In conclusion the M-SAA3 shows a clear potential to improve the early stages of the dry period, independently of LPS traces, not only stimulating the mammary gland involution and immune system but also reducing bacterial infection.

Key Words: dry period, immune, infection

84 Lack of circulating serotonin (5-HT) in TPH1-deficient mice down-regulates serum calcium and mammary gland gene expression of calcium transporters. J. Laporta*, K. E. Merriman, S. Weaver, C. Cronick, T. L. Peters, and L. L. Hernandez, *University of Wisconsin, Madison.*

Serotonin (5-HT) is a homeostatic regulator of lactation and is known to play a role in calcium homeostasis. 5-HT is synthesized in a 2-step reaction from L-tryptophan (L-TRP), with the rate-limiting step catalyzed by tryptophan hydroxylase (TPH1) to form 5-hydroxytryptophan (5-HTP), which is then further converted to 5-HT by aromatic amino acid decarboxylase. We recently demonstrated increasing circulating 5-HT up-regulates mammary gland expression of calcium transporters in rats. To demonstrate that 5-HT is responsible for regulating calcium transport in the mammary gland, we performed an experiment in lactating mice that are genetically deficient for TPH1 (−/−, n = 7) and compared them to wild-type mice (+/+, n = 7). On d 1 and 10 of lactation blood samples were collected to measure serum 5-HT and calcium concentrations. All animals were euthanized on d10 of lactation and mammary gland tissue was harvested. Total RNA was isolated from mammary gland tissue to measure the mRNA expression of TPH1, 5-HT transporter (SERT) and the following calcium transporters: plasma membrane Ca^{2+} ATPases 1 and 2 (PMCA1, 2), sodium-Ca^{2+} exchanger 1 (NCX1), secretory Ca^{2+} ATPase 1 and 2 (SPCA1, 2), and sarco(endo)plasmic reticulum Ca^{2+} ATPase 2 (SERCA2), by real-time RT-PCR. Total protein was also isolated from mammary gland tissue to measure 5-HT content. Serum 5-HT concentration were decreased in the −/− dams compared with +/+ dams on both d1 and 10 of lactation ($P < 0.036$) as was mammary gland 5-HT content on d10 of lactation ($P = 0.0039$). Serum calcium was decreased on both d1 and 10 of lactation in −/− dams compared with +/+ dams ($P < 0.023$). Mammary gland TPH1 and SERT mRNA expression was decreased in −/− dams compared with +/+ dams ($P < 0.011$). Mammary gland mRNA expression of NCX1, SERCA, SPCA1 and 2, PMCA1 and 2, were decreased in −/− dams compared with +/+ dams ($P < 0.038$). These results demonstrate that 5-HT is critical for regulation of circulating calcium concentrations and calcium transport within the mammary gland during lactation.

Key Words: serotonin, calcium, lactation

85 Importance of progesterone and prolactin profiles, and of parturition on the composition of colostrum obtained before and after parturition. J. J. Gross[1], E. C. Kessler[1], V. Bjerre-Harpoth[2], and R. M. Bruckmaier*[1], *[1]Veterinary Physiology, Vetsuisse Faculty University of Bern, Bern, Switzerland, [2]Department of Animal Science, Aarhus University, Foulum, Denmark.*

Progesterone (P4) and prolactin (PRL) are key regulators that mediate the initiation of both parturition and onset of lactation including colostrum formation. The hypothesis was tested that colostrum formation is regulated by changes of P4 and PRL but independent of the actual time

of parturition. To achieve this goal, 23 multiparous cows were randomly assigned to 2 groups: control (PP, postpartum only, n = 11) milked for the first time 4 h post-calving, and a treatment (AP, ante- and postpartum, n = 12) group that was already milked approximately 1 d before calving and again at 4 h after parturition. Colostrum yield before and after parturition was recorded and proportional samples were analyzed for total IgG, fat, protein and lactose. Blood samples for the analyses of P4 and PRL were collected at 8 h intervals for 4 d pre-partum until calving, and another sample was taken at 4 h after parturition. Total IgG mass increased with increasing time span between the P4 drop and first milking ($P < 0.05$). Total IgG mass and milk yield tended to increase with decreasing time span between PRL peak and first milking ($P < 0.1$), and also with increasing time between parturition and first milking ($P < 0.1$). Protein concentration in colostrum decreased with increasing interval between drop of P4 and PRL peak ($P < 0.05$). Milk yield, fat, protein and lactose concentration did not differ between PP and AP at the first milking. However, total IgG mass was higher in AP than in PP ($P < 0.05$) which is obviously due to the low milk yield in AP. In AP cows, milk protein decreased between pre- and postpartum milking, while lactose concentration increased ($P < 0.05$). In colostrum obtained at 4 h postpartum, milk fat was increased in AP compared with PP, while protein, total IgG concentration and mass were decreased ($P < 0.05$). Milk yield and lactose were not different between AP and PP at 4 h postpartum. These data suggest that synthesis and secretion of constituents into first colostrum do not only depend on changes in PRL and P4.

Key Words: colostrum, composition, lactogenesis

86 Feeding entrainment of the mammary circadian rhythm in FVB mice. L. Ma*, Y. Ying, A. Clarke, P. Bartell, and K. J. Harvatine, *Penn State University, University Park.*

Food entrainment of adipose and liver circadian rhythms is well established, but little is known about the regulation of the circadian rhythm of the mammary gland. Food entrainment of circadian rhythm of milk fat synthesis was investigated in wild-type FVB mice. Treatments were ad libitum feed intake and 7 h feed restriction during the day (DR; 1100 to 1800 h) or night (NR; 2300 to 0600 h) from d 7 to 14 of lactation. Dam intake and body weight and litter gain were recorded 2×/d. On d 14 of lactation, dams were euthanized at 0600, 1200, 1800, or 2400 h (n = 6 per treatment per time point) and dam mammary tissue and pup stomach milk clots were collected. Data were analyzed using ANOVA with treatment, time, and the interaction of treatment and time as fixed effects and second by fitting to a cosine function with a 24 h period for rhythm analysis. In control mice, no overt rhythm was observed for feed intake, milk fat synthesis or mammary gene expression, which is expected as FVB mice commonly do not express a robust circadian rhythm. Dams from DR treatment consumed more than 70% of daily intake during the dark phase, while NR mice consumed more than 76% of daily intake during the light phase (treatment by time, $P < 0.01$). Litters from DR and NR gained the most weight during the light (65%) and dark (72%) phase, respectively (treatment by time $P < 0.01$). Day restriction entrained a rhythm in de novo milk FA synthesis and the peak (amplitude 1.57 and 4.52% FA for DR and NR, respectively) was advanced about 10 h for NR ($P < 0.01$). Inverted rhythms (shifted by 11.3 h) were also observed for preformed FA between DR and NR treatments ($P < 0.01$). The mammary expression of core clock genes (BMAL1, CRY1 & 2, and PER1 & 2), lipogenic regulators (SREBP1c and Spot 14), and milk fat synthetic enzymes (FASN and SCD1) showed a rhythm in the mice with restricted feeding and the phase was shifted by 5.5 to 12.3 h ($P < 0.01$). In conclusion, timing of feed intake entrains the circadian rhythm in the mammary gland and milk fat synthesis by entraining the expression of mammary clock genes as well as regulators and enzymes involved in milk fat synthesis.

Key Words: FVB mice, feed restriction, circadian rhythm

87 Proteomic profiling of bovine mammary gland response to milk removal or increased milking frequency indicates roles for prolactin and leptin signaling. M. G. H. Stevens*[1], E. H. Wall[2], P. A. Bentley[3], A. Ruiz-Sanchez[3], and T. B. McFadden[1,3], *[1]University of Missouri, Columbia, [2]University of Vermont, Burlington, [3]University of Alberta, Edmonton, AB, Canada.*

Milking dairy cattle 4-times (4X) instead of twice-daily (2X) during early lactation increases milk yield and persistency. Our objective was to identify physiological processes involved in the mammary response to milk removal or increased milking frequency. Six cows were assigned at parturition to unilateral frequent milking (2X milking of left udder half, 4X milking of right udder half) and biopsies were taken from both udder halves at 5 DIM. In the first study (n = 2) the effect of milk removal was investigated by taking biopsies immediately after milking only the 4X udder half. In the second study (n = 4) biopsies were obtained at 2.5h after milking both udder halves to quantify the sustained effect of 4X. Proteins were quantified by iTRAQ and proteomes of paired udder halves were compared. Proteins differentially expressed by ≥1.5 fold were used for Ingenuity Pathway Analysis (IPA). The response to milk removal was characterized by differential expression of 479 peptides, mapped to 38 proteins; 35 were eligible for IPA. The top ranked network comprised 17 proteins (Score = 42) and associated with post-translational modification, carbohydrate and lipid metabolism. A weak activation of prolactin signaling is predicted as an upstream regulator and associated with 6 of the differentially expressed proteins (activation score: 0.686; $P < 0.001$). The sustained response to 4X-milking was associated with differential expression of 1302 peptides, mapping to 97 proteins; 67 were used for IPA. The top network was associated with cellular assembly and organization, molecular transport and protein trafficking (Score = 46). Activation of leptin signaling is predicted as an upstream regulator and associated with 19 differentially expressed proteins (activation score: 2.200; $P = 0.003$). Data suggest that the response to milk removal involves proteins associated with mammary metabolism, and may be driven by prolactin signaling. The sustained response to 4X appears to modulate proteins involved in cellular organization and function, and may be regulated by leptin.

Key Words: proteomics, bovine mammary gland, lactation biology

Meat Science and Muscle Biology: Effects of Nutrients and Supplements on Animal Growth Performance and Meat Quality

88 Effect of dietary vitamin D_3 supplementation on meat quality of naked neck chickens. M. Mabelebele*[1,2], J. W. Ngambi[2], D. Norris[2], and O. J. Alabi[2], *[1]University of New England, New South Wales, Armidale, Australia, [2]University of Limpopo, Polokwane, South Africa,*

Consumers' interest in indigenous chicken meat is increasing. An experiment was conducted to determine the effect of vitamin D_3 supplementation on meat quality of indigenous male naked neck chickens. Two hundred 13-wk-old male naked neck chickens with a mean live weight of 1200 ± 3 g were supplemented with vitamin D_3 levels of 0, 2000, 4000, 6000 and 8000 IU per kg dry matter (DM) of feed for a period of 7 d before slaughter. A 2 (postmortem agings of 0 or 24 h) × 5 (vitamin D_3 levels) factorial arrangement in a complete randomized design was used for shear force and sensory evaluation of cooked chicken meat. Twenty chickens were used in each treatment. The meat samples were cooked and prepared according to an oven-broiling method using direct radiant heat. A quadratic equation was used to determine vitamin D_3 supplementation levels for optimum shear force value and sensory attributes. Vitamin D_3 supplementation and Vitamin D_3 and postmortem aging interaction did not improve ($P > 0.05$) shear force values of unaged or aged cooked naked neck chicken meat. Shear force values of unaged and aged cooked meat were optimized at different levels of 2512 ($r^2 = 0.669$) and 4249 ($r^2 = 0.873$) IU of vitamin D_3 per kg DM feed, respectively. Vitamin D_3 supplementation and its interaction had no effect ($P > 0.05$) on unaged meat tenderness, juiciness and flavor. However, vitamin D_3 supplementation improved ($P < 0.05$) aged meat tenderness and flavor. Postmortem aging did not improve ($P < 0.05$) sensory attributes of naked neck chicken meat. Tenderness, juiciness and flavor of aged naked neck chicken meat were optimized at supplementation level of 6830 ($r^2 = 0.839$), 6894 ($r^2 = 0.683$) and 9795 ($r^2 = 0.657$) IU of vitamin D_3 per kg DM. It was concluded that vitamin D_3 supplementation improved tenderness and flavor of aged naked neck chicken meat, however, shear force was not improved.

Key Words: shear force, postmortem aging, sensory attributes

89 Effects of supplemental lysine and methionine with zilpaterol hydrochloride on feedlot performance, carcass characteristics on finishing feedlot cattle. A. D. Hosford*[1], W. Rounds[2], J. E. Hergenreder[1], M. J. Anderson[2], M. A. Jennings[1], T. L. Harris[1], S. N. Aragon[1], and B. J. Johnson[1], *[1]Department of Animal and Food Science, Texas Tech University, Lubbock, [2]Kemin Industries Inc., North America, Des Moines, IA.*

Feeding zilpaterol hydrochloride (ZH) with encapsulated amino acids (AA) was evaluated in a feeding trial. Crossbred steers (n = 180; initial BW = 366 kg) were blocked by weight and then randomly assigned to treatments (45 pens; 9 pens/treatment). Treatment groups consisted of: no ZH and no AA (Cont−), ZH and no AA (Cont+), ZH and an encapsulated lysine supplement (Lys), ZH and an encapsulated methionine supplement (Met), and ZH and encapsulated lysine and methionine Lys+Met, (LysiPEARL, MetiPEARL). Zilpaterol hydrochloride (8.3 mg/kg DM basis) was fed for the last 20 d with a 3 d withdrawal. Lysine and Met were top dressed daily for the 134-d feeding trial to provide 12 and 4 $g \cdot hd^{-1} \cdot d^{-1}$, respectively, to the small intestine. Carcass characteristics were collected following harvest. Cattle treated with Met and Lys+Met had increased final BW of 15 and 14 kg ($P = 0.02$ and 0.03) as compared with Cont−. Average daily gain increased ($P < 0.05$) for Met and Lys+Met fed cattle as compared with Cont− and Cont+ for the entire 134 d feeding period. The supplementation of Lys, Met and Lys+Met improved G:F ($P < 0.05$) as compared with Cont− during the ZH feeding period (d 111 to 134) as well as the entire feeding period ($P < 0.05$). Zilpaterol hydrochloride increased carcass ADG ($P < 0.05$) when compared with non-ZH fed cattle. Lysine + methionine treated cattle tended to have increased carcass ADG ($P = 0.09$) as compared with Cont+. Methionine and Lys+Met treatments had heavier hot carcass weight (HCW, $P < 0.05$) as compared with Cont−. Yield grade was decreased ($P < 0.05$) for Cont+ cattle compared with Lys, Lys+Met, and Cont− treated cattle. There was a higher proportion of yield grade one carcasses ($P < 0.05$) with Cont+ treatment compared with any AA treatment. Supplementation of Met in conjunction with ZH feeding increased ADG and HCW. These findings indicated that cattle fed ZH may require additional AA absorbed from the small intestine to maximize performance, and supplementing encapsulated AA may actually increase the ZH response as compared with ZH alone.

Key Words: beef cattle, lysine/methionine, zilpaterol hydrochloride

90 Effects of supplemental lysine and methionine with zilpaterol hydrochloride administration on finishing feedlot cattle tenderness. A. D. Hosford*[1], W. Rounds[2], J. E. Hergenreder[1], M. J. Anderson[2], M. A. Jennings[1], T. L. Harris[1], S. N. Aragon[1], and B. J. Johnson[1], *[1]Department of Animal and Food Science, Texas Tech University, Lubbock, [2]Kemin Industries Inc., North America, Des Moines, IA.*

Steaks from beef steers that were fed encapsulated amino acids and zilpaterol hydrochloride were tested for tenderness using the Warner Bratzler shear force (WBSF) method. Crossbred steers (n = 180; initial BW = 366 kg) were blocked by weight and then randomly assigned to treatments (45 pens; 9 pens/treatment). Treatment groups consisted of: no ZH and no AA (Cont−), ZH and no AA (Cont+), ZH and an encapsulated lysine supplement (Lys), ZH and an encapsulated methionine supplement (Met), and ZH and encapsulated lysine and methionine Lys+Met, (LysiPEARL, MetiPEARL). Zilpaterol hydrochloride (8.3 mg/kg DM basis) was fed for the last 20 d with a 3 d withdrawal. Lysine and Met were top dressed daily for the 134 d feeding trial to provide 12 and 4 $g \cdot hd^{-1} \cdot d^{-1}$, respectively, to the small intestine. Cattle were slaughtered at a commercial facility and longissimus muscle samples were collected following fabrication. Four steaks (2.54 cm thick) from each strip loin were aged for 7, 14, 21 or 28 d, and WBSF was determined as an indicator of tenderness. Tenderness was reduced ($P < 0.05$) with ZH regardless of AA supplementation. Lysine, Met, Lys+Met, and Cont+ had less tender steaks ($P < 0.05$) throughout all aging groups as compared with Cont−. Steaks from Lys treated cattle were less tender ($P < 0.05$) than Cont+ during the 7 and 14 d aging periods. After 21 d of aging all steaks from AA's fed animal had similar WBS ($P > 0.05$) as Cont+. Control− also had the highest percentage of tender steaks after 21 d of aging ($P < 0.05$). Supplementation of encapsulated AA's in conjunction with ZH feeding resulted in decreased tenderness even after aging for 28 d when compared with steaks from Cont- cattle. Supplementation of encapsulated lysine and ZH resulted in less tender steaks up to 14 d of aging when compared with ZH alone. Further research is needed to determine if this decrease in tenderness can be detected by the consumers.

Key Words: lysine/methionine, tenderness, zilpaterol hydrochloride

91 Influence of multi exogenous enzymes on performance and carcass characteristics in growing rabbits. H. Gado*[1] and A. Z. M. Salem[2], *[1]Animal Production Department, Faculty of Agriculture, Ain Shams University, Qalubia, Egypt, [2]Facultad de Medicina Veterinaria y Zootecnia, Universidad Autonoma del Estado de Mexico, Mexico.*

This study was conducted to investigate productivity of growing rabbits fed different levels of multi exogenous enzymes of ZADO (EZ) in diets. One hundred twenty Hy-Plus 30-d-old weaned rabbits were used in the study. Animals were divided into 4 comparable experimental groups (30 growing rabbits in each group) in a completely random design. The first group was fed a commercial diet and kept without treatment as a control group. The 2nd; 3rd and 4th groups were fed the same diets but supplemented with 1(EZ1), 3 (EZ3) and 5 (EZ5) kg ZADO/ton of diet, respectively. The experimental period lasted for 30 d and was carried out during growing period (from weaning to marketing at 60 d). Daily body weight gain; feed efficiency, feed conversion and final body weight of growing rabbits increased ($P < 0.05$) with increasing the EZ levels in diets compared with control ones. Feed intake was not affected by EZ supplementation. Supplementation of rabbit diet with EZ increased ($P < 0.05$) dressing percentage, carcass weight and absolute and relative internal organs weight to carcass weight. Post-weaning mortality decreased ($P < 0.05$) compared with those unsupplemented rabbits. The improvement in rabbit performance and carcass characteristics was more in EZ3 or EZ5 than EZ1 group. It can be concluded that supplementation of ZADO to rabbit diets showed enhanced growth performance, carcass traits and decreasing mortality rate, during growing period. At the economic point 3 kg ZADO/ton diet is recommended for growing rabbits

Key Words: carcass, growth, productive

92 Influence of different forms of lipid supplements and frequencies of fed on physical characteristics of heifer meat. M. C. A. Santana*[1], R. A. Reis[2], A. V. Pires[3], T. T. Berchielli[2], V. C. Modesto[2], P. H. M. Dian[4], M. A. A. Balsalobre[5], and G. T. Pereira[2], *[1]EMATER, Goiânia, Goiás, Brazil, [2]São Paulo State University, Jaboticabal, Sao Paulo, Brazil, [3]Sao Paulo University, Piracicaba, São Paulo, Brazil, [4]Camilo Castelo Branco University, Descalvado, São Paulo, Brazil, [5]Bellman, Mirassol, São Paulo, Brazil.*

This research aimed to evaluate by physical quality of meat (color – a*, b*, L*; shear force–WBSF; water-holding capacity – WHC; pH and cooking loss percentage –CLoss) the effects of different fat sources on meat attributes of heifers finished in pasture. The experiment was designed as a completely randomized, using a 3x2 factorial arrangement of treatments, replicated 7 times, in which 17 mo-old crossbred heifers (1/4 Nellore x 1/4 Santa Gertrudis x 1/2 Braunvieh) were fed for 135 d according to the treatments: soybean grain (SG), soybean oil (SO), and rumen-protected fat, Megalac-E (MEG), and the 2 supplement feeding frequencies (Monday, Wednesday and Friday – MF; and daily –DL). At slaughter, LM muscle pH measurements were taken, and samples between 12th and 13th were harvested and frozen at −20°C for meat evaluation. Samples of LM were evaluated for color interface in the L*a*b* color space and LM steaks were thawed and roasted to evaluated WBSF. The WHC was obtained by determining the difference of the LM sample weights under 10 kg of pressure for 5 min. The CLoss value was determined according to the reduced percentage rate before and after the meat was cooked. All variables were not different ($P > 0.05$) among treatments. The results of this research suggest that the physical indicators of meat quality were not influenced by the supplements and its feeding frequencies.

Table 1. Means for shear force (WBSF), water-holding capacity (WHC), and percentage cooking loss (CLoss), the colors a, b and L, and meat pH of heifers fed with different lipid supplement (SG. SO, MEG) and supply frequencies [Monday, Wednesday and Friday (MF) or daily (DL)].

	Supplement and frequency					
Item	SG	SO	MEG	MF	DL	SD
WBSF (kgf/ cm3)	8.3	8.8	7.6	8.0	8.3	1.9ns
WHC (%)	72.0	72.3	72.9	73.2	71.8	3.1ns
CLoss (%)	33.9	33.7	32.6	33.2	33.6	2.1ns
L (%)	36.4	36.0	36.9	36.9	36.0	1.7ns
a (%)	17.9	17.6	18.3	18.2	17.7	1.0ns
b (%)	3.4	3.3	4.1	3.8	3.5	0.8ns
pH	5.7	5.7	5.8	5.7	5.7	0.1ns

Key Words: soybean, soybean oil, protect fat

93 Performance, carcass, economics of production, hematological status, and organoleptic evaluation of broilers fed with graded levels of cowpea testa-based diets. P. O. Fakolade*[1], B. O. Alabi[1], A. A. Amao[1], and A. H. Ekeocha[2], *[1]Osun State University, Osogbo, Osun, Nigeria, [2]University of Ibadan, Ibadan, Oyo, Nigeria.*

Nutritional challenge of today is to provide for the worlds' present inhabitants without degrading resources needed to meet the greater nutritional challenges of tomorrow. Now, livestock producers focus on agro- industrial by-products and wastes, which are not utilized by man in underdeveloped country; an example is cowpea testa meal (CTM). Cowpea testa meal has been reported to be a cheaper alternative (waste) to soybean meal in poultry nutrition, but contains some anti-nutritional factors, which could limit its usage. The objective of this study focus on digestibility status, carcass and organoleptical evaluation, economics of production and the hematological status, of 3 hundred and 60 broiler birds (Arbor acre) randomly allotted into 4 dietary groups with 3 replicates in a completely randomized design. Four diets were formulated with CTM replacing soybean meal at 0%, 15%, 30%, and 50% grade levels for 56 d. There were significant ($P < 0.05$) differences between diets in final weight gain, average daily feed intake, feed to gain ration. Birds on control (0%) and (15%) CTM diet had significant ($P < 0.05$) weight gained than those fed with 30% and 50% CTM inclusion level. Panelist rated T_1 and T_2 with highest values; for color, flavor, tenderness, juiciness, texture and overall acceptability, while color, tenderness and juiciness were seen to have no significance differences ($P > 0.05$) among all the treatments. For carcass evaluation, organs and primal cut, were seen to have significant differences for lungs, gizzard, proventriculus, and chicken back, while ($P > 0.05$) was not observed in others organs or cuts. Hematology studies had no significant differences ($P > 0.05$) but cost of production was lower in broiler fed 15% CTM compare with 0% and other inclusion levels. Therefore, cowpea testa can be used to substitute soybean at 15% in broilers diet at both starter and finisher phase for effective growth performance and good carcass quality at a reduced cost of production.

Key Words: cowpea testa, digestibility, organoleptic properties.

94 Effects of feeding flaxseed or sunflower-seed in high forage diets on biohydrogenation intermediates in adipose tissues of yearling steers. C. Mapiye*[1], T. D. Turner[1], D. C. Rolland[1], J. A. Basarab[2], V. S. Baron[1], T. A. McAllister[3], H. C. Block[4], and B. Uttaro[1], J.L. Aalhus[1], and M. E. R. Dugan[1], *[1]Agriculture and Agri-Food Canada, Lacombe Research Centre, Lacombe, AB, Canada, [2]Alberta Agriculture*

and Rural Development, Lacombe Research Centre, Lacombe, AB, Canada, [3]Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, AB, Canada, [4]Agriculture and Agri-Food Canada, Brandon Research Centre, Brandon, Manitoba, Canada.

Supplementing high forage diets with oilseeds can increase deposition of biohydrogenation intermediates in adipose tissues; however, the effects of forage type have not been widely studied. This study examined the effects of feeding 70:30 forage:concentrate diets to yearling steers for 205 d, with either grass hay (GH) or red clover silage (RC) as the forage source, and concentrates containing either sunflower-seed (SS) or flaxseed (FS), each providing 5.4% oil to diets. Two pens of 8 animals were fed per diet. At harvest, perirenal fat (PF) closest to the cranial-central part of the whole PF and subcutaneous fat (SF) adjacent to the 12th rib were collected, methylated with sodium methoxide, and analyzed using a combination of GC (100 m highly polar column) and Ag^{+}-HPLC. Data were analyzed using PROC MIXED procedure of SAS including oilseed, forage and their interaction as the main effects. Pen was the experimental unit. Overall, fatty acid (FA) profiles in PF and SF followed similar trends when feeding FS or SS in high forage diets but SF compared with PF had greater ($P < 0.05$) proportions of n-3 FA, conjugated linoleic acids, mainly rumenic acid (RA), atypical dienes (AD), and less ($P < 0.05$) proportions of n-6 FA and *trans*-18:1 isomers, mainly vaccenic acid (VA). Feeding diets containing SS versus FS elevated ($P < 0.05$) adipose tissues proportions of VA, RA and linoleic acid (LA). Steers fed diets containing GH versus RC or FS versus SS had greater ($P < 0.05$) adipose tissue proportions of total n-3 FA, mainly α-linolenic acid (ALA) and total AD. A forage × oilseed type interaction ($P < 0.05$) was found for total conjugated linolenic acid (CLNA), with their greatest adipose tissues proportions being produced when feeding the RC-FS diet. Overall, feeding SS containing diets was more effective in increasing adipose tissues proportions of VA, RA and LA while enrichment of ALA, CLNA and AD were achieved by feeding diets containing FS. Feeding forages also affected adipose tissue FA profiles, but their effects were generally of less magnitude compared with oilseed effects.

Key Words: adipose tissue, forage, oilseed

95 Growth, carcass traits and meat color stability in steers finished on a potato-based versus a corn-based ration. K. J. Thornton*, M. J. Colle, J. A. Macumber, M. E. Doumit, R. Richard, C. W. Hunt, and G. K. Murdoch, *University of Idaho, Moscow.*

Increasing feed prices and competition for available commodities has driven beef producers to consider alternate feedstuffs. However, it is imperative that these alternate feeds do not negatively affect growth, carcass traits, or end product quality. In the Northwestern US potato by-product is used as a corn substitute. We compared growth, carcass traits and color stability in steers fed either a conventional finishing ration containing corn and barley as the grains (CB, n = 20) or a ration with 10 percent potato by-product substituted for corn (PB), balanced for energy and nitrogen. No differences ($P > 0.05$) were observed in ADG, FCR, DMI, HCW, PYG, REA, KPH, FYG, quality grade or marbling score. Steers finished on a PB ration produced strip loin steaks with lower ($P = 0.04$) WBSF values. No significant differences were observed in the L*, a* or b* values in the longissimus dorsi (LD) measured at 0, 1, 3, 5, 7 and 9 d of simulated retail display . Gluteus medius (GM) steaks from steers finished on a PB ration had a higher a* value on d 5 ($P = 0.03$). No differences were observed in L* or b* values in the GM. American Meat Science Association (AMSA) evaluation guidelines were used to evaluate browning, discoloration, color uniformity and surface discoloration in the LD and GM muscles. The LD steaks from steers finished on a CB ration had numerically less; browning, discoloration, surface discoloration and more uniformity during simulated retail display. However, the amount of browning ($P = 0.01$) and the discoloration ($P = 0.05$) were significantly different on d 7. No visual color differences in color were observed in the GM. While steers finished on either a PB or CB finishing ration exhibited no difference in carcass quality, steers fed a PB ration had more tender strip steaks. In contrast, color stability may be increased in the LD of steers finished on a CB ration. Overall, subtle differences in meat quality exist between steers finished on either a CB or PB ration, but both rations result in high quality beef products.

Key Words: potato by-product, end-product quality, color stability

96 Influence of *Salix babylonica* extract and exogenous enzymes on meat quality in growing lambs. J. Cayetano[1], A. Z. M. Salem*[1], H. Gado[2], and R. Rojo[3], *[1]Facultad de Medicina Veterinaria, Universidad Autonoma del Estado de Mexico, Mexico, [2]Animal Production Department, Faculty of Agriculture, Ain Shams University, Qalubia, Egypt, [3]CU-UAEM Temascaltepec, Universidad Autonoma del Estado de Moxico, Mexico.*

The objective of the present study was to determine the effect of the addition of extract of *Salix babylonica* and exogenous enzymes in combination or individually on the quality of meat in lambs. Suffolk lambs of 6 to 8 mo-old were used in the study. Lambs were divided into 4 groups of 5 animals each in a completely randomized design and the treatments were (1) Control: fed a basal diet of concentrate (30%) and corn silage (70%); (2) EZ: fed the basal diet plus 10 g of enzyme; (3) SB: fed the basal diet plus 30 mL of *S. babylonica* extract, and (iv) EZSB: fed the basal diet plus 10 g enzyme and 30 mL of *S. babylonica* extract. Lambs were housed in individual cages for 60 d as experimental period. The SB was given orally while the EZ was mixed with a small amount of the concentrate, while the corn silage was offered ad libitum. At the end of experimental period, all lambs were slaughtered and samples of Longissimus dorsi muscle were taken. Samples were analyzed for crude protein, crude fat, ash and dry matter. Some parameters of meat quality were determined (color parameters, PH, carcass temperature and average daily gain). There were no significant differences between the 4 treatments ($P < 0.05$) in meat color coordinates (L*, a*, b*), temperature, average daily gain. Meat pH was lower ($P < 0.05$) in EZSB compared with other treatments. L* (lightness) was highest in EZSB ($P < 0.05$) compared with the other treatments. In conclusion, administration of EZSB in the diet improves measured meat quality parameters by reducing the pH and increase meat lightness compared with EZ and SB individually.

Key Words: exogenous enzyme, lamb, meat quality

97 Effects of alternative cattle finishing strategies on meat quality characteristics. K. J. Phelps*[1], K. A. Miller[1], C. L. Van Bibber-Krueger[1], A. K. Sexten[1], J. S. Jennings[2], J. S. Drouillard[1], and J. M. Gonzalez[1], *[1]Kansas State University, Manhattan, [2]Alltech Inc., Nicholasville, KY.*

Effects of alternative finishing strategies on fresh meat quality were examined in beef steers (64 pens; 8 steers/pen) using a randomized complete block design with a 2 × 2 factorial treatment arrangement. For factor 1, diets with inorganic trace mineral supplement, vitamins A and E, Rumensin, and Tylan (C) were compared with diets with PN Beef supplement (PN; Alltech, Inc.). The PN treatments were fed the basal diet with PN Beef Receiver from d 1–20, and PN Beef Finisher

from d 21 to harvest. Factor 2 consisted of the presence or absence of exogenous growth promotants (+GP vs. –GP). Steers in the +GP treatments were implanted initially with Component E-S, reimplanted with Component TE-S, and fed 400 mg/steer daily of ractopamine-HCl (Elanco Animal Health) for the final 28 d before harvest. The basal diet consisted of steam-flaked corn, wet corn gluten feed, wheat straw, and supplement. Steers were harvested on d 175, strip loins were removed from 2 carcasses selected at random from each pen, transported to Kansas State University, weighed, vacuum packaged, and aged for 14 d. On d 14, loins were reweighed to assess purge loss and fabricated into 2.54-cm-thick steaks for determination of Warner-Bratzler shear force and color stability during a 7-d retail display. There were no interactions ($P > 0.05$) between feeding strategy and exogenous growth promotants. Purge loss was less for PN compared with C loins ($P < 0.01$). Use of GP increased moisture loss during cooking ($P < 0.05$), while feeding PN decreased moisture loss during cooking ($P < 0.05$). Steaks from +GP were less tender ($P < 0.01$) than –GP steaks, but C and PN were not different ($P > 0.05$). Initial values for L* were less for C than for PN ($P < 0.05$), but changes in color, surface percentages of oxymyoglobin and metmyoglobin, and metmyoglobin reducing ability were unaffected by feeding strategy ($P > 0.05$). In conclusion, alternative feeding strategies can favorably affect meat tenderness and water-holding capacity without compromising retail display characteristics.

Key Words: implant, beta agonist, feed additive

98 Gene expression of lipogenic enzymes present in muscle of young bulls fed ground soybean or rumen-protected lipid with or without ionophore. M. M. Ladeira[1,2], D. M. Oliveira[1], A. Chalfun Junior[1], M. L. Chizzotti[1], H. G. Barreto[1], T. C. Coelho[1], P. D. Teixeira[1], C. C. Coelho[1], and D. R. Casagrande*[1], *[1]Federal University of Lavras, Lavras, MG, Brazil, [2]Purdue University, West Lafayette, IN.*

The objective of this study was to evaluate the gene expression of lipogenic enzymes in the muscle of young bulls fed soybean grain (SB) or rumen protected lipid (RPL), with or without the supplementation of monensin (M). Forty bulls were allotted in a completely randomized design using a 2 × 2 factorial arrangement. The diets had 6.6% EE and the corn silage was used as forage. Half of the bulls fed SB or RPL was supplemented with 230 mg/hd/d of monensin. The bulls were harvested with on average 497 kg. The genes evaluated were acetyl coA carboxylase (ACC), adipocyte-type fatty acid binding protein ($FABP_4$), stearoyl coA desaturase (SCD), lipoprotein lipase (LPL), glutathione peroxidase (GPX), peroxisome proliferator activator receptor (PPAR-α), and sterol regulatory element binding protein (SREBP-1c). The gene expression was analyzed using the qPCR technique and the evaluation of relative quantification was carried out by formula $2^{-\Delta\Delta C_T}$. The data were analyzed using PROC GLM of SAS 9.1. There was no difference ($P > 0.05$) in gene expression for ACC and SREBP-1c between diets. However, the LPL was 4 times more expressed ($P < 0.05$) in the muscle of bulls fed SB than RPL. The gene expression of $FABP_4$ also presented similar performance when SB was used, being around twice more expressed ($P < 0.05$). The largest difference in gene expression was observed for SCD. Muscle of bulls fed SBM, RPL, and SB, presented, respectively, 12, 6 and twice more SCD gene expression ($P < 0.05$) compared with the RPLM diet. The GPX was 2.5 times more expressed ($P < 0.05$) in the muscle of bulls fed SBM than the other 3 diets. Similar result occurred in the gene expression of PPAR-α. The gene expression of the enzymes FABP and LPL were influenced ($P < 0.05$) by the monensin only when RPL diet was used. For the first enzyme ionophores reduced the gene expression, and for the second, it increases the gene expression. The use of soybean grain or rumen protected lipid, with or without monensin, changed the gene expression of the lipogenic enzymes, and the main affected enzymes were LPL and SCD.

Key Words: nutrigenomics, monensin, soybean

99 Effect of enterotoxigenic *Escherichia coli* on Na^+-dependent glucose transporter-1 mRNA abundance in piglet jejunal segments infused with customized glycans. A. D. Woodward*, X. Chen, M. G. Gänzle, and R. T. Zijlstra, *University of Alberta, Edmonton, Alberta, Canada.*

Enterotoxigenic *Escherichia coli* (ETEC) induces diarrhea and reduces absorption of water and nutrients, yet effects of ETEC on glucose transport in pigs are poorly understood. Exopolysaccharides reuteran and levan from *Lactobacillus reuteri*, but not related glycans dextran and inulin, reduce the occurrence of ETEC-induced diarrhea, and may thus also influence the expression of glucose transporters. We hypothesized that ETEC infection reduces mRNA abundance of Na^+-dependent glucose transporter-1 (SGLT1) in ETEC-challenged piglets. Weanling gilts (5-wk-old; 10.2 ± 1.8 kg BW; n = 4) were prepared for small intestine segment perfusion with 10 jejunal segments. Five segments were infected with ETEC K88 (5×10^9 cfu/mL); remaining segments were treated with saline. Five pairs of segments, 1 ETEC and 1 non-ETEC infected each, were infused with 65 mL of 10 g/L of glucans (dextran, reuteran) or fructans (levan, inulin) or saline (control) for 8 h. After infusion, mRNA was extracted from mucosa, and cDNA was manufactured for quantitative reverse transcription-PCR. Gene expression was calculated as fold change, using the $2^{-\Delta\Delta C}{}_T$ method with β-actin and GAPDH as reference genes, and analyzed with PROC-MIXED in SAS. Overall, SGLT1 decreased (0.6 vs. 1.0 ± 0.2; $P < 0.05$) with ETEC infection but did not differ among glycan and saline treatments. Within treatments, ETEC-infection decreased SGLT1 expression in segments infused with saline (0.3 vs. 1.0 ± 0.4; $P < 0.05$), dextran (0.5 vs. 1.0 ± 0.4; $P < 0.05$), and reuteran (0.4 vs. 1.0 ± 0.4; $P < 0.05$) compared with non-ETEC-infection; however, SGLT1 did not differ between ETEC- and non-ETEC infection for inulin or levan. In conclusion, ETEC-infection decreased SGLT1 abundance. Reduction in SGLT1 abundance in response to ETEC-infection was eliminated with infusion of fructans inulin and levan, but not glucans reuteran and dextran. Thus, effects of ETEC pathogenesis on SGLT1 mRNA abundance in ETEC-infected pigs may depend on glycan composition or their degradation products rather than their effect on diarrhea.

Key Words: enterotoxigenic *Escherichia coli*, glucose transporter, pig

100 Effect of glycan infusion on cytokine expression in piglet jejunal segments challenged with enterotoxigenic *Escherichia coli*. A. D. Woodward*, X. Chen, M. G. Gänzle, and R. T. Zijlstra, *University of Alberta, Edmonton, Alberta, Canada.*

Adhesion of enterotoxigenic *Escherichia coli* (ETEC) to small intestine enterocytes causes release of toxins that stimulate cytokine release. The exopolysaccharides reuteran and levan produced by *Lactobacillus reuteri* may reduce inflammatory responses caused by ETEC-infection. We hypothesized that these exopolysaccharides also reduce mRNA abundance of cytokines interleukin-1β (IL1β), interleukin-6 (IL6), and tumor necrosis factor-α (TNFα) in ETEC-challenged piglets. Weanling gilts (5-wk-old; 10.2 ± 1.8 kg BW; n = 4) were surgically prepared for small intestine segment perfusion with 10 jejunal segments. Five segments were infected with ETEC F4 (K88) (5×10^9 cfu/mL); the rest were treated with saline. Five pairs of segments, 1 ETEC infected and 1 not, were infused with 65 mL of 10 g/L glucans (dextran, reuteran), fructans (inulin, levan), or saline (control) for 8 h. After infusion, mucosa was collected, mRNA extracted, and cDNA manufactured before quantitative reverse transcription-PCR. Contrasts between ETEC- and non-ETEC-infection were analyzed as fold change using the $2^{-\Delta\Delta C}{}_T$ method with β-actin and GAPDH as reference genes. The ETEC-infection increased IL1β (8.2 vs. 1.0 ± 0.2; $P < 0.01$) and IL6 (4.1 vs. 1.0 ± 0.6; $P < 0.01$), but did not affect TNFα, compared with control. Without ETEC, IL6 tended to increase for levan (6.3 vs. 1.0 ± 1.5; $P = 0.09$) and reuteran (7.1 vs. 1.0 ± 1.5; $P = 0.07$) compared with saline. With ETEC-infection, inulin decreased IL1β (0.4 vs. 1.0 ± 0.5; $P < 0.05$) and IL6 (0.1 vs. 1.0 ± 1.2; $P < 0.05$) compared with saline. With ETEC-infection within treatments, IL6 was increased (22.3 vs. 1.0 ± 1.3; $P < 0.01$) for dextran and tended to increase (5.6 vs. 1.0 ± 1.3; $P = 0.07$) for reuteran, but did not differ between inulin or levan, compared with non-ETEC-infection. In conclusion, ETEC-infection increased inflammatory responses based on tissue IL1β and IL6 expression. Luminal fructan infusion may reduce these inflammatory responses whereas luminal glucan infusion did not. Thus, effects of glycans on ETEC-induced cytokine release in pigs may depend on glycan composition.

Key Words: cytokine, enterotoxigenic *Escherichia coli*, pig

101 Dietary inclusion of low doses of microencapsulated zinc oxide affects inflammatory cytokine and tight junction protein expression in the ileum of piglets . E. Grilli*[1], B. Tugnoli[1], F. Vitari[2], and A. Piva[1], *[1]DIMEVET, University of Bologna, Ozzano Emilia, Italy, [2]Department of Health, Animal Science and Food Safety, University of Milan, Milan, Italy.*

Aim of this study was to investigate the expression of inflammation markers and tight junctions protein (TJ) in the ileum of piglets fed with low doses of microencapsulated zinc oxide (ZnO; Zincoret, Vetagro SpA, Italy) in comparison with either a pharmaceutical dose of free ZnO (positive control) or a negative control. Twenty-four pigs weaned at 28 d and divided in 4 groups, received either a basal diet (NC) or the basal diet added with zinc oxide at 2850 mg/kg (PC), or lipid encapsulated ZnO at 187 or 437 mg/kg (Zn200 and Zn400). After 15 d, 6 pigs per group were euthanized and ileal samples were collected for cytokines (IL-6, IL-10, TNF-a, and IFN-g), zonula occludens-1 (ZO-1), occludin (OCC) and claudin-1 at both mRNA and protein level. Data were analyzed with 1way ANOVA. Both groups receiving microencapsulated ZnO tended to have a reduced expression of IL-6 (−25%, $P = 0.1$), compared with both NC and PC. IFN-g expression was the lowest in Zn400 group ($P = 0.02$), and the protein tended to be lower in Zn400 than in PC ($P = 0.07$). Microencapsulated ZnO tended also to downregulate TNF-a expression compared with NC and PC ($P = 0.1$) and TNF content in ileal samples ($P = 0.07$). OCC gene expression was the lowest in Zn400 ($P = 0.04$), though the protein amount was 2–4 fold higher in Zn400 group compared with NC and PC, respectively ($P < 0.001$). ZO-1 expression was not affected by the treatments but ZO-1 amount in Zn400 group was 1.3–1.5 fold higher than in NC and PC, respectively ($P < 0.001$). Claudin-1 gene expression was 1.7–2.4 higher in Zn400 compared with NC and PC, respectively ($P = 0.01$). Overall, Zn200 group tended to have intermediate values between PC and Zn400. The results suggest that ZnO released from a lipid matrix is available in the ileum of piglets where it modulates the local immune response which, in turn, affects the intestinal permeability via the TJ proteins. In this respect, lipid encapsulated ZnO was effective at relatively low concentrations whereas free ZnO fed at 6–15 higher doses failed to be, probably because of a rapid metabolization in the upper gut.

Key Words: microencapsulation, piglet, zinc oxide

102 Effects of dietary clays on performance and barrier function of chicks challenged with *Salmonella enterica* serovar Typhimurium. J. A. S. Almeida*, J. J. Lee, P. Utterback, R. N. Dilger, and J. E. Pettigrew, *University of Illinois, Urbana.*

An experiment was conducted to test for beneficial effects of dietary clays on young chicks challenged with pathogenic *Salmonella* and to explore potential mechanisms through which clays may produce benefits, with emphasis on barrier function. Two hundred forty 1-d-old male commercial broiler chicks (initial BW: 41.6 ± 0.4 g; Ross × Ross) were allotted in a randomized complete block design with level on the battery as the block and pen as the experimental unit. Six replicates of 5 chicks/pen were assigned to each treatment. Pens were randomly assigned to 1 of 2 infection treatments (with or without *Salmonella* challenge at 2 wk of age) and 4 dietary treatments: basal, 0.3% smectite A (SMA), 0.3% smectite B (SMB) and 0.3% zeolite (ZEO). The *Salmonella* challenge reduced ($P < 0.05$) the growth rate of chicks fed the basal diet by 11% during d 3–7 post-inoculation (PI), but the clays prevented this reduction. The interaction between challenge and diet occurred ($P < 0.05$) for ADFI d7–10 PI and ADFI and ADG during the overall period (d0–14 PI), and the pattern was similar but not significant for other measures. Goblet cell number and size were increased ($P < 0.05$) by the *Salmonella* challenge in chicks fed the basal diet, and were reduced ($P < 0.05$) in *Salmonella*-challenged chicks by feeding SMA. Villus height was reduced by the *Salmonella* challenge in the chicks fed dietary clays ($P < 0.01$) but not in chicks fed basal diet (interaction $P < 0.05$). The mRNA expression of IFFN-γ, a canonical inflammatory marker, in cecal tissues remained low in all treatments. Clays did not alter the concentration of α-1 acid glycoprotein in the sham-challenged group but increased it in the *Salmonella*-challenged group. In conclusion, clays restored performance of *Salmonella*-challenged chicks, SMA had effects consistent with strengthening of the mucosal barrier, and the pattern of response suggests that different clays produce benefits through different mechanisms.

Key Words: goblet cell, chick, clay

103 *Bacillus licheniformis* and sodium butyrate protective effects on oxidative stress-induced inflammation in IPEC-J2 porcine intestinal epithelial cells. A. Ortiz*[1], P. Gálfi[2], E. Paszti-Gere[2], A. Jerzsele[2], M. Puyalto[1], and J. J. Mallo[1], *[1]Norel S.A., Madrid, Spain, [2]Szent István University, Budapest, Hungary.*

To determine whether sodium butyrate (SB) and *Bacillus licheniformis* (BL) spent culture supernatant (SCS) could exert protective effects under oxidative stimuli, IPEC-J2 porcine intestinal epithelial cells were treated simultaneously with hydrogen peroxide and the above mentioned active ingredients (AIs). Transepithelial electrical resistance (TER) measurement of monolayers was performed using epithelial tissue volt/ohmmeter (EVOM) to elucidate the effect of 0.5 m*M* peroxide and AIs on cell membrane integrity. Occurrence of cell death was monitored using 2 staining methods, Trypan blue exclusion assay (TB) and Neutral Red uptake test (NRU) by counting 300 cells per flask in 3 parallels. Administration of sodium butyrate at 2 m*M* significantly ($P < 0.05$) increased TER values compared with positive controls (84.09% vs. 67.55%), this barrier strengthening property remained elevated after an 24-h recovery period (174.41% vs. 143.16%). SCS of *Bacillus licheniformis* in 10% solution significantly ($P < 0.05$) elevated TER values compared with control (90.10% vs. 69.32%). Sodium butyrate at 2 m*M* significantly ($P < 0.05$) elevated the number of viable cells with NRU staining compared with H_2O_2 treated samples (68.71% vs. 58.37%). SCS of *Bacillus licheniformis* in 10% solution also increased cell viability significantly (79.60% vs. 58.37; $P < 0.05$) as a reduced number of dead cells was found. Sodium butyrate at 2 m*M* significantly ($P < 0.05$) elevated the number of viable cells compared with H_2O_2 treated samples (82.20% vs. 55.48%) with the TB assay. It is concluded that both SB at 2 m*M* and BL SCS in 10% solution have a protective effect on IPEC-J2 porcine intestinal epithelial cells.

Table 1.

		Mean TER (OHM·cm2)		
		Before treatment	After treatment	After 24 h
Trial 1	0.5 mM H2O2	7367	4976b	10535b
	0.5 mM H2O2 + 2mM SB	5688	4783a	9920a
Trial 2	0.5 mM H2O2	6254	4335b	—
	0.5 mM H2O2 + 10% BL	7224	6509a	—

Key Words: stress, butyrate, licheniformis

104 Effect of acute water and feed deprivation event on mucin, cytokine, and tight junction gene expression in weaned pigs. N. Horn*[1], G. Miller[3], K. M. Ajuwon[1], F. Ruch[2], and O. Adeola[1], *[1]Purdue University, West Lafayette, IN, [2]Enzyvia LLC., Sheridan, IN, [3]Biomatrix, Princeton, MN.*

The effect of acute water and feed deprivation events on mucin, cytokine, and tight junction gene expression in weaned nursery pigs were evaluated. Pigs (6.21 ± 0.29 kg) were allotted in a randomized complete block design to 4 post-weaning treatments on the basis of body weight at the time of weaning which consisted of a control, 24-h feed deprivation event, 24-h water deprivation event, and a 24-h feed and water deprivation event. There were 8 pigs per pen and 12 replicate mixed-sex pens per treatment. Following the deprivation events pigs were returned to normal management procedures. On d 2 and 7 post weaning one pig per pen was euthanized and ileal and jejunal mucosal samples were taken for gene expression analyses by RT-PCR for mucin (MUC2), cytokines interleukin 1 (IL-1β), interleukin 6 (IL-6), and tumor necrosis factor (TNF-α), and tight junction proteins claudin 4, occludin, and zonula occludens 1 (ZO-1). In the jejunum there was a decrease in TNF-α expression the day following the feed stress event ($P = 0.011$) and a significant feed x water interaction ($P = 0.017$). Furthermore, there was a decrease in occludin gene expression the day following the water stress event ($P = 0.019$). There were no differences in MUC2, tight junction, or cytokine gene expression in the jejunum 7 d post weaning. In the ileum there was a decrease in claudin 4 gene expression 7 d post weaning in water stressed pigs ($P = 0.008$). There was also a tendency for a decrease in ZO-1 gene expression with the water stress event ($P = 0.081$) and a tendency for a feed × water interaction ($P = 0.096$) was observed 7 d post weaning. There were no differences in MUC2, cytokine, or tight junction gene expression in the ileum 2 d post-weaning. The results from the current trial show a decrease in tight junction gene expression in the gastrointestinal tract of nursery pigs on d 2 and 7 post-weaning following a 24-h water deprivation event at weaning although expression of cytokines and MUC2 were largely unaffected by the stress events.

Key Words: tight junction gene expression, nursery pig, stressor

105 Effect of dietary fructo-oligosaccharide with different polymerization degree on the cellular immune response in weaned pigs. V. Halas*[1], I. Nochta[2], T. Tuboly[3], Cs. Szabó[1], and L. Babinszky[4], *[1]Kaposvár University, Kaposvár, Hungary, [2]Provimi, Zichyújfalu, Hungary, [3]Szent István University, Budapest, Hungary, [4]University of Debrecen, Debrecen, Hungary.*

Fructo-oligosaccharide (FOS) supports the beneficial microbiota that affects the immune status, particularly at weaning. However, it is not clear if degree of FOS polymerization can alter the animal response. Therefore the aim of the trial was to study the effect of different FOS supplementation on cellular immune response and growth performance of nursery pigs. A total of 464 piglets (7.9 kg BW) were assigned into 4 dietary treatments (6 flat deck pens/treatment) at weaning (28 d). The negative control (NC) diet was a commercial feed without growth promoter (basal diet), the basal diets was supplemented with 40 ppm avilamycin (treatment PC), 0.5 g/kg of FOS (3–5 degree of polymerization; Profeed, Allied Nutrition Ltd., South Africa; treatment FOS) or 0.5 g/kg of inulin (10 degree of polymerization; Fibrulin, Warcoing, S.A. Belgium; treatment IN). Pigs were immunized by inactivated Aujeszky's disease virus vaccine at d1 and 14 of the trial (28- and 43 d-age). Blood samples were taken at d1, 8, 15, 22 and 32 from 2 pigs/pen for lymphocyte stimulation tests (LST) with nonspecific mitogens (concanavalin A, pokeweed mitogen, phytohemagglutinin) and with specific mitogen (Aujeszky's virus). All piglets were individually weighed on d1, 15 and 32. Data were analyzed by ANOVA. Feed additives enhanced the nonspecific cellular immune response at d32 ($P < 0.05$), but no treatment effect was observed on specific LSTs at any time. At the first 2 weeks of the trial ADG was lower in FOS and IN groups (207 and 201 g/d, resp.) compared with the NC and PC groups (234 and 228g/d, resp; $P < 0.05$). However, there were no differences in growth rate among treatments ($P > 0.05$) either in the last 18 d (NC, PC, FOS, IN: 358, 361, 339, 346 g/d, resp) or in the whole nursery period (NC, PC, FOS, IN: 300, 299, 277, 278 g/d, resp). The ADFI and FCR values were similar in each period. In conclusion, fructo-oligosaccharide supplementation results in better non-specific cellular immune response regardless of degree of polymerization ranging from 3 to 10, even if no growth promoting effect is present.

Key Words: FOS polymerization, immune response, piglet

106 Astragalus polysaccharide reduces inflammatory response by decreasing permeability of LPS-stimulated Caco2 cells. X. Wang, Y. Li, X. Yang, and J. Yao*, *College of Animal Science and Technology, Northwest A&F University, Yangling, Shaanxi, China.*

As the major constituent of Radix Astragali, astragalus polysaccharide (APS) is known for its anti-inflammation and immunomodulatory functions. The objective of this study was to investigate the effect of APS on inflammatory response and structural changes in lipopolysaccharide (LPS)-stimulated Caco2 cells. Caco2 cells were cocultured with APS and LPS, with APS added after the addition of LPS (post-addition), before the addition of LPS (pre-addition), or simultaneously with the addition of LPS (simultaneous addition). The mRNA expression of inflammatory indicators (TNF-α, IL-1β and IL-8) and tight junctions (zonula occludens-1 (ZO-1) and occludin) was measured by RT-qPCR. Short circuit current (Isc) was recorded by an Ussing chamber system. Data were subjected to one-way ANOVA using the GLM procedure of SAS, version 8.02. Means were separated by Fisher's least significant difference multiple-range test. Addition of APS downregulated the expression of TNF-α, IL-1β and IL-8 ($P < 0.05$) and the Isc levels ($P < 0.05$) of LPS-stimulated Caco2 cells for all 3 administration treatments. The minimum anti-inflammatory concentration of APS was 50, 100, and 100 μg/mL for pre-, post-, and simultaneous additions of APS, respectively. The mRNA expression of ZO-1 and occludin was upregulated for post- and pre-additions of APS, respectively ($P < 0.05$). Results suggested that APS had context-dependent anti-inflammatory and tight junction protective properties for LPS-stimulated Caco2 cells, and may be used as a preventative treatment against LPS stimulation for intestine cells.

Key Words: astragalus polysaccharide, inflammatory response, tight junction

107 Oxygen consumption and respiratory control ratio (RCR) of broilers with and without growth enhancing levels of mineral supplementation challenged with *Eimeria maxima*. G. Acetoze*[1], R. Kurzbard[1], J. J. Ramsey[2], K. C. Klasing[1], and H. A. Rossow[3], *[1]Department of Animal Science, University of California, Davis, [2]School of Veterinary Medicine, University of California, Davis, [3]School of Veterinary Medicine, University of California, Tulare.*

Respiratory control ratio (RCR, State3/State4) provides an indication of mitochondrial coupling and efficiency of oxidative phosphorylation. However, the effect of dietary minerals fed at growth enhancing levels on mitochondrial function represented by RCR is unknown. Sixteen 7-d-old broilers were randomly assigned to 4 treatments: an infected control diet (Cu 15 ppm and Zn 60 ppm) + *Eimeria maxima* (Ei), 245 ppm Cu from tribasic copper chloride (TBCC) + Ei, negative control (Cu 15 ppm and Zn 60 ppm) - Ei and 2000 ppm Zn from ZnO + Ei. The diet was composed of 49% corn, 40% soybean meal, 6.2% vegetable oil (DM = 90.62%, CP = 21.37%, Fat = 7.7%, ME = 2.89Mcal/day) and were fed for 14 d. Mitochondria O_2 consumption was performed on isolated liver mitochondria (1g liver tissue) according to Ramsey et al. (2004). Statistical analysis was performed in R (version 2.15.1) using ANOVA. There was a trend of State 4 (leak-dependent O_2 consumption) being higher for infected birds fed 2000 ppm ZnO and infected birds fed Zn and Cu at the requirement levels ($P = 0.08$). However, State 3 (maximum ATP stimulated respiration) did not differ between treatments ($P = 0.51$). RCR values were 4.27, 2.40, 2.54 and 2.65 for the negative control group, the positive control group, 245ppm of Cu from TBCC group and 2000 ppm ZnO group, respectively and were different ($P = 0.02$). With the exception of birds not infected with Ei and not treated with high levels of minerals, birds that were fed levels of Cu from TBCC and Zn from ZnO above the requirement had higher RCR's compared with infected birds not treated with high minerals (2.54 and 2.65 versus 2.40, respectively). Levels of minerals (245ppm Cu as TBCC and 2000ppm Zn as ZnO) could possibly be decreasing the activity of Ei by acting as anticoccidials, protecting the cells from inflammation and therefore mitochondria uncoupling, loss of integrity and membrane disruption. Damage to the mitochondria membrane would interfere with proton leak kinetics which is highly related to H^+ gradient build up during electron transport chain and affects efficiency of H^+ use for ATP production.

Key Words: broilers, mitochondria, RCR

108 Retention and digestibility of Zn, Cu, Mn, and Fe in pigs fed diets containing inorganic or organic minerals. Y. Liu*[1], Y. L. Ma[2], J. M. Zhao[2], M. Vazquez-Añón[2], and H. H. Stein[1], *[1]University of Illinois, Urbana, [2]Novus International Inc., St. Charles, MO.*

The objective of this experiment was to measure the apparent total tract digestibility (ATTD) and retention rate of Zn, Cu, Mn, and Fe in pigs fed either inorganic micro minerals (IMM) or organic micro minerals (OMM). Thirty 2 barrows (BW: 38.4 ± 10.17 kg) were housed in metabolism cages and assigned to 4 treatments with a 2 × 2 factorial arrangement and 8 replicates per treatment. Semi-synthetic (SS) or corn-soybean meal (CS) diets were formulated with the inclusion of IMM ($ZnSO_4 \cdot 7H_2O$, $CuSO_4 \cdot 5H_2O$, $MnSO_4 \cdot H_2O$ and $FeSO_4 \cdot H_2O$), or OMM [$Zn(HMTBa)_2$, $Cu(HMTBa)_2$, $Mn(HMTBa)_2$ and FeGly] premix. The Zn, Cu, or $Mn(HMTBa)_2$ (MINTREX®, Novus International Inc., St. Charles, MO) is a chelate of 1 mineral with 2 2-hydroxy-4-methylthio butanoic acid and FeGly (MAAC®) is a chelate of 1 mineral with 1 glycine. Pigs were fed the SS diet without added micro mineral for 2 wk and then randomly assigned to 1 of 4 treatment diets. Fecal and urine samples were collected for 5 d following a 5-d adaptation period. The inclusion of OMM increased ($P < 0.05$) the ATTD and retention rate of Zn, Cu, Mn, and Fe in pigs. No difference was observed between SS and CS diets, except pigs fed CS diets had greater ($P < 0.05$) ATTD of Zn than pigs fed SS diets. Compared with IMM, adding OMM increased ($P < 0.05$) the ATTD and retention of Cu, Mn, and Fe to a lesser extent in SS diets than in CS diets (interaction, $P < 0.05$). This may be due to the greater concentration of phytate in CS diets than in SS diets. Results indicate that organic forms of micro minerals have better digestibility and retention rates compared with inorganic forms.

Table 1. Apparent total-tract digestibility (ATTD) of Zn, Cu, Mn, and Fe in pigs fed diets containing inorganic (IMM) or organic micro minerals (OMM)

	Semi-synthetic		Corn-soybean meal		
	IMM	OMM	IMM	OMM	SEM
Zn					
ATTD, %	49.11	57.63	44.04	53.60	1.75
Retention, %	40.65	48.44	38.61	49.55	1.37
Cu					
ATTD, %	42.93	44.61	35.64	50.46	2.37
Retention, %	39.58	40.83	33.14	47.88	2.31
Mn					
ATTD, %	37.90	40.79	29.50	44.31	2.60
Retention, %	34.12	36.55	27.22	41.67	2.23
Fe					
ATTD, %	38.57	42.03	30.16	47.37	1.88
Retention, %	36.48	40.41	28.00	45.48	1.94

Key Words: apparent total-tract digestibility, micro mineral, pig

109 Microencapsulated zinc oxide on piglets growth performance and intestinal architecture. E. Grilli*[1], B. Tugnoli[1], F. Vitari[2], A. Piva[1], and A. Prandini[3], *[1]DIMEVET, University of Bologna, Ozzano Emilia, Italy, [2]Department of Health, Animal Science and Food Safety, University of Milan, Milan, Italy, [3]ISAN, Università Cattolica Sacro Cuore, Piacenza, Italy.*

The aim was to compare low doses of microencapsulated zinc oxide (ZnO; Zincoret) in the diet of piglets with pharmacological level of ZnO on growth and ileal architecture. 144 weaned piglets, divided in 36 pens (n = 9), received a basal diet (NC; Zn at 45 mg/kg) or the basal diet with ZnO at 2850 mg/kg (PC), or with lipid microencapsulated ZnO at 187 or 437 mg/kg (Zn200 and Zn400). After 15 and 49 d, 6 pigs/group/time were euthanized to collect ileal mucosa for immunohistochemistry, histomorphology, and Na-dependent glucose transporter (SGLT-1) gene expression. Pigs BW and feed intake were recorded at 0, 14 and 42 d and ADG and FCR were calculated. Data were analyzed with 1 way ANOVA. At 14d the PC group had a 32% and 7% higher ADG and BW and a lower FCR compared with NC ($P < 0.05$), whereas Zn200 and Zn400 had intermediate values. At 42d both groups receiving microencapsulated ZnO had higher BW than NC and did not differ from PC ($P = 0.01$). ADG was on average 20% higher for PC and Zn400 than the NC ($P = 0.01$) and FCR was lower

in all treated groups compared with NC (−22%; $P < 0.01$). At 14 d, villi length in Zn400 pigs was 9% and 6% higher than in NC and PC, respectively ($P < 0.01$) and the villi:crypts ratio (V:C), as well as % of mitotic cells, were higher in all treated groups compared with NC ($P < 0.01$). SGLT-1 gene expression was the lowest in Zn400 pigs. At 49d villi length and V:C ratio were the highest for PC compared with all of the other groups (+10% than NC; $P = 0.01$). Mitotic cells were the highest in Zn400 group compared with other groups (+3% compared with NC and PC; $P < 0.01$), whereas SGLT-1 expression tended to be lower in Zn200 and Zn400 groups compared with NC and PC ($P = 0.06$). Pigs receiving low doses of microencapsulated ZnO had performance comparable to those receiving pharmacological level of ZnO overall the post-weaning phase. Moreover, in the first 2 weeks, microencapsulated ZnO improved the ileal architecture as reflected by the increased V:C ratio and the % of mitotic cells. The reduced SGLT-1 m-RNA abundance might suggest a reduced availability of glucose in the lumen of ileum, therefore suggesting a lower amount of undigested nutrients.

Key Words: microencapsulation, piglet, zinc oxide

110 Effect of dietary zinc and copper sources on wean-to-finish pig performance. J. Morales[1], C. Rapp*[2], and T. L. Ward[3], *[1]Pig Champ Pro Europa, Segovia, Spain, [2]Zinpro Animal Nutrition Inc., Boxmeer, the Netherlands, [3]Zinpro Corporation, Eden Prairie, MN.*

A total of 288 weanling pigs (7.5 kg BW; 28 d of age) were used to determine the effect of dietary Zn and Cu source on wean-to-finish growth performance by employing a 2 X 2 factorial arrangement of treatments and randomized complete block design. At weaning (d 1), pigs were blocked by BW and randomly assigned to 1 of 2 treatments for 35 d: (1) 2360 ppm Zn as ZnO + 150 ppm Cu as $CuSO_4$ [HZCS] or (2) 50 ppm Zn as zinc amino acid complex + 60 ppm Zn as ZnO + 150 ppm Cu as copper amino acid complex [COZC]. At the end of the nursery phase (d 35), one-half of the pigs from each treatment were assigned to 1 of 2 fattening treatments on which they were maintained until the end of the study (d 151): 1) 100 ppm Zn as ZnO [IZ] or 2) 50 ppm Zn as zinc amino acid complex + 50 ppm Zn as ZnO [CZ]. In the nursery, each treatment was replicated 24 times and in fattening, 9 times, with equal numbers of female and male pigs in each pen. Pigs were fed a phase 1 (d 1 to 14), phase 2 (d 15 to 35) and fattener diet (d 36 to 151). In phase 1, ADG and ADFI were increased (157, 130, 233, 202 g/d; $P < 0.05$) and proportion of pigs that needed therapeutic antibiotic treatment decreased (23, 48%; $P < 0.05$) in pigs fed HZCS compared with pigs fed COZC. In phase 2 and in the overall nursery period, ADFI and FCR were lower (646, 703, 467, 519 g/d; 1.47, 1.63, 1.49, 1.60; $P < 0.05$) in pigs fed COZC than pigs fed HZCS. Data were analyzed using the GLM procedure of SAS. No significant ($P > 0.13$) interactions between treatment in nursery and fattening period were observed. From d 131 to 151, ADG was increased (896, 829 g/d; $P < 0.05$) and FCR decreased (2.46, 2.70; $P < 0.05$) in animals consuming CZ compared with IZ. In the fattening period (d 36 to 151), FCR was lower (2.33, 2.41; $P < 0.06$) in pigs fed COZC than in pigs fed HZCS. Overall (d 1 to 151), FCR was decreased (2.22, 2.32; $P < 0.05$) in pigs fed COZC compared with HZCS. High levels of ZnO and $CuSO_4$ were more effective in mitigating negative effects of weaning immediately post-weaning than complexed Zn and Cu. However, supplementing complexed Zn and Cu in nursery improved feed conversion ratio over the entire nursery and fattening period.

Key Words: swine, growth, trace mineral

111 Effects of selenium-enriched exopolysaccharides produced by *Enterobacter cloacae* Z0206 on growth performance, antioxidant status, and immune functions in weaning piglets. Z. Q. Lu*, G. X. Wu, M. Huang, F. Q. Wang, and Y. Z. Wang, *Institute of Feed Science, Zhejiang University, Hangzhou, Zhejiang, China.*

This study was conducted to investigate the effects of Se-enriched exopolysaccharides (Se-Exo, 536 mg/kg Se) on growth performance, antioxidant status and immune functions in weaning piglets. A total of 150 piglets [(Landrace × Yorkshire) × Duroc] weaned at 28 d of age with an initial BW of 8.11 ± 0.12 kg were randomly allocated into 5 groups of 3 replicates each. The 5 treatments were: basal control diet (CON), Na_2SeO_3 diet (CON + 0.30 mg/kg Na_2SeO_3), Na_2SeO_3+ astragalus polysaccharide (APS) diet (CON + 0.30 mg/kg Na_2SeO_3 + 560 mg/kg APS), Na_2SeO_3+ EPS diet (CON + 0.30 mg/kg Na_2SeO_3 + 560 mg/kg EPS) and Se-Exo diet (CON + 560 mg/kg Se-Exo). On d 58, samples were taken for analysis: blood for total antioxidant content (T-AOC), glutathione peroxidase (GSH-Px), superoxide dismutase (SOD), tumor necrosis factor-α (TNF-α), interleukin-6 (IL-6), immunoglobulin G and M (IgG, IgM); liver, jejunum and ileum for gene expression of proline-arginine rich 39-amino acid peptide (PR-39), Hepcidin and porcine β-defensin-2 (pBD-2). Compared with CON group, ADG was enhanced in the Na_2SeO_3+APS, Na_2SeO_3+EPS and Se-Exo groups (+8.9%, +9.9% and + 12.3%, resp., $P < 0.05$) and F:G was decreased (−10.2%, - 8.4 and −10.2%, resp., $P < 0.01$). There were no differences in ADG between pigs fed the Na_2SeO_3+APS, Na_2SeO_3+EPS and Se-Exo diets. The Se-Exo group had higher serum T-AOC (+29.6%), GSH-Px (+25.6%) and SOD (+18.6%) activities than the CON group ($P < 0.05$), and the T-AOC activity in Se-Exo group was higher than the Na_2SeO_3 group ($P = 0.035$). Increases ($P < 0.05$) in serum IgG (+54.0%;), IgM (+56.1%), TNF-α (+61.6%) and IL-6 (+47.5%) were observed in the Se-Exo group compared with the CON. Pigs fed Se-Exo diet had higher PR-39 and Hepcidin gene expression levels in liver ($P < 0.001$) and pBD-2 gene expression levels in jejunum and ileum ($P < 0.05$) compared with the CON group. These results implicated that the combined effects of Se and exopolysaccharide are responsible for the bioactivity of Se-Exo which would be expected to be a new immunopotentiator in weaning piglets.

Key Words: exopolysaccharide, immunity, weaning piglet

112 Effects of chromium-loaded chitosan nanoparticles on growth, carcass characteristics, pork quality, and lipid metabolism in finishing pigs. M. Q. Wang*, Y. D. He, C. Wang, H. Li, S. Y. Chen, W. J. Tao, and S. S. Ye, *Animal Science College of Zhejiang University, Hangzhou, Zhejiang, China.*

Numbers of researches have been conducted to study the effects of Cr from different chemical forms. The study was conducted to evaluate the effects of chromium-loaded chitosan nanoparticles (Cr-CNP) on growth, carcass characteristics, pork quality and lipid metabolism in finishing pigs. A total of 160 barrows (66.1 ± 1.01 kg BW) were randomly divided into 4 groups, each group with 4 pens, 10 pigs per pen. Pigs were fed same basal diet(CP 17.98%, DE 13.2MJ/kg, Lys 1.05%, Met 0.45%)supplemented with 0, 100, 200, or 400 μg/kg Cr from Cr-CNP, respectively. All pigs were given free access to feed and water for 40 d. Average daily gain, feed intake and feed gain ratio were collected. Eight pigs from each treatment were slaughtered to measure carcass lean ratio, longissimus muscle area (LMA), backfat thickness, 45 min pH, Hunter L, a, b value, 24-h drip loss, and some serum parameters and enzymatic activities. The results showed that feed gain ratio of pigs fed supplemental Cr-CNP was decreased ($P < 0.05$). Dietary Cr-CNP increased the carcass lean ratio ($P < 0.01$) and LMA ($P < 0.01$), decreased carcass fat ratio ($P < 0.001$) and backfat thickness (P

< 0.001) with linear and quadratic manner. The 24 h drip loss was linear and quadratic decreased ($P < 0.01$), while 45 min pH value and Hunter L, a, b values in longissimus muscle were unaffected. Supplemental Cr-CNP linearly increased serum free fatty acids ($P < 0.001$), lipase activity ($P < 0.01$) and serum insulin-like growth factor I ($P < 0.01$), while linearly decreased serum insulin ($P < 0.001$). Dietary supplementation of Cr-CNP also linearly decreased activities of fatty acid synthase ($P < 0.01$) and malate dehydrogenase ($P < 0.01$), while increased the activity of hormone-sensitive lipase ($P < 0.05$) in subcutaneous adipose tissue with linear and quadratic manner. The present results suggested that dietary supplementation of Cr as Cr-CNP had beneficial effects on growth, carcass characteristics and pork quality, and positively affected on lipid catabolism in finishing pigs.

Key Words: chromium, carcass characteristics, lipid metabolism

Ruminant Nutrition Symposium: Advancements in Enhancing Cell Wall Digestibility and its Contribution to Improve Ruminant Production

113 Improving cell wall digestion and animal performance with fibrolytic enzymes. A. T. Adesogan*, J. J. Romero, and Z. X. Ma, *Department of Animal Sciences, IFAS, University of Florida, Gainesville.*

The objective of this paper is to summarize published responses to treatment of cattle diets with exogenous fibrolytic enzymes (EFE), to discuss reasons for variable EFE efficacy in animal trials and to recommend strategies for improving enzyme testing and enzyme efficacy in ruminant diets. A review of 24 dairy cow studies with 69 treatments revealed that dietary addition of exogenous fibrolytic enzymes (EFE) increased milk production and feed efficiency 20 and 23% of the time by 2.45 kg/d (7.6% increase) and 0.13 (9% increase) on average, respectively. This variability is attributable to several enzyme, feed, animal, and management factors that will be discussed in this paper. The variability reflects our limited understanding of the synergistic and sequential interactions between exogenous glycosyl hydrolases, autochthonous ruminal microbes and endogenous fibrolytic enzymes that are necessary to optimize ruminal fiber digestion. An added complication is that many of the standard methods of assaying EFE activities may over or underestimate their potential effects if they are based on pure substrate saccharification or if they do not simulate ruminal conditions. Our recent evaluation of 18 commercial EFE showed that 78 and 83% of them exhibited optimal endoglucanase and xylanase activities at 50°C and 77 and 61% had optimal activity at pH 4–5, respectively. Hence, most would not be optimally active under ruminal conditions. Of the many fibrolytic activities that act synergistically to degrade forage fiber, only a few are typically assayed, and of the latter endoglucanase and xylanase typically account for most the variability in fiber digestion. Yet, neither of these can hydrolyze the recalcitrant phenolic acid–lignin linkages that are the main constraints to ruminal fiber degradation. These factors highlight the futility of random addition of EFE to diets. This paper will discuss animal responses to fibrolytic enzymes, advance explanations for the variability in the response and suggest strategies to improve enzyme testing and enzyme efficacy in ruminant diets.

Key Words: fibrolytic enzyme, cow, digestion

114 Effects of neutral detergent fiber concentration and digestion characteristics on energy intake and partitioning of lactating cows. M. S. Allen*, *Michigan State University, East Lansing.*

Neutral detergent fiber (NDF) comprises from less than 28% to more than 40% of dietary dry matter for lactating cows. The concentration and digestion characteristics of NDF in diets affect dry matter intake, digestibility, and energy partitioning and can greatly affect productive performance of lactating cows. Ruminal turnover rate of NDF varies depending upon initial particle size, digestion kinetics and particle fragility. Longer retention time increases digestibility as well as digesta mass and volume. Increased digesta mass in the rumen can reduce risk of ruminal acidosis and abomasal displacement but can also limit feed intake. Signals to brain feeding centers from ruminal distension control feed intake when the drive to eat is high and metabolic control of feed intake is diminished (e.g., cows at peak lactation) while signals derived from metabolism of fuels dominate the control of feed intake when signals from distension decrease (e.g., cows in late lactation). Therefore, NDF turnover rate is an important consideration for diet formulation; a higher turnover rate is desirable when feed intake is limited by ruminal distention. Over half of the ruminal mass of NDF is in particles that are below the threshold size for passage. Ruminal retention of small particles is from entrapment by the pool of large particles in the rumen and passage rate is positively related to particle density. Forage family (e.g., legumes, grasses) and maturity at harvest affect digestion characteristics and ruminal retention time and therefore the filling effect of forages. Non-forage fiber sources (NFFS) contribute little to the filter bed of large particles but function to displace dietary starch. Substitution of fermentable fiber for starch can maintain milk yield while decreasing gain in body condition for cows with lower requirement for glucose. This presentation will discuss the effects of dietary NDF concentration and digestion characteristics on energy intake and partitioning of cows and how they change throughout the lactation cycle.

Key Words: physiological state, digestion kinetics, fiber fragility

115 Nutritional strategies to optimize feeding brown midrib corn silage to dairy and beef cattle. J.-S. Eun*, M. S. Holt, A. J. Young, and D. R. ZoBell, *Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan.*

Digestibility of forage fiber affects many aspects of dairy and beef cattle production. In addition, providing adequate concentrations of digestible fiber in cattle ration is essential for animal health, as it is required to support an appropriate rumen function. Brown midrib corn silage (BMRCS) is characterized by its lower lignin concentration and higher fiber digestibility than conventional corn silage (CCS). Several, but not all experiments feeding BMRCS, have reported improved lactational performance of dairy cows. Inconsistent effects of BMRCS have been caused by various factors, including cows differing in physiological state and duration of experiment. Our recent study indicated that feeding BMRCS in high-forage diets can have beneficial effects to lessen body fat mobilization in fresh cows without limiting DMI around peak lactation, resulting in longer peak milk production. Similarly, another lactation study reported that feeding BMRCS during the transition period resulted in increased feed intake for the last 2 wk of gestation as well as the first 3 wk postpartum, leading to an increase in milk yield during the 3-wk postpartum period. When all cows were fed a CCS-based diet, a carryover effect occurred from the feeding of BMRCS during the transition period, resulting in increases in the yields of protein, lactose, and solids in these cows from wk 4 to 15 of lactation. Feeding BMRCS in growth-phase diets of beef steers resulted in increased DMI and improved digestibility of DM and fiber, whereas it did not result in improved ADG compared with those fed CCS. Feeding BMRCS at 24% of diet DM by replacing corn did not negatively affected growth rates in finishing beef cattle, implying that feeding BMRCS in a relatively higher dietary concentration can be a cost-effective alternative method to raising beef. Understanding interactive effects of dietary sources of fiber with BMRCS at various dietary proportions, physiological conditions of animals, and control of feed intake is needed to optimize potential benefits of feeding BMRCS in cattle diets.

Key Words: brown midrib corn silage, growth performance, lactational performance

116 The utility of lipid extracted algae as a protein source in forage or starch-based ruminant diets. S. L. Ivey* and L. N. Tracey, *New Mexico State University, Las Cruces.*

Microalgae are unicellular organisms that live and reproduce in many forms of water and use sunlight, CO_2 and added nutrients to produce carbohydrates, proteins and lipids. Algal biomass has shown many different advantages as a feedstock for the biofuel industry, including: (1) high biomass yield per unit cultivation; (2) minimal competition for land used for traditional agriculture; (3) uses various water sources such as waste, saline, and produced water; and (4) biomass from algae could potentially produce both fuel and valuable co-products. Co-products resulting from the algal biofuel industry may be a source of protein for ruminant livestock. It is widely recommended that the algal biofuel industry not trivialize co-product value but consider it an additional source of revenue in an effort to gain industry sustainability and food security in the US by using geographic areas and resources not used for traditional food production. The cattle industry consumes approximately 40 million tons of protein feeds annually; therefore, the potential exists for the ruminant feeding industry to be a consistent, large-volume outlet for high protein algal co-product. In addition to proteins and lipids microalgae utilize photosynthesis to produce carbohydrates. Carbohydrates are used for energy storage and structure by the algal cell and the types of carbohydrates present are species-dependent but may include cellulose, glycogen, starch and other monosaccharides. The algal biofuel industry will potentially use a variety of algal strains, growth conditions, and harvesting and oil extraction methods. All of these factors may influence the utility of the final co-product. This presentation will address ongoing research to evaluate LEA produced from various algal strains, cultivation methods, and harvesting and extraction protocols. Currently, oil extraction protocols coupled with multiple algal strains have yielded inconsistent coproduct that ranges in protein from 15 to 50%, 3 to 47% ash and an uncharacterized carbohydrate fraction.

Key Words: ruminant, algae, biofuel

117 Dietary protease increases amino acid digestibility of various proteinaceous feedstuffs in growing pigs. J. Escobar*, J. Lunnemann, J. Xue, K. Eckert, N. Odetallah, and M. Vazquez-Añón, *Novus International Inc., St. Charles, MO.*

Supplementing diets with an exogenous protease to increase amino acid (AA) digestibility may be used to reduce feed cost, decrease protein fermentation in the hindgut, or both. The objective of this study was to quantify apparent ileal AA digestibility (AID) in soybean meal (SBM), corn-derived distillers dried grain with solubles (DDGS), meat and bone meal (MBM), and poultry byproduct (PBP) without or with exogenous protease (Cibenza DP100 at 500 ppm, PROT). Eight growing barrows (initial BW: 56.1 ± 0.6 kg) were individually housed and surgically fitted with a simple T-cannula in the distal ileum. The test order of feedstuffs was randomized and they were the only source of AA in each diet, which included 0.4% of TiO_2 as an indigestible marker. For each feedstuff, pigs were randomly allotted to a 2-period crossover design to give n = 8 per diet. Each independent feedstuff trial consisted of 5 d of diet adaptation and 2 d of ileal digesta collection. Results indicate that supplementation with PROT increased AID of Arg, Cys, His, Ile, Leu, Lys, Met, Thr, Phe, and Val in PBP ($P < 0.04$) and SBM ($P < 0.006$). In DDGS, PROT increased ($P < 0.05$) AID of Cys, Leu, Met, Thr, Phe, and Val, as well as, Lys ($P = 0.06$) and Ile ($P = 0.08$). In MBM, PROT increased AID of Met ($P = 0.04$), Lys ($P = 0.06$), Leu and Thr ($P = 0.07$), and Arg ($P = 0.08$). Results from a meta-analysis of the 4 independent trials indicate that PROT supplementation increased ($P < 0.05$) AID of Ala, Arg, Cys, Glu, Ile, Leu, Lys, Met, Ser, Thr, Phe, and Val, as well as Asp ($P = 0.08$) and Gly ($P = 0.10$). The increase in percent AID points was 6.2 for Lys, 5.8 for Met, and 7.6 for Thr. Collectively from these results, it can be concluded that PROT is an effective protease that increases in vivo AA digestibility of animal- and plant-derived proteinaceous feedstuffs.

Key Words: enzyme, amino acid digestibility, swine

118 Protease and carbohydrase supplementation increased carcass weight and profit of finishing pigs. J. Escobar*, Y. Ma, N. Odetallah, and M. Vazquez-Añón, *Novus International Inc., St. Charles, MO.*

Inclusion of alternative ingredients and byproducts is a viable strategy to reduce the cost of diets. However, the combination of lower digestible ingredients and their higher content of anti-nutritional factors (e.g., fiber) compared with a corn-soy diet may contribute to reduce growth performance, carcass weight, and profit. The objective of this study was to evaluate the effect of enzyme supplementation of corn (TYP) and wheat (ALT) based diets with dietary protease and carbohydrases (Cibenza DP100 and Cibenza CSM, respectively, NZ) on growth performance, carcass weight, and profit. All diets contained 30% corn-derived DDGS and were formulated to contain equal content of ME and standardized ileal digestible amino acids. Barrows (TR-4 × C-22, PIC, Hendersonville, TN; 144 in total) were housed 2/pen and had free access to feed and water at all times. After a 7-d acclimation period, pigs were weighed (84.8 ± 2.9 kg BW) and randomly assigned to a 2 × 2 factorial arrangement of treatments in a complete randomized block design with n = 18 per treatment. Pigs were fed in 2 phases for 21 and 20 d each, and then transported to a commercial harvesting facility. Data were analyzed using the mixed procedure (SAS Institute, Cary, NC). Diet type or NZ inclusion had no effect ($P = 0.15$ to 0.71) on dressing percent, lean content percent, jowl iodine value, or last rib loin and backfat depths. No diet*NZ interactions were found ($P = 0.11$ to 0.92) for growth performance or carcass traits. A diet*NZ interaction ($P = 0.006$) was found for fecal DM content. Thus, NZ increased fecal DM in TYP but had not effect on ALT diets. Inclusion of NZ increased final body weight (+1.7%, $P = 0.001$), ADG (+6.3%, $P < 0.001$), ADFI (+1.9%, $P = 0.05$), GF (+2.7%, $P = 0.03$), hot carcass weight (HCW, +1.8%, $P = 0.009$), HCW-ADG (+5.6%, $P = 0.002$), HCW-GF (+4.3%, $P = 0.006$), carcass income (+5.6%, $P = 0.002$), and income-over-feed (+19%, $P = 0.03$) compared with CON. In conclusion, dietary enzyme supplementation can be a viable solution to increase growth performance, carcass weight, and profitability of swine enterprises.

Key Words: enzyme, growth performance, swine

119 Causes of in-transit losses of pigs. K. Zurbrigg*[1] and A. van Dreumel[2], [1]*Ontario Ministry of Agriculture, Food and Rural Affairs, Elora, ON, Canada,* [2]*Animal Health Laboratory, University of Guelph, Guelph, ON, Canada.*

The cause of death for hogs that die in transit to a packing plant is an economic and welfare concern to producers, transporters, abattoirs and consumers. The increase in shipping mortalities observed during the summer months in Canada and the United States is commonly attributed to heat exhaustion or heat stress. However few studies have identified the specific cause of death for these hogs. The objective of this study is to determine if there are underlying physiologic risk factors that predispose a market hog to death during transport to slaughter. Post-mortems on 62 hogs that died in transit were completed at the abattoir or at the Animal Health Laboratory, University of Guelph. Fifty hearts were collected from hogs that did not die in transit. Each heart was examined blindly by one veterinary pathologist (TVD) grossly and histologically. Heart weights for hogs that died in transit were compared with the controls. Heart failure was the cause of death for 68% (42/62) of the hogs that died during transport. Heart lesions were chronic in nature. In 21% of the hogs, the only findings on gross post-mortem examination were pulmonary congestion and edema of the lungs. In 11% of the hogs, lesions unrelated to heart failure were identified (e.g., respiratory or gastrointestinal disease, fractures). No lesions were found on the gross examination of the control hearts. Average total heart weight for hearts with lesions (451.50 g ± 63.33) was greater than hearts without lesions (380.75 g ± 40.27) ($P = 0.0001$). Final analysis of histologic results is pending. Compared with most other mammals, a pig's heart is small in relation to its body size (Friendship and Henry. 1998. Cardiovascular system, hematology and clinical chemistry. Pages 3–5 in Diseases of Swine. 7th ed.). As a result, hearts with compromised function have little reserve capacity to respond to challenges. The compensatory hypertrophy of defective hearts resulted in greater heart weights. In this study the majority of hogs that died in transit had a pre-existing cardiac abnormality resulting in hogs that were unable to survive standard transport practices.

Key Words: transportation, swine, death

120 Effect of pig insemination technique and semen preparation on profitability. D. Gonzalez-Pena*, N. V. L. Serão, J. Pettigrew, R. Knox, and S. L. Rodriguez-Zas, *University of Illinois at Urbana-Champaign, Urbana.*

Intrauterine (IUI) and deep intrauterine (DUI) artificial insemination (AI) require lower boar semen counts compared with conventional (CON) AI. Fresh (FRE) or frozen (FRO) semen preparation and AI technique affect boar utilization efficiency and selection pressure, genetic dissemination, and biosecurity. The combined effect of 3 AI techniques and 2 semen preparations on the net profit of a pig crossbreeding system was evaluated. A 3-tier system was simulated starting with the cross of nucleus breeds A and B (500 sows/breed) that generated 200,000 AB sows at the multiplier level. The AB sows were mated to breed C terminal boars (from 500 nucleus sows) at the commercial level resulting in 4,500,000 weaned pigs/year. The combinations of preparation and techniques were represented by distinct boar:sow ratios in the AB x C cross. To understand the effects of technique and preparation, the ZPAN simulation assumed 2.1 semen doses/estrus, 2.25 farrowings/year, 50 collection/boar/year, 3 sperm counts (CON = 3×10^9, IUI = 1×10^9 and DUI = 15×10^7). Sow stayability ranged from 1 year (nucleus) to 3 years (commercial) and involuntary culling was 32%. A range of farrowing rates (75–85%) and number of piglets alive/litter (9–12) was tested. A significant ($P < 0.0001$) improvement in the average net profit was observed in FRO (and FRE) from CON to IUI by 12.6% (4.0%) and to DUI by 17.8% (6%). There was a significant ($P < 0.0001$) reduction on the average cost in FRO (and FRE) from CON to IUI by 6.6% (3.3%) and to DUI by 9.4% (4.5%). Lower total costs in IUI and DUI were driven by lower fixed costs (60%) across preparations. The variable cost of boar maintenance decreased from CON to IUI and DUI by 66% and 95%, respectively across preparations. The variable cost of sow increased for FRE (and FRO) from CON to IUI by 8.56% (4%) and to DUI by 15% (7%). Synergistic effects of AI technique and semen preparation on the net profit of pig crossbreeding systems (−0.94 $/sow for CON, 0.24 $/sow for IUI, 0.70 $/sow for DUI, 0.95 $/sow for FRE, and −0.95 $/sow for FRO) were demonstrated.

Key Words: intrauterine insemination, deep uterine insemination, fresh semen

121 Use of exogenous hormones on estrus synchronization and the reproductive life of female pigs. L. J. Parazzi*[1], T. A. Del Santo[1], A. Arruda[2], S. M. M. K. Martins[1], A. F. C. Andrade[1], and A. S. Moretti[1], *[1]University of São Paulo (FMVZ-VNP), Pirassununga, São Paulo, Brasil, [2]University of Guelph, Guelph, Ontario, Canada.*

Estrus induction and synchronization in gilts using exogenous hormones can bring advantages to the productive life of the female. The objective of this study was to evaluate the use of exogenous gonadotropins before puberty and its effects on the reproductive life of the female until the seventh parity. Ninety-six hybrid gilts from a commercial herd were enrolled in this study. The mean age, weight and backfat thickness were 152.42 ± 4.46 d, 99.83 ± 8.12 kg and 11.90 ± 3.06 mm, respectively. The experimental design was a randomized trial with 2 treatments: use of an intramuscular injection of 600 IU of eCG (Novormon, Sintex S.A., Argentina) followed by an intramuscular injection of 2.5 mg of porcine LH (Lutropin Vetrepharm Canada Inc., Canada) 72 h later (Treatment H) and male stimuli only (Treatment M). Diet composition met NRC (1998) recommendations and was based on corn and soybean meal. Estrus was recorded for both groups until first artificial insemination. Data were collected through a computer program in place in the herd (Pig CHAMP software). A higher percentage of synchronization of estrus was observed on group H compared with group M ($P > 0.05$). There was no effect of treatment on litter size, number of piglets born alive, number of stillbirths or number of mummified fetuses ($P > 0.05$). There was a tendency effect for treatment H to farrowing interval ($P = 0.069$), with a lower value observed for this group. In conclusion, the use of exogenous hormones in gilts does not affect the productivity of the female regarding litter size; however it might bring advantages regarding number of non-productive days and facilitate female introduction in the sow herd.

Key Words: exogenous gonadotropin, longevity, productivity

122 Gestational heat stress alters postnatal thermoregulation. J. S. Johnson*[1], M. V. Sanz-Fernandez[1], S. K. Stoakes[1], M. Abuajamieh[1], J. W. Ross[1], M. C. Lucy[2], T. J. Safranski[2], R. P. Rhoads[3], and L. H. Baumgard[1], *[1]Department of Animal Science, Iowa State University, Ames, [2]Division of Animal Sciences, University of Missouri, Columbia, [3]Department of Animal and Poultry Sciences, Virginia Polytechnic Institute and State University, Blacksburg.*

Gestational heat stress (GHS) is a teratogen that negatively affects development in a variety of species, but how it alters postnatal thermoregulation is not well-understood. Study objectives were to characterize postnatal thermoregulation indices in pigs from differing in-utero thermal environments. First-parity gilts (n = 13) were exposed to 1 of 4 ambient temperature treatments [HS (cyclic 28 to 34°C) or TN (18 to 22°C)], applied for the entire gestation (HSHS; TNTN), the first half (HSTN), or second half (TNHS) of gestation. Of the resultant offspring, 24 barrows (30 ± 3 kg BW; n = 6 HSHS, n = 6 TNTN, n = 6 TNHS, n = 6 HSTN) were housed at the ISU Zumwalt Climactic Chambers in TN (21.7 ± 0.7°C) conditions and then exposed to 2 separate but identical HS periods (HS1 = 6 d; HS2 = 6 d; cycling 28 to 36°C). Core body temperature (T_{core}) was assessed hourly using Thermochron iButtons (Dallas Semiconductor), surgically implanted in the intraperitoneal cavity. Respiration rate (RR) was measured daily (0800, 1300, 1600, 2000 h). In TN conditions, all GHS pigs had elevated ($P < 0.01$; 0.35°C) T_{core} compared with TNTN pigs. Regardless of gestational treatment, both RR and T_{core} increased from TN to HS periods ($P < 0.01$; 61 bpm and 0.70°C, respectively). During HS1, HSHS and HSTN pigs had increased T_{core} ($P < 0.01$; 0.30 and 0.39°C, respectively) compared with TNTN pigs, and tended to have increased T_{core} compared with TNTN during HS2 ($P < 0.08$; 0.25°C). No gestational area under the T_{core} response curve differences were detected in either HS period ($P > 0.80$). No gestational differences were detected for either ADG or feed intake. In summary, pigs originating from in-utero heat stress (especially the first half of gestation) had increased T_{core} compared with controls, and this magnitude of differential was maintained in both TN and HS conditions. This suggests that in-utero HS increases (0.33°C) the thermoregulatory set-point, but how this influences whole body bioenergetics remains unknown.

Key Words: gestational heat stress, pig, thermal imprinting

123 Comparison of cathelicidin expression, cytokine and gut microbes between Jinhua and Landrace pigs experimentally challenged with *Escherichia coli* K88. Y. Gao*[1,2], X. Huang[1,2], H. Yi[1,2], Y. Rong[1,2], and Y. Wang[1,2], *[1]Institute of Feed Science/College of Animal Science, Zhejiang University, [2]Key laboratory of Animal Nutrition and Feed Science, Ministry of Agriculture, Hangzhou, China.*

This study was conducted to determine the possible role(s) of cathelicidins in the porcine immune system by comparing the cathelicidin expression, cytokine, gut microbes between Chinese Jinhua pigs and European landrace experimentally challenged with *Escherichia coli* K88. The *E. coli* challenge resulted in decreased growth rate and increased diarrhea rate in both breeds. Average daily gain (ADG) of Jinhua and Landrace pigs decreased by 25% and 28.6%, respectively. The ADG of Jinhua

pigs was significantly higher ($P < 0.05$) compared with Landrace pigs post-challenge. However challenged Jinhua pigs showed relatively lower rates of diarrhea compared with those in Landrace. Pigs challenged with *E. coli* showed different levels of expression for PR-39 and protegrin-1 between the 2 breeds examined. Jinhua pigs had a higher level of PR-39 in the bone marrow and spleen post-challenge compared with Landrace ($P < 0.05$). Additionally, pro-inflammatory cytokines were induced, while anti-inflammatory cytokines (IL-4 and IL-10) were attenuated in all challenged pigs. Jinhua pigs had significantly higher IFN-γ, IL-6 and IL-10 levels, but lower TNF-α and IL-4 levels compared with Landrace post-challenge. Moreover, *E. coli* challenge significantly increased the colonic quantity of *E. coli* in both breeds, and challenged Landrace had higher quantity of colonic *E. coli* compared with Jinhua pigs ($P < 0.05$). Our findings revealed that porcine cathelicidin expression could be upregulated by *E. coli* challenge, indicating that endogenous cathelicidin expression may relate to disease resistance in pigs. Jinhua pigs exhibited higher level of cathelicidins and were associated with higher growth rate, lower diarrhea rate and colonic *E. coli* number post-challenge compared with Landrace, which were probably due to Jinhua pigs had higher disease resistance and were less susceptible to *E. coli* challenge. These results, in concert with the antibacterial properties of cathelicidins, suggest that they may play a crucial role in porcine immune responses to bacterial infection.

Key Words: cathelicidin, *Escherichia coli* K88, Jinhua pigs

124 Whole-genome association analysis for feed efficiency traits in Duroc pigs. S. Jiao*[1], J. Cassady[1], C. Maltecca[1], K. Gray[2], and J. Holl[2], *[1]North Carolina State University, Raleigh, [2]Smithfield Premium Genetics, Roanoke Rapids, NC.*

Improvement of feed utilization is expected to significantly increase efficiency of production given that feed costs represent the largest variable cost in pork production. The objective of this study was to identify genomic regions associated with variation in feed efficiency and its component traits in a Duroc terminal sire population. Traits analyzed were ADFI (Average daily feed intake), ADG (Average daily gain), FCR (Feed conversion ratio) and RFI (Residual feed intake). Individual feed intake and serial pig body weights were recorded using the FIRE system on 1047 individuals. Feed intake data were edited by linear mixed model to adjust errors of individual visits to the feeders. Subsequent measures were estimated from both linear and robust regression. Genotyping was performed using Illumina PorcineSNP60K Bead Chip. After quality control 40,008 SNPs remained for analysis. Missing SNP genotypes were imputed for all available boars (n = 1022) with pedigree information. Single trait association analyses were performed using a Bayes-B model. The proportion of phenotypic variance explained by markers was 0.268 for ADFI, 0.175 for ADG, 0.187 for FCR and 0.076 for RFI. Significant regions were identified by using 3 different significance tests; posterior windows variance, Bayes factor and bootstrapping. Significance was declared for regions where tests significance overlapped. Regions associated with ADFI were mapped to chromosome 1 and 10. Similarly, regions associated with ADG mapped to chromosome 1, 4, 11, and 14. A significant region was found for FCR on chromosome 4 while no QTL were identified for RFI. In conclusion, we have identified several genomic regions associated with traits affecting nutrient utilization that could be considered for future genomic prediction to improve feed utilization.

Key Words: genomics, Duroc, feed efficiency

Teaching/Undergraduate and Graduate Education Symposium: Graduate Education in a Shifting Research Landscape

125 Mentoring graduate students for success in a shifting research landscape. R. Randel*, *Texas A&M AgriLife Research, Overton.*

The purpose of the educational process for graduate students is to develop scientists and educators who will be successful in their area of expertise. They must be capable of creating new knowledge and be able to impart this knowledge to appropriate end users. The research landscape is always shifting as economic change occurs and the technology of today will be replaced with new technology tomorrow. The scientific method will remain constant through technological and economic change. Scientists and educators grounded in the fundamental sciences as well as application to agriculture will remain in demand and will be successful in this shifting research landscape. Students require a blending of fundamental science with application to agriculture. Each student is a unique individual and will need a program designed to eliminate weaknesses and to amplify strengths. For animal agriculture each student must have a background in statistics and biochemistry. These 2 fundamental sciences should be included early in the educational process. It is never too early to involve a student in their own research. Early ownership of research data and with use of the scientific process is crucial for future success. Each graduate student should be involved in collaborative and interdisciplinary research. To be successful in a shifting research landscape requires having the ability to work and collaborate across disciplinary lines. With a well-designed program emphasizing fundamental science and use of the scientific method supported by understanding the application of science to agriculture, graduate students will have the tools needed to become successful in the shifting research landscape.

Key Words: mentoring, graduate student

126 Adjusting to the other side of the table: Experiences as a newer mentor. B. J. Bradford* and L. K. Mamedova, *Kansas State University, Manhattan.*

Effective graduate student mentoring is a crucial but under-recognized component of launching a research program. Advice for new faculty members is typically focused on research topics, teaching methodology, extension programming, and grant writing, and with the many tasks facing a new faculty member, mentoring can too easily be forgotten. However, effective mentoring is critical to student success, program visibility, and new student recruitment. Mentoring graduate students often requires a delicate balance between conflicting goals: providing guidance while fostering independence, offering broad experiences without loss of focus, and identifying weaknesses while building confidence. In our experience, striking the right balance is aided by some key practices, which we have learned through mistakes as much as success. First, the fit of a prospective student in the group must be considered, rather than selecting students based on academic merit alone; this can be a particular challenge for new faculty members who may not have lots of applicants. Second, expectations should be as clear as possible. Often students transitioning from BS to MS programs, or even from MS to PhD programs, fail to fully grasp the differences. Third, mentors must have adequate availability to provide constructive and timely feedback. This can be accomplished in a variety of ways, and we rely on both technology and team mentoring to help address this challenge. Finally, graduate training should develop "soft skills" in addition to technical knowledge. Research projects can offer excellent opportunities to develop abilities in personnel management, task/time management, communication skills, conflict resolution, and professional networking that will serve students well regardless of their career path. Key to all of these is a mindset that, while the graduate student is responsible for contributing to the research program, the mentor is also responsible for helping the student to grow personally and professionally. Despite its many challenges, mentoring is one of the most rewarding aspects of a professorial career if it is approached as a worthwhile endeavor.

Key Words: graduate education, mentorship, training

127 Making the transition from academia to industry researcher: Perspectives on similar and unique skill sets. A. E. Wertz-Lutz*, *ADM Alliance Nutrition, Quincy, IL.*

The objective of this presentation is to discuss skill sets that are similar and those that are unique to conducting research in an academic setting compared with an industry setting. Animal agriculture is dynamic, and with recent changes in the landscape of animal agriculture research, opportunities have arisen for suited individuals to transition from research in an academic to an industry environment. Making the transition from academic to industry research requires careful consideration. Evaluation of career goals, innate skills, and intended purpose are essential to making an informed decision and having a smooth transition. Additional factors such as opportunities for collaboration, expectation for research outcomes, and potential for research impact should all be considered when making a move from academic to industry research. The fundamental skills of written communication, sound experimental design, proper use of controls, ethical interpretation of the resulting data, and integrity are common to research in both an academic and industry setting. Beyond the commonality of these fundamentals, research within an industry setting has the added facet of interfacing with the business front. Issues such as product commercialization, compliance and regulatory, ethical use of science in marketing, and return on invested capital begin to emerge when taking a demonstrated biological response to marketable product. Strong interpersonal communication skills are needed to bridge the gap between business and research within an industry setting. Factors such as securing research funding, travel expectations, work pace, research focus, confidentiality, and student mentoring differ between research in the academic compared with industry setting. This presentation is intended to compare and contrast the role of academic and industry researcher, and to provide, based on personal experience, some guidance to current graduate students weighing the option of an academic or industry career with an advanced degree in animal science.

Key Words: Academic research, industry research, skill sets

128 An undergraduate research experience: Team dynamics and mentoring. B. J. Bequette*, *University of Maryland, College Park.*

The undergraduate research experience often exposes students to their first opportunity to see the scientific process up close. This first-time exposure can have a lasting impact on student's career options, and so the process should be designed carefully to instill a sense of research ownership and accomplishment by students, and the value of their

research to current and future societal issues. The Gemstone Program at the University of Maryland is a multidisciplinary 4-year research program for undergraduate honors students of all majors. Under guidance of faculty mentors and Gemstone staff, teams of students (6–15) design, direct and conduct research exploring the interdependence of science and technology with society. As freshman, students learn to explore current topics in science, technology and society, and the essentiality of team building to research success. During the year, students naturally migrate around a topic of mutual interest. In sophomore year, teams meet with their selected mentor when the process of teaching the scientific process begins in earnest for the mentor. As a mentor, patience is essential to guiding the team. Guiding the team toward a testable hypothesis and well-defined and achievable objectives must be step by step. To ensure team ownership, mentors should resist leading the team too far from their initial interests. As sophomores, students have yet to take courses that fill their heads with the basic knowledge required to write their proposal and initiate experimentation. Thus, the mentor should make use of the limited, yet valuable, time in team meetings to lecture, teach and discuss basic concepts and current literature. Take every opportunity to encourage and engage all team members; leave no student behind. Team and experimental challenges will arise, as they often do in research, and so mentors must use these instances as teaching moments of the essentiality of teamwork and the realities of conducting research. In the fourth year, teams present their research in the form of a thesis to experts selected by the students, and the students complete the program with a citation and a sense of accomplishment.

Key Words: undergraduate, research, mentoring

129 Effective personal development planning for scientists and graduate students. B. Rittgers*, *Elanco Animal Health, Greenfield, IN.*

Effective Development Planning is paramount in all aspects of business and academia as the workforce evolves and people are looking to grow professionally and personally. The saying "Help them Grow or Watch them Go" could not be more true. Effective Development Planning does not happen for a variety of reasons. These may include individuals not knowing what aspects of their scientific or transferable skill set to develop. (A lack of coaching and feedback); skill development and career planning are looked at separately or not at all. Personal development planning may be nothing more than a "check the box" exercise. No accountability on the part of students/scientists or supervision to prioritize development planning. Emphasis is put on class room training versus relationships and experiences to drive development; in other words, the 70–20–10 Principle of Effective Development is not followed. The 70–20–10 Principle was developed by the Center for Creative Leadership. The concept is based on findings that personal development occurs from 70% Experience: On the job experiences of in-place assignments that allow individuals to utilize and grow the aspects of performance or skills needed for success. These can happen on the job (55%) or through off-the-job experiences (15%) in the community, industry affiliations or faith based organizations; 20% Relationships: Relationships that provide individual feedback, coaching, personal insights and mentoring contribute to 20% of development; 10% Training: Although most prevalent when planning for development, training only contributes to 10% of actual development. To be sure, it is important but true development comes most frequently from experiences and relationships. Development Planning should be done around the congruence of personal interest and growth needs and the business or academic needs of the larger organization. By assessing and understanding the needs of both, individuals can develop a good balance of development that will help them develop their careers as well as further the goals of their organizations.

Key Words: development, coaching, training

Breeding and Genetics: Applications and Methods in Animal Breeding—Dairy I

130 The correlation analysis between Holstein body conformation traits and milk production traits in the Shanghai region. K. Zhu[1,2], G. L. Liu*[1,2], L. M. Huang[1], C. B. Zhang[2], and F. S. Fu[2], *[1]State Key Laboratory of Dairy Biotechnology, Shanghai Bright Holstan Co. Ltd., Shanghai, China, [2]Shanghai Dairy Breeding Center Co. Ltd., Shanghai, China.*

The objective of this study was to analyze the correlation between Holstein body conformation traits and milk production traits in the Shanghai region. In total, 871 Holstein cows were randomly chosen from 28 dairy farms in Shanghai at second stage of lactation as the object of our study. Five milk production traits, including 305-d milk yield, butter fat percentage, milk protein percentage, peak lactation days and peak milk production were obtained from dairy Herd Improvement (DHI) project of Shanghai Dairy Breeding Center. The quantitative values of 7 body conformation traits were recorded by 9-point methods and the model of multiple linear regressions was used here to analyze the correlation between the body conformation traits (as independent variable) and the milk production traits (as dependent variable). The results showed that the total score of body conformation were extremely significantly positively correlated with the 305-d milk yield, butterfat percentage, Peak milk production ($P < 0.01$), significantly positively correlated with the peak lactation days ($P < 0.05$), and weak correlation with the milk protein percentage (not significant). The body hindquarters capacity was significantly positively correlated with the milk yield. The cow hoofs character was extremely significantly positively correlated with the peak milk production, the butterfat percentage, and the milk protein percentage; and was significantly positively correlated with milk yield. The hip character was significantly positively correlated with the butterfat percentage. The lactation system and udder traits were significantly positively correlated with the peak lactation days. We concluded that the body hindquarters capacity, the hoofs character, the hip character, the lactation system and udder traits were the most important factors that influenced the milk production traits of Holstein cows. The identification and scoring of body conformation traits might provide significant guiding on screening high-yield, excellent producing Holstein cows as well as selection and assortative mating.

Key Words: Holstein cow, body conformation trait, milk production trait

131 Heterosis and effect of breed proportion for milk production traits in crosses between Danish Holstein, Danish Red, and Danish Jersey. E. Norberg*[1], K. Byskov[2], and M. Kargo[1,2], *[1]Centre for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark, [2]Knowledge Centre for Agriculture, Agro Food Park 15, Aarhus N, Denmark.*

During the last decade the use of systematic crossbreeding in dairy cattle herds has been increasing in Denmark. The aim of this study was to estimate the effect of breed proportion and heterosis on milk production traits. The study was based on records on milk yield (MY), protein yield (PY) and fat yield (FY) from 52,165 first lactation cows born in 2004 or later from 104 herds using systematic crossbreeding. More than 50% of the cows were crosses between Danish Holstein (DH), Danish Red (DR) and /or Danish Jersey (DJ) and the remaining were pure DH, DR or DJ. Cows with less than 45 DIM and/or a calving age below 18 or above 40 mo were omitted. The statistical model included a fixed effect of herd-year and calving month, a regression on calving age, a regression on the proportion of DH, DR and DJ genes, a regression on the degree of heterozygosity between DH and DR, DH and DJ and DR and DJ, a random genetic effect of the cow and a residual. Data was analyzed using AI-REML in the DMU package. The effect of breed proportions was estimated relatively to a pure DH. For MY, a pure DR was estimated to give 259 kg less than a pure DH, while a pure DJ gave 1838 kg less than a pure DH. For PY there was no significant difference between DH and DR. Danish Jersey produced 40 kg less PY than DH and 35 kg less than DR. There was no significant effect of breed proportion for FY between the 3 breeds. Heterosis was significant in all combination of breeds for all 3 milk production traits. Heterosis for crosses between DH and DR was estimated to 177 kg, 5.8 kg and 8.4 kg for MY, PY and FY, respectively. Corresponding figures for crosses between DH and DJ was 320 kg, 13.4 kg and 17.5 kg, while crosses between DR and DJ gave heterosis estimates of 380 kg, 14.3 kg and 20.2 for MY, PY and FY, respectively. The results obtained in this study demonstrate the existence of heterosis on milk production traits in crosses between the 3 Danish dairy breeds.

Key Words: heterosis, breed effects, milk production

132 Genetic parameters for body condition score and body weight in Canadian Holsteins. A. Sewalem*[1], R. Cue[2], K. Wade[2], H. Delgado[2], D. Lefebvre[3], R. R. Lacroix[2], J. Dubuc[4], and E. Bouchard[4], *[1]Agriculture and Agri-Food Canada, Guelph, ON Canada, [2]Department of Animal Science, McGill University, Montreal, QC, Canada, [3]Department of Research and Development, Valacta, Centre d'Expertise en Production Laitière, Bellevue, Québec, Canada, [4]University of Montreal, St-Hyacinthe.*

The objective of this study was to characterize and determine the association between body weight (BW) and body condition score (BCS) in Canadian dairy Holsteins. Body weight was calculated from a heart girth circumference measurement and then converted to an estimated body weight (kg). A total of 75,443 BW and 22,899 BCS records were obtained from first lactation first records of Holstein cows that calved between 2002 to 2008. The average BW was 601.6 ± 34.1 kg. Body condition score was recorded by producers using a subjective scale of 1 to 5 (0.13, 16.51, 72.35, 10.79, and 0.23%, respectively). The data were analyzed using a multiple-trait animal model, including fixed effects for herd, calving year, calving season, age at first calving; linear and quadratic regressions of days in milk; and random effects for animal and residual. The data was analyzed using DMU software. Results yielded a heritability for BW and BCS of 0.19 ± 0.01 and 0.17 ± 0.16, respectively. The genetic and residual correlations between BW and BCS were low (0.195 ± 0.06 and 0.23 ± 0.01, respectively). A subsequent analysis of these data will be carried out using a random regression approach by including all available records.

Key Words: body weight, body condition score, genetic parameter

133 Lactation profile and genetic parameters of locomotion score and lameness in dairy cattle. A. Kougioumtzis[1], G. E. Valergakis[1], G. Oikonomou[1,2], G. Arsenos[1], and G. Banos*[1,3], *[1]Faculty of Veterinary Medicine, Aristotle University of Thessaloniki, Thessaloniki, Greece, [2]College of Veterinary Medicine, Cornell University, Ithaca, NY, [3]SRUC/Roslin Institute, Edinburgh, UK.*

Lameness greatly concerns the dairy cattle industry because of its high prevalence and associated costs. This study aims to investigate the profile and genetic parameters of lameness before and after calving and throughout lactation in primiparous Holstein cows. The study was carried out in a large commercial in Greece and included 237 cows that calved between 2008 and 2010. Cows were locomotion scored weekly on a 5-point scale, starting 6 weeks before calving and throughout lactation. Cows with a score greater than or equal to 2 were considered lame. These records were matched with weekly body condition score, liveweight and milk yield. Total number of repeated records amounted to 9,643. Traits were analyzed with bivariate random regression models that included the effects of year-season of calving, country of origin, calendar month, barn, calving age, a fixed regression on week from calving, and random regressions on week from calving associated with the additive genetic profile and the permanent environment of cow. Fixed curves for the 2 traits illustrated an increase in their relative levels up to mid-lactation. Weekly estimates of genetic variance were highest before calving and during the 4 weeks following calving and then decreased gradually; all estimates were statistically greater than zero ($P < 0.05$) demonstrating the presence of genetic factors that control the animal's capacity for uninhibited movement and resistance to lameness. Consistent with the genetic variance, heritability estimates were highest before calving and decreased with lactation stage; average estimates were 0.39 ± 0.06 and 0.26 ± 0.06 for locomotion score and lameness, respectively. Statistically significant ($P < 0.05$) genetic correlations were found of weekly locomotion score and lameness with body condition score ranging from -0.31 to -0.65 and from -0.44 to -0.76, respectively. It is concluded that locomotion score and lameness are amenable to improvement with genetic selection and body condition score can be used as an auxiliary trait for this purpose.

Key Words: genetics, locomotion, lameness

134 Multi-trait analysis of bovine leukosis incidence, somatic cell score, and milk yield in US Holstein cattle. E. A. Abdalla*[1], G. J. M. Rosa[1], K. A. Weigel[2], and T. Byrem[3], *[1]Department of Animal Sciences, University of Wisconsin-Madison, Madison, [2]Department of Dairy Science, University of Wisconsin-Madison, Madison, [3]Antel BioSystems Inc., Lansing, MI.*

Bovine leukosis (BL) can be defined as a retroviral disease caused by the bovine leukosis virus (BLV) which affects only cattle. Positive BL dairy cows produce less milk and have more days open compared with those that are negative. In addition, the virus also affects the immune system and causes a weak response to vaccines in infected animals. The objectives of this study were to estimate the heritability for BL incidence and its genetic correlations with BL, milk yield (MY) and somatic cell score (SCS). Results of a commercial ELISA assay used to detect BLV antibodies in milk samples were obtained from Antel BioSystems Inc. (Lansing, MI). The data included continuous milk ELISA scores and binary milk ELISA diagnosis as well as MY and SCS for 11,554 cows from 112 dairy herds across 16 US states. Continuous and binary ELISA results were analyzed jointly with MY and SCS using linear and threshold animal models, respectively. Estimates of heritability obtained with the 2 approaches were very similar and around 8%, indicating that there is a non-negligible genetic component underlying BL disease incidence. Estimated genetic correlations of BL incidence with MY were 0.14 and 0.17 using the threshold and linear model, respectively, whereas with SCS such correlations were 0.17 and 0.20. In summary, results of this study indicated that selection could be used to improve resistance to BL in Holstein cattle. In addition, selection for increased MY may also increase BLV susceptibility, such that higher infection rates may be expected in high-performing dairy herds. Nevertheless, selection for reduced SCS may increase the resistance to BLV. Hence, simultaneous selection for improved MY and BLV resistance using an appropriate index may lead to improvement of both traits.

Key Words: bovine leukosis, multi-trait analysis, heritability

135 Effect of genetic selection for Johne's disease resistance on the prevalence in dairy cattle using an epidemiological model. K. J. E. van Hulzen[1], A. P. Koets[1], M. Nielen[1], H. C. M. Heuven*[1,2], J. A. M. van Arendonk[2], and D. Klinkenberg[1], *[1]Faculty of Veterinary Medicine, Utrecht University, Utrecht, the Netherlands, [2]Animal Breeding and Genomics Centre, Wageningen University, Wageningen, the Netherlands.*

Johne's disease in dairy cattle is an important issue in the dairy industry. Genetic variation exists therefore genetic selection could be an additional approach to control this disease. The objective was to study the effect of different selection strategies on the prevalence of john's disease taking epidemiological aspects into account, using deterministic simulation. Three strategies were compared: (1) dam-selection, i.e., selection of cows only based on their ELISA test (current test and cull surveillance program); (2) sire-selection, i.e., using only the top 80% of the sires based on their EBV for resistance; (3) combining both strategies. Three parameters in the model were affected by genetic selection: length of latent period, susceptibility and length of susceptible period. The effect of selection on the parameter under selection was 'translated', using an epidemiological model, to an effect on prevalence to assess the effect of a selection strategy. For dam-selection, responses to selection for Johne's disease resistance were small, irrespective of the parameter that was varied in the model. For sire-selection, responses to selection were much larger for all 3 parameters that were varied. The largest effect was observed for length of susceptibility period, followed by susceptibility and then length of the latent period. Sensitivity analysis of the parameters showed that this ranking did not depend on the disease prevalence. The conclusion of this simulation study was that genetic selection for Johne's disease resistance on the sire level could contribute to the control of the disease.

Key Words: Johne's disease, genetic-epidemiological model, selection response

136 Genetic analysis of processed in-line mastitis indicator data. L. P. Sørensen* and P. Løvendahl, *Aarhus University, Department of Molecular Biology and Genetics, Center for Quantitative Genetics and Genomics, Tjele, Denmark.*

The aim of this study was to estimate heritability of elevated mastitis risk (EMR), a trait derived from in-line measurements of cell counts expressing risk of mastitis on a continuous scale, and its genetic correlation with in-line somatic cell counts. Log-transformed somatic cell counts (SCC; n = 855,181) based on in-line measurements (OCC, DeLaval, Sweden) in automatic milking systems were collected from 2007 to2013 in 7 herds from a total of 1986 first and second parity cows (5 to 305 d in milk). Only data from the lactation with most measurements was used from each cow. A bio-model based on exponential smoothing of the SCC values followed by factor analysis for estimation of the latent variable EMR was used. Finally, EMR was expressed as a continuum on the interval [0;1] using sigmoid transformation. Thus, an EMR value close to zero indicates low risk of mastitis and a value close to one indicates high risk of mastitis. The EMR values were summarized for each cow using the log-transformed median EMR. A second trait

was defined as the median of the log-transformed SCC values from 5 to 305 d in milk. A bivariate animal model was used for estimation of co-variance components for the 2 traits. The fixed part of the model included herd and parity. Estimates of heritability were 0.08 (SE = 0.04) and 0.14 (SE = 0.05) for EMR and SCC, respectively. The genetic correlation between the 2 traits was 0.97 (SE = 0.08). The high genetic correlation indicates that the 2 traits are influenced by common genes, as expected because EMR values are based on SCC measurements. The heritability of SCC is reduced when SCC measurements are processed into EMR values but with similar standard errors. The EMR values are useful in a management context for early mastitis detection and health surveillance; however the present results suggest that SCC values are preferable to EMR values for estimation of breeding values.

Key Words: mastitis, genetic parameter, dairy cow

137 Effects of mesenteric infusion of 0, 61, and 120 mmol/h of volatile fatty acids on hepatic metabolism in fasted pigs. U. Krogh*, A. C. Storm, and P. K. Theil, *Aarhus University, Department of Animal Science, Foulum, Tjele, Denmark.*

The aim of the study was to quantify hepatic metabolism of precursors potentially used as fuels in pigs in a post absorptive phase. Four fasted (18 h) pigs (BW 58 kg ± 2; Mean ± SD) were fitted with indwelling catheters in the portal vein, hepatic vein, mesenteric vein and -artery. VFA was infused into the mesenteric vein of anesthetized pigs to mimic effects of increased consumption of dietary fibers. Infusion 0 (INF0: 0 mmol/h VFA, 0.9% saline) was infused for 30 min followed by 45 min of infusion 61 (INF61: 61 mmol/h VFA) and 45 min of infusion 120 (INF120: 120 mmol/h VFA), with the consequence of a potential confounding effect of time. INF61 and INF120 contained 70, 20 and 5% of acetate, propionate and butyrate, respectively. Para-aminohippuric acid was infused to quantify blood flow and net hepatic flux of nutrients (NHF). Eight sets of blood samples were simultaneously drawn from the artery, portal-, and hepatic veins at 15 min intervals. Statistical analysis included fixed effects of infusion, sampling times (ST), random effect of pig, and interaction between infusion and ST, with ST included as repeated measure. Results of incremental change in NHF (ΔNHF) (i.e., INF61- INF0 and INF120-INF0) are shown in Table 1. Glucose ΔNHF tended to be higher at INF120 vs. INF61 ($P = 0.07$), while no effect was observed for lactate. Urea NHF increased ($P = 0.04$) from INF0 to INF61 and from INF0 to INF120, and ΔNHF of urea at INF120 vs. INF61 did not differ ($P = 0.74$). Oxygen ΔNHF tended to be higher at INF120 vs. INF61 ($P = 0.07$). The data indicate that VFA infusion levels influence hepatic glucose metabolism and oxidation pattern in the pig.

Table 1. Incremental change in net hepatic flux (ΔNHF) of glucose, lactate, urea, oxygen and carbon dioxide (mmol/h) in fasted mesenteric-infused pigs at 61 (INF61) and 120 (INF120) mmol/h of volatile fatty acids

Metabolite	INF611	INF1201	SEM	*P*-value
Glucose	5.1	28.2	16.5	0.07
Lactate	−3.8	−8.2	5.5	0.57
Urea	15.7	17.8	4.4	0.74
Oxygen	38.5	−66.9	67.7	0.07
Carbon dioxide	−97.9	−55.6	59.4	0.42

[1]INF61 = NHF61 − NHF0; INF120 = NHF120 – NHF0.

Key Words: gluconeogenesis, liver, VFA

138 Leucine pulse stimulates protein synthesis and suppresses protein degradation pathways in muscle of neonatal pigs fed continuously. C. Boutry*[1], S. El-Kadi[2], A. Suryawan[1], S. Wheatley[1], R. Orellana[1], H. Nguyen[1], and T. Davis[1], *[1]USDA/ARS Children's Nutrition Research Center, Houston, TX, [2]Virginia Tech, Blacksburg.*

Using neonatal pigs as a dual-model for animal agriculture and biomedicine, we have shown that muscle protein synthesis is enhanced with intermittent bolus feeding (BOL) to a greater extent than continuous feeding (CON). Leucine can act as a nutrient signal to stimulate muscle protein synthesis; limited evidence suggests leucine suppresses protein degradation. To determine if leucine can enhance protein anabolism during CON feeding, pigs (n = 20; 8-d-old) received formula by orogastric tube for 24h CON or by BOL (every 4 h for 15 min). For the CON+LEU group, leucine was pulsed parenterally (800 $\mu mol \cdot kg^{-1} \cdot h^{-1}$) every 4h. Plasma was collected at intervals during the last 4-h feeding cycle. At 25.25 h, muscle protein synthesis was measured by flooding dose methodology and intracellular signaling protein activation by Western blot. Data were analyzed by one-way ANOVA and mixed models for repeated-measures analysis. Plasma insulin increased 15min after a bolus meal and returned to baseline by 2h ($P < 0.001$); insulin was unchanged in CON and CON+LEU. In CON+LEU, plasma leucine was higher after the leucine pulse (+192% 1 h after pulse, $P < 0.0001$). LEU during CON feeding decreased plasma essential amino acid levels compared with CON ($P < 0.0001$). Muscle protein synthesis was greater in CON+LEU (+24%) and BOL (+56%) than CON ($P < 0.0001$). Muscle ribosomal protein S6 kinase 1 and 4E-binding protein 1 phosphorylation and eukaryotic initiation factor (eIF)4E•eIF4G formation were higher in CON+LEU and BOL than CON ($P < 0.05$). AMP-activated protein kinase-α, eIF2-α and eukaryotic elongation factor 2 phosphorylation was unaffected by treatment. Microtubule-associated protein 1 light chain 3 (LC3)-II to total LC3 ratio was lower in CON+LEU and BOL than CON ($P < 0.001$). There were no differences in Atrogin-1 and MURF-1 abundance and FoxO3 phosphorylation. These results suggest that administration of leucine pulses during continuous feeding increases skeletal muscle protein synthesis by stimulating translation initiation and suppressing autophagy-lysosome, but not the ubiquitin-proteasome, degradation pathways in neonatal pigs (NIH AR444474 and USDA/ARS 6250–51000–055).

Key Words: leucine pulse, protein synthesis, pig

139 Temporal proteomic analysis reveals defects in small intestinal development of porcine fetuses with intrauterine growth restriction during gestation. X. Wang[1], C. Liu[1], G. Lin[1], C. Feng[2], T. Wang[1], D. Li[1], G. Wu[1,3], and J. Wang*[1], *[1]State Key Laboratory of Animal Nutrition, China Agricultural University, Beijing, China, [2]Department of Obstetrics and Gynecology, China-Japan Friendship Hospital, Beijing, China, [3]Department of Animal Science, Texas A&M University, College Station.*

The fetus/neonate with intrauterine growth restriction (IUGR) has a high perinatal mortality and morbidity rate, as well as reduced efficiency for nutrients utilization, which predisposes the offspring to malfunction and jeopardize the postnatal development of small intestine. Our previous studies showed a significant alteration of small intestinal proteome in IUGR piglets at birth and continuous impairment during nursing periods. With the consideration of fetal programming for intestinal development during gestation and the dramatically increase in volume and nutrients concentration of amniotic fluid from d 60 of gestation in pigs, the analysis is extended to IUGR porcine fetuses from d 60 to d 110 of gestation (mid- to late-gestation in pig) with a purpose of disclosing the mechanisms responsible for developmental programming of fetal gut. In total, 59 differentially expressed small intestinal proteins that are related to gut growth, development and reprogramming were identified. Results reveal increased levels of proteins and enzymes associated with oxidative stress, apoptosis and protein degradation, as well as decreased levels of proteins required for maintenance of cell structure and motility, absorption and transport of nutrients, energy metabolism and protein synthesis in fetal small intestine during mid- and late-gestation. Moreover, IUGR interfere with expression of fetal small intestinal proteins associated with gene regulation and signal transduction starting from middle to late gestation. Collectively, these changes in the proteome profile indicate alterations in the expression of some of the proteins in

the small intestinal tissue of IUGR porcine fetuses, which may predispose the gut to metabolic defects during gestation as well as disruption of fetal gut developmental programming.

Key Words: intrauterine growth restriction, intestine, pig

140 Identification of porcine short-chain fatty acid receptors, GPR41 and GPR43, and their expression pattern in different development stages. G. Li*, H. Su, Z. Zhou, and W. Yao, *Laboratory of Gastrointestinal Microbiology, Nanjing Agricultural University, Nanjing, Jiangsu, China.*

In addition to supplying energy, short chain fatty acids also play a regulatory role in various physiological processes. Current researches revealed that SCFAs functioned as natural ligands for GPR41 and 43. To date, there is no systemic research about porcine GPR41 and 43. In this study, we tried to identify porcine GPR41 and 43 and determine their tissue distribution. Each 3 of Duroc × Landrace × Yorkshire pigs were slaughtered when 1, 25, 35, 70, 115 and 160 d old. Various tissues (liver, spleen, ileum, colon, heart, kidney, adipose tissue and skeletal muscle) were collected for RNA extraction. RT-PCR, Western blot and immunohistochemistry was used to detect GPR41 and 43 expressions in different tissues. The rapid amplification of cDNA ends was used to amplify the 3′ and 5′ end regions of porcine GPR41 and 43 mRNA. The qPCR was carried out to investigate expression pattern of GPR41 and 43 in different tissues and different development stages. A search of the pig genome database in GenBank revealed pig genome contains GPR41 and 43 genes, located on chromosome 6, highly similar to these genes in human and rodents. The RT-PCR, Western blot and immunohistochemistry analysis indicated that both GPR41 and 43 mRNA were detected in the tested tissues. A 2219bp and 1908bp nucleotide sequences representing the full-length cDNA sequence of procine GPR41 and GPR43 was obtained and encoded 335 and 329 amino acid sequence, respectively. The qPCR results showed that GPR43 was most highly expressed in spleen, while GPR41 was in ileum. The highest expression level of GPR41 in ileum and colon was on 70d and 1d, respectively. GPR43 expression in ileum and colon was on 25d and 70d, respectively. Furthermore, porcine GPR41 and 43 was expressed in adipose tissue with a significant time-dependent manner. Their expression level was upregulated after birth with a peak at 70d, and then decreased, suggesting that these 2 receptors may exert function mainly in early stage. However, further studies are essential to clarify their function in different development stages and different physiological processes.

Key Words: GPR41 and 43, short-chain fatty acids, pig

141 Effect of breed on the expression of sirtuins (Sirt1-7) and antioxidant capacity in porcine brain. Y. Ren*, T. Shan, L. Zhu, J. Huang, and Y. Wang, *Institute of Feed Science, Zhejiang University, Hangzhou, Zhejiang Province, China.*

Sirtuins, nicotinamide adenine dinucleotide (NAD)-dependent histone deacetylase (HDAC), play important roles in a variety of biological processes including metabolism, apoptosis, oxidative stress, cytokine responses and further influencing aging. In brain, aging increased the risk of psychiatric disorders and vascular diseases caused by age-related oxidative damage. Sirtuins are highly expressed in brain, indicating that they may play critical roles in cerebral development and nervous system. Sirt1 and Sirt3 have been proved to protect brain from oxidative stress. Furthermore, obesity may lead to oxidative stress and the plasma total antioxidative capacity (T-AOC) is different between obese and healthy people. Therefore, the aim of this study was to determine breed differences of porcine sirtuins expression and antioxidant capacity in brain between Jinhua pig (a fatty breed of China) and Landrace pig (a lean breed). The effect of age on sirtuins expression was also investigated. At the age of 180 d, the mRNA levels of Sirt1 ($P < 0.05$) as well as Sirt2 ($P < 0.01$) and Sirt4 ($P < 0.05$) were greater in Jinhua pig, but the mRNA levels of Sirt3, Sirt5, Sirt6 and Sirt7 were lower ($P < 0.01$) compared with Landrace pig. Likewise, the mRNA levels of sirtuins were significantly greater in Jinhua pig except for Sirt5 and Sirt7 at the same BW of 64 kg. Meanwhile, Jinhua pig had higher antioxidants activity than Landrace pig either at the same age ($P < 0.05$) or at the same BW ($P < 0.05$). In addition, mRNA levels of sirtuins were decreased with age in brain in both breeds from 30 d to 120 d. These results indicated that sirtuins expression was different between fatty and lean pigs in brain and may correlate to antioxidant capacity. Sirtuins expression could be also downregulated by age in porcine brain. These results may provide useful information for better understanding of the physiological roles of sirtuins and for further regulating metabolism and antioxidant stress in pig.

Key Words: antioxidant, brain, sirtuin

Undergraduate Student Competition: ADSA-SAD Undergraduate Competition: Dairy Foods

142 Goat milk: An alternative to cow milk. C. A. Becker*, N. D. Schock, and J. M. Bewley, *University of Kentucky, Lexington.*

Goat milk is still a niche market in the United States, but in many other countries, it is preferred over cow milk. Dairy goat products are not usually marketed in mainstream grocery stores. Rather, they are more often sold at specialty food stores and farmer's markets. As the consumer health craze continues to steadily increase, dairy goat milk and other dairy goat products are starting to see slow, steady growth trends. Goat milk is used to make many products including cheese, yogurt, and ice cream. Some dairy goat producers sell their products directly to retail stores or restaurants. Restaurants use goat cheese on menu items from pizza to dessert. Consuming goat milk can be very beneficial to a person's health. Goat's milk is a good source of protein, tryptophan, vitamin A, riboflavin and potassium, which all are associated with health benefits. The vitamin A in goat's milk is in pure form so that it can be readily absorbed by the body. Contrastingly, cow milk vitamin A is in the form of carotenoids that the body has to convert before it can be absorbed. Consumers who are unable to digest cow milk are often able to tolerate goat milk. Cow milk contains a protein, α_{S1}-casein, that is known to be a major allergen. However, goat milk contains much lower values of this protein, if any, allowing people with cow milk allergies to drink goa milk. The fat globules in goat milk are significantly smaller than the fat globules found in cow milk, making goat milk easier for intestinal enzymes to digest. Goat milk contains a high amount of short-chain and medium-chain triglycerides that aid in speeding up metabolism and help lower cholesterol levels, and make goat's milk easier to digest. Although goat milk is not the only alternative to cow milk, it may be considered the best alternative due to all the potential health and consumption benefits.

Key Words: goat milk, digestion

143 Dairy options for lactose intolerant consumers. A. R. Davis*, D. R. Winston, and B. A. Corl, *Virginia Tech, Blacksburg.*

Lactose intolerance is a condition in which the small intestine does not make adequate amounts of the enzyme lactase to break down the milk sugar lactose. It is characterized by bloating, diarrhea, flatulence, nausea, and cramps. Lactose intolerance must be diagnosed by a physician, but it is commonly misunderstood and many consumers self-diagnose. Between physician diagnosis and self diagnosis, an estimated 12% of consumers are lactose intolerant. Of that 12%, most avoid dairy products all together; however, exclusion of dairy from the diet is not necessary and has many health consequences, including higher incidence of osteoporosis and increased risk of developing diabetes and hypertension. According to a study led by the American Academy of Pediatrics, clarifying lactose intolerance misconceptions at a young age is essential. The best defense against osteoporosis is to establish peak bone mass before age 27, and dairy products have been shown to provide 77% of recommended dietary calcium. In a separate study, odds of developing diabetes or hypertension were significantly reduced by increased intake of calcium from dairy foods. The dairy industry should educate lactose intolerant consumers about what lactose intolerance actually is, the health consequences of a dairy-free diet, and how they can incorporate dairy foods into their diet for their overall health. This could lead to increased per capita consumption of milk by this group of consumers.

Key Words: lactose intolerance

144 Addition of Fiber to dairy foods. R. E. Brown* and C. C. Williams, *Louisiana State University, Baton Rouge.*

Many Americans do not meet the required amount of fiber needed in the diet, with women needing 25 g and men needing 38 g per day. According to the International Food Information Council Foundation's "2010 Food & Health Survey," only 5% of Americans meet the required intake of fiber with the average person consuming about 15 g of fiber. Fiber offers a variety of health benefits including, lowering body weight, preventing diverticulitis, and preventing type 2 diabetes. These statistics are important to the dairy foods industry, because processors have now found a way to incorporate fiber into dairy products to allow more consumers to meet their daily requirements. This is possible by adding isolated fibers such as inulin to ice cream, yogurt, and milk. Inulin is a low-caloric fructo-oligosaccharide that offers a blend of short-chained and longer-chained oligosaccharides that are soluble prebiotic fibers. The addition of fiber to dairy products has been met with some opposition. Some scientists believe that fortified fibers are not beneficial to the health of consumers, and can even cause harm if too much fiber is consumed. Although, most food consumed today has been processed research shows that isolated fibers can be added to dairy food products without changing the texture or taste. Therefore, giving consumers the fiber needed to meet their daily requirements without giving up the taste of dairy products would provide an additional health benefit to those already provided by milk and dairy foods.

Key Words: dairy food, fiber, diet

145 Pulsed electric field: A novel method of dairy product processing. C. Widener* and J. Fain, *Clemson University, Clemson, SC.*

Most Americans consume some type of heat-pasteurized dairy product daily. These traditional methods require a large energy input that is difficult to reclaim or recycle. With the movement toward sustainable agricultural production systems, food processing systems will need to follow suit. As consumers become more aware of the energy costs associated with dairy product processing, the industry needs to look toward alternatives that both lower energy costs and inputs. One of these alternatives is known as pulsed electric field (PEF). Traditionally, PEF works by using small bursts of electricity to inoculate microorganisms in liquid and semi-liquid foods. PEF has been applied commercially in fruit juices, and researchers across the country and internationally have begun to study its use in dairy products. Combination of this system with thermal methods allow processors to use lower temperatures and keep a shorter time frame, around 149°F for a total of 10 s, than traditional pasteurization, and thus a lower energy input. Additionally, PEF products have experienced a longer shelf life, in some cases as high as 24 additional days, with less of a "cooked milk" flavor associated with ultra-pasteurization methods. Raw milk processed through this method also maintained larger protein micelles and fat globules than milk processed with thermal methods while also successfully degenerating the enzymes that cause off flavors. Before this method could be implemented commercially, there would need to be a streamlining of parameters for both the temperature and the intensity of PEF. While there is still work and research to be done before commercial use, PEF

mixed with heat offers an energy efficient and nutritious option for the future of dairy processing.

Key Words: pasteurization, pulse electric, processing milk

146 Innovations in milk packaging. L. M. Kapanick* and D. R. Olver, *Pennsylvania State University, University Park.*

The first major development in fluid milk packaging was established at the end of the last century when the glass bottle became the most widely used container for distribution and storage. The glass bottle was the main method of milk packaging until 1933 when the first milk carton was introduced. This carton was made of wax paper and was widely used until the plastic bottle was developed in 1940. Together the plastic milk bottle and paper carton have created a wide range of containers suitable for milk packaging. Today consumers are offered more beverage alternatives, and fluid milk is being passed by in favor of other options such as bottled water. This can be seen in fluid milk consumption data. US fluid milk consumption declined 33% per capita from 1970 to 2011. New innovations in milk packaging are being developed to help reverse this trend. Factors such as convenience, environmental impact, and product quality are at the forefront of these new packages. Manufacturers have begun to rise to meet the challenge by producing smaller milk bottles in the shapes of animals for children and offering single-serve milk bottles for on-the-go adults. New designs have been launched in Israel that are capable of keeping milk fresh for 30 d. This packaging has a specific set of coatings that creates an electrical charge that kills bacteria. As the majority of consumer economic spending power shifts from "Baby Boomers" to "Millennials," it is crucial for the milk packaging industry to change and use methods that are appealing for the next generation. For example, a study commissioned by Tetra Pak concluded that 77% of their respondents would purchase one product over another because "the packaging would be better for the environment." As a result, manufacturers are constructing packages made of more easily recycled materials. Factors such as attractiveness, convenience, and increased shelf life are also important to these consumers, and milk packaging manufacturers are changing their products to meet these market needs.

Key Words: milk packaging, fluid milk

Undergraduate Student Competition: ADSA-SAD Undergraduate Competition: Dairy Production

147 Cow comfort: An important element of the 21st century dairy operation. A. Gibson* and L. Fox, *Washington State University, Pullman.*

Cow well-being is becoming an essential element of management in the modern dairy business. Cows that are given adequate and clean space to rest and eat appear more comfortable and will produce more milk. Cow well-being is also a societal concern. The public wants to be satisfied that their milk comes from healthy and well-treated animals. Producers can use cow well-being assessment tools such as the body condition score, locomotion score, and hygiene scores. Dairy managers can also observe cattle handling, and adjust the surroundings for heat stress to create the most ideal environment for the cow. Through careful observation of factors that can cause stress in the cow's life farmers can then locate the bottleneck that prevents optimum cow comfort and then alleviate that bottleneck. Inherently, cow well-being is an important aspect of the modern dairy. Uncomfortable cattle are less productive as they have decreased feed intake, and thus decreased production, and increased reproduction and disease problems. Minimizing stressful conditions for dairy cows is not only important economically but it is also good for public perception.

Key Words: cow comfort, welfare, cow well-being

148 Thermal variation effect on dairy calf rearing. A. C. Thompson*, D. M. Amaral-Phillips, and J. M. Bewley, *University of Kentucky, Lexington.*

Calves are the future productive units of a dairy herd. The herd's future performance, current and future earnings are based on their growth. Dairy calves are expected to double their birth weight from birth to 2 mo. Fluctuations in environmental temperatures and humidity affect how well a calf grows. One key to raising well-grown calves is a clean, draft-free, and well-ventilated environment. Temperature extremes outside of a calf's thermal neutral zone negatively affect growth and immune function. Calves begin to experience heat stress at temperatures exceeding 21°C. To reduce the effects of heat stress, ventilation, shade, and water need to be provided. According to Hill et al. (2011), ventilation with fans increased ADG ($P < 0.05$) and feed efficiency ($P < 0.05$). Shade allows the calf to grow while reducing the amount of energy expended to curtail heat effects (Spain and Spiers, 1996). Any energy that a calf uses to maintain their thermal neutral zone is energy diverted from growth. As ambient temperatures drop below 15°C, newborn calves begin to experience cold stress because they lack the fat stores necessary to stay warm. Calves older than 3 wk begin to experience cold stress at temperatures below 7°C because they develop fat stores as they age. During cold stress, the calf's energy requirement for maintenance increases. Additional dry bedding and draft-free ventilation alleviate the added stress. A calf provided deep bedding will nest creating a warmer microenvironment in contrast to bedding with sand or sawdust (Lago et al., 2006). This lowers the amount of energy the calf expends staying warm. According to Nonnecke et al. (2009), extra nutrients are needed for calves in cold environments to maintain growth similar to a warm environment. With colder temperatures, additional milk or milk replacer is needed to maintain growth. Minimization of environmental effects and additional nutrients from milk ensures that a calf doubles her birth weight by 2 mo.

Key Words: environmental temperature, stress, dairy calf

149 A survey on the challenges and opportunities regarding the transition from conventional to automatic milking systems in the northeastern United States. A. R. Ervin*, R. Peters, T. McCoy, and K. M. Moyes, *University of Maryland, College Park.*

As herd size increases, new technology that allows small-to-medium-sized dairy farmers to remain sustainable is greatly desired. Automatic milking systems are one way farmers can remain competitive and sustainable via improving management and production efficiency, as well as enhancing quality of life and business attractiveness to successors. The objective of this survey was to identify the interest and factors that are important to small-to-medium-sized dairy farmers when considering transitioning from conventional milking systems to AMS in the Northeast region. In January 2013, over 1330 questionnaires were sent to Maryland and Pennsylvania dairy producers having between 80 and 250 lactating dairy cows. The response rate was approximately 35%. Of the producers that completed the surveys, 33% expressed interest in transitioning to an AMS. Of the producers that expressed interest, 53% were between the ages of 50 and 64 and 45% possessed a high school diploma or graduate equivalency degree (GED). Return on investment/profitability, improving management of family time and improving herd management were the most important factors regarding their interest in AMS. Return on investment/profitability, financing/cash flow and barn design are the top 3 factors influencing dairy farmers' interest and concern when considering transitioning to AMS. Twenty-one percent of producers said they have access to information regarding changes in barn design, whereas 18.0% said they have access to information regarding changes in animal health/productivity and financing. Producers said more information on barn design, animal health/productivity and economic impact would be helpful when considering a transition to AMS. Results will serve as the basis for education programs designed to provide farmers with the decision-making tools required to estimate and quantify economic impacts, performance outcomes and lifestyle changes associated with AMS.

Key Words: dairy cow, survey, automatic milking system

150 Sexed semen, genomics, and crossbreeding as tools for increasing the value of dairy herd genetics and cull dairy animals. T. L. Boyd*, D. R. Winston, and B. G. Cassell, *Virginia Tech, Blacksburg.*

Sexed semen and genomic testing are recent developments in the dairy industry that have gained in popularity since their introduction, both in registered and commercial herds. As many farmers look for new ways to increase profitability in the face of increasing production costs, the cost-benefit ratio of these technologies is sometimes questioned. To maximize their value, crossbreeding has been suggested as a third tool to create a more valuable end product— cull dairy calves—while increasing the genetic value of those animals remaining in the milking herd. This is achieved by breeding genomically inferior heifers to beef semen, which creates a marketable product (half-beef, half-dairy bull and heifer calves) while keeping bad genetics from remaining in the herd. It can also reduce some semen costs, since good, expensive dairy bulls are not wasted on poor females, in addition to reduced health costs

due to fewer incidences of dystocia. The downside is that it requires expenditures in time and effort to implement, and it is a relatively new concept for commercial herds. The value of such a system was analyzed via meta-analysis by comparing traditional cull values with those produced by this system. The value of these culls was determined by comparing both the costs incurred by increased semen costs, genomic testing, and decreased fertility and the benefits of greater more valuable cull calves, more accurate culling, and superior replacement heifers. The analysis indicates a cost of approximately $20 per contemporary member of the breeding group, although management techniques can turn this into a net profit.

Key Words: sexed semen, genomics, crossbreeding

151 What lies within the rumen? S. M. Vignes* and C. C. Williams, *Louisiana State University, Baton Rouge.*

Subcute ruminal acidosis (SARA) is characterized by a sustained rumen fluid pH below the normal 5.8. Many factors can attribute to the pH dropping below this level including diet particle size, dietary carbohydrate concentration, limited saliva production, and water intake. Rumen microorganisms break down readily fermentable carbohydrates which lead to the production of volatile fatty acids (VFA) and lactic acid. In turn the ruminal fluid's pH is lowered. Acidosis can lead to the microorganisms in the rumen being harmed or becoming obsolete altogether as well as the absorptive papillae being damaged. SARA is of concern in mature dairy cattle but also in the growing calves. It is widely known that the first 24 to 36 h after a calf is born is the most crucial time to feed colostrum to ensure passive immunity. Once calves are transitioned onto their liquid feeding program, they should also be provided with high quality calf starter not only to provide nutrients but to promote rumen development. The starch and sugars provide the readily fermentable carbohydrates for production of VFA which help develop the rumen. With this practice though, subacute acidosis could occur as production of the VFA and lactic acid lead to the decrease in pH. This is a problem because the earlier weeks are the most vital time for initiating rumen development, and a fine line is being walked between beneficial and detrimental. The rumen must be provided for, but too much grain could result in SARA due to low rumen pH. Low rumen pH impairs fiber digestion by inhibiting the growth of cellulolytic microorganisms. Research has shown subacute rumen acidosis to be common among calves, but has it become a normal event?

Key Words: acidosis, calves

152 Rumination monitoring: A management tool for early detection of metabolic disorders. K. Carraway*, M. Brauneis, N. Engwall, and J. Fain, *Clemson University, Clemson, SC.*

Rumination monitoring is an important tool for dairy herd management as it is a direct reflection of cow health. Monitoring rumination rate has the potential to be utilized in an array of practices from heat detection to metabolic disorder diagnosis. Until recently, monitoring rumination has been achieved by visually monitoring cow activity, which is time consuming and lacks accuracy. Recently, SCR Engineers Ltd. of Israel released the HR-Tag, a rumination collar that has changed the way producers can manage their herds. The neck color is equipped with a built in motion sensor, microphone, and processor for recording rumination rates, chewing rhythm, and general movements. A scanner then transmits the recordings to a computer data system that keeps an activity report of the entire herd. By sensing a drop in rumination rates, the rumination collar is able to detect metabolic disorders such as ketosis, acidosis, displaced abomasums, as well as mastitis. This tool is especially useful in transition animals, a phase corresponding to a time when these disorders are most prevalent. Early detection allows producers to quickly begin remedial therapies that in turn reduce the costs associated with potential advanced treatment and production loss. Additional cost reduction may be realized through identification of a disorder's subclinical manifestations. There are some limitations that hold back the HR-Tag from its full potential. The cows must be near the transmitter to allow data to be sent to the computer, and any data not sent is lost in 24 h. Decreases in rumination are not always associated with illness or heat, and must be crossed checked with milk records for validation. Additionally, the cause of the drop in rumination is something that must be further investigated, for the exact disease or reason is not given. Proper placement of the tag is crucial for accurate readings, and that is difficult to achieve with some animals. Despite these minor setbacks, studies show that with proper training and experience, rumination monitoring is a highly effective and accurate way of detecting early illness, making it a valuable tool for herd management.

Key Words: rumination monitor, metabolic, management

153 The Fodder System. K. Supa* and B. Richards, *Delaware Valley College, Doylestown, PA.*

The Fodder System is a hydroponic system used to produce a fresh feed source for domestic animals. This new system was developed in Australia and introduced into the United Stated in 2009. The system will convert grain or legume seeds into a fresh feed source in 6 d. The end product or mats consist of the roots and the greens of the plants. The seeds are grown in a controlled and sterile environment which decreases the development of fungus or molds. A wide variety of seeds can be grown in the Fodder System to maximize the benefits of feeding the product. This unique management style using this system allows agricultural producers to deliver a feed source to their animals that is consistent and nutritious. Animals are fed a mat that includes the roots, which makes the feed source 70% digestible, according to the Fodder Systems website. This type of system is labor efficient and reasonably priced for the system. The cost of the system is affordable when compared with the high cost of equipment to make traditional forages. Less equipment also means less money for repairs on harvesting equipment. Another benefit to the fodder system would be the ability to farm on a smaller land base, thus allowing us to produce more quality feed with less foot print on the environment. The Fodder System provides a high quality feed product that can offer many benefits to agricultural producers in the United States.

Key Words: Fodder System, hydroponic, legume seeds

154 Effects of group housing and pairing calves before weaning. D. L. Grove* and D. R. Olver, *Pennsylvania State University, University Park.*

In the United States, the traditional way of raising calves has often been to house them individually until weaning and then group them together. This was thought to prevent the spread of disease and allow management of each individual calf. With the advent of automated feeders, group housing of calves before weaning has become more popular. Research from British Columbia showed that calves housed in pairs spent more time eating and had higher intakes of starter shortly after weaning. Pair-housed calves in the study vocalized 3 times less at weaning than individual calves, indicating that the pair-housed calves exhibited less stress. The individually-housed calves took on average 40 h longer

to start eating starter when mixed with other calves at weaning. They concluded pair-housing calves reduces behavioral responses to weaning and improves weaning performance. In another British Columbia study, calves housed in groups struggled less when handled than individually housed calves. These scientists also showed paired calves on a typical plane of nutrition spent more time playing than individually-housed calves with the same nutrition level. This is a positive sign of animal well-being. In a Spain study where calves were grouped either before weaning or else 6d after weaning, calves were 2 times less likely to have respiratory problems if they were grouped earlier. The early-grouped calves had higher starter intake at weaning in this study. The researchers believe that group housing allows more space for the calves, which reduces stress and leads to fewer health problems. A Canadian study agreed that more access to space may be beneficial to calf health and lead to reduced stress at weaning. All of these studies found a positive increase in animal well-being in group-housed calves.

Key Words: calf, housing

Graduate Student Competition: ADSA Production Division Oral Competition, MS Division

155 Effects of urea on uterine response to interferon-tau in presence of progesterone. J. Spencer*[1], K. Austin[2], K. Carnahan[1], and A. Ahmadzadeh[1], *[1]University of Idaho, Moscow, [2]University of Wyoming, Laramie.*

High blood and uterine urea concentrations, associated with high dietary protein, can reduce fertility in dairy cows. In an in vitro steroid free culture, urea did not affect bovine endometrial (BEND) cell expression of Mx1 and ISG15 in response to the ruminant maternal recognition protein (IFN-tau). However, uterine protein secretions are altered in response to IFN-tau in the presence of progesterone (P_4). Therefore, the objective of this study was to determine the direct effects of urea on protein expression of the endometrial cells of the bovine uteri in response to IFN-tau in the presence of P_4. Using BEND cells as a model, the effects of urea on the production of 2 IFN-tau stimulated proteins, ISG15 and Mx1, were examined. Bovine endometrial cells were grown to 80% confluency and further incubated for additional 24 h in culture media containing P_4 (10^{-7} *M*). Cells (90% confluent) were then treated with urea at final concentrations of 0, 5, 7.5, or 10 mM urea and subsequently, challenged with 0 or 10,000 antiviral units of recombinant IFN-tau and incubated for an additional 24 h. Once harvested, BEND cells were lysed and the cell supernatant was analyzed and quantified for Mx1 and ISG15, using SDS-PAGE, Western blot and immunoblotting protocols. Based on optical density, regardless of urea treatment, IFN-tau increased ($P < 0.01$) Mx1 and ISG15 by 11 and 4 fold, respectively. There was no effect of any urea treatment or urea by IFN-tau interaction on Mx1 and ISG15 production after 24 ($P = 0.9$) of culture. These results show that there is no disruption of IFN-tau stimulated Mx1 or ISG15 production, when BEND cells are exposed to varying concentrations of urea in the presence of P_4 in vitro.

Key Words: urea, interferon, bovine endometrial cells

156 Effect of bedding surface on the welfare of preweaned Jersey calves. C. A. Kurman* and P. D. Krawczel, *University of Tennessee, Knoxville.*

Previous research on the effect of the bedding surface on the welfare of dairy calves has produced mixed results with indication that calves prefer a soft, dry surface and others suggesting that bedding or flooring have no effect on behavior and performance. The objective of this study was to determine the effect on the behavior and performance of Jersey calves housed using individual hutches bedded with gravel, sand, or rubber mat. It was hypothesized that sand or rubber mat would increase lying time, decrease lying bouts, but not affect BW gain or feed intake in preweaned calves. Twenty-eight Jersey calves were blocked by birth date and randomly assigned to 1 of 3 bedding treatments (gravel, sand, or rubber mat). Lying time and lying bouts were assessed with dataloggers, recording at 1-min intervals for 3 consecutive days each week. Performance was determined by weight gain (calculated from birth weight and weekly BW) and grain intake (calculated as daily difference between grain offered and refused over 3-d). Data were collected for 8 wk following birth. Data were analyzed using a mixed model in SAS with repeated measures. Mean lying time (15.2 ± 0.3 h/d) was not affected by trt ($P = 0.51$), wk ($P = 0.16$), or trt × wk interactions ($P = 0.54$). Lying bouts were affected by trt ($P = 0.01$) and trt × wk interactions ($P = 0.05$) but not by wk ($P = 0.20$). Calves on mats engaged in more lying bouts/d (12.1 ± 0.7 n/d) than gravel (9.8 ± 1.0; $P = 0.01$) or sand (9.0 ± 0.7 n/d; $P < 0.001$). An effect of week was evident in BW gain (2.2 ± 0.2 kg/wk; $P = 0.002$), but trt ($P = 0.41$) or trt × wk interactions ($P = 0.19$) effects were not evident. Grain intake (gravel = 386.9 ± 59.8 g/d, mat = 413.3 ± 50.0 g/d, sand = 479.1 ± 52.7 g/d) increased from 0 g/d in wk 1 to 1095.8 g/d in wk 8 ($P < 0.001$) but there was no trt effect ($P = 0.48$) or trt × wk interaction ($P = 0.21$). There were no biological significant differences in behavior or performance among treatments. This suggests that, on a well-managed farm, any of these beddings may be used without compromising the welfare of preweaned Jersey calves.

Key Words: dairy calf, behavior, bedding

157 The effects of D-α-tocopherol and dietary energy on growth and health of dairy calves. L. A. Krueger*[1], K. Onda[1], M. Osman[1], M. R. O'Neil[1], R. L. Stuart[2], H. D. Tyler[1], B. Nonnecke[3,1], and D. C. Beitz[1], *[1]Department of Animal Science, Iowa State University, Ames, [2]Stuart Products Inc., Bedford, TX, [3]Ruminant Diseases and Immunology Research Unit, National Animal Disease Center, Agricultural Research Service, USDA, Ames, IA.*

To understand the effects of dietary vitamin E in relation to dietary energy on growth and immune status in dairy calves, 32 newborn Holstein bull calves were assigned to one of 4 treatments for 5 weeks in a 2 ×2 factorial randomized complete block, split plot design. Calves received one of 2 all-milk diets formulated to provide 70% or 100% of the dietary energy recommendation for milk-fed calves according to the NRC's Nutrient Requirements of Dairy Cattle. Calves in these 2 groups were either injected subcutaneously with 5 mL Vital E-A+D on d 1 and administered 200 IU vitamin E (Emcelle Tocopherol) orally via milk daily, or were not supplemented during the study period. Weight gain of calves receiving the 100% diet was greater than that of calves receiving the 70% diet. Calves receiving vitamin supplementation demonstrated elevated concentrations of plasma α-tocopherol, retinol, and 25-(OH)-vitamin D_3, but calves receiving the 100% diet demonstrated decreased concentration of plasma α-tocopherol. Serum haptoglobin, an acute phase protein, was higher at wk 2 for non-supplemented calves receiving the 100% diet. Serum amyloid A, also an acute phase protein, was not different among groups and was elevated from baseline during wk 1 through 3 before a return to baseline by wk 4. Plasma IgG_1 concentration was higher in vitamin-supplemented calves than in their non-supplemented dietary counterparts, while plasma IgG_2, IgA, and IgM concentrations were not different. In summary, dietary supplementation of vitamin E did not affect growth, but improved plasma α-tocopherol status, decreased serum haptoglobin associated with acute inflammation in calves fed the 100% diet, and slightly improved adaptive immune status. Consumption of the 100% diet increased weight gain in calves, but decreased plasma α-tocopherol and increased serum haptoglobin, indicating a role for vitamin E supplementation in prevention of inflammatory stimuli such as oxidative stress associated with accelerated growth and onset of infectious disease.

Key Words: tocopherol, haptoglobin, dairy calf

158 Metabolic and oxidant profiles of periparturient pastured dairy cows milked in an automatic milking system. M. F. Elischer*, J. M. Siegford, and E. L. Karcher, *Michigan State University, East Lansing.*

The periparturient period is a physiologically stressful time for dairy cows where an increase in energy expenditure paired with a decrease in feed intake leaves the cow highly susceptible to health issues, especially metabolic disorders and impaired immune function. Metabolic and oxidative status are related, though the precise linkage is unknown. Metabolic and oxidative stress profiles for cows in traditional milking and feeding are well documented, but little research has examined these health parameters in automatic milking systems (AMS) or with pasture-based diets. The objective of this study was to characterize metabolic and oxidative profiles for periparturient dairy cows milked in an AMS and consuming a pasture-based diet. Fourteen multiparous Friesian cows were sampled weekly from −21 to 21 d relative to calving. Eight primiparous cows were sampled weekly from calving to 21 d. Multiparous cows milked more frequently (2.60 milkings/d ± 0.24 vs. 1.93 ± 21; P kg/d ± 1.52 vs. 13.3 ± 1.37; P compared with primiparous cows. Blood was collected weekly and analyzed for nonesterified fatty acids (NEFA), β-hydroxybutyrate (BHBA), insulin, glucose, antioxidant potential (AOP), and reduced glutathione (GSH). NEFA concentrations declined from d 1 through 21 for both groups ($P < 0.05$). There was no significant effect of day or parity on BHBA concentrations. Insulin values did not differ significantly between the 2 groups. Glucose concentration was elevated on d 7 and 14 in primiparous compared with multiparous cows ($P < 0.05$). Primiparous cows had significantly higher AOP at 14 and 21 d postpartum, suggesting that primiparous cows had less oxidative stress as serum lipids were better protected. Lower concentrations of GSH, a major antioxidant, were exhibited in primiparous than multiparous cows, though this was not significant. Overall, blood analyses indicate primiparous cows experienced less metabolic and oxidative stress than multiparous cows, likely due to lower milk yield and frequency.

Key Words: oxidative stress, metabolism, robotic milking

159 Nutritional value and silage fermentation parameters of leaves and roots of yacón (*Smallanthus sonchifolius*) mixture as alternative supplementation of cattle in Colombia. L. Bernal*, *Universidad de La Salle, Bogotá, Colombia.*

In this study the nutritional value and fermentation parameters of silage leaves and roots of yacón (*Smallanthus sonchifolius*) was evaluated. Yacón is a native plant of the Andes. The leaves of yacón are not harvested for feeding ruminants. This forage does not compete with human food and has not been extensively studied in the country, in terms of animal nutrition. Samples were taken from the existing planting on the campus of La Salle University in Bogotá. Six treatments were evaluated with different inclusion rates of leaves and roots of yacón. T1: leaves 100%, T2: root 100%, T3: leaves 90: root 10; T4: leaves 80: root 20; T5: leaves 70: root 30 and T6: leaves 60: root 40. These mixtures were stored at ambient temperature in small plastic bags of around 1 kg fresh matter for a period of 56 d. At the end of the fermentation period, samples were taken for analysis of nutritional quality (dry matter DM, crude protein CP, neutral detergent fiber NDF, acid detergent fiber ADF and gross energy GE) and fermentation parameters (pH, ammonia nitrogen and its relation with total nitrogen). The experimental design was completely randomized, 6 treatments and 4 replicates. Variables were analyzed by the GLM procedure by SAS. There was a significant effect of the mixture ratio. The values of DM and CP were higher in leaves than in roots. The part of plant had a significant effect on values NDF, ADF and GE. The fermentation parameters were significantly different. The values of pH, ammonia nitrogen and the relationship between ammonia nitrogen/total nitrogen were better for mixed silages than for leaves and roots only. Finally, the result of nutritional value and silage fermentation parameter showed that it is better to use the mixture with up to 70% leaves, which is good option for feeding cattle.

Key Words: *Smallanthus sonchifolius*, roots, silage

160 Low cost on-farm predictors of individual cow risk for ketosis and fatty liver. Z. Sawall* and N. B. Litherland, *University of Minnesota, St. Paul.*

Early lactation data from 3 studies (n = 176 cows) were composited to determine on farm prediction tools for cows at risk for elevated serum BHBA and NEFA and liver triglycerides (TG). The objective of this retrospective analysis were to determine if low-cost, on-farm measures of colostrum yield (CY), colostrum specific gravity (CSG) and body condition score (BCS) at calving are good predictors of cow health and production in early lactation. Pearson correlation coefficients were calculated for CY, CSG, BCS, BHBA, NEFA and ME 305d milk production. CY is a significant predictor of serum BHBA on d 1 and d 7 postpartum. Serum NEFA can be predicted on d 1, 7 and 14 by CSG using Brix refractometer. Both CY and CSG are significantly correlated with liver TG on d 7 and CY and CSG help predict DMI during the first week postpartum. BCS is negatively correlated with serum calcium 24 h postpartum and can identify cows at risk for hypocalcaemia. BCS is positively correlated with serum BHBA at d 1 and d 14, serum NEFA at d 7 and d 14 and ME 305 d milk production. Low cost, on-farm measures of CY, CSG and BCS provides insight into rates of body reserve mobilization without blood or liver sample collection. The implementation of these tools together can allow dairy producers to quickly identify cows at risk for hypocalcaemia, ketosis, and low DMI shortly after parturition. Rapid, low cost identification of cows at high risk for these disorders allows for early treatment or implementation of tailored feeding and management strategies to minimize the incidence and severity of subclinical fresh cow disorders.

Table 1. Pearson correlations between colostrum yield (CY), colostrum specific gravity (CSG) and BCS on cow health parameters

	CY	CSG	BCS
Ca 12H	0.005	−0.14	−0.03
Ca 24 H	−0.06	−0.20	−0.31*
NEFA d 1	0.20*	0.17*	−0.04
NEFA d 7	0.11	0.29***	0.39**
NEFA d 14	0.03	0.20**	0.29*
BHBA d 1	0.19*	0.01	0.38**
BHBA d 7	0.16*	−0.02	0.13
BHBA d 14	0.02	−0.01	0.39**
Liver TG 7	0.20*	0.13**	0.23
Liver TG 14	0.15†	0.07	0.16
DMI wk 1	−0.18 *	0.32***	−0.16
ME 305-d milk	−0.08	0.08	0.29†

†$P < 0.1$, *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$.

Key Words: transition cow, cow health

161 Mass loading of antibiotic resistance genes in feces of prophylactically treated dairy cattle. B. F. Willing*, L. R. Caudle, A. Pruden-Bagchi, and K. F. Knowlton, *Virginia Polytechnic Institute and State University, Blacksburg.*

Prophylactic antibiotic treatment has the potential to increase excretion of antibiotic resistance genes (ARGs) by dairy cattle through selection pressure on the gut microbiome. The objective of this study was to evaluate the effect of cephapirin on establishment and persistence of antibiotic resistance genes in dairy cattle during the dry period. To examine temporal variation in fecal excretion of ARGs, 32 end-of-lactation cows were used. Treatment cows (22) received cephapirin benzathine as an intramammary infusion before dry-off and control cows (10) received no antibiotics. Fecal grab samples were collected for each cow on d −2 or −3 (baseline, used as covariate), and d 1, 3, 5, 7, and once per week until d 56. Fecal samples were collected in sterile containers using a new glove for each cow, then freeze-dried. DNA was extracted from freeze-dried samples using a commercially available FastDNA SPIN KIT for Soil (MP Biomedical). The abundance of ARGs (Tet, Sul), integrase-specific gene (Int), and 16S rRNA were quantified using qPCR. Non-normal data were log-transformed and data were statistically analyzed using PROC GLIMMIX in SAS 9.2.There were significant interactions between treatment and day for all genes. In dry-treated cows, relative abundance (log gene copies/16S rRNA) of TetO, Sul1, and Int1 increased ($P < 0.0001$, $P < 0.001$, and $P < 0.0001$, respectively) from d 1 to d 56 following antibiotic treatment while relative abundance decreased ($P < 0.0001$, $P < 0.001$, and $P < 0.0001$, respectively) in untreated cows across the same time period. Relative abundance of TetW increased ($P < 0.0001$) during the dry period in both dry-treated and control cows. Administering long-acting antibiotics as intramammary dry therapy to dairy cows increases the selection pressure and subsequently increases the abundance and persistence of selected ARGs excreted during the dry period. Increased relative abundance of Int1 indicates increased potential of ARG dissemination by horizontal gene transfer.

Key Words: antibiotic resistance gene, cephapirin, prophylactic

162 Effect of oral administration of *Megasphaera elsdenii* on performance of Holstein cows during early lactation. K. D. Stevens*, M. L. Eastridge, S. K. Finney, and S. N. LeShure, *The Ohio State University, Columbus.*

Transition cows have a high risk for metabolic disease within the first 30 DIM. Administration of direct-fed microbials (DFM) may reduce the adverse effects that fresh cows experience during this transition period. *Megasphaera elsdenii* (*M. elsdenii*) is a lactic acid-utilizing bacterium that has shown promise as a potential DFM during the transition period. Primi- and multiparous Holstein cows (n = 162) at a commercial dairy herd in Ohio were assigned to 1 of 4 treatments: (1) control (no dose) (n = 44), (2) 200 mL Lactipro (*M. elsdenii*, 1×10^8 cfu/mL; MSBiotec, Littleton, CO) when cows entered (~−14 DIM) the close-up pen (n = 45), (3) 200 mL Lactipro at calving (n = 39), and 4) 200 mL Lactipro prepartum and 200 mL at calving (n = 34). Close-up cows were fed 71% forage (57:43 corn silage and wheat straw), and upon calving, cows entered the high group and were fed 41% forage (93:7 corn silage:wheat straw). All cows were body condition scored (BCS) prepartum and at 30, 60, and 90 DIM. Urine ketones (Ketostix; Bayer Corp., Leverkusen, Germany) were measured at 7 to 14 DIM. Cows were milked 3 times daily, and yield was recorded daily until 90 DIM using Afimilk (Kibbutz Afikim, Israel). Milk composition data were from monthly DHI (DHI Cooperative, Inc., Columbus, OH) samples taken from the first daily milking during the first 2 test dates postpartum. There was no difference in milk yield among treatments (39.8, 39.2, 39.7, and 40.3 ± 1.1 kg/d), and the test-day milk fat and protein percentages were similar among treatments. Test-day milk fat and protein were higher ($P < 0.001$) for the first (3.88%) versus second (3.38%) test-day, reflective of the low incidence of ketosis discussed below. Neither a difference in BCS by treatment nor a treatment by time interaction occurred. Based on urine ketones, only 2.5% of the cows in the study experienced clinical ketosis, but cows with ≥5 mg/dL were 31.8, 35.6, 25.6, and 17.6% for treatments, respectively. Concentrations of dietary starch and NDF fed both prepartum and postpartum may affect animal response to dosing with *M. elsdenii*.

Key Words: firect fed microbial, early lactation, *Megasphaera elsdenii*

163 Effect of heat stress in utero on calf performance and health through the first lactation. A. P. A. Monteiro*, S. Tao, I. M. Thompson, and G. E. Dahl, *University of Florida, Gainesville.*

Calves born to cows exposed to heat stress during the dry period have lower birth weight and weaning weight and compromised passive immune transfer compared with those born to dams that are cooled. However, it is unknown if heat stress in utero has carryover effects after weaning. The objective was to evaluate the effect of heat stress during late gestation on growth, fertility and milk production in the first lactation of the offspring. Data of animals obtained from previous experiments conducted during 5 consecutive summers were pooled and analyzed. Cows were dried off 46 d before expected calving and randomly assigned to either cooling (CL) or heat stress (HT). CL cows were housed under sprinklers, fans and shade, whereas only shade was provided to HT cows. Within 4 h after birth, 3.8 L of colostrum was fed to calves from both groups of cows. All calves were managed in the same manner and weaned at 49 d of age. Birth weight and survival of 147 calves (HT = 74; CL = 72) and body weight and growth rate from 72 heifers (HT = 34; CL = 38) were analyzed. Additionally, fertility and milk production in the first lactation from 38 heifers (HT = 17; CL = 21) were analyzed. As expected, HT calves were lighter (39.1 ± 0.7 vs. 44.8 ± 0.7 kg, $P < 0.01$) at birth than CL calves. CL heifers were heavier (200.2 ± 3.4 vs. 190.9 ± 3.7 kg, $P < 0.05$) up to one year old, but had similar weight gain (305.8 ± 5.9 vs. 299.1 ± 6.3 kg) compared with HT heifers. No differences in age at first AI or age at first parturition was observed, but HT heifers had a greater number of services per conception than CL heifers (2.6 ± 0.3 vs. 1.8 ± 0.3, $P = 0.03$). HT heifers tended to produce less milk up to 35 weeks of the first lactation compared with CL heifers (26.9 ± 1.9 vs. 29.3 ± 1.8 kg, $P = 0.11$), but no difference in body weight during lactation was observed (HT: 565.4 ± 12.0 kg; CL: 554.1 ± 11.0 kg). These data suggest that heat stress during the last 6 weeks of gestation negatively affects fertility and milk production up to and through the first lactation of offspring.

Key Words: calves, heat stress, postnatal performance

164 Association between dairy calf management practices and calf immune status. A. Bartier*, C. Windeyer, and L. Doepel, *University of Calgary, Calgary, Alberta, Canada.*

Dairy calves are at high risk of failure of passive transfer of immunity (FPT) if consumption of colostral IgG within hours of birth is inadequate. The objectives of this study were to determine (1) the incidence of FPT on Alberta dairy farms, (2) which neonatal calf management practices are used, and (3) the relationship between these practices and FPT. Fourteen commercial dairy farms were visited weekly from February to September, 2012. At each visit, blood samples were collected from

calves <7d old. Total serum protein (TSP) was determined with a refractometer and serum IgG was determined quantitatively by RID. Producers completed a survey for each calf outlining the management practices that were followed (e.g., amount of colostrum fed, time calf left with dam) in the first 7 d of life. A sample of first feeding colostrum was analyzed by RID for IgG content. A mixed linear models regression procedure was performed using TSP and serum IgG as response variables, management practices and colostrum IgG as predictor variables and 'farm' as a random effect. Data were obtained from 199 bull calves and 557 heifer calves. Minimum, maximum and mean ± SEM for TSP were 3.0, 10.0 and 5.39 ± 0.03 g/dL; for serum IgG, values were 0.35, 58.0 and 18.95 mg/ml. FPT was 44.7% based on TSP <5.2 g/dL and 27.7% based on IgG <10 mg/mL. Univariate analysis showed type of colostrum (e.g., pooled, dam) fed in the first 6 h and from 6 to 12 h of life, and amount of IgG consumed in the first 6 h of life to be significant predictors of serum IgG and TSP ($P < 0.0002$). Univariate analysis showed that type of milk (e.g., sale, waste) fed after colostrum, use of medications in the first week of life and if fresh or frozen colostrum was fed were significant only for serum IgG ($P < 0.03$); method of feeding in the first 6 h of life was significant only for TSP ($P < 0.003$). For the multivariate analysis all possible predictor variables were offered in the model and nonsignificant ($P > 0.05$) predictors were removed by backward elimination. IgG consumed in the first 6 h of life was the most important predictor variable ($P < 0.0001$) associated with both high serum IgG and TSP.

Key Words: IgG, calf management, FPT

165 Effects of acute feed restriction combined with targeted use of increasing LH in FSH preparations on superovulation and embryo quality in lactating dairy cows. R. W. Bender*, K. S. Hackbart, A. R. Dresch, P. D. Carvalho, L. M. Vieira, P. M. Crump, J. N. Guenther, R. D. Shaver, D. K. Combs, and M. C. Wiltbank, *University of Wisconsin-Madison, Madison.*

Superovulatory programs have multiple metabolic and hormonal factors that potentially affect success. This study evaluated the effect of acute feed restriction and increased luteinizing hormone (LH) content in the superovulatory preparation on superovulation response and embryo quality from lactating dairy cows. In each of 2 experiments, 16 lactating Holstein cows were superovulated in a Latin square design while exposed to a 2 × 2 factorial arrangement of treatments: feed restriction (FR; 25% reduction in DMI during 6 d before AI) vs. ad libitum (AL) feeding combined with high (H) vs. low (L) LH in the last 4 injections of the 8 injection superovulatory protocol. Embryos were flushed 7 d after AI. As expected, FR reduced circulating insulin concentrations ($P < 0.05$). Follicle numbers, ovulation rates, and corpora lutea on d 7 were not different. There was an interaction between FR and amount of LH on fertilization rates, percentage of structures that were Quality 1 and 2 embryos, and number of structures that were degenerate. In the first period analysis of experiments 1 and 2, fertilization rates were greater ($P < 0.01$) for the AL-L (89.4%) and FR-H (80.1%) treatments compared with the AL-H (47.9%) and FR-L (59.9%) treatments. Similarly, the proportion of total structures designated as Quality 1 and 2 embryos was greater ($P < 0.01$) for AL-L (76.7%) and FR-H (73.4%) treatments compared with AL-H (35.6%) and FR-L (47.3%) treatments. In addition, the number of degenerate embryos was lower ($P = 0.03$) for AL-L (1.3) and FR-H (0.4) treatments than AL-H (2.6) and FR-L (2.3) treatments. Thus, cows with either too low (FR-L) or too high (AL-H) of insulin and LH stimulation have lower embryo production following superovulation due to reduced fertilization rate and increased percentage of degenerate embryos. The interaction of the gonadotropin content of the superovulatory preparation with the nutritional program of the donor cow needs to be considered to optimize superovulatory success.

Key Words: superovulation, feed restriction, LH

166 Description of weighing errors and times during preparation of a ration. Y. Trillo*[1], A. Lago[2], and N. Silva-del-Rio[1], *[1]Veterinary Medicine Teaching and Research Center, University of California Davis, Tulare, [2]DairyExperts, Tulare, CA.*

The objectives of this study were to describe weighing errors, time intervals between loading ingredients, length of ration preparation, and dropping times for the high cow ration prepared in 4 California dairies (A, B, C, and D) ranging in size from 2,500 to 6,000 cows. Records from Jan to Dec 2012 were extracted from the feeding management software FeedWatch 7.0. The variables included were: date, drop number, recipe, ingredient, feeder, loading sequence, loading start-time, loading end-time, loading errors, dropping start-time, dropping end-time, and dropping sequence. Descriptive statistics were conducted with SAS 9.3. The high cow ration included 13 (A), 14 (B), 18 (C) and 12 (D) ingredients. All dairies had a main feeder and one (A), 2 (D) or 3 (B, C) relief feeders. The main feeder prepared 85% (n = 3,319), 64% (n = 2,547), 64% (n = 1,162) and, 83% (n = 1,949) of the high cow ration loads in dairy A, B, C and D respectively. The frequency in which ingredients were loaded with errors ≥ |2|% of the expected weight was 35.9% (A), 67.6% (B), 46.4% (C), and 44.0% (D) for the main feeders and 33% (A), 66% (B), 46% (C), and 48% (D) for the relief feeders. The frequency in which ingredients were loaded with errors ≤ |0.5|% of the expected weight was 22% (A), 8% (B), 13% (C), and 21% (D) for the main feeders and 22% (A), 9% (B), 15% (C), and 19% (D) for the relief feeders. Short intervals between loading of ingredients (<45 s) might indicate that the feeder was wrongly dropping leftovers from the previous ingredient in the next ingredient load. Intervals between loading of ingredients <45 s occurred in 12% (A), 14% (B), 1% (C) and 36% (D) of the loads done by the main feeder and in 7% (A), 16% (B), 1% (C) and 27% (D) of the loads done by the relief feeder(s). The first drop of the day had an interquartile range (Q0.25 – Q0.75) of 10 (C), 14 (A, B), and 20 (D) min whereas for the last drop of the day was 9 (D), 24 (C), 52 (A) and 54 (B) min. Feeding management software could be used to identify opportunities to improve the feeding process. Future research should define achievable goals on feeding management practices for dairies.

Key Words: dairy cow, feeding management, software

167 Evaluation of multiple ancillary therapies utilized in combination with an antimicrobial in newly received high-risk calves treated for bovine respiratory disease. B. K. Wilson*[1], C. L. Maxwell[1], D. L. Step[2], C. J. Richards[1], and C. R. Krehbiel[1], *[1]Department of Animal Science, Oklahoma State University, Stillwater, [2]Department of Veterinary Clinical Sciences, Oklahoma State University, Stillwater.*

This experiment evaluated 3 commonly used ancillary therapies in combination with an antimicrobial in high-risk calves treated for bovine respiratory disease (BRD). Crossbred steers (n = 516; initial BW = 217 ± 20 kg) were monitored daily for clinical signs of BRD. Calves that met treatment criteria (n = 320) were randomly assigned to 1 of 4 experimental treatment groups: intravenous flunixin meglumine injection (NSAID), intranasal viral vaccination (VACC), intramuscular vitamin C injection (VITC), or no ancillary therapy (NOAC). Mortality attributed to BRD was 13%. Data were analyzed using the GLIMMIX procedure (SAS 9.3) with pen (n = 16; 4 per experimental treatment) serving as the experimental unit. Steers receiving VACC tended (P = 0.10) to require a second BRD treatment less frequently than steers receiving NSAID or NOAC. Calves receiving NSAID or VITC tended (P = 0.09) to require a third BRD treatment less often than calves receiving NOAC. Of calves treated 3 times for BRD, those receiving NOAC had lower (P = 0.05) severity scores than those receiving VACC or VITC and heavier (P = 0.02) BW than those receiving NSAID, VACC, or VITC at the time of third treatment. Between the second and third BRD treatments, calves receiving NOAC also had greater (P = 0.03) ADG than those receiving VACC or VITC and tended (P = 0.06) to have greater ADG than those receiving NSAID. Calves receiving NOAC tended (P = 0.07) to have heavier BW on d 28 than NSAID, VACC, or VITC with mortalities and removals excluded. When contrasted with the average of NSAID, VACC, and VITC calves, NOAC calves tended (P < 0.10) to have heavier BW on d 56, greater ADG and DMI from first BRD treatment through d 28, greater DMI from d 28 through d 56, and had greater (P = 0.05) DMI from first BRD treatment through d 56 with mortalities and removals excluded. Responses to ancillary therapy were negligible in this experiment. The use of NSAID, VACC, and VITC appears to have minimal benefits and could potentially be detrimental to animal performance in severely challenged calves.

Key Words: ancillary therapy, bovine respiratory disease, high-risk calf

168 Interactions of rectal temperature status and vaccine type with sire on weight gain and feed intake in *Bos indicus* crossbred steers following Bovine Viral Diarrhea Virus challenge. C. A. Runyan*[1], X. Fang[1], E. D. Downey[1], T. B. Hairgrove[2], J. E. Sawyer[3], J. G. Moreno[1], J. F. Ridpath[4], and A. D. Herring[1], *[1]Texas A&M University, College Station, [2]Texas Agrilife Extension, College Station, [3]Texas Agrilife Research, College Station, [4]USDA-ARS, Ames, IA.*

Half-blood (F_2 and F_3), yearling Angus-Nelore steers (n = 106) were evaluated in 2012 for weight gain, feed intake, and rectal temperature after vaccination for Bovine Respiratory Disease (BRD) pathogens and subsequent intranasal challenge with Bovine Viral Diarrhea Virus (BVDV). Steers were confirmed free of BVD persistent infection and stratified by sire over 3 vaccine groups of killed (KV; n = 35), modified-live (MLV; n = 35), and non-vaccinated (NON; n = 36). KV steers received immunizations at d −49 and d −28, and MLV steers received a single immunization at d −28. On d 0 all steers were challenged via intranasal ingestion of BVDV Type 1b strain CA0401186a. Weights and rectal temperatures were collected on d 0, 3, 7, 10, 14, 28, 42. Steers were housed in 4 pens (balanced across vaccine groups) with daily feed intake (DFI) collected via a Growsafe system. A rectal temperature threshold over 40°C on evaluation days was used to classify steers for rectal temperature status (RTEMP). Mixed model procedures, with repeated measures were used to analyze DFI with a model that included fixed effects of vaccine group (VAC), pen, day, sire, RTEMP, and 2-factor interactions for VAC × RTEMP, sire × RTEMP, Sire × VAC and day × VAC; all were significant except VAC. ADG was calculated for the three 14-d periods as well as the 42-d period and was analyzed with a model containing similar fixed effects plus d-0 weight as a covariate; pen, Sire x VAC, and Sire × RTEMP were significant. For the Sire × RTEMP interaction (DFI, P < 0.01; ADG from d 0–42, P = 0.03), most sires had progeny rank higher for DFI and ADG when below RTEMP threshold, but some had higher DFI and ADG for progeny above RTEMP threshold. There was not a consistent trend across sires for the Sire × VAC interaction for DFI (P < 0.01) or ADG from d 0–42 (P = 0.05), implying that DFI and ADG may be affected quite differently across genetic backgrounds following BRD vaccination and subsequent pathogen exposure.

Key Words: BVDV, feed intake, ADG

169 Using DNA paternity testing to evaluate commercial bull performance. D. J. Drake[2], K. L. Weber[1], and A. L. Van Eenennaam*[1], *[1]Department of Animal Science, University of California, Davis, [2]University of California Cooperative Extension, Yreka.*

DNA markers for paternity identification were used to evaluate the breeding performance of bulls in multisire natural service breeding pastures on 3 large ranches in northern California for 3 consecutive years. All bulls passed breeding soundness examinations and were grouped with bulls of similar age. Two of the ranches had both fall- and spring-calving herds, while the third ranch had only a single fall calving herd. Breeding seasons ranged from ~90 d to 120 d depending upon the ranch. The cow:bull ratio was approximately 25 cows to 1 although the size of the group varied, giving bulls in larger groups access to a larger number of cycling females on any given day. Birthdate records and DNA samples were collected on 5,382 individually identified calves enrolled in the trial. Of these 5,272 (98%) were assigned to an individual sire. Bulls present per season (n = 296) produced 17.8 ± 13.1 progeny per calf crop, ranging from 0 to 63. Bulls with reduced breeding seasons due to injury or lack of condition produced fewer calves 9.1 ± 2.2 compared with full breeding season bulls 18.9 ± 0.78 progeny (P < 0.01). Bulls produced similar numbers of progeny across ranches (18.5 ± 1.2, 20.4 ± 1.8, 18.5 ± 1.4, P = 0.63), years (19.6 ± 0.4, 19.2 ± 1.4, 17.9 ± 1.4, P = 0.68), and season (20.3 ± 1.5, 18.3 ± 0.9, P = 0.27). The maximum number of calves sired by one bull in one day was 11 when placed with naturally cycling, unsynchronized females. The more prolific bulls sired more early calves (d 1–21 of the calving season) than low prolificacy bulls (P = 0.05). SC EPD was positively related to prolificacy (R^2 = 0.05, P < 0.01). There was a trend (R^2 = 0.01, P = 0.14) for older bulls to sire an increased number of progeny. Although most bulls in the study were Angus, the calves that were sired by South Devon (n = 217) and Hereford (n = 145) bulls were on average 20.4 kg and 16.4 kg heavier (P < 0.01) at weaning respectively, due to heterosis in these herds with high percent Angus commercial females. Prolificacy was the main driver of bull contribution to ranch income explaining 98.4% of the variation, whereas the individual calf value explained only another 0.88% of the variation.

170 Field assessment of progeny from sires with divergent residual feed intake genetic test results. K. L. Weber*[1], B. Welly[1], J. A. Rendon[2], C. Antwi[3], G. Acetoze[1], E. Kebreab[1], E. D. M. Mendes[4], and A. L. Van Eenennaam[1], *[1]University of California, Davis, Davis, [2]Universidad Autonoma de San Luis Potosi, San Luis Potosi, Mexico, [3]Kwame Nkrumah University of Science & Technology, Kumasi, Ghana, [4]Embrapa, Corumba, MS, Brazil.*

Due to the high cost of feed in beef production systems, there is interest in selecting cattle for feed efficiency, or ability to convert feed to marketable product. One measure of feed efficiency is residual feed intake (RFI), defined as the difference between observed feed intake and that predicted from metabolic body weight and rate of gain. The objective of this demonstration project was to assess the RFI in progeny derived from 2 Angus sires (HIGH, LOW) whose RFI breeding values differed by 0.32 kg/d based on the HD 50K MVP genetic test (Zoetis, Kalamazoo, MI). At 8 mo of age, 8 steer progeny from each sire, selected by live weight, were fed a growing ration (NEm 0.915 MJ/kg, NEg 0.525 MJ/kg). The steers' feeding intake and behavior were measured over 70 d using the GrowSafe System (Airdrie, AB Canada), and RFI calculated (RFI-GROW). The steers were finished in individual pens at the UC Davis feedlot, and finishing ration (NEm 1.76 MJ/kg, NEg 1.18 MJ/kg) feed intake was manually recorded. Body weights and ultrasound measures were taken every 2 weeks. Finishing RFI (RFI-FINISH) was calculated over an average of 91 d (70–105 d). Slaughter end point was determined based on ultrasound backfat thickness (11 mm), and a variety of carcass measurements were collected. Significance testing was performed using GLM procedures in R. Steers from the LOW RFI sire tended toward lower RFI-GROW (−0.64 kg/d, $P = 0.087$), with reduced visits to the bunk ($P < 0.05$) and increased visit duration ($P < 0.01$) when group-housed with GrowSafe. RFI-FINISH was significantly lower for LOW steers (−0.56 kg/d, $P < 0.05$). During the finishing period, LOW steers had heavier mid-test weights ($P < 0.05$), and a trend toward higher ADG ($P = 0.078$) and higher mid-test weight/hip height ($P = 0.083$). At slaughter, LOW steers had heavier empty body weights ($P < 0.01$) and increased carcass specific gravity ($P < 0.05$), suggesting LOW animals were leaner than HIGH animals for their carcass weight. These data showed a consistent trend of improved feed efficiency during both the growing and finishing phase in the steer progeny derived from the LOW RFI MBV Angus sire.

Key Words: beef, feed efficiency, genomic prediction

171 Relationships between residual feed intake EPD and metabolic variables of progeny from Red Angus sires divergent for maintenance energy EPD. C. M. Welch*[1], S. E. Speidel[2], W. J. Price[1], J. K. Ahola[2], J. B. Hall[1], G. K. Murdoch[1], D. H. Crews Jr.[2], C. S. Schneider[1], and R. A. Hill[1], *[1]University of Idaho, Moscow, [2]Colorado State University, Fort Collins.*

The Red Angus Association of America has developed the maintenance energy (ME_M) EPD as an estimator of maintenance requirements. Due to the associations among energy expenditure, performance, and feed intake, it has been proposed that ME_M EPD may be associated with residual feed intake (RFI). Postweaning RFI and other performance measures were recorded in 3 birth year contemporary groups from the progeny (n = 222) of sires (n = 12) divergent for ME_M EPD. The objectives of this study were to 1) identify relationships between sire RFI EPD and progeny serum IGF-I concentration and myogenic gene expression, and 2) identify the relationship between sire ME_M EPD and RFI EPD. Sires were partitioned into high (inefficient) and low (efficient) RFI groups based on their RFI EPD. For modeling purposes, RFI groups were considered as fixed effects while contemporary groups were random effects. Serum IGF-I concentration (collected at weaning) was higher ($P < 0.05$) in the high RFI group. In addition, serum IGF-I concentration was positively correlated (r = 0.34; $P < 0.0001$) with RFI EPD. Using biopsy samples collected from the biceps femoris, the relationship between key genes in various regulatory pathways and RFI EPD were evaluated, and no associations ($P > 0.05$) were detected for gene expression and RFI EPD. Furthermore, sire ME_M EPD was found to be negatively correlated (r = −0.26; $P < 0.003$) with sire RFI EPD. Therefore, our data analyses indicate (1) serum IGF-I concentration may be an underlying metabolic indicator of RFI due to its relationship with RFI EPD, (2) evaluation of myogenic gene expression offered no insight into the physiological mechanisms associated with the RFI phenotype, and (3) the negative correlation between RFI EPD and ME_M EPD may suggest that a properly weighted selection index tool could be developed to improve efficiency of feed utilization.

Key Words: EPD, IGF-I, residual feed intake

172 Factors influencing feed efficiency of beef cows of varying proportion of Brahman influence. S. W. Coleman* and J. P. S. Neel, *USDA ARS, El Reno, OK.*

Feed constitutes the greatest proportion of costs in cow-calf production. Therefore, genetic merit for feed efficiency has received interest from producers, but has generally been assessed in growing animals. The objectives of this study were to determine the main factors that contribute to variance in feed intake and determine whether proportion Brahman genetics (B) interacts with those factors. Ninety cows, varying in proportion Brahman influence (0, 1/4 and 1/2), were fed in groups of 30 over 3 seasons (S; 2 spring- and 1 fall-calving) in pens designed to determine individual feed intake. Within about 3 wk postpartum, cows and their calves were evaluated throughout lactation. Cow and calf weights and milk production and composition were determined at monthly intervals. Sorghum silage was the primary dietary component for cows, being supplemented with a grain and cottonseed mix to mimic forage from rangeland. Calves were offered whole oats in separate creep feeders. Diet samples were taken at weekly intervals and analyzed for CP and IVDMD while refusals were taken as needed. The diets averaged 8.2, 7.6, and 8.8% CP and 55.7, 50.3, and 48.9% IVDMD for each of the seasons, respectively. Digestible dry matter intake (DDMI) of cows was the variable of interest and analyzed using GLM of SAS. The model included class effects of S and B, continuous variables average daily milk energy produced, calf ADG, cow weight, and season-long weight change, and interactions of S and B with the continuous variables. Season ($P < 0.01$), milk energy ($P = 0.07$), calf ADG ($P < 0.01$), and the interaction of B with calf ADG ($P < 0.08$) and cow weight ($P = 0.06$) influenced DDMI ($R^2 = 0.9$). Each additional kg of calf ADG required 1.13 kg DDM, but cows with either 0 or 1/2 Brahman required less than those with 1/4 Brahman influence. A kg of milk energy required 1.32 kg additional DDM. Cows generally lost weight over the lactation on these diets, but the level of loss did not influence variation in intake. Dry matter intake of these cows was greater than that predicted by the NRC equation.

Key Words: feed efficiency, cow-calf, Brahman influence

173 The effect of heterosis of dam and crossbreeding on progeny's feed efficiency, performance and carcass characteristics. K. M. Retallick*[1], D. B. Faulkner[2], S. L. Rodriguez-Zas[1], J. D. Nkrumah[3], and D. W. Shike[1], *[1]University of Illinois, Urbana, [2]University of Arizona, Tucson, [3]Pfizer Animal Genetics, Kalamazoo, MI.*

Two experiments (1: n = 577) (2: n = 158) were conducted to analyze maternal effects and crossbreeding on subsequent steer performance,

carcass, and feed efficiency traits. Steers were early weaned at 78 ± 24 d of age and randomly pen allotted. Steers were managed similarly before weaning and fed a common finishing diet. In experiment 1, Angus (AN) and/or Simmental (SM) maternal dam breeds were represented: (1) 100% AN (AN), (2) 75% AN (75AN), (3) 50% AN (50AN), and (4) 25% AN (25AN). The remaining percentage was SM. Results from experiment 1 showed that DMI was 0.22 kg/d lower ($P < 0.05$) for progeny of 75AN and 50AN indicating a positive influence of maternal heterosis. Consequently, residual feed intake (RFI) had a tendency to improve ($P = 0.06$) for 75AN and 50AN compared with AN and 25AN dams. Residual BW gain of progeny tended to improve ($P = 0.07$) as percent of AN decreased in the dams. Steers whose dams had a decreased percentage of AN also had more desirable ($P < 0.05$) LM area, backfat, and yield grade. In conclusion, experiment 1 showed that dams of varying AN breed composition produce offspring that perform differently in the feedlot with progeny that were from 75AN dams excelling in the feedlot. In experiment 2, purebred AN and SM sires and dams were utilized. Experiment 2 resulted in progeny from SM dams having a more desirable RFI ($P < 0.05$). An improved HCW, backfat, LM area, and consequently yield grade was shown by progeny of SM dams ($P < 0.05$); however, marbling score was 80 units higher for progeny of AN dams ($P < 0.05$). When compared, sire breeds had no difference in HCW ($P = 0.82$), but SM-sired progeny had an advantage in LM area, backfat, and yield grade ($P < 0.05$). The only sire by dam breed interaction was for marbling score ($P = 0.05$). Experiment 2 showed both maternal and paternal effects on progeny in the feedlot with the maternal advantage in RFI given to progeny of SM dams. Overall, maternal breed effects on performance, feed efficiency measures, and carcass traits of resulting progeny appear to be important.

Key Words: feed efficiency, feedlot, maternal breed effect

174 Relationship among performance, carcass, and feed efficiency characteristics and their ability to predict economic value in the feedlot. K. M. Retallick*[1], D. B. Faulkner[2], S. L. Rodriguez-Zas[1], J. D. Nkrumah[3], and D. W. Shike[1], *[1]University of Illinois, Urbana, [2]University of Arizona, Tucson, [3]Pfizer Animal Genetics, Kalamazoo, MI.*

A 4-year study was conducted utilizing 736 steers of known Angus, Simmental, or Simmental × Angus genetics to determine performance, carcass, and feed efficiency factors explaining variations in economic performance. Steers were pen-fed and individual DMIs were recorded using the GrowSafe feeding system (GrowSafe Systems Ltd., Airdrie, Alberta, Canada). All steers received similar diet and management. Feed efficiency values investigated were: feed conversion ratio (FCR), residual feed intake (RFI), residual BW gain (RG), and residual BW gain and intake (RIG). Data were analyzed using stepwise option of PROC REG in SAS (SAS Inst., Inc., Cary NC) to determine regression intercept, slope, and model fit (R^2) explaining variation within each pricing scenario. Dependent variables were carcass value ($/steer), profit ($/steer), feed costs ($/steer*$d^{-1}$), and cost of gain ($/kg). Independent variables were year, DMI, ADG, HCW, LM area, marbling, yield grade, dam breed, and sire breed. A 10% improvement in RG ($P < 0.05$) yielded the most favorable cost of gain (−0.09 $/kg) and carcass value (17.92 $/steer). Carcass value increased ($P < 0.05$) as feed efficiency improved by 10% for FCR, RG, and RIG. Profit increased with a 10% improvement feed efficiency ($P < 0.05$) with FCR at 34.65 ($/steer), RG at 31.21 ($/steer), RIG at 21.66 ($/steer), and RFI at 11.47 ($/steer). The model for carcass value explained 96% of the variation among carcasses and included HCW, marbling score, and yield grade. Average daily gain, marbling score, yield grade, DMI, HCW, and year born constituted 81% of the variation for the prediction of profit. Variation in cost of gain was mainly explained by ADG and DMI ($R^2 = 0.78$). Prediction equations were developed that excluded ADG and DMI and included feed efficiency values. Cost of gain was explained primarily by FCR ($R^2 = 0.71$). Seventy-three percent of profitability was explained with RG and marbling accounting for 55% of this total explained variation. These models represent the relative importance of factors contributing to economic success in feedlot cattle based on current prices.

Key Words: feedlot economics, feed efficiency

175 Grass-finishing high-value beef: A pilot project in northern United States. P. Lammers*[1], M. Honeyman[2], R. Dewell[2], and S. Millman[2], *[1]Illinois State University, Normal, [2]Iowa State University, Ames.*

Grass-finished beef is a growing niche market but producer adoption of this feeding strategy has been limited. Consistently producing high-value beef on forage alone is challenging. Intramuscular fat (IMF) is a key factor in beef quality grading; both diet and genetics influence IMF. Ultrasound scanning of growing cattle can be used to identify cattle with high-IMF potential and predict carcass quality. This pilot study examined the potential for producing USDA Quality grade Choice beef by combining scanned IMF data with pasture management. Yearling Angus heifers (22 hd) were blocked by scanned IMF and body weight. Blocks of cattle were allotted to either pasture or feedlot on May 7, 2012 at the Armstrong Research Farm, Lewis, IA (41°N 95°W). The 10.5 ha pasture was a mix of alfalfa (*M. sativa*) and smooth brome (*B. inermis*). Initially, grazing cattle were moved to a fresh paddock every 3–4 d with surplus forage harvested to maintain pasture quality. In mid-July, overly dry conditions prevailed and cattle were given access to the entire pasture until marketing. Feedlot cattle were fed a mixed ration of 45% corn grain, 32% modified distillers grain, 20% ground hay, and 2% supplement that included monensin (DM basis). No cattle were implanted, fed hormones, or antibiotics. Cattle were weighed every 28-d until the average BW of the treatment group reached 453.5 kg. Cattle were weighed and scanned before harvest at a commercial abattoir where carcass data was collected. Initial BW and IMF and final BW were not different for the 2 treatments ($P > 0.5$). Feedlot cattle grew faster (1.78 vs. 0.94 kg/d, $P < 0.001$), had 0.41 cm more fat cover ($P = 0.02$), and produced a 7% larger carcass ($P = 0.05$). Yield grade, LMA, and scanned IMF at market were similar ($P \geq 0.08$) for both groups. All cattle increased IMF content during finishing and based on final scanned IMF, ≥90% of cattle in both treatments were expected to grade Choice. Ultimately 92% of feedlot heifers but only 60% of pasture heifers graded Choice or better. Fat cover of the pasture cattle was yellow which may explain why the scanned IMF did not predict the quality grade at the abattoir.

Key Words: beef quality, grass-finished, grazing

Bioethics Symposium II: Is Modern Animal Agriculture Ethically Defensible?

176 The food morality movement: The race to the moral high ground. K. Murphy*, *Food-Chain Communications LLC, Lees Summit, MO.*

Many critics of modern, intensive farming and food production have shifted their criticism to one based upon questions of religion, ethics and morality. We term this "the food morality movement" (FMM). The FMM often employs the language of science, food-safety, environmental impact and socio-economics to entice the general public into debate regarding ethical questions involving social justice, environmental justice, economic equality, animal rights, and others. Animal scientists and others who must respond to FMM-based criticism must adapt their response to incorporate several elements of a morality-focused defense, including reclaiming the farmer's moral heritage, relearning communication strategies based on morality, avoiding internecine strife caused by misunderstanding of FMM motives, and shedding lingering guilt based on moral uncertainty. The modern food system needs an agricultural apologia to answer the FMM in the race to the moral high ground.

Key Words: food morality movement, modern food system, animal science

177 Consumer perception of production process attributes for pork and lunchmeat products. M. G. S. McKendree*, N. J. O. Widmar, and C. C. Croney, *Purdue University, West Lafayette, IN.*

Livestock producers are facing a changing marketplace. Consumers are increasingly focused on the practices used to produce their food and are especially interested in the treatment of livestock. An online survey of 798 US consumers was conducted in June 2012. One objective of this study was to determine consumer purchasing patterns of meat and dairy products, and perceptions of hog rearing and livestock product attributes. Fourteen percent of respondents reported reduced overall pork consumption due to animal welfare/handling concerns in the past 3 years. Of those included in the survey, concern for pig rearing practices was highest for intensive housing practices; fewest respondents were concerned about castration and ear notching. Although concern for livestock animals is often discussed, consumers' actual shopping decisions focus on individual products. Lunchmeat purchasing and preferences for lunchmeat attributes were assessed. Inconsistencies were found between which lunchmeat attributes consumers associated with high quality and which attributes they actually considered during purchase. Over 73% of respondents agreed that "produced on farms with animal welfare and handling standards in place" and "produced by farmers certified in animal welfare techniques" were associated with higher quality lunchmeats. Of those purchasing lunchmeat, only 47% and 45% of respondents, respectively, reported considering these attributes during purchase. When asked about concern for animal welfare and food safety, the majority of products studied elicited concern from more respondents for food safety. Staple products (milk, eggs and ground beef) generated concern for the largest number of respondents. Numbers of respondents indicating concern varied across products, even when they were produced by the same animal species (i.e., steak versus roast beef lunchmeat). This work suggests that consumers' values and beliefs influence their perceptions of important product attributes (such as food safety and animal welfare/handling) and potentially their purchasing behavior. However, high variation exists in concerns as a function of the product type and attribute.

Key Words: consumer demand, animal welfare, pork

178 An analysis of perceived obligations by consumers across animal species: Livestock, pet, or neither? M. G. S. McKendree*, C. C. Croney, and N. J. O. Widmar, *Purdue University, West Lafayette, IN.*

Do perceived concerns about and obligations to animals vary based on their classification as a pet, livestock animal, or neither? An online survey (n = 798) was conducted with an objective of determining consumers' classification of animal species, the relationship between classification and opposition to eating those species, and the relationship between pet ownership/crating and their perceived obligations to animals. The survey collected information on household demographics, pet ownership and perceptions of pets, and perceptions of traditional and non-traditional livestock animals. One interesting species classification was the horse, with 55% selecting pet, 27% livestock and 18% neither. Respondent opposition to eating animals varied by animal species; 81 respondents opposed eating a beef cow while 151 opposed eating a dairy cow. Respondents opposed to eating certain animal species were less opposed to others eating them. Tying classification with opposition to eating animals, those classifying a beef cow as non-livestock more often reported opposition to eating animals than those classifying a beef cow as livestock. Sixty-six percent of respondents reported having at least one household pet. At the 95% confidence level, respondents with cats and/or dogs more frequently reported concern about livestock animal welfare than those without cats and dogs. Of those with cats and/or dogs, 20% reported using cages/crates. However, no statistical differences were found between those who used crates/cages and those who did not regarding their level of concern for pig housing and management practices (including gestation crates, farrowing crates, group housing, and indoor confinement). Dog and/or cat owners more frequently reported having a source for animal welfare information (51% of dog and cat owners vs. 32% without a cat/dog). Understanding consumers' views of different livestock species, their perceived obligations to animals and sources of relevant information is an important step in facilitating constructive discussions of agricultural animal care, welfare and ethics that incorporates layperson's beliefs and values.

Key Words: animal welfare, pet, livestock

179 Industry stakeholder views on dairy cattle welfare. B. A. Ventura*, M. A. G. von Keyserlingk, and D. M. Weary, *Animal Welfare Program, Faculty of Land and Food Systems, University of British Columbia, Vancouver, BC Canada.*

Increasing stakeholder engagement is important as the dairy industry seeks to address societal concerns about the welfare of farm animals. The aim of the current study was to facilitate engagement among stakeholders and to describe their perspectives on key issues affecting the welfare of dairy cattle. Five heterogeneous focus groups were conducted during a dairy cattle industry meeting in Guelph, Canada in October 2012. Each group contained between 7 and 10 participants and consisted of a mix of dairy producers, veterinarians, researchers, students, and industry specialists. The 1 h facilitator-led discussion focused on participants' perceptions of the key welfare issues and the role of different groups in addressing these concerns. Discussions were

audio-recorded and transcribed verbatim, and the resulting transcripts coded and the themes identified. Lameness was uniformly recognized as the most important welfare issue facing dairy cattle; cow comfort, painful procedures (such as dehorning) and other production diseases (such as mastitis) were also commonly discussed. Participants had mixed views on the roles of different stakeholders in formulating solutions; many felt that producers and others working within the dairy industry should be primarily responsible, but some believed that members of the general public also had an important role. Participants agreed that improved knowledge translation from researchers to producers and from dairy industry groups to the public was required to develop solutions to these concerns. These results illustrate the value of stakeholder engagement in developing solutions to dairy cattle welfare concerns.

Key Words: stakeholder attitudes, animal welfare, engagement

Breeding and Genetics: Applications and Methods in Animal Breeding—Pigs

180 Survival analysis of mice divergently selected for heat loss. A. S. Bhatnagar* and M. K. Nielsen, *University of Nebraska-Lincoln, Lincoln.*

Improvement in feed efficiency was achieved by reducing maintenance energy requirement without changing output in mice divergently selected for heat loss (MH = high, ML = low, MC = control). In 3 replicates of selection, feed intake at the same mature weight differs greatly (MH/ML~1.38). However, correlated decline in reproductive stayability may negate the benefit in reduced feed intake. For each line by replicate combination, 21 mating pairs were sampled at 7 wk of age (189 pairs). Pairs were culled due to death or illness of either member, no first parity by 42 d cohabitation, 2 consecutive litters with none born alive, 3 consecutive litters with none weaned, 42 d between parities, or average size of most recent 2 litters less than half the average of first 3 litters. All pairs were culled by 1 yr cohabitation. Survival curves were produced from Kaplan-Meier estimates and hazard ratios were produced using Cox proportional hazard model. Data were analyzed over the entire study and in 2 periods (P1: ≤ 5 parities, P2: > 5 parities). A competitive risk analysis was performed to explore risk of culling for each criterion. Log-rank tests of survival curves and hazard ratios showed similar trends. Overall, there was no difference in hazard rates between MH and ML mice. However, MH mice were 2.57 more likely to be culled than ML mice in P1 ($P < 0.04$) but 0.55 times less likely in P2 ($P < 0.04$). MH and ML mice had an increased hazard over MC mice ($P < 0.03$ and $P < 0.01$, respectively). MH mice carried an increased risk of 3.49 ($P < 0.02$) in P1, while ML mice carried an increased risk of 2.58 ($P < 0.01$) in P2 compared with MC mice. There were no differences found in the competitive risk analysis between MH and ML mice for any culling criteria. Results indicate that MH mice are more likely to be culled early and ML mice later, but MC mice have greater survival rates. For systems where smaller maximum parities are desirable, ML mice have less involuntary losses and thus enhanced efficiency in addition to their lower maintenance. But this advantage erodes in systems allowing larger numbers of parities.

Key Words: survival, feed efficiency, mice

181 Genome-wide association mapping including phenotypes from relatives without genotypes for three traits in broiler chickens. H. Wang*[1], I. Misztal[1], I. Aguilar[2], A. Legarra[3], W. Muir[4], R. Fernando[5], and R. Hawken[6], *[1]University of Georgia, Athens, [2]INIA, Las Brujas, Uruguay, [3]INRA, Toulouse, France, [4]Purdue University, West Lafayette, IN, [5]Iowa State University, Ames, [6]Cobb-Vantress Inc., Siloam Springs, AR.*

The purpose of this study is to extend genome-wide association studies using a single-step method (ssGBLUP) for a multi-trait model in broiler chickens. Data set consisted of 2 pure lines (L1 and L2) across 5 generations for 3 traits: body weight at 6 wk (BW6), ultrasound measurement of breast meat (BM), and leg score (LS) coded 1 = no and 2 = yes for leg defect. In total, there were 294,632 and 274,776 individuals in pedigree for L1 and L2, of which 4667 and 4553 were genotyped using a SNP 60k panel. After standard quality control, 40,615 SNP markers remained for analyses. For BM, there were ~74% missing phenotypes in both lines. Pedigree, phenotypic and genomic information were combined, and a multi-trait linear model was used through ssGBLUP. Genomic breeding values were calculated for all individuals in pedigree and converted to SNP effects. Variances of markers were calculated from SNP solutions and included as weights in a new genomic relationship matrix. The last step was repeated 5 times. Manhattan plots were constructed as proportion of genetic variance explained by each region consisting of 20 consecutive SNP markers. Several peaks explaining >1% of the genetic variation were found for BW6; however, peaks for L1 and L2 are on different chromosomes. No strong peaks have been observed for BM and LS, and each region for these traits explained <1% of total genetic variance. BM and LS seem to follow the infinitesimal model. Different peaks for the 2 lines for BW6 suggest different selection goals. The ssGBLUP approach allows for simple GWAS with complex models and easy accommodation of information from genotyped animals.

Key Words: chicken, genome-wide association, multi-trait model

182 Accuracy of estimation of genomic breeding values in pigs using low density genotypes and imputation. Y. M. Badke*[1], R. O. Bates[1], C. W. Ernst[1], J. Fix[3], and J. P. Steibel[1,2], *[1]Department of Animal Science, Michigan State University, East Lansing [2]Department of Fisheries & Wildlife, Michigan State University, East Lansing, [3]National Swine Registry, West Lafayette, IN.*

Genomic selection has the potential to increase genetic progress. Genotype imputation of high density SNP genotypes can improve cost efficiency of genomic breeding value (GEBV) prediction for pig breeding. Consequently, the objectives of this work were to (1) estimate accuracy of GEBV in a Yorkshire population and (2) quantify the loss in accuracy of GEBV prediction when genotypes were imputed (accuracy = 0.95) in selection candidates. Phenotypes (Table) and genotypes obtained with the PorcineSNP60 BeadChip were available for 965 Yorkshire boars. Genotypes of selection candidates were masked and imputed using tagSNP in the GeneSeek Genomic Profiler (10K). Imputation was performed with BEAGLE using 128 haplotypes as reference panel. SNP effects were estimated with ridge regression using de-regressed breeding values as response variables. Accuracy of GEBV was estimated as the squared correlation between estimated breeding values (EBV) and GEBV in a 10-fold cross validation design. Accuracy of GEBV prediction from observed genotypes (r^2_{obs}) ranged from 0.03 for LBW to 0.47 for BF (Table). Variation in accuracy between traits largely depended on the number of boars (N) with usable EBV. Using imputed genotypes for GEBV estimation caused a slight decrease in the accuracy of GEBV (r^2_{imp}) with the proportion of r^2_{imp} to r^2_{obs} ranging from 0.87 to 0.99. GEBV prediction from imputed genotypes is a cost efficient alternative for implementation of genomic selection in pigs. Furthermore, genotyping animals at lower cost and low density, followed by imputation, can result in increased accuracy by allowing more animals into the training panel.

Table 1. Accuracy of genomic prediction

	Backfat thickness	Days to 250 lb	Litter birth weight	Loin muscle area	Litter weaning weight	No. born alive	No. weaned	Wean to estrus
Boars with usable EBV (no.)	965	936	302	938	612	532	482	332
h^2	0.45	0.26	0.19	0.47	0.065	0.08	0.02	0.33
r^2obs	0.47	0.45	0.03	0.45	0.25	0.18	0.21	0.14
r^2imp	0.45	0.44	0.06	0.40	0.23	0.16	0.18	0.13
r^2imp/r^2obs	0.95	0.99	NA	0.89	0.91	0.93	0.87	0.90

Key Words: genomic prediction, pig, imputation

183 Estimation of US Yorkshire breed composition using genomic data. Y. Huang*[1], R. O. Bates[1], C. W. Ernst[1], J. S. Fix[2], and J. P. Steibel[1,3], *[1]Department of Animal Science, Michigan State University, East Lansing, [2]National Swine Registry, West Lafayette, IN, [3]Department of Fisheries and Wildlife, Michigan State University, East Lansing.*

White coat color, as an indication of breed purity has been a long-time selection requirement for the Yorkshire breed. Currently, color verification is completed using a test mating program, which creates an inefficient use of time and resources. In this study, genomic information from local chromosomal regions surrounding the positions where coat color genes are physically mapped, as well as the whole genome were applied to estimate breed composition of purebred Yorkshire animals. Genotypes for ~60,000 SNP from the Illumina PorcineSNP60 Beadchip (60K), including ~8,500 SNP from the GeneSeek Genomic Profiler for PorcineLD (GGP) (GeneSeek, Lincoln, NE) were available for reference animals, in which the genetic background was known, and study animals, that included Yorkshire sires (Tes_York, n = 889), and known crossbred animals that had Yorkshire heritage (Tes_U, n = 12). Haplotypes of 9 SNPs flanking the KIT gene (Dominant white) were developed for reference animals for the Duroc (n = 60), Hampshire (n = 52), Landrace (n = 56), Yorkshire (n = 64) and Pietrain (n = 15) breeds. Haplotypes observed in white reference breeds (Yorkshire and Landrace) were detected in 97% and 62% of haplotypes from Tes_York and Tes_U, respectively. Therefore, multi-SNP haplotypes flanking KIT can be used to classify animals that are not of Yorkshire or Landrace breed origin. In addition, whole genome SNP information was used in regression analyses to further differentiate breed composition. Using 60K SNP, regression coefficients for Yorkshire, indicating relative Yorkshire composition, ranged from 0.79 to 1.07 and 0.52 to 1.06 in Tes_York and Tes_U, respectively. Regression coefficients for Hampshire ranged from −0.029 to 0.052 and −0.005 to 0.38 in Tes_York and Tes_U, respectively. Animals in Tes_U were likely of Yorkshire and Hampshire breed origin. Correlation of regression coefficients for breed composition obtained by using the 60K and GGP SNP panel was 0.99. Genomic information can be used as a tool to describe an animal's breed composition and reduce the need for progeny testing for white coat color verification.

Key Words: haplotype, regression, SNP

184 Genome-wide association for human nose score of boar taint using single-SNP analysis. Y. G. Tesfayonas*[1,2], *[1]Wageningen University, Wageningen, the Netherlands, [2]Swedish University of Agriculture Sciences, Uppsala, Sweden.*

Human nose score (HNS) is one method used to reduce boar taint without castration. It involves the scoring of the level of boar taint in boars by sensory panel. The objective of this study was to identify SNPs that are associated with HNS and to determine the phenotype variation explained by the SNPs. Boar taint is the unpleasant odor released when cooking meat from entire male pigs. It is mainly caused by increased accumulation of androstenone and skatole in adipose tissue. Producers castrate male pigs to remove boar taint; however, this practice has raised animal welfare concerns from consumers. HNS of 1835 intact boars from 5 purebred (1,438) and 3 crossbred (397) lines genotyped with Porcine 60K SNP Bead chip, and 46,751 SNPs were used for the genome wide association study; boars that were part of the purebred and crossbred both contained sire and sow lines. The design of the study was population based. GRAMMAR approach in R package-GenABEL was employed for the genome wide association analysis. This study revealed genome wide SNP (FDR ≤0.05) on SSC5. The SNP had minor allele frequency of 0.04% and it explained 19% of the phenotype variation. In addition, Boars heterozygous for the SNP had a mean score (0.72) higher than the 2 homozygous genotypes (0.56 and 0.63) which suggests over dominance. Moreover, chromosome wide significant SNPs (FDR ≤0.05) were found on SSC2, SSC7 and SSC17. Some of the SNPs correspond to QTLs of androstenone and skatole. Therefore, HNS can be used to alleviate boar taint through breeding.

Key Words: human nose score, boar taint, SNP

185 Identification of a major QTL associated with N-specific IgG response in piglets experimentally infected with porcine reproductive and respiratory syndrome virus. A. S. Hess*[1], B. R. Trible[2], Y. Wang[2], N. J. Boddicker[1], R. R. R. Rowland[2], J. K. Lunney[3], and J. C. M. Dekkers[1], *[1]Iowa State University, Ames, [2]Kansas State University, Manhattan, [3]USDA, ARS, BARC, APDL, Beltsville, MD.*

Porcine reproductive and respiratory syndrome virus (PRRSv) costs the US pork industry $664 million annually; therefore, much emphasis has been placed on identification of genomic markers and pathways associated with host response. Serum level of immunoglobulin G (IgG) likely contributes to observed variability in health when infected with PRRSv. This study examined serum virus N protein-specific IgG levels, measured by fluorescent microsphere immunoassay. Serum and other data were collected on 462 Large White × Landrace piglets infected with PRRSv isolate NVSL 97-7895. 1:400 dilutions of sera, collected 42 post-infection, were added to virus N protein coupled beads. Antibody was detected by addition of biotin-conjugated goat anti-swine IgG, followed by addition of streptavidin-conjugated phycoerythrin. MAGPIX was used to obtain mean fluorescence intensity (MFI). Three standards were run on each plate: a negative control (no pig serum), a medium positive (serum with a median MFI), and a high positive (serum with a high MFI). Subtraction of the background and standardization using high positive resulted in a sample:positive ratio with the least between plate variation (4.6 ± 4.2% of total variance) and was used for analysis. Pedigree-based heritability was 13.5 ± 13.2%. In a genome-wide association study using 60k SNP data, the proportion of markers with no effect (π) was estimated to be 0.9999 using BayesCPi in GenSel. The 1-Mb region that explained the most genetic variation was on chromosome 7 in a region harboring the major histocompatibility (MHC) class I antigen genes, and was estimated to explain 54.2% of genetic variation. Analysis with Bayes B supported these results, indicating the presence of a major QTL associated with IgG levels. This is indicative of response to the N protein of PRRSv and is consistent with the presence of the MHC class I genes in the region, which play a direct role in immune response to viruses. Supported by NPB grant #12–120, Genome Canada, the National Pork Board and breeding companies of the PRRS Host Genetics Consortium.

Key Words: PRRSv, pig, antibody

186 eQTL analysis of blood RNA from pigs challenged with PRRSV reveal numerous differentially expressed transcripts associated with viral load QTL region. J. P. Steibel*[1], I. Choi[4], M. Arceo[1,3], C. W. Ernst[1], N. Raney[1], Z. Hu[2], C. K. Tuggle[2], N. Boddicker[2], J. Dekkers[2], R. R. R. Rowland[5], and J. K. Lunney[4], *[1]Michigan State University, East Lansing [2]Iowa State University, Ames, [3]North Carolina State University, Raleigh, [4]BARC-USDA, Belltsville, MD, [5]Kansas State University, Manhattan.*

This study's aim was to assess differentially expressed (DE) genes in pigs segregating for SNP WUR10000125 on SSC4, which has been reported as associated with porcine reproductive and respiratory syndrome virus (PRRSV) load post infection. Healthy pigs (n = 39) from a PRRS Host

Genetics Consortium (PHGC) trial were inoculated with PRRSV isolate NVSL 97–7985. RNA was prepared from blood Tempus tube samples collected at 0, 4, and 7 d post-infection. Pigs were assigned into 4 phenotypic groups according to the pigs' serum viral level and weight gain: (1) high viral level (Hv)-high growth (Hg), (2) Hv-low growth (Lg), (3) low viral level (Lv)-Hg and (4) LvLg. RNA was hybridized to the 20K 70-mer oligonucleotide Pigoligoarray in a blocked reference design with time 0 of each individual animal as the reference sample. Microarray data was analyzed using a linear mixed model with fixed effects of dye, time, phenotypic group (viral load × weight gain), WUR10000125 SNP genotype, interactions of SNP genotype × time and time × group, and random effects of array and pig. Nine oligonucleotides representing genes close to the WUR10000125 SNP were tested separately to assess cis-effects; a suggestive cis-acting association was detected for GBP4 ($P = 0.007$). A total of 107 oligonucleotides spanning 99 known genes across the genome were DE with respect to genotype within time effects (FDR <10%). Enrichment analyses for these 99 genes were performed with Ingenuity Pathways Analysis software. Top biological functions were Inflammatory Response, Cell-mediated Immune Response, and Lymphoid Tissue Structure And Development. Top canonical pathways included CCR5 Signaling in Macrophages, Cytotoxic T Lymphocyte-mediated Apoptosis of Target Cells, Calcium-induced T Lymphocyte Apoptosis and T Cell Receptor Signaling. Finally, TRAT1 and IL15 were identified as the top upstream regulators. These results provide insight into potential eQTL and mechanisms involved in the genetic control of gene expression in relation to PRRSV infection. A larger sample size is being processed to confirm these results in a broader eQTL scan.

Key Words: porcine reproductive and respiratory syndrome (PRRSV), eQTL, PRRS Host Genetics Consortium (PHGC)

187 Include birth weight in your breeding goal in the right way. R. Bergsma* and E. F. Knol, *TOPIGS Research Center IPG B.V., Beuningen, the Netherlands.*

The objective of our study was to examine optimal use individual birth weight (IBWT) observations to improve the genetic model for average daily gain (ADG). Data on ± 25,000 crossbred finishers were collected at TOPIGS Research farm in Beilen (NL). Pigs weighing 0.9 kg at birth had a grow-finish ADG of 828 g/d, while their 1.8-kg littermates gained 885 g/d, resulting in a reduction of 7 d to market. Pig breeding companies have been successful in selecting for increased litter size. As litter size increased, average birth weights tended to decline (b = −37 g/pig). When pig birth weight drops, the probability of preweaning death increases. Increasing birth weight by genetic selection seems, therefore, to be an attractive alternative. Several studies show that the heritability of IBWT is 0.30 or higher. A similar estimate was found in this data set. Birth weight, however, is not a characteristic of the piglet, but a characteristic of the sow. Analyzing IBWT with a direct–maternal genetic model reduced the heritability for the direct effect to 0.02 while the heritability for the maternal component was 0.15. The statistical properties of the latter model showed that this model is, by far, preferable to a direct genetic model. A bivariate model for IBWT and ADG showed that ADG and the direct effect of IBWT were uncorrelated and that ADG and the maternal component of IBWT had a moderate genetic correlation ($r_g = 0.34$). Since sows with a high genetic merit for ADG are heavier when giving birth (Bergsma et al., 2008), this genetic correlation showed that these sows give birth to heavier piglets because they are heavier themselves. As a bonus the genetic variance for ADG increased by 9%. The low heritability for the direct effect for IBWT also means that the sire of the litter hardly affects IBWT. This, together with the observation that IBWT and ADG are genetically uncorrelated, justifies the conclusion that selection for IBWT in sire lines is not relevant. Add IBWT as a direct–maternal effect to your genetic evaluation of ADG. This improves the perspective for selection for ADG and allows you to select for increased average birth weight (in dam lines) via increased litter weight.

Key Words: pig breeding, birth weight, daily gain

188 Genetic analysis of pig survival in a crossbred population. M. Dufrasne*[1,2], I. Misztal[3], S. Tsuruta[3], K. A. Gray[4], and N. Gengler[1], *[1]Gembloux Agro-Bio Tech, University of Liege, Gembloux, Belgium, [2]FRIA, Brussels, Belgium, [3]Department of Animal and Dairy Science, University of Georgia, Athens, [4]Smithfield Premium Genetics Group, Rose Hill, NC.*

The aim of this study was to estimate genetic parameters for survival traits at different steps of the fattening period and their relationships with final weight in a commercial crossbred population of pigs. The edited data set consisted of 24,376 crossbred pigs from 197 purebred Duroc sires and 1,671 non-pedigreed Large White x Landrace dams. Traits analyzed were preweaning mortality (PWM); farrow dock (FAD) defined as culling between farrowing and nursery site; nursery dock (NUD) defined as culling between nursery and finisher site; finisher dock (FID) defined as culling before packing plant; hot carcass weight (HCW). Genetic parameters were estimated with a threshold-linear sire model because of the combination of categorical (PWM, FAD, NUD, and FID) and continuous (HCW) traits. Fixed effects were sex and dam parity. Random effects were year × month of birth, sire, litter and residual. The PWM was 16.99%, FAD was 0.71%, NUD was 0.90%, and FID was 1.02%. The mean HCW was 93.4 kg. Estimates of heritability were low to moderate (0.04 for PWM, 0.02 for FAD, 0.14 for NUD, 0.07 for FID, 0.12 for HCW). The sire genetic effects, defined as the ratio between the estimated sire variance and the total variance, were even lower and followed the same pattern than heritability. Estimates of common litter effect were higher and decreased with time for survival traits (0.11 for PWM, 0.19 for FAD, 0.10 for NUD, 0.04 for FID). Estimate of genetic correlation was 0.10 between PWM and FAD. Estimates of genetic correlations were negatives between PWM and NUD (−0.51), between PWM and FID (−0.10), between FAD and NUD (−0.50), and between FAD and FID (−0.21); NUD was positively correlated with FID (0.41). Estimates of genetic correlation between survival traits and HCW were 0.08 for PWM, −0.11 for FAD, 0.03 for NUD, and −0.27 for FID. Survival at the beginning of the fattening period (PWM and FAD) is not a good predictor for survival until harvesting and high market weight. Docking at nursery and finisher stages are more similar traits than docking at farrowing stage. The influence of the sire line on the survival of crossbred pigs is small.

Key Words: genetic parameter, pig, survival

189 Survival from birth to weaning in gilts. A. J. Cross*[1], M. Knauer[1], A. DeDecker[3], K. Gray[2], J. Holl[5], S. Callahan[4], and JP Cassady[1], *[1]North Carolina State University, Raleigh, [2]Smithfield Premium Genetics, Rose Hill, NC, [3]Murphy-Brown LLC, Rose Hill, NC, [4]Virginia Polytechnic Institute and State University, Blacksburg, [5]PIC North America, Hendersonville, TN.*

The aim of this study was to evaluate the influence of birth weight on gilt survival. For the US pig industry to remain globally competitive production efficiencies must continue to be improved. Improved methods for producing pork that reduce inputs, minimize environmental impact, maximize pig well-being, and ensure a safe, nutritious pork supply are

needed. To improve reproductive efficiency, pigs have been genetically selected for increased litter size at birth. However as number born alive increases, individual piglet birth weight decreases. Low piglet birth weights can result in increased pre-weaning mortality and reduced wean-to-finish growth performance. Information on 12,968 gilts from 2 genetic multiplier farms in eastern North Carolina was recorded. Gilts were individually tagged and birth weights were recorded within 24 h of birth. Mortality was recorded based on date of death and reason. Average birth weight was 1250 g (±320). From the 12,968 gilts that were born, 10,742 (82.8%) survived to weaning. The average wean age of the gilts is 22.06 d (±2.74). Glimmix procedure was used to examine the effect of birth weight on survivability in gilts. A binomial distribution was used for death (1 = alive, 0 = dead). Birth week, parity, cross-foster, and farm were fixed effects. Number born, birth weight, and number nursed were covariates. All effects in the model were significant ($P <$ 0.05). Piglets with a 100g increase in birth weight are 1.16 times more likely to survive. When increasing number born and number nursed by one piglet, the odds of survival are 0.84 and a 0.95, respectively. Survival decreased 9.5% when piglets were cross-fostered. Producers should develop genetic and management strategies to select on birth weight and survivability. It was concluded that cross-fostering piglets decreased survivability.

Key Words: pig, survival, cross-fostering

190 Genetic parameters of maternal traits related to sow feed efficiency during lactation. D. M. Thekkoot*[1], R. A. Kemp[2], M. F. Rothschild[1], and J. C. M. Dekkers[1], *[1]Iowa State University, Ames, [2]Genesus Inc., Manitoba, Canada.*

Over the past few decades, the productivity of commercial sows has increased and this has resulted in higher energy requirements and greater mobilization of body reserves, which can negatively affect the longevity and later production performance of sows. One way to overcome this is to increase feed efficiency during lactation. The objective of this study was to estimate genetic parameters for traits related to feed intake and efficiency of sows during lactation. The data were provided by Genesus Inc. and included data on 1239 farrowings from 478 Yorkshires and 457 Landrace sows recorded between July 2011 and December 2012. Sow body weight and back fat were measured ~5 d before farrowing, and at weaning. Daily feed intake was recorded using the Gestal feed recording system. Heritabilities were estimated separately for each breed using a single trait linear mixed model analysis using ASReml. All models included fixed effects of parity (5 levels), contemporary group (farrowing year and season–7 levels), random animal and permanent environmental effects. Sow residual feed intake (RFI) and lactation energy balance (EB) were used to evaluate the overall efficiency of sows during lactation. Heritability estimates for RFI and EB were 0.21 and 0.12 for Landrace and 0.25 and 0.06 for Yorkshire sows. The major traits that contribute to the calculation of RFI and EB are total feed intake of sow (FI), Protein loss (PL), fat mass loss (FML), sow body weight loss (WL), litter birth weight (LBW) and litter weaning weight (LWW) and these traits exhibited moderate heritabilities (0.18, 0.36, 0.20, 0.32, 0.41 and 0.11 for Landrace and 0.33, 0.24, 0.12, 0.24, 0.32 and 0.10 for Yorkshire). Proportions of variance due to permanent environmental effects ranged from 0 to 0.10 for all traits except LWW, for which it was 0.24 and 0.18 for Landrace and Yorkshire sows respectively. These results suggest that for the population studied, selection based on these traits can result in reasonable genetic improvement for feed efficiency during lactation.

Key Words: sow lactation, feed efficiency, genetic parameter

191 Random regression models for daily feed intake in Danish Duroc pigs. A. B. Strathe*[1,2], T. Mark[1], J. Jensen[3], B. Nielsen[2], D. N. Do[1], and H. N. Kadarmideen[1], *[1]Department of Clinical Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Frederiksberg C, Denmark, [2]Danish Agriculture & Food Council, Pig Research Centre, Copenhagen V, Denmark, [3]Department of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark.*

The objective of this study was to develop random regression models and estimate covariance functions for daily feed intake (DFI) in Danish Duroc pigs. A total of 476201 DFI records were available on 6542 Duroc boars between 70 to 160 d of age. The data originated from the National test station and were recorded using ACEMO electronic feeders in the period of 2008 to 2011. The pedigree was traced back to 1995 and included 17222 animals. The phenotypic feed intake curve was decomposed into a fixed curve, being specific to the barn-year-season effect and curves associated with the random pen-year-season, permanent, and animal genetic effects. The functional form was based on Legendre polynomials (LP). A total of 64 models for random regressions were initially ranked by BIC to identify the approximate order for the LP using AI-REML. The parsimonious model included Legendre polynomials of 2nd order for genetic and permanent environmental curves and a heterogeneous residual variance, allowing the daily residual variance to change along the age trajectory due to scale effects. The parameters of the model were estimated in a Bayesian framework, using the RJMC module of the DMU package, where weakly informative priors were derived from preliminary AI-REML analysis. We used a burn-in of 10k followed by 90k rounds, interleaving every 10th sample. Posterior mean heritabilities were low for DFI, but increased from 0.07 to 0.12 at 100 d of age and then decreased fluctuating to around 0.08. The low heritabilities were due to a higher residual variance when using individual DFI records compared with average DFI records over the entire test period. The heritability of DFI for the entire test period was 0.28, corresponding closely to the estimate derived from analysis of average DFI records. Eigenvalues of the genetic covariance function showed that 33% of genetic variability was explained by the individual genetic curve of the pigs. This proportion was covered by linear (27%) and quadratic (6%) coefficients. Genetic eigenfunctions revealed that altering the shape of the feed intake curve by selection may be an option in Danish Duroc pigs.

Key Words: random regression model, Gibbs sampling, genetic parameter

192 Proteolysis and texture development in Prato cheese made with different coagulants. C. Merheb-Dini*[1], L. S. Alves[1], E. Gomes[2], R. da Silva[2], and M. L. Gigante[1], *[1]Faculty of Food Engineering, University of Campinas - UNICAMP, Campinas, SP, Brazil, [2]Instituto de Biociências, Letras e Ciências Exatas, UNESP - Univ Estadual Paulista, São José do Rio Preto, SP, Brazil.*

This work had the aim of comparing the effect of different coagulants on the ripening of a typical Brazilian cheese. Prato cheese was made using the following coagulants: laboratory obtained protease, from the fungus Thermomucor indicae-seudaticae N31, recently isolated in Brazil (Thermomucor cheese) and commercial coagulant from *Rhizomucor* sp. (Alternative, Bela Vista) (Control cheese). Fifty liters of milk were enzymatic coagulated in vats with heating-cooling jacket, stirrers and speed control. After cutting, the mass was cooked (42°C) and washed and, after whey drainage, chesses were pressed. For both chesses the amount of enzyme added was calculated to achieve milk clotting in ≈35 min. Cheese ripening was periodically monitored for 50 d. A 2 × 6 factorial design with 3 replications was performed and the results were evaluated by ANOVA and mean values were compared by Tukey's test ($P < 0.05$). Proteolysis (NS pH 4.6 (%NT)) and firmness were affected by coagulant type and by ripening time. Thermomucor cheese exhibited lower proteolysis and higher firmness and Control cheese exhibited higher proteolysis and lower firmness. For both cheeses, proteolysis increased and firmness decreased throughout ripening. However, the interaction between coagulant type × ripening time was not significant for the evaluated parameters. The capillary electropherograms showed that the protein hydrolysis profile of both cheeses was very similar exhibiting degradation of casein fractions α_{S1}-CN 8P, α_{S1}-CN 9P, β-CN A^1, β-CN A^2 and formation of hydrolysis products α_{S1}-I-CN 8P, α_{S1}-I-CN 9P and γ-CNs. This behavior was equivalent to the classic and expected profile of chymosin made cheeses: hydrolysis of α_{S1}-CN, by the residual coagulant during initial stages of ripening on the bond Phe23-Phe24, resulting in the formation of α_{S1}-I-CN and hydrolysis of β-CN by plasmin, resulting in the formation of γ-CNs. The data showed that ripening developed in the same way for both cheeses suggesting the potential of protease from Thermomucor indicae-seudaticae N31 as milk clotting agent for industrial scale cheese production. Acknowledgments: FAPESP, CNPq.

Key Words: ripening, capillary electrophoresis

193 Application of an improved powder X-ray diffraction method to evaluate cheese crystals. G. Tansman*[1], P. S. Kindstedt[1], and J. M. Hughes[2], *[1]Department of Nutrition and Food Sciences, University of Vermont, Burlington, [2]Department of Geology, University of Vermont, Burlington.*

Cheese crystals have been studied for over a century, often with the goal of eliminating visible crystals. With the resurgence of artisan cheese making in America and globally, the incidence and morphological diversity of visible crystals appear to be on the rise. During the 1930s through 1970s several investigators used powder x-ray diffraction (PXRD) to identify cheese crystals. However, attempts to optimize analyses using newer advanced PXRD instrumentation are limited. The objectives of this research were to develop an improved PXRD method for cheese crystal analysis and to demonstrate test capabilities by identifying major and minor components of crystal complexes in Cheddar, Gouda and Asiago cheeses. Cheese samples were obtained from commercial sources. Crystals were physically removed from the cheese surface or cheese interior using a dissecting needle, razor blade, and tweezers. Crystalline species were fractionated and purified through differential solubility in water and acetone, which enabled the identification of minor crystal components that might otherwise go undetected due to a lack of instrumental resolution and baseline noise. Purified crystals were dried in a desiccator for 12 h and ground into power using a mortar and pestle for analysis using a Rigaku MiniFlex II x-ray diffractometer. Surface crystals from aged Cheddar cheese contained crystalline calcium lactate pentahydrate, tyrosine, calcium phosphate and an unidentified crystalline component (UCC). Crystals from the interior of Cheddar contained only calcium lactate pentahydrate. In aged Gouda, interior crystals consisted mostly of tyrosine with lesser amounts of the same UCC found on Cheddar; crystals from the surface of interior eyes contained both tyrosine and the UCC. Interior crystals from Asiago were exclusively tyrosine. Powder x-ray diffractometry, combined with crystal separation though differential solubility, provides a rapid and sensitive means to identify crystalline species that comprise complex visible deposits in cheese. Such information may help to inform future studies aimed at elucidating mechanisms of co-crystallization in cheese.

Key Words: crystal, cheese, X-ray diffraction

194 The effect of the exopolysaccharide producing cultures and adjunct cultures isolated from the Egyptian dairy environment on the texture and sensory characteristics of fat-free Cheddar cheese. M. El Soda* and N. Ahmed, *Faculty of Agriculture, Alexandria University, Alexandria, Egypt.*

Low fat cheeses often suffer from undesirable texture and flavor properties, the exopolysaccharide producing cultures were used in the manufacture of low fat cheeses to increase yield and improve texture. The objective of this communication is to assess the effect of EPS producing cultures and adjunct cultures isolated from the Egyptian dairy environment on the texture and flavor characteristics of fat-free Cheddar cheese. Pilot-scale fat-free Cheddar cheeses were manufactured using commercial Cheddar starter in addition to selected EPS producing cultures and adjunct cultures obtained from our culture collection. Modifications to the cooking temperature, cheddaring conditions and pressing were also performed. The obtained results revealed that the best cheese was obtained using 2 mesophilic lactobacilli producing exopolysaccharides in addition to a 1:1 ratio of 2 strains of *Lactobacillus paracasei* exhibiting debittering activity. The obtained yield for the experimental fat free Cheddar was 8.3%, the values for moisture; fat and protein were 52% ± 0.5, 0.7% and 38% ± 0.8 respectively after 6 mo of ripening. The rheological parameters of full-fat Cheddar were compared with those of the experimental fat-free Cheddar. The obtained data reveal 80% similarity between the 2 cheeses for hardness, chewiness and gumminess, whereas fat-free cheeses showed more cohesiveness and springiness when compared with the full-fat cheese. The use of *Lactobacillus paracasei* strains led to a considerable reduction of bitterness and to the development of the characteristic Cheddar notes in the fat-free cheese. In conclusion, the use of EPS producing lactobacilli, *Lactobacillus paracasei* adjunct and the different modifications to the make procedure led to the production of a fat free Cheddar cheese exhibiting flavor and texture characteristics comparable to the full fat product.

Key Words: fat-free Cheddar, adjunct, exopolysaccharide

195 Effect of milk protein concentration on the microstructure and properties of full-fat Cheddar cheese during ripening. K. Soodam*[1,2], L. Ong[1,2], S. E. Kentish[1], and S. L. Gras[1,2], *[1]Department of Chemical and Biomolecular Engineering, The University of Melbourne, Melbourne, Victoria, Australia, [2]Bio21 Molecular Science and Biotechnology Institute, The University of Melbourne, Melbourne, Victoria, Australia.*

Ultrafiltered retentate (UF) can be used to standardize cheese milk and can potentially affect cheese yield but few studies have examined the effect of added UF on the microstructure of the cheese and linked these to the properties observed during ripening. This study investigated the effect of increasing the milk protein concentration on the microstructure, as well as the biochemical changes that occur during the ripening of Cheddar cheese. Advanced microscopy techniques, including confocal scanning laser microscopy and cryo-scanning electron microscopy (cryo-SEM) were coupled with textural, sensory and chemical analyses and applied during ripening. The milk protein level was found to significantly affect the hardness of the cheese. A possible link was also established between the protein level, stretchability and the microstructure of the cheese, as observed with cryo-SEM. Several changes were also observed during ripening for all protein treatments. The protein network within cheese contained fewer branches, as observed by the number of intersections (vertices), as a result of ripening. A significant correlation was also found between the microstructure of the cheese and level of proteolysis as well as the microstructure of the cheese and the cheese texture. Our findings provide new insights into the effect of processing conditions and the effect of the maturation process on the development of cheese microstructure and functional properties.

Key Words: cheese ripening, microstructure

196 Evaluation of an alternative method for the rapid and direct determination of sodium in cheese. J. A. Stankey*, C. Akbulut, J. Romero, and S. Govindasamy-Lucey, *Wisconsin Center for Dairy Research, Madison.*

Currently, Na in cheese is routinely determined via an indirect method using the Cl Analyzer. A direct and rapid method of Na detection is needed in the industry due to the increasing use of Na replacers. An x-ray fluorescence spectroscopy (XRF) method for the determination of Na in cheese was developed and compared with inductively coupled plasma-optical emission spectroscopy (ICP) and Cl Analyzer. Sodium quantification was performed by multi-point calibration with standard cheeses (n = 7) (Cheddar, Gouda, Mozzarella, pizza, nonfat and processed) over the range of 0–5% Na (wt/wt). Amount of Na in the each of cheese standard (cheese discs: 7 × 30 mm) was quantified with the XRF equipment. Method validation was performed and the results for linearity, precision, limit of detection and limit of quantification were determined. Linearity ($R^2 \geq 0.99$) was observed in calibration curves obtained for different cheese standards. Procedure was tested by quantifying the amount of Na in a wide range of commercial cheese samples. Na data obtained by XRF were in good agreement with those from ICP and Cl Analyzer for most commercial cheeses. Lowest concentration of Na (LOQ) that can be determined with an acceptable level of repeatability, precision, and trueness was about 245 mg/100g cheese. Calibration graph for Na quantification in the presence of increasing K levels was created using natural cheeses made with different ratios of Na:K and it was able to predict Na content in cheeses manufactured with K-based salt replacers. The Cl analyzer was less accurate than the XRF when Na-replacers may be present, due to the indirect quantification of Na (by the Cl Analyzer). If quantifying Na in the presence of K using XRF method, it was critical that the calibration plot should be created with standards in the presence of K. The XRF method enables the rapid and direct measurement of Na content in a variety of cheeses.

Key Words: Na, X-ray fluorescence spectroscopy, cheese

197 Proteolysis and microstructure of salt-reduced Cheddar cheese. A. Sheibani*, M. M. Ayyash, T. Vasiljevic, and V. Mishra, *Victoria University, Melbourne, Victoria, Australia,*

The effects of salt reduction on proteolysis and microstructure of Cheddar cheese was investigated. Four levels of dry salting including control (2.5%) and 3 treatments (1, 1.5 or 2% salt) were applied followed by storage for 8 weeks at 4°C. Samples were taken at fortnightly intervals and subjected to chemical composition, proteolysis rate and microstructure analysis. Except 12% trichloroacetic acid-soluble nitrogen (TCA-SN), water-soluble nitrogen (WSN) and 5% phosphotungstic-soluble nitrogen (PTA-SN) significantly ($P < 0.05$) differed among cheeses samples. There was no significant ($P > 0.05$) difference in the release of major peptides among samples during storage, whereas hydrophilic peptides differed substantially. Total free amino acids (TFAA) showed significant difference between experimental cheeses at the same storage time ($P < 0.05$). Significant differences in chemical composition except fat content were observed between cheese samples at every sampling point. There was a significant difference between pH of control cheese comparing with other experimental cheeses. pH values of all treatments increased significantly from about 4.8 to 5.1 after first 2 weeks of storage. In compare with control, microstructures of treatments 1, 2, and 3 were smooth, small voids and close structure. During storage, the structure of Cheddar cheeses became more close and homogenous. Salt reduction treatment significantly influenced cheddar cheese characteristics during storage period.

Key Words: salt reduction, proteolysis, microstructure

Companion Animals: Companion and Captive Exotic Animals

200 Ingredient composition of diets offered to black-and-white ruffed lemurs (*Varecia variegata*) from surveyed United States zoological institutions. B. C. Donadeo*[1], K. R. Kerr[1], C. L. Morris2,3, and K. S. Swanson[1], [1]*University of Illinois at Urbana-Champaign, Urbana,* [2]*Omaha's Henry Doorly Zoo & Aquarium, Omaha, NE,* [3]*Iowa State University, Ames.*

Fifty-eight US zoological institutions are registered with the International Species Information System (ISIS) as housing black-and-white ruffed lemurs (*Varecia variegata*), but little data are available on their captive diets. Our objective was to identify feed items and inclusion amounts of diets offered to captive *V. variegata* at US zoological institutions. Institutions were contacted via the Prosimian Taxon Advisory Group listserv and direct email contact to request participation in the study. Diet information (i.e., type and amount of diet items) was collected utilizing a survey (created on SurveyMonkey.com). Respondents were prompted to indicate inclusion level for items expected to be common, including fruits, vegetables, biscuits (and other commercial products), greens, and browse (i.e., twigs, shoots, leaves), and to provide information on items not specifically listed. Thirty-five institutions provided diet information utilizing the survey between July 27 and December 31, 2012, including 33 of the 58 ISIS listed institutions (57%). Data presented here are from 33 institutions which have provided complete information for analysis. The most commonly included items (30 of 33 zoos) were bananas (<5% to 30% of diet). Most institutions offer either Marion Zoological's Leaf Eater biscuit (10 zoos; <5% to 70% of the diet), Mazuri's Leaf-Eater biscuit (14 zoos; <5% to 50% of the diet), or Mazuri's Primate Browse biscuit (10 zoos; <5% to 25%). -seven institutions use browse (<5% to 10%); of these institutions, 10 indicated little to no consumption of browse offered. While *V. variegata* is a frugivorous species, research in our lab shows that Madagascan fruits available to wild *V. variegata* are higher in fiber and lower in carbohydrates than diets offered at US zoos. Therefore, high inclusion of fruit in captive lemur diets may be inappropriate. Further research is needed on the effects of different captive diet types and ingredient inclusions on lemur health.

201 Amino acid composition and standardized digestibility of whole prey diet items intended for captive exotic and domestic felids. K. R. Kerr*[1,2], P. L. Utterback[2], C. M. Parsons[2], and K. S. Swanson[1,2], [1]*Division of Nutritional Sciences, University of Illinois, Urbana,* [2]*Department of Animal Sciences, University of Illinois, Urbana.*

Whole prey diets are popular for captive exotic and domestic felids. However, research on whole prey has primarily focused on non-nutritive benefits. Our objective was to evaluate the amino acid (AA) composition and bioavailability of 20 whole prey sources: mice (1 to 2 d, 10 to 13 d, 21 to 25 d, 30 to 40 d, and 150 to 180 d of age); rats (1 to 4 d, 10 to 13 d, 21 to 25 d, 33 to 42 d, and >60 d of age); rabbits (still born, 30 to 45 d, > 65 d with skin, and >65 d of age with skin removed); chicken (1 to 3 d of age, ground adult); duck (ground adult); and quail (1 to 3 d, 21 to 40 d, and >60 d of age). We measured AA composition of each whole prey item and evaluated standardized AA digestibility utilizing the cecectomized rooster assay. We calculated the amino acid score (AAS) and protein digestibility corrected AAS (PDCAAS) utilizing the growth requirements for domestic cats as a reference value (AAFCO, 2012). For most the whole prey, AA concentrations were greater than the recommendations for domestic cats: AAS were greater than 88 for all species except rabbits (AAS: 6 to 56). The first limiting AAs were Cys + Met, Met, Tau, and Trp. In the 30 to 45 d-old rabbit, taurine concentration (0.01% DM) was lower than that recommended for domestic cats (0.10% DM). Standardized digestibility coefficients were quite high, but variable (Arg: 85 to 95%; His: 87 to 96%; Ile: 82 to 92%; Leu: 84 to 94%; Lys: 85 to 93%; Met: 89 to 97%; Phe: 83 to 94%; Thr: 80 to 95%; Trp: 84 to 94%; Val: 80 to 93%). The PDCAAS were 3 to 13 units lower than AAS. Given the AA digestibilities and high protein concentrations in whole prey, meeting the requirements likely would not be an issue for Cys + Met, Met, and Trp. However, some whole prey had Tau concentrations below the recommendations for domestic cats. If Tau concentrations are not measured before feeding, supplementation of whole prey may be beneficial. Standardized AA digestibility coefficients of 80 to 97% are expected.

Key Words: protein digestibility corrected amino acid score, cat

202 The effects of L-carnitine on energy expenditure and fuel selection in adult Miniature Dachshunds, Beagles, and Labrador Retrievers measured using indirect calorimetry. D. Minikhiem*, K. Shoveller, J. DiGennaro, and L. Fortener, *Procter and Gamble, Mason, OH.*

Despite the common incorporation of L-carnitine (LC) in dog food there is little research on the effects of LC on energy expenditure (EE) and fuel selection in healthy, lean dogs. In the present study indirect calorimetry was used to determine if dogs consuming 50 ppm LC (LC+) had lower RQ and greater EE compared with dogs fed control (CON). This study was a 2 × 2 Latin Square with baseline measurements before each period. A total of 16 dogs (6 Labrador Retrievers [Labs], 4 Miniature Dachshunds [Dachshunds], and 6 Beagles) were pseudo-randomly allocated to LC+ and CON diets and balanced for BW and food intake. Dogs were fed Iams ProActive Health MiniChunks with (LC+) and without (CON) 50 ppm added LC (as fed basis) to maintain BW. Indirect calorimetry was conducted during fasting and for 8 h post feeding at baseline, 3, and 6 wk. Area under the curve (AUC) for RQ and EE, and AUC for RQ and EE divided into 4 postprandial time periods (0–120 min, 120–240 min, 240–360 min, and 360–480 min) were analyzed using a random mixed model with breed and diet-by-breed interaction as covariates. There were no differences in RQ between treatments at baseline ($P > 0.05$). RQ tended to increase (contrary to expected results) from baseline at wk 3 and 6 for Dachshunds and Beagles fed LC+ ($P = 0.07$). There were no differences between treatments in EE at baseline for each breed. EE increased in Labs fed LC+ after 3 and 6 wk. Specifically, Labs fed LC+ had greater EE ($P < 0.05$) than Labs fed CON during the last 3 postprandial periods at wk 3 and 6. Fasted EE tended ($P = 0.08$) to be greater in Labs fed LC+ at 6 wk. There were no differences between treatments for Beagles or Dachshunds. In conclusion, effects of LC on dog metabolism are breed-specific. Dogs consuming a maintenance diet supplemented with 50 ppm LC exhibited an apparent increase in carbohydrate metabolism (Dachshunds and Beagles) and an increase in total energy expenditure (Labs).

Key Words: L-carnitine, dog, indirect calorimetry

203 Effect of photoperiod on feline adipose transcriptome profiles as assessed by RNA sequencing (RNA-seq). A. Mori*[1], K. L. Keppen[1], and K. S. Swanson[1,2], [1]*Department of Animal Sciences, University of Illinois, Urbana,* [2]*Division of Nutritional Sciences, University of Illinois, Urbana.*

Photoperiod is known to cause physiological changes in seasonal mammals, including body weight (BW), physical activity, and reproductive status. Because cats are seasonal breeders, we recently tested the effects of day length on resting metabolic rate (RMR), voluntary physical activity, and food intake. In that study, RMR, physical activity, and food intake to maintain BW were greater in cats exposed to long days (LD) vs. short days (SD). Because photoperiod has also been demonstrated to affect adipose tissue gene expression in several species, including dairy cows, sheep, and Siberian hamsters, the objective of this study was to determine the effects of day length on the adipose transcriptome profile of cats as assessed by RNA-seq. Ten healthy adult neutered male domestic shorthair cats were used in a randomized crossover design study. During two 12-wk periods, cats were exposed to either SD (8 h light:16 h dark) or LD (16 h light:8 h dark). Cats were fed a commercial diet to maintain baseline BW. Subcutaneous adipose biopsies were collected at wk 12 of each period for RNA isolation and sequencing. A total of 578 million sequences (28.9 million/sample) were generated by Illumina sequencing. Using a raw *P*-value of $P < 0.005$, 170 mRNA transcripts were differentially expressed between SD- and LD-housed cats. Of the 170 transcripts highlighted, 25 annotated transcripts were upregulated, while 116 annotated transcripts were downregulated by LD. Another 29 un-annotated transcripts (name and function not known) were also different between groups. In general, adipose tissue of LD-housed cats had greater expression of genes involved with cholesterol trafficking, fatty acid synthesis and immune function, and lower expression of genes involved with cell growth and differentiation, cell development and structure, and protein processing, when compared with SD-housed cats. This study has highlighted molecular mechanisms that may contribute to seasonal metabolic changes in cats. Although this area requires more research, these data may be used to develop strategies for feline obesity prevention or treatment.

Key Words: adipose tissue, cat, photoperiod

205 Potato pulp as a dietary fiber source in high quality dog foods. M. R. Panasevich*[1], R. N. Dilger[1,2], K. S. Swanson[1,2], L. Guérin-Deremaux[3], G. L. Lynch[4], and G. C. Fahey Jr.[1,2], *[1]University of Illinois Department of Animal Sciences, Urbana, [2]University of Illinois Division of Nutritional Sciences, Urbana, [3]Roquette Fréres, Biology and Nutrition Department, Lestrem, France, [4]Roquette America Inc., Geneva, IL.*

Dietary fiber is important in companion animal diets because of its positive effects on gut and systemic health. Potato pulp (PP), a co-product of potato starch processing (Roquette Frères, France), was evaluated as a potential novel fiber source in dog foods. The PP substrate was evaluated for chemical composition and in vivo responses. Ten female dogs with hound bloodlines (5.4 ± 0.0 yr; 22 ± 2.1 kg) were each provided 5 diets with graded levels (0, 1.5, 3, 4.5, or 6%; added in place of cellulose) of PP on an as-is basis in a replicated 5 × 5 Latin square design. Fresh fecal samples were collected to measure fecal pH and fermentation end products. Chemical composition results revealed that raw and cooked PP contained 55% total dietary fiber, with 32% insoluble fiber and 23% soluble fiber, as well as 4% crude protein and 2% acid-hydrolyzed fat. No differences were observed in total tract digestibility coefficients for dry matter (81.3 to 82.7%), organic matter (84.1 to 85.5%), crude protein (81.7 to 80.2%), acid-hydrolyzed fat (94.1 to 94.6%), or energy (84.9 to 85.7%). Total dietary fiber digestibility was greater ($P < 0.01$) for dogs fed the 3, 4.5, and 6% PP diets compared with dogs fed the 0% PP diet. Fecal pH was lower ($P < 0.01$) when dogs were fed the 4.5 and 6% PP diets compared with the 0% PP diet. Fecal acetate, propionate, and total SCFA were higher when dogs were fed the 3, 4.5, and 6% PP diets, and fecal butyrate was higher when dogs were fed 4.5 and 6% diets compared with the 0% PP diet ($P < 0.05$). Overall, with increasing PP inclusion, linear increases ($P < 0.01$) were observed for all SCFA, with a concomitant linear decrease ($P < 0.01$) in fecal pH. Fecal protein catabolites were physiologically low or undetectable, with the exception of spermidine, which was greater ($P < 0.05$) when dogs were fed the 6% PP diet compared with the 0% PP diet. These findings suggest that increased inclusion of PP elicited favorable fermentation characteristics without negatively affecting nutrient digestibility. Collectively, these data suggest that PP could be a functional dietary fiber in high quality dog foods.

Key Words: potato, fiber, dog

206 Mannoheptulose has acute effects on post-prandial energy expenditure, respiratory quotient and insulin response in adult Beagles fed diets with different macronutrient contents. L. L. McKnight*[1], E. A. Flickinger[2], J. France[1], G. Davenport[2], and A. K. Shoveller[2,1], *[1]University of Guelph, Guelph, ON, Canada, [2]Procter & Gamble Pet Care, Mason, OH.*

Overweight dogs are treated with nutritional management strategies that involve therapeutic diets and/or total calorie restriction (CR). As CR strains the human-animal bond, calorie restriction mimetics (CRM) [i.e., mannoheptulose (MH)] are being investigated. The objective of this study was 2-fold: (1) determine the effects of low carbohydrate CHO; high fat (32% CP; 30.6% CHO; 27.9% fat) and high CHO; low fat (27.0% CP; 53.6% CHO; 11.2% fat) diets on energy expenditure (EE), respiratory quotient (RQ) and glycemic response in adult beagles, and (2) determine whether these outcomes were affected by supplementing the diets with mannoheptulose (MH; 8 mg/kg). This study was designed as a 4 × 4 repeated Latin square with each dog (n = 8) randomly allotted to each dietary treatment (high CHO, HC; high CHO with MH, HC+; low CHO, LC; low CHO with MH, LC+). As indirect calorimetry methodology only allowed for 4 dogs to be measured per day, dogs were divided into 2 groups with each diet × MH combination represented on each day. Fasting and postprandial (24 h) EE and RQ were determined by indirect calorimetry (d 12 or 14). Glycemic and insulinemic responses (24 h) to the treatment meal were determined on the alternate day (d 12 or 14). Dietary CHO level did not affect fasting or postprandial EE, serum insulin or glucose:insulin as would be expected in lean dogs receiving these diets for 14 d. Dogs fed HC had higher postprandial RQ (indicating an increase in CHO oxidation) but lower serum glucose than dogs fed LC. MH acutely increased postprandial RQ (25 – 75 min, $P < 0.05$) and EE (5 – 7 h, $P < 0.05$) and decreased serum glucose:insulin (14 – 22 h, $P < 0.10$) (implying improved insulin sensitivity) irrespective of dietary CHO content. These findings suggest that MH elicits changes in pathways related to energy sensing and that these effects are at least partly mediated by changes in insulin signaling and not related to the macronutrient content of the diet. This study was funded by Procter & Gamble Pet Care.

Key Words: energy expenditure, macronutrient, mannoheptulose

207 In vitro fermentation characteristics of coconut endosperm and chicory pulp fibers using canine fecal inoculum. M. R. C. de Godoy*[1], Y. Mitsuhashi[2], L. Bauer[1], G. C. Fahey[1], P. R. Buff[2], and K. S. Swanson[1], *[1]Department of Animal Sciences, University of Illinois, Urbana, [2]The Nutro Company, Franklin, TN.*

The objective of this experiment was to determine the effects of in vitro fermentation of coconut endosperm fiber (CEF), chicory pulp (CHP),

and selective blends of these substrates on short chain fatty acid (SCFA) production and changes in microbiota using canine fecal inocula. A total of 6 individual substrates, including short-chain fructooligosaccharide (scFOS; a well-established prebiotic source), pectin (PEC; used as a positive control), pelletized cellulose (PC; used as a negative control), beet pulp (BP; considered the gold standard fiber source in pet foods), CEF, and CHP, and 3 CEF: CHP blends [75% CEF: 25% CHP (B1); 50% CEF: 50% CHP (B2); 25% CEF: 75% CHP (B3)] were tested. Triplicate samples of each substrate were fermented for 0, 8, and 16 h after inoculation. A significant substrate × time interaction ($P < 0.01$) was observed for pH change and acetate, propionate, butyrate, and total SCFA concentrations. After 8 and 16 h, pH change was greatest for scFOS (−2.0 and −3.0, respectively) and smallest for PC (0.0 and −0.1, respectively). After 16 h, CEF had the highest butyrate production among all the CEF: CHP blends, and it was not different than PEC. The substrate × time interaction was significant for bifidobacteria ($P = 0.013$) and lactobacilli ($P < 0.001$). After 8 h, bifidobacteria was highest for BP and lowest for PC; 12.7 and 10.0 $\log_{10}$ cfu/tube, respectively. After 16 h, PC had the lowest and scFOS had the highest bifidobacteria; 6.7 and 13.3 $\log_{10}$ cfu/tube, respectively. In general, CEF, CHP and their blends had similar bifidobacteria populations after 8 and 16 h of fermentation when compared with BP and scFOS. After 16 h, lactobacilli populations were highest for B1, B2, B3, BP, and scFOS, intermediate for PEC, and lowest for PC ($P < 0.05$). Overall, our data suggest that CEF had a butyrogenic effect and that CEF, CHP and their blends had similar bifidobacteria and lactobacilli populations as popular prebiotic and fiber substrates. Future research should investigate the effects of CEF, CHP, and their blends on gastrointestinal health and fecal quality in dogs.

Key Words: dog, fiber, in vitro

208 Pheromones and an interomone change the physiology and behavior of anxious dogs. W. G. Thompson* and J. J. McGlone, *Texas Tech University, Lubbock.*

Pheromones are species-specific odors used in communication and have been shown to have both behavioral and physiological effects. Interomones are pheromones in one species, but have diverse effects on other species. The objective of this study was to assess the efficacy of pheromones/interomones to modulate heart rate (HR) and behavior in adult anxious dogs (trembling, cowering, shy). The dogs (10.2 ± 4.2 kg; estimated 5–10 yr old, intact males) and were professionally diagnosed as anxious. Each dog was housed in a separately-ventilated room with a minimum of 12 m^2 of floor space. Heart rate was measured using a telemetry system (Data Science International, St. Paul, MN). Behavior was recorded and later processed by a trained individual (blind to treatment group) using a scan sample with a recording interval of 5 min over a 24 h baseline period. At the end of 24 h with a treatment or control pheromone collar, each dog was startled with a 110 db fog horn while behavior and HR were recorded. Each dog received each treatment in a Latin square design with repeated measures over time. This model allowed evaluation of effects of treatment, dog, treatment by dog, time, treatment by time and dog by time effects. Treatments were given in the form of a collar containing each pheromone/interomone and included Placebo, Sergeant's Formula H (SERG), 2-methylbut-2-enal–Rabbit Pheromone (RP), or Dog Appeasing Pheromone (DAP) collar. During baseline 24 h, DAP increased HR in 1 dog and decreased HR in 2 dogs; SERG increased HR in 2 dogs and decreased HR in 1 dog and RP increased HR in 2 dogs and decreased HR in 2 dogs (dog by trt, $P < 0.0001$). Dog lying behavior changed with SERG and RP but not DAP. After startle, each treatment changed dog HR in at least one dog (dog by trt, $P = 0.002$). Treatments caused one dog to increase while another decreased lying (dog by trt, $P < 0.001$) after startle. Individual dogs changed behavior and HR differentially in response to the pheromones/interomones evaluated. The pheromones/interomones tested clearly changed dog heart rate and behavior. However, anxious dogs did not respond uniformly to each pheromone/interomone tested.

Key Words: pheromone, interomone, behavior

Dairy Foods Symposium: New Approaches to Lower Sodium in Cheese and Techniques to Address Quality Challenges

209 Sodium reduction and public health—Why, how much, and current trends. J. Nicholls*, *National Dairy Council, Rosemont, IL*

To address sodium overconsumption, public health programs aimed at reducing sodium intakes of Americans have gained momentum in recent years. These include public education campaigns, regulatory approaches, standards for marketing and advertising to children, and voluntary industry programs for sodium reduction. The Dietary Guidelines for Americans recommends intakes of 2,300 mg sodium per day for most Americans and 1,500 mg per day for certain population groups. These recommendations are based on the links between high sodium intake, high blood pressure, and increased risk for cardiovascular disease. Sodium intakes of the majority of Americans exceed recommendations with average intakes of about 3,300 mg sodium per day. The Dietary Guidelines also recommend Americans consume 3 servings of dairy foods per day including milk, yogurt and cheese, and based on national survey data, cheese is among top sources of sodium in the diets of Americans. To understand what sodium reduction and public health efforts mean for cheese, dairy's role in the diet, key efforts underway to reduce sodium in the food supply, specific sodium reduction guidelines, and what to expect in coming years will be reviewed. Authoritative reports including the 2010 Institute of Medicine on Strategies to Reduce Sodium Intake in the United States and the Dietary Guidelines for Americans will be reviewed and put into context. Voluntary sodium reduction programs and regulations including USDA regulations for sodium reduction in school meals and proposed regulations for sodium content of "competitive" foods sold in schools will also be reviewed. Emphasis will be placed on policies and programs to reduce sodium intake by Americans and an understanding of the current environment relevant to dairy foods.

Key Words: sodium reduction, cheese, Dietary Guidelines for Americans

210 Lower sodium cheeses—Consumer acceptance and flavor differences. M. A. Drake*, *North Carolina State University, Raleigh.*

Sodium reduction is a key issue in the dairy industry as salt plays a crucial role in flavor and ripening of Cheddar cheese. This presentation will address the effect of sodium reduction on cheese flavor, studies to minimize these effects and consumer perception of sodium reduction in Cheddar cheese. Salt reduction as little as 30% alters cheese ripening and flavor development with increased development of sulfur, brothy and rosy flavors and bitter taste concurrent with volatile compound changes. Off-flavors are magnified in lower sodium reduced fat cheeses due to changes in volatile compound thresholds due to fat reduction. Sodium reduction effects vary with different starters suggesting that careful selection of starter culture strains can alleviate some of these effects. Sodium cation substitution with other cations such as potassium controls water activity similar to sodium chloride. Volatile compound effects were not evident up to 50% substitution although trained sensory panelists documented increased bitter taste and metallic mouthfeel with 25% substitution. Consumer interest in sodium reduction was lower than interest in fat reduction emphasizing the need for parity in sensory properties. Consumer liking scores were not different up to 50% substitution of potassium for sodium with either full fat or 50% reduced fat cheeses. These results suggest that a 25–30% sodium reduction in Cheddar cheese is readily achievable by substitution of potassium for sodium.

Key Words: cheese, sodium reduction, flavor

211 Lower sodium cheeses—Changes in the microbiology and safety. D. J. McMahon*, *Western Dairy Center, Utah State University, Logan.*

With the interest in reducing sodium content of foods for dietary reasons there has been a concern expressed about how reducing sodium content of cheese affects its microbiology and consequent safety. Lowering the level of salt addition to cheese changes the amount of whey expulsion after salting and so cheese manufacturing needs to be altered to maintain moisture targets. Cheddar cheese with 33% reduction in salt will lower the salt-in-moisture (S/M) content from ~4.7% to 3.2%, while a cheese with salt reduction to meet low sodium food regulations will have S/M <2.0%. This greatly reduces the use of salt content of cheese as a microbiology hurdle for controlling bacterial growth. This presentation will address the impact of sodium reduction on cheese microflora from the aspect of cheese ripening and survival of pathogens. When S/M is lowered in either full fat or low fat cheddar cheese, the lactococcal starter cultures survive for a longer time and the nonstarter lactic acid bacteria take longer to reach high levels and become the predominant culturable bacteria in cheese. Similarly, when potassium chloride was substituted for sodium chloride, there is a tendency for the lactococci to remain dominant for longer times, which is indicative of potassium ions subjecting the starter bacteria to less stress than high levels of sodium ions. There are also various metabolic pathways that can be expected to be upregulated or downregulated when potassium is substituted for sodium. When cheddar cheese was made with normal (1.8% salt) and low (0.7%) salt contents and then inoculated with *Listeria monocytogenes* and stored at 4, 10 and 21°C (for 3, 3 and 1 mo, respectively) the viable count decreased by about one log at regular salt levels and 0.5 log in low salt cheese at all temperatures, and at both high and low pH. When similar cheese was inoculated with *Salmonella* there was about 3 log reduction in *Salmonella* counts in all cheeses.

Key Words: cheese, salt, microbiology

212 Process cheese products—Approaches to manufacturing consumer acceptable process cheese products with less sodium. L. E. Metzger* and A. Kommineni, *South Dakota State University, Brookings.*

Process cheese products are an integral part of the American diet. However, these products contain a substantial amount of sodium (1265 to 1540 mg/100 g). The major sources of sodium in process cheese products are sodium based emulsifying salts, sodium chloride, and natural cheese. In a typical formulation emulsifying salts contribute 45% of the sodium whereas natural cheese and sodium chloride contribute 30 and 25% of the sodium, respectively. Consequently, various strategies that target one or more of the sodium sources in process cheese products can be used to decrease the level of sodium. The simplest and first strategy is to remove sodium chloride in the formulation. In a typical formulation if all of the sodium chloride is removed, the sodium content can be reduced from 1500 mg/100g to approximately 1100 mg/100 g. In addition to removing sodium chloride from the formulation, a variety of salt substitutes can be used to increase the perceived salty flavor of process cheese products with less than 1100 mg of sodium/100 g. Salt

substitutes utilize potassium chloride in combination with a masking agents or bitterness blockers. Masking agents and bitterness blockers are required when potassium chloride is used in a formulation because potassium chloride can result in bitter off-flavors. To produce process cheese with a sodium content below 1100 mg/100 g a portion of the sodium based emulsifying salts in the formulation must also be replaced with a potassium based emulsifying salt. Using a combination of removal of sodium chloride and addition of potassium based salt substitutes and potassium based emulsifying salts it possible to produce process cheese products with a sodium content below 1100 mg/100 g. However, process cheese products with this level of sodium have an extremely bland flavor and are perceived by consumers as having a flavor that is not typical of process cheese.

Key Words: process cheese, reduced sodium, salt substitutes

213 Unwanted gas formation in cheese—Newer information on causes and determining the composition of the cheese microbiota.
J. Steele*, *University of Wisconsin-Madison, Madison.*

Cheese contains microorganisms that are not intentionally added during manufacture. The organisms present in this adventitious microbiota can have significant, beneficial and detrimental effects on cheese quality. One detrimental impact this microbiota can have is the production of slits and cracks, which is related to gas production by the adventitious microbiota. A wide variety of microorganisms have been associated with this defect, including yeasts, *Clostridium tyrobutyricum*, obligately heterofermentative lactobacilli, *Leuconostoc* sp., *Propionibacteria* sp., and coliforms. However, recently cheeses with slits and cracks not containing detectable levels of these organisms have been sporadically observed. This research project evaluated the ability of *Lactobacillus curvatus* LFC1, a facultatively heterofermentative lactobacilli, to cause this defect. *L. curvatus* LCF1 when present at 4.5 log cfu/g in cheese on d 1 of ripening resulted in slits and cracks within 3 mo. Chemical analysis of the cheeses indicate that the addition of *L. curvatus* LCF1 resulted in higher levels of acetate and lactic acid and accelerated reductions in the levels of citrate and galactose. Culture independent analysis of the influence of *L. curvatus* LCF1 addition on the cheese microbiota was conducted by automated ribosomal intergenic spacer analysis and high throughput DNA sequencing. The results demonstrate that the addition of *L. curvatus* LCF1 resulted in a greater microbial diversity within the cheese matrix. Model fermentations conducted with added citrate and lactose demonstrated that these 2 substrates contribute to gas production by *L. curvatus* LCF1. Collectively, these results suggest that *L. curvatus* is capable of causing slits and cracks in cheese, when present at high levels and if the cheese contains sufficient levels of lactose and citrate.

Key Words: cheese defects, lactobacilli, cheese composition

Milk Protein and Enzymes Symposium: Role of Enzymes in Dairy Processing

214 Enzymes in milk—A dynamic system. D. E. Otter*, *AgResearch Ltd., Palmerston North, New Zealand.*

What are they? Where do they come from? Why are they there? How can we use them? The presence of over 70 enzymes encompassing a wide range of activities including lipases, proteinases and lysosomal enzymes have been described in milk. The most highly characterized enzymes include lactoperoxidase, lysozyme, plasmin, lipoprotein lipase and xanthine oxidoreductase. The levels of the different enzymes are species-specific and may relate to the immune maturity of the new-born offspring; for example, in human milk the levels are generally greater than in bovine milk. Milk and colostrum also contain several antimicrobial factors, which exert both specific and non-specific bacteriostatic and bactericidal activity. Enzymes may be present for several reasons, including happenstance, "spill over" from epithelial mammary cells or serum during milk secretion and/or during inflammation or infection of the mammary gland. With the evolution of the lactation process; for example, during cattle domestication and breeding for milk production, it is highly unlikely that their presence is random and indeed some enzymes have essential roles in lactogenesis regulation and are necessary elements of the innate immune system of milk. The enzymes are predominately associated with the MFGM (milk fat globule membrane) and vesicle membranes in milk and the activity of many enzymes can vary significantly due to the metabolic activity of cells, stage of lactation, uninfected or infected glands (mastitis), subclinical infection and inflammation and the hormonal, nutritional and metabolic status of the producing animal (e.g., diet, stress). Enzymes are active in the udder before milk let-down, during the refrigerated storage stage both on the farm and in the factory and may also be present in the final dairy product e.g., plasmin, lipases and phosphatases. They can be exploited in several ways during processing including as an index of the thermal treatment of milk and for consumer health and food safety, e.g., to combat bacterial invasion and growth. The effects of processing and the impact on product quality need to be explored further including the partitioning of enzymes into different milk fractions and the assay methods used to quantify them.

Key Words: enzyme, milk, review

215 Use of phospholipases to modify phospholipid functionality in dairy processing. R. Ipsen*, *Department of Food Science, University of Copenhagen, Frederiksberg C, Denmark.*

Phospholipids (PL), despite constituting only approximately 0.5% of the total lipid in bovine milk, have a critical role in stabilizing milk fat globules against coalescence. They also have different technologic roles in dairy products, e.g., by coating powder particles, providing higher foam volumes in aerated products and acting as co-emulsifiers. In addition, phospholipases can be used to modify phospholipid functionality in dairy processing by improving fat stability or increasing product yield. We have been shown that partial hydrolysis of PL increases cheese yield. In manufacture of part-skim Mozzarella cheese manufactured from milk hydrolyzed with fungal phospholipase A1 before renneting, reduced fat loss in whey and cooking water as well increased cheese yield was found as a result of improved fat and moisture retention. The mechanism of yield improvement due to phospholipases has been found to be complex and not only due to better O/W emulsification of lyso-PL, but also caused by the interaction of lyso-PL with protein and the increased water binding of lyso-PL. When extra phospholipid was added to cheese milk, increased yield also resulted, but the effect of phospholipase was more pronounced than the effect of adding PL. Phospholipase can also be used in the dairy industry to improve the foaming properties of whey protein as we have shown. In general the surface properties of milk and whey are dramatically changed by application of phospholipase and our results have also shown that the reaction between lyso-PL and whey proteins (β-lactoglobulin) increased the heat stability of the whey proteins and show promise for making more heat stable emulsions. It is known that PL influence milk fat crystallization and we have recently started investigating the effect of phospholipase treatment on water-in-oil emulsions of dairy origin. Our preliminary results indicate that the source of milk phospholipids (e.g., buttermilk, whey protein concentrate) has a major effect on the functional behavior.

Key Words: phospholipase, phospholipid, functionality

216 Oligosaccharides from lactose: Enzymatic synthesis and nutritional functionality. M. Gänzle*, *University of Alberta, Edmonton, Canada.*

Oligosaccharides produced from lactose are functional food ingredients to exploit specific biological functions, including low caloric value and prebiotic activity. Galacto-oligosaccharides are synthesized on a commercial scale from lactose by microbial β-galactosidases. Lactose acts as galactosyl-donor as well as galactosyl-acceptor to convert lactose to indigestible oligosaccharides. High lactose concentrations favor oligosaccharides synthesis by β-galactosidases over hydrolysis and high oligosaccharide yields are obtained at lactose concentrations of 30% or higher. Galacto-oligosaccharides are indigestible, stimulate colonic fermentation to short-chain fatty acids, and increase the abundance of intestinal bifidobacteria, and are thus recognized as prebiotic compounds. Transgalactosylation by β-galactosidases with acceptor carbohydrates other than lactose yields a large diversity of oligosaccharides. Lactulose and lactosucrose are produced with fructose and sucrose as acceptor carbohydrates, respectively; both compounds find commercial application as functional food ingredients to stimulate colonic fermentation and to alleviate constipation. *N*-Acetylglucosamine, mannose, fucose, or chitin-oligosaccharides also are galactosyl-acceptors for microbial β-galactosidases to produce novel galactosylated oligosaccharides. Experimental evidence obtained in vitro indicates that galacto-oligosaccharides and related compounds prevent the adhesion of enteric pathogens to mucosal surfaces. Their activity is likely mediated by specific interaction with bacterial glycan recognition proteins that are involved in early steps of pathogenesis. Oligosaccharide synthesis from lactose is an established process to produce galacto-oligosaccharides as functional food ingredients. Health benefits of galacto-oligosaccharides are mainly based on their colonic fermentation to short chain fatty acids. Emerging evidence indicates that lactose can also be used to produce novel oligosaccharides that benefit host health by complementary mechanisms, i.e., the prevention of pathogen adhesion.

Key Words: lactose, β-galactosidase, galacto-oligosaccharide

217 Utilization of enzymes to influence the functionality of milk proteins. U. Kulozik*, *Technische Universität München, Chair for Food Process Engineering and Dairy Technology, Freising-Weihenstephan, Bavaria, Germany.*

The objective of work presented in is paper was to develop new methods for the enhancement of structures in fermented dairy products, to make use of milk proteins in the production of microencapsulated sensitive microorganisms (probiotics) and to produce peptides from milk proteins with functionalities related to bioactivity and surface activity. The report will focus on the following subjects: (1) Strengthening gel firmness in stirred yogurt by Transglutaminase and investigation (avoidance) of structure changes along shelf life, using 3 approaches of enzymatic crosslinking of milk proteins in yogurt milk before fermentation, simultaneously with fermentation, only in supplementary milk used to increase dry matter and protein contents. (2) Microencapsulation of sensitive ingredients and probiotics in enzymatically crosslinked milk protein matrices using an emulsification method producing droplets of highly concentrated dairy proteins containing the core material with subsequently induced crosslinking reaction by Transglutaminase or Chymosin. (3) Selective enzymatic hydrolysis of whey proteins to eliminate individual components based on their individual sensitivity against action of various hydrolyzing enzymes. Targeted enzymatic hydrolysis of whey proteins or enzymatic crosslinking for the production of bioactive peptides, surface active peptides for the manufacture of foams and emulsions, caseinomacropeptide depleted cheese whey with upstream separation of precursor proteins and downstream fractionation of peptide mixtures using novel chromatographic methods

Key Words: transglutaminase, chymosin, trypsin

218 Use of digital infrared thermography to measure the skin temperature changes in estrus synchronized dairy cows. S. Talukder*[1], L. Ingenhoff[1], K. L. Kerrisk[1], S. C. Garcia[1], and P. Celi[1,2], *[1]The University of Sydney, Narellan, Australia, [2]The University of Melbourne, Parkville, Victoria, Australia.*

The primary aim of this study was to explore the potential use of digital infrared thermography for estrus detection in dairy cows. Twenty cows were synchronized using controlled internal drug release (CIDR, progesterone 1.9g) and prostaglandin $F_{2\alpha}$ ($PGF_{2\alpha,}$ cloprostenol sodium 500µg). Vulva and muzzle skin temperatures were measured every 12 h from CIDR insertion to 32 h post $PGF_{2\alpha}$ injection and then every 4 h until ovulation occurred. Thermal images obtained with a FLIR T620 series infrared camera were analyzed using ThermaCAM Researcher Professional 2.9 software. All the images of vulva and muzzle were averaged for the following 5 periods: 1) 24 h before PG injection (B-PG), 2) 32 h after PG injection (A-PG), 3) 36 h after PG injection to 1st sign of estrus (PG-E), 4) time from estrus to ovulation (E-OV) 5) 4 h interval in which ovulation occurred (OV). The relationship of vulva and muzzle temperature at different periods was analyzed by linear mixed model using Genstat version 14. Temperature humidity index and time of the day were included as covariates. Vulva and muzzle temperature changed significantly ($P < 0.01$) between time periods. Muzzle skin temperature increased from A-PG to E-OV after which temperature decreased. A positive ($P < 0.01$, r = 0.74) relationship was noted between muzzle and vulva skin temperature. The mean time of onset of estrus and ovulation were 54.7 ± 14.4 and 87.3 ± 19.1 h respectively after $PGF_{2\alpha}$ injection. Ovulation occurred 30.7 ± 9.8 h after onset of estrus. Muzzle and vulva temperature also changed significantly ($P < 0.01$) as ovulation approached. The most distinct increase in vulva and muzzle temperature was observed 22 and 16 h respectively before ovulation. Therefore, digital infrared thermography could be a promising tool for estrus detection or prediction of ovulation in dairy cows. Further biometrical analyses are required to build prediction models and to test the accuracy with hormonal assay.

Key Words: infrared thermography, estrus, dairy cow

219 Presynchronizing $PGF_{2\alpha}$ and GnRH injections before a fixed-time artificial insemination CO-Synch + CIDR program. S. L. Hill*[1], S. L. Pulley[1], KC Olson[1], J. R. Jaeger[1], R. M. Breiner[1], V. R. G. Mercadante[2], G. C. Lamb[2], and J. S. Stevenson[1], *[1]Kansas State University, [2]University of Florida.*

We hypothesized that pregnancy outcomes may be improved by inducing luteal regression and ovulation before a timed AI (TAI) program in suckled beef cows. This hypothesis was tested by presynchronizing estrous cycles before initiating a TAI program with the objective to increase the proportion of cows starting the program in a high (≥1 ng/mL) progesterone status and increase pregnancy per TAI (P/TAI). Cows were assigned randomly to 2 treatments after stratification by breed, parity, and days postpartum. Cows at 4 locations (n = 803) were assigned to either: (1) control (100 µg GnRH i.m. and insertion of a progesterone-releasing intravaginal controlled internal drug release (CIDR) insert on d –10, 25 mg $PGF_{2\alpha}$ i.m. and CIDR insert removal on d –3, and 100 µg GnRH i.m. plus TAI on d 0); or (2) PrePGG (same as control with a pre-$PGF_{2\alpha}$ injection at d –20 and a pre-GnRH injection at d –17). Blood was collected on d –20, –17, –10, –3, and 0 for progesterone assays. Ovarian structures in cows at 1 location were scanned. Binomial data were analyzed by procedure GLIMMIX. The PrePGG cows were more likely ($P < 0.05$) than controls to have luteolysis after the initial $PGF_{2\alpha}$ injection (42.2 vs. 14.4%) and had reduced ($P < 0.05$) concentrations of serum progesterone (0.37 vs. 0.71 ng/mL) at the time of the presynchronizing GnRH injection. On d –10 and –3 more ($P < 0.05$) PrePGG cows had at least 1 CL than controls (63.9 vs. 41.9% and 62.7 vs. 45.3%, respectively) indicating that ovulation had occurred in response to pre-GnRH. The P/TAI at d 35 did not differ between PrePGG and control (44.4 vs. 44.0%, respectively). Final pregnancy outcome (82.6 vs. 82.6%) and pregnancy loss (5.4 vs. 3.6%) did not differ between PrePGG and control, respectively. Cows having BCS >5.0 at d –20 were more ($P < 0.01$) likely to become pregnant than thinner cows (49.8 vs. 38.8%). Cows that were ≥70 d postpartum also had a greater ($P < 0.01$) P/TAI than cows with fewer days postpartum at TAI (52.6 vs. 36.1%). In summary, luteal regression and ovulation were enhanced by presynchronization before the 7 d CO-Synch program; however, P/TAI was not increased.

Key Words: timed AI, presynchronization, luteolysis

220 Influence of estrus at fixed-time AI on accessory sperm numbers and embryonic development. E. L. Larimore*[1], S. G. Kruse[2], B. J. Funnell[2], S. L. Bird[2], O. L. Swanson[1], G. A. Bridges[2], and G. A. Perry[1], *[1]Department of Animal Science, South Dakota State University, Brookings, [2]North Central Research and Outreach Center, University of Minnesota, Grand Rapids.*

Increased accessory sperm numbers have been correlated with increased embryo quality, and estrous expression before timed-AI (TAI) resulted in increased pregnancy success. Thus, the objective of this experiment was to determine if estrous expression before TAI affected accessory sperm numbers and embryonic development. Beef heifers at UMN (Rep 1; n = 44, Rep 2; n = 44) and SDSU (Rep 3; n = 50) were developed in a dry-lot and fed approximately 125% NRC requirements from weaning to AI. Ovulation was synchronized using the 5 d CO-Synch + CIDR with TAI on d 0. Estrous expression was assessed twice daily with the aid of EstroTect patches. Immediately following TAI, half the heifers continued on the pre-insemination diet and the remaining heifers were restricted fed. On d 6 embryos were collected and evaluated to determine quality (IETS standards; 1 = excellent, 5 = degenerate) and stage (1 = unfertilized, 9 = expanded hatched blastocyst). Embryos were stained and evaluated to determine the number of dead blastomeres (propidium iodide), total blastomeres, and number of accessory sperm (Hoechst 33342). Data was analyzed using the Mixed procedures of SAS. There were no treatment by replication or treatment by estrus interactions for any data evaluated, thus all data were pooled. Estrous expression before TAI did not affect the percent of embryos recovered ($P = 0.21$; n = 61 and 26 for heifers that did and did not exhibit estrus, respectively), number of dead cells ($P = 0.86$), or total cells ($P = 0.13$). However, embryos from heifers that exhibited estrus had improved embryo quality ($P = 0.03$; 2.2 ± 0.1) and advanced embryo stage ($P < 0.01$; 4.4 ± 0.1) compared with heifers that did not exhibit estrus (2.8 ± 0.3 and 3.7 ± 0.2, respectively). Heifers that exhibited estrus also tended to have increased numbers of accessory sperm ($P = 0.06$; 23.2 ± 3.6) and percentage of cells alive ($P = 0.08$; 81.1 ± 2.4%) compared with heifers that did not exhibit estrus (12.1 ± 2.8 and 69.7 ± 6.4%). In summary, initiation of standing estrus before TAI resulted in improved embryo stage and quality and tended to improve accessory sperm numbers and percentage of live cells.

Key Words: embryo, estrus, accessory sperm

221 Reducing handling in the 5-day timed AI program in dairy cows. J. S. Stevenson*, S. L. Pulley, and S. L. Hill, *Kansas State University, Manhattan.*

We hypothesized that 50 mg of prostaglandin $F_{2\alpha}$ (PG) on d 6 (not d 5 as previously tested) would induce luteolysis in a traditional 5-d Ovsynch-72 program (GnRH 5 d before [d 0] and 72 h after [d 8] 25-mg PG doses [d 5 and 6 after GnRH]; timed AI on d 8). Experiment 1 monitored luteal regression of original and GnRH-induced luteal tissue (CL) and blood progesterone (P4) after either of the 25-mg doses of PG (d 5 and 6; control; n = 31) or a single 50-mg dose of PG on d 6 (1 × 50 mg; n = 30). Estrous cycles were presynchronized (GnRH 7 d before 25 mg of PG) and 11 d later (62 to 71 d in milk) cows were enrolled in a 5-d Ovsynch-72 program and treatments were administered. Blood was sampled for P4 and luteal structures were measured by ultrasonography on d 0 (original CL) and d 5 through 9 to monitor new GnRH-induced CL. Data were analyzed as repeated measures using procedure MIXED. Control PG reduced ($P < 0.01$) luteal tissue area of original CL on d 6 and 7, but no difference was detected by d 9. In contrast, no differences were detected in luteal tissue area of the induced CL on d 5 through 9. Serum P4 on d 5 through 9 averaged: 5.6 vs. 6.0, 1.2 vs. 6.0 ($P < 0.01$), 0.29 vs. 0.65, 0.16 vs. 0.59, and 0.14 vs. 0.46 (±0.3 ng/mL), respectively, for control and 1 × 50 mg dose. Luteolysis occurred in all 31 controls, but luteolytic failure occurred in 2 of 30, 1 × 50 mg cows in which no CL were present on d 0 (1 or 3 new CL were present on d 5). Experiment 2 monitored luteolysis in non-pregnant repeat-service cows subsequently treated with the same 2 treatments as in Exp. 1. Serum P4 in 57 cows on d 5, 6, and 8 was: 5.4 vs. 6.6, 1.7 vs. 5.8 ($P < 0.01$), and 0.29 vs. 0.35 (±0.5 ng/mL), respectively, for control and 1 × 50 mg dose. Luteolysis occurred in 28/30 controls and in 26/26, 1 × 50 mg treated cows. Pregnancy outcome 32 d after AI for both experiments was 30/60 (50%) vs. 26/56 (46%) for control vs. 1 × 50 mg dose, respectively. We concluded that the single 50-mg dose was equivalent to the control based on actual luteal tissue regression, decreased P4, and pregnancy outcome.

Key Words: luteolysis, luteal, pregnancy

222 Effect of presynchronization using Ovsynch or a single GnRH injection 7 d before an Ovsynch56 protocol on fertility of lactating dairy cows at first service. P. D. Carvalho*, J. N. Guenther, M. J. Fuenzalida, M. C. Amundson, M. C. Wiltbank, and P. M. Fricke, *Department of Dairy Science, University of Wisconsin-Madison, Madison.*

Presynchronization strategies such as Presynch Ovsynch and Double Ovsynch increase fertility to timed artificial insemination (TAI); however, simpler presynchronization strategies could reduce costs and simplify reproductive management. Lactating Holstein cows (n = 400) were randomly assigned to one of 2 presynchronization treatments before beginning an Ovsynch56 protocol (GnRH (G1) at 70 ± 3 DIM; PGF 7 d later; GnRH 56 h after PGF; TAI 16 h later at 80 ± 3 DIM) for first TAI. Cows (n = 208) in the first treatment (Double Ovsynch; DO) were presynchronized using a modified Ovsynch protocol (GnRH at 53 ± 3 DIM, 7 d later PGF, 3 d later GnRH) ending 7 d before G1 of Ovsynch56. Cows (n = 192) in the second treatment (GGPG) were presynchronized using a single injection of GnRH 7 d before G1 of Ovsynch56 at 63 ± 3 DIM. Blood samples were collected at G1 and the PGF injection of the Ovsynch56 protocol to determine progesterone (P4) concentration and pregnancy diagnosis was performed by ultrasonography. Temperature humidity index (THI) was calculated based on data from a station located near the farm, and data were analyzed using PROC GLIMMIX of SAS. Overall, DO cows had greater ($P = 0.03$) pregnancies per AI (P/AI) compared with GGPG cows 32 d after TAI (50.2% vs. 40.8%). Treatment was not affected by parity (primiparous vs. multiparous), and pregnancy loss did not differ between treatments or parities. Interestingly, P/AI was similar for DO and GGPG cows during cool weather (THI < 72; 47.2% vs. 45.1%, respectively), whereas P/AI was greater ($P = 0.02$) for DO cows during heat stress (THI ≥ 72; 52.0% vs. 34.8%). Based on P4 at G1, more ($P < 0.001$) DO cows had P4 in a medium range (>0.5 to < 4 ng/mL) compared with GGPG cows (81.9% vs. 58.7%). In addition, more ($P < 0.001$) DO cows had high P4 (>4 ng/mL) at the PGF injection of Ovsynch56 compared with GGPG cows (69.0% vs. 36.8%). In conclusion, presynchronization with a modified Ovsynch protocol increased P/AI by increasing synchrony to the Ovsynch56 protocol particularly during heat stress compared with presynchronization with a single injection of GnRH.

Key Words: synchronization, timed AI, dairy cow

223 Relationship of follicle size and concentrations of estradiol among cows that do and do not exhibit estrus during a fixed-time AI protocol. O. L. Swanson*[1], E. L. Larimore[1], B. L. Perry[1], G. D. Djira[2], R. A. Cushman[3], and G. A. Perry[1], *[1]Department of Animal Science, South Dakota State University, Brookings, [2]Department of Mathematics and Statistics, South Dakota State University, Brookings, [3]USDA-ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Cows that exhibited estrus around the time of fixed-time AI had greater pregnancy success compared with cows that did not. The objective of this study was to determine the relationship between follicle size and peak estradiol concentration between cows that did or did not exhibit estrus during a fixed-time AI protocol. Beef cows were synchronized with the CO-Synch protocol [GnRH (100 µg) on d −7, $PGF_{2\alpha}$ (25 mg) on d 0, and a second injection of GnRH 48 h after $PGF_{2\alpha}$ (d 2)] in 3 replicates (n = 80, 22 and 24). Follicle size (d 2) and ovulation (d 4) was determined by ultrasonography. Blood samples were collected every 3 (replicates 1 and 2) or 4 (replicate 3) h from $PGF_{2\alpha}$ injection to h 56. Estrus was detected by visual observation with the aid of estrus detection patches, and cows that ovulated were classified as exhibited estrus (n = 46) or did not exhibit estrus (n = 63). Data were analyzed using the GLM procedure in SAS with replicate as a co-variate. Among all cows ($P < 0.01$) and among cows that exhibited estrus ($P < 0.01$), there was a significant positive relationship between follicle size and peak estradiol concentration, but there was no relationship ($P = 0.60$) between follicle size and peak estradiol concentration among cows that did not exhibit estrus. Cows that exhibited estrus had a larger ($P = 0.02$) follicle (13.4±0.25 mm) and greater ($P < 0.01$) peak estradiol concentration (12.4 ± 0.54 pg/mL) compared to cows that did not exhibit estrus (12.6 ± 0.22 mm and 7.8 ± 0.46 pg/mL). There was no relationship between follicle size and estradiol concentration at the second GnRH injection among all cows ($P = 0.27$), cows that exhibited estrus ($P = 0.34$), and cows that did not exhibit estrus ($P = 0.34$), but cows that exhibited estrus (8.9 ± 0.56 pg/mL) had greater ($P < 0.01$) concentrations of estradiol compared to cows that did not exhibit estrus (5.8 ± 0.45 pg/mL). In summary, follicle size had a positive relationship with peak concentrations of estradiol, but only among cows that exhibited standing estrus.

Key Words: follicle size, estradiol, estrus

224 Progesterone supplementation to dairy cows lacking a corpus luteum (CL) at the initiation of the Ovsynch protocol. R. S. Bisinotto*, N. Martinez, F. S. Lima, T. L. C. Pinto, R. S. Surjus, G. C. Gomes, E. S. Ribeiro, L. F. Greco, W. W. Thatcher, and J. E. P. Santos, *University of Florida, Gainesville.*

Objectives were to evaluate the effects of supplemental progesterone (P4) on fertility responses of Holstein cows lacking a CL at the initiation of the Ovsynch-56 program (d-10 GnRH, d-3 $PGF_{2\alpha}$, h-16 GnRH, d0 AI). Cows had their ovaries evaluated by ultrasonography on d-10 and those without CL were assigned randomly to receive 0 (Control; n = 270) or 2 controlled internal drug-release (CIDR) inserts containing P4 from d-10 to d-3 (2CIDR; n = 261). Cows with CL on d-10 were used as positive controls (Diestrus; n = 756). Cows had their ovaries scanned on d-3 to detect newly formed CL. Blood was sampled on d-10, −9, −7, −5, −3, and 0 and P4 concentrations determined by RIA. Estrus was detected based on removal of tail chalk. Pregnancy was evaluated 32 and 60 d after AI. The LOGISTIC and GLIMMIX procedures of SAS were used to analyze binomial and continuous responses. The use of 2 CIDR inserts increased ($P < 0.001$) P4 concentrations between d-9 and −3 compared with Control (2.57 vs. 0.75 ng/mL), but concentrations were less than those of Diestrus (4.45 ng/mL). Ovulation to the first GnRH was greater ($P < 0.001$) for Control and 2CIDR compared with Diestrus (61.9, 57.1, and 35.9%, respectively), which resulted in a greater ($P < 0.001$) proportion of cows bearing a new CL on d-3 (71.5, 65.9, and 39.0%, respectively). Nonetheless, a greater proportion of Diestrus cows had CL on d-3 compared with Control and 2CIDR (89.6, 71.5, and 65.9%, respectively). Pregnancy per AI was less for Control than for Diestrus and intermediate for 2CIDR cows (Table 1). However, this trend was observed only in cows that were not in estrus at AI.

Table 1. Fertility responses (%; no.) to treatment

	Treatment			
	Control	2CIDR	Diestrus	*P*-value
Estrus at AI	59.3 (270)	66.7 (261)	55.8 (756)	0.70
Pregnant d 32				
Overall	26.7 (270)^{b,B}	31.8 (261)^{A}	33.6 (756)^{a}	0.002
Estrus at AI	35.0 (160)	36.2 (174)	35.8 (422)	0.93
Not in estrus at AI	14.6 (110)^{b}	23.0 (87)^{a}	30.8 (334)^{a}	0.001
Pregnant d 60				
Overall	23.0 (270)^{b}	27.7 (260)^{b}	31.5 (752)^{a}	0.002
Estrus at AI	29.4 (160)	32.2 (174)	33.4 (419)	0.62
Not in estrus at AI	13.6 (110)^{b}	18.6 (86)^{B}	29.1 (333)^{a,A}	0.002
Pregnancy loss	13.9 (72)^{a}	12.2 (82)^{a}	5.2 (250)^{b}	0.03

Key Words: anestrus, progesterone, dairy cow

225 Resumption of postpartum ovarian cyclicity in dairy cows and its relationship with acute phase proteins, uterine health and lipolysis during the transition period. C. C. Brauner*[1], A. R. T. Krause[1], M. E. Lima[1], E. G. Xavier[2], A. Schneider[1], E. Schmitt[3], E. Schwegler[1], M. M. Weschenfelder[1], P. Montagner[1], F. A. B. Del Pino[1], M. N. Corrêa[1], and L. F. M. Pfeifer[3], *[1]Universidade Federal de Pelotas, NUPEEC, Pelotas, RS, Brazil, [2]Granjas 4 Irmãos S/A, Rio Grande, RS, Brazil, [3]Empresa Brasileira de Pesquisa Agropecuária EMBRAPA, Porto Velho, RO, Brazil.*

The aim of this study was to evaluate the resumption of postpartum cyclicity and its relationship with acute phase proteins, uterine health and lipolysis during the transition period of dairy cows. Twenty multiparous Holstein cows were enrolled in this study from a commercial dairy farm with annual rolling herd average of 7,891 ± 1.18 kg of milk. To assess the cyclicity resumption, blood samples were collected weekly from 16 to 44 d during the postpartum period to evaluate the concentration of progesterone. Cows were classified as either ovulatory (OC group), consisting of cows that ovulated up to 44 ± 2 d (n = 12) or anovulatory (AC group), those cows that did not ovulate in the same period (n = 8). Blood samples were collected weekly from day −21 relative to calving to 30 d postpartum aiming to evaluate the concentration of acute phase proteins (haptoglobin, paraoxonase and albumin), as well as, glucose and NEFA. Endometrial cytology was performed at 37 ± 2 postpartum days, to assess the uterus health considering the polymorphonuclear (PMN) cells count, using uterine low volume flushing. Data were analyzed by MIXED PROCEDURES of SAS. The OC had lower ($P = 0.05$) PMN percentage in endometrial cytology than AC with 26.3% vs. 53.4% PMN cells in the uterine flushing, respectively. The AC had lower ($P = 0.03$) concentrations of albumin during the prepartum (2.42 ± 0.07 vs. 2.64 ± 0.05 g/dL) and postpartum period (2.22 ± 0.09 vs. 2.52 ± 0.07 g/dL $P = 0.01$), and higher ($P = 0.04$) concentrations of haptoglobin during the prepartun (0.69 ± 0.16 vs. 0.23 ± 0.13 g/L) and tended ($P = 0.09$) to have lower activity of paraoxonase during the postpartum period (87.81 ± 9.11 U/L vs. 108.41 ± 7.45 U/L) than the OC group. No differences ($P > 0.05$) were observed of NEFA and glucose concentrations during the transition period. In conclusion, cows that return earlier to estrous cyclicity have reduced concentrations of haptoglobin and proportion of PMN in endometrium, and increased concentrations of albumin, but no differences in blood NEFA were observed between OC and AC.

Key Words: inflammation, ovulation, NEFA

226 A missense mutation in growth differentiation factor-9 (GDF9) increases ovulation rate in sheep. M. P. Mullen* and J. P. Hanrahan, *Animal and Grassland Research and Innovation Centre, Teagasc, Athenry, Co. Galway, Ireland.*

The Finnish Landrace is a well-known high prolificacy sheep breed and has been used in many countries to increase fecundity of local breeds. All of the evidence adduced to date suggests that mutations with a large effect on ovulation rate are not responsible for the exceptional prolificacy of Finnsheep. The objectives of this study were 1) to ascertain if any of the 10 established mutations with large effects on ovulation rate in sheep or 2) if any other DNA sequence variants within the candidate genes GDF9 and BMP15, are implicated in the high prolificacy of the Finnish Landrace breed using material from lines developed by divergent selection on ovulation rate. Genotyping results showed that none of 10 known mutations, $FecX^{G}$, $FecX^{B}$, $FecG^{H}$, $FecB^{B}$, $FecX^{I}$, $FecX^{H}$, $FecX^{L}$, $FecT^{T}$, $FecG^{E}$ or $FecX^{R}$, were present in the set of 108 Finnsheep tested and thus do not contribute to the exceptional prolificacy of Finnsheep. However, DNA sequence analysis of GDF9 identified a previously known mutation, V371M, segregating at significantly different frequencies between high and low ovulation rate lines. Subsequently analysis of Belclare sheep revealed a significant association V371M and ovulation rate ($P < 0.001$). Heterozygous carriers of V371M, a missense mutation in GDF9, exhibited increased ovulation rate (0.24 s.e. 0.084) relative to the wild type. This finding brings to 11 the number of mutations that exhibit large effects on ovulation rate in sheep and to 3, including $FecB^{B}$ and $FecG^{E}$, the number of known mutations within the TGFβ superfamily with a positive effect on prolificacy in the homozygous state without any associated sterile phenotype. These results further highlight the central role of members of the TGFβ superfamily in the control of fertility in mammals.

Key Words: fecundity, growth differentiation factor-9 (GDF9), control of fertility

227 Effect of exogenous FSH on endogenous FSH secretion and testicular development in prepubertal bulls. B. R. Harstine*[1], L. H. Cruppe[1], F. M. Abreu[1], M. D. Utt[1,3], R. S. Cipriano[1], C. Premanandan[2], J. M. DeJarnette[3], and M. L. Day[1], *[1]Department of Animal Sciences, The Ohio State University, Columbus, [2]Department of Veterinary Biosciences, The Ohio State University, Columbus, [3]Select Sires Inc., Plain City, OH.*

In prepubertal bulls, FSH facilitates testis maturation and a transient proliferation of Sertoli cells. Two experiments (Exp) examined the effects of exogenous FSH on hormone secretion and testis development of Angus-cross bulls. Exogenous FSH treatment consisted of IM injection of 30 mg NIH-FSH-P1 (Folltropin-V) in a 2% hyaluronan solution (pFSH). In Exp 1, bulls (50 ± 6.5 d age; d 0) received either pFSH (FSH, n = 5) or saline (control, n = 5) on d 0 and 3.5. Blood samples to assess FSH and testosterone (T) concentrations (CONC) were obtained every 6 h for 24 h after pFSH and every 12 h thereafter. Peripheral FSH CONC measured using a bovine FSH RIA were greater ($P < 0.05$) in the FSH than control treatment 6 h after pFSH and tended to be greater ($P \leq 0.08$) 12 h after pFSH. FSH CONC from 18 to 84 h after pFSH and T CONC throughout did not differ between treatments. In Exp 2, bulls were treated with pFSH (FSH, n = 11) or saline (control, n = 11) every 3.5 d from 35 ± 2 to 91 ± 2 d age. Blood samples were collected before each treatment to quantify T and FSH CONC. Body weight (BW) and scrotal circumference (SC) were measured weekly. Bulls were castrated at 93 ± 2 d age. Seminiferous tubule diameter, testis composition, and number of Sertoli cells per tubule cross section (GATA-4 positive staining) were determined from fixed and stained histological sections. FSH CONC did not differ between treatments from 35 to 67.5 d age, but increased ($P < 0.05$) in the FSH treatment at 70 d age and remained elevated and greater than control bulls through 91 d age. CONC of T, BW, SC, testis wt and volume, percent of parenchyma comprised of tubules, and tubule diameter did not differ between treatments. However, number of Sertoli cells per round tubule cross section was greater ($P < 0.05$) in the FSH than control (33.35 ± 0.9 vs. 28.27 ± 0.9 cells) treatment. In summary, exogenous pFSH treatment from 35 to 91 d of age increased endogenous FSH secretion and the number of Sertoli cells at 93 d of age. It is suggested that exogenous FSH altered endocrine mechanisms regulating endogenous FSH secretion and augmented Sertoli cell proliferation in young bulls.

Key Words: FSH, Sertoli cell, testes

228 Effect of estradiol benzoate on estrus intensity, estrus response and fertility in CIDR-treated crossbred heifers. M. U. Mehmood*[1], A. Y. Qamar[1], N. Ahmad[1], A. Sattar[1], and M. Abdullah[2], *[1]Department of Theriogenology, University of Veterinary and Animal Sciences, Lahore, Punjab, Pakistan, [2]Department of Livestock Production, University of Veterinary and Animal Sciences, Lahore, Punjab, Pakistan.*

Crossbred dairy animals are capable of sustaining higher levels of production than native buffalo, Sahiwal, Cholistani and Desi breeds, but also more environmentally adaptable to the harsh climates of Pakistan when compared with exotics (Friesian or Jersey). Unfortunately as replacement heifers are not lactating, they are often ignored by the owners in terms of feeding and evaluating the onset of puberty. Therefore, the objectives of the present study were to determine the effect of estradiol benzoate (EB) on estrus response, intensity and fertility in CIDR (Controlled Internal Drug Releasing Device; 1.38g Progesterone; Pfizer, USA) treated crossbred heifers. Crossbred (Sahiwal × Friesian) heifers with average body condition score of 2.5 ± 0.5 (1–5), were placed at 4 different farms near Lahore, Pakistan. All the heifers were treated with CIDR on d 0 and were injected $PGF_{2\alpha}$ (Dalmazine, FATRO, Italy; 0.075 mg/mL, im), on d 6 followed by removal of CIDR on d 7. Estradiol benzoate (100 µg/mL, im Sigma Aldrich Germany) was administered 24 h after the CIDR removal (n = 50) treated with EB (group-I) while the other group (n = 50) was without EB treatment (group-II). Estrus detection was carried out by visual observation; twice daily for at least 30 min. All heifers were artificially inseminated 48 and 60 h after CIDR removal. Pregnancy status was determined by ultrasonography (HS 1500V; Honda; Japan, with 7.5 MHz probe) between d 30 and 40 post-AI. Estrus response and pregnancy rate were analyzed using Chi-squared, while estrus intensity scored by Mann-Whitney test. Estrus response was 100% in both groups. Estrus intensity was scored at the time of AI as 1 = Low, 2 = Medium, 3 = High based upon the heat signs. Estrus intensity was highly significant ($P = 0.01$) in group I (2.9 ± 0.1) compared with group II (2.0 ± 0.7). Pregnancy rate was 54% (27/50) in group I and 36% (18/50) in group II heifers ($P = 0.07$). It is concluded that estradiol benzoate in CIDR protocol intensified signs of estrus and pregnancy rate. It is implied that CIDR could be a good tool to enhance fertile estrus.

Key Words: crossbred heifers, CIDR, estradiol benzoate

Physiology and Endocrinology Symposium: The Next Generation of Metabolic Endocrinology

229 Novel insights in to the biology of the emerging metabolic regulator FGF21. A. C. Adams* and A. Kharitonenkov, *Eli Lilly & Co., Indianapolis, IN.*

Fibroblast growth factor 21 (FGF21) is a multifaceted metabolic regulator which has potential applications in the treatment of diseases such as obesity, diabetes and fatty liver. When administered in vivo either peripherally or centrally FGF21 has a plethora of beneficial activities. To date the mechanism and site of action underlying these effects remains unknown with recent studies suggesting some of its effects may be mediated indirect and occur via modulation of other factors such as adiponectin and leptin. Using tissue specific knock out mouse models lacking either the FGF receptor (FGFR1) or the critical co factor β-Klotho (KLB) we sought to determine the tissue upon which FGF21 acts and receptor complex responsible for FGF21 its mediating in vivo efficacy. Importantly, when KLB is ablated from all tissues FGF21 action is completely abrogated. To determine the precise tissue of action we created 2 tissue specific lines harboring deletion of FGFR1 in neurons and in adipose tissue, respectively. Surprisingly, in animals with neuronal FGFR1 loss there was no change in the metabolic activity of FGF21 suggesting direct central FGF21 action is not required for its physiological endpoints. In contrast, when we examined the adipose FGFR1 mutants we found significant attenuation of metabolic efficacy. Importantly, the action of FGF21 via adipose tissue results in alterations in adipokine secretion and systemic sensitivity to these factors. Therefore, while FGF21 itself may not directly act on the CNS, leptin and other adipokines are likely be mediators of FGF21's secondary central effects downstream of direct adipose tissue engagement. Further studies are required to delineate the precise mechanistic basis underlying central FGF21 mediated physiology.

Key Words: FGF21, metabolism, diabetes

230 Biology of the novel hormone fibroblast growth factor-21 in the transition dairy cow. Y. R. Boisclair*, S. L. Giesy, and L. S. Caixeta, *Cornell University, Ithaca, NY.*

The modern dairy cow reaches near maximal productivity soon after parturition despite a substantial nutritional deficit. This ability is underpinned by coordinated adaptations that are most obvious in liver, adipose tissue and skeletal muscle and affect the metabolism of all major organic nutrients. Over the last 2–3 decades, most research in dairy cattle has focused on the roles played by growth hormone, insulin-like growth factor-I and insulin in driving these adaptations. The last 10–15 years, however, have witnessed the discovery of novel hormones with potent metabolic actions. Among those, the hormone fibroblast growth factor-21 (FGF21) appears relevant on the basis of its ability in laboratory animals to regulate mobilization of lipids from adipose tissue and their oxidation in liver, 2 processes that are crucial to the efficient utilization of lipid reserves in early lactating dairy cows. These observations led us to examine the regulation of the FGF21 system in high yielding dairy cows over the last 4 weeks of pregnancy (LP) and the first 8 weeks of lactation (EL). Plasma FGF21 was nearly undetectable in LP, peaked on the day of parturition and then stabilized at lower, chronically elevated concentrations during the energy deficit of EL. Gene expression studies showed that liver was the major source of plasma FGF21 in EL with little or no contribution by adipose tissue, skeletal muscle and mammary gland. Finally, we identified liver and adipose tissue as the only 2 major tissues with meaningful expression of β-Klotho, a co-receptor that is absolutely essential for FGF21 signaling. These results suggest that FGF21 may be a key metabolic hormone in early lactating dairy cows and provide impetus to identify factors triggering its production as well as FGF21-dependent liver and adipose tissue responses.

Key Words: periparturient period, liver, adipose tissue

231 Role of adiponectin and visfatin in chicken growth and reproduction. R. Ramachandran*, S. Krzysik-Walker, O. Ocon-Grove, R. Vasilatos-Younken, G. Hendricks III, and J. A. Hadley, *Department of Animal Science, Pennsylvania State University, University Park.*

Adiponectin and visfatin are 2 endocrine factors that affect metabolism in domestic animals. Adiponectin, a 30 kDa adipokine hormone, improves carbohydrate and lipid metabolism in humans and rodent animal models by activating 2 distinct transmembrane receptors (AdipoR1 and AdipoR2) that are widely expressed in various tissues in the chicken. We have cloned and characterized the chicken genes that encode for adiponectin, AdipoR1, and AdipoR2. While adipose tissue is the primary site of adiponectin expression in the chicken, we found that adiponectin and its receptors are ubiquitously expressed in other tissues. Adiponectin undergoes multimerization during biosynthesis in the adipose tissue and circulates as a unique heavy molecular weight isoform that is larger than 669 kDa mass. Plasma adiponectin levels were found to be significantly lower in 8-wk-old compared with 4-wk-old male chickens and inversely related to abdominal fat pad mass. In vitro studies using hepatocytes and ovarian follicular cells revealed that recombinant chicken adiponectin (rcADN) increased the abundance of phosphorylated adenosine monophosphate-activated protein kinase, phosphorylated acetyl coenzyme A carboxylase, and phosphorylated Erk 1/2, as well as increased glucose uptake. Future studies will focus on regulating the signal transduction pathways of adiponectin for improving growth and reproductive efficiency. Nicotinamide phosphoribosyltransferase (Nampt/visfatin/PBEF) has been identified as a rate-limiting NAD^+ biosynthetic enzyme and an adipokine/myokine found within the cells and circulation. Human and chicken skeletal muscles are reported to have the highest level of Nampt expression among various tissues. We found that plasma levels of visfatin dramatically increases 28-fold in pubertal broiler breeder chickens compared with pre-pubertal chickens. Furthermore, recombinant visfatin was found to alter the expression of key myogenic transcription factors in satellite cells suggesting that visfatin may influence postnatal myogenesis. Future studies will focus on elucidating the functional role of circulating visfatin in growth and reproduction of farm animals.

Key Words: adiponectin, visfatin, chicken

232 Characterization of serum adiponectin during lactation in dairy cows supplemented with conjugated linoleic acids. S. P. Singh*[1], S. Häussler[1], S. Dänicke[2], M. Mielenz[3,1], and H. Sauerwein[1], *[1]Institute of Animal Science, Physiology and Hygiene Group, University of Bonn, Bonn, Germany, [2]Institute of Animal Nutrition, Friedrich-Loeffler-Institute (FLI), Federal Research Institute for Animal Health, Braunschweig, Germany, [3]Leibniz Institute for Farm Animal Biology (FBN), Department of Nutritional Physiology, Dummerstorf, Germany.*

The adipokine adiponectin (Aq) is known for its insulin sensitizing effects. The metabolic profile of dairy cows may be affected by conjugated linoleic acids (CLA). The objectives of our study were to characterize serum Aq concentrations throughout lactation and to test whether dietary CLA supplementation affects this time course in multiparous (MP) and primiparous (PP) dairy cows. Thirty 3 pregnant German Holstein cows (22 MP and 11 PP) were included in the study from d 21 antepartum (ap) until d 252 postpartum (pp). From d 21 ap until calving, all animals received same diet. From d 1 to d 182 pp, animals received same lactation diet but were either fed CLA (100 g/d Lutrell Pure, BASF, Ludwigshafen, Germany; group CLA: 11 MP and 5 PP cows) or a control fat supplement (100 g/d Silafat; BASF; group CON: 11 MP and 6 PP cows). After d 182 pp, all animals were continuously fed with same lactation diet but without CLA or control fat supplement for further 12 wk. Blood samples were collected for determining serum Aq by ELISA (Mielenz et al., 2013, doi:10.1016/j.domaniend.2012.10.04). Data were analyzed by mixed model (SPSS). Treatment and parity were considered as fixed factors and sampling days as repeated effects. Serum Aq (μg/mL; means ± SEM) decreased from 21 d ap reaching a nadir at calving [18.5 ± 1.6 (mean for all groups together)] and increased gradually thereafter until d 21 pp in PP cows [35.9 ± 3.7 (CON), 25.8 ± 2.7 (CLA)] and until d 49 pp in MP cows [34.6 ± 2.2 (CON), 28.2 ± 2.1 (CLA)], respectively and remained unchanged thereafter. Serum Aq were lower ($P < 0.05$) in CLA than in CON cows; this difference emerged 4 wk earlier in PP cows than MP cows. Circulating Aq tended ($P = 0.09$) to be higher in MP cows of both CLA and CON groups compared with respective PP cows. Our results indicate that major changes in circulating Aq occur peripartum and that dietary CLA decreases serum Aq in both PP and MP dairy cows albeit at different times. In view of the insulin sensitizing actions of Aq described in monogastrics, the CLA effects observed herein point to a CLA-induced decrease in insulin sensitivity.

Key Words: adiponectin, conjugated linoleic acid, dairy cow

233 Daily injection of tumor necrosis factor alpha in the first week of lactation decreases milk production and promotes health disorders in Holstein dairy cows. J. K. Farney*, K. Yuan, L. K. Mamedova, and B. J. Bradford, *Kansas State University, Manhattan.*

Inflammation may contribute to transition disorders in dairy cattle. The objective of this study was to determine the production responses to administration of an inflammatory cytokine, tumor necrosis factor a (TNFα), in the first week of lactation. At calving, 33 Holstein cows (n = 9 primiparous, n = 24 multiparous) were blocked by parity and alternately assigned to either control (CON; 0 μg TNFα/kg BW), low dose (LOW; 1.5 μg TNFα/kg BW), or high dose (HIGH; 3.0 μg TNFα/kg BW) s.c. injections daily for 7 d. Daily DMI, water intake, and health disorder data were recorded; plasma samples were also collected daily for metabolite analyses. Data were analyzed using mixed models with repeated measures over time and significance was declared at $P < 0.05$ and tendencies at $P < 0.10$. Preplanned contrasts evaluating CON vs. TNFα treatments and LOW vs. HIGH were evaluated. Plasma TNFα concentrations tended to be increased in cows receiving TNFα injections ($P = 0.09$, 64% increase), but there were no differences observed between HIGH and LOW treatments. DMI was significantly reduced in cows receiving TNFα injections (18% decrease). Similarly, water intake was decreased 13% with TNFα. Milk production was reduced in TNFα treated cows as evidenced by 15 to 18% decreases in yields of milk, milk fat, milk protein, milk lactose, energy-corrected milk, and solids-corrected milk. Milk fat yield and SCM tended to be further depressed in HIGH cows, but no differences were observed between LOW and HIGH for any other milk variable. No treatment differences were observed for plasma glucose, β-hydroxybutyrate, nonesterified fatty acid, or triglyceride concentrations. Daily injection of TNFα increased total diagnosed health disorders in the first week of lactation, due in part to a tendency for an increased incidence of ketosis in cows injected with TNFα. The results of this study indicate that low grade inflammation induced by daily injection of TNFα negatively affects milk production and increases physiological stress on the transition dairy cow as evidenced by increased health disorders.

Key Words: inflammation, anorexia, metabolism

234 Inflammation and endoplasmic reticulum (ER) stress gene network expression in liver of peripartal Holstein cows fed two levels of dietary energy prepartum. M. J. Khan*[1], E. Trevisi[2], D. E. Graugnard[1], G. Bertoni[2], and J. J. Loor[1], *[1]University of Illinois, Urbana, [2]Universita Cattolica del Sacro Cuore, Piacenza, Italy.*

The peripartal period is characterized by marked changes in inflammatory status that are functionally related with impaired immune and metabolic responses in the cow. We examined blood metabolites and expression of genes related to inflammation and ER stress in cows assigned (6/diet) to a control (high-straw, CON; NEL = 1.34 Mcal/kg) or moderate-energy (OVE; NEL = 1.62 Mcal/kg) diet during the entire dry period. All cows were fed a common lactation diet (NEL = 1.69 Mcal/kg) postpartum. Blood was collected on d (±3) −14, −5, −2, −1, 0, 1, 2, 5, 7, 10, 14 and 21 d relative to parturition. A percutaneous liver tissue biopsy was harvested at −14, 7, 14, and 30 d relative to parturition for transcript profiling via quantitative PCR. Estimated prepartal energy balance (EBAL) OVE was greater ($P < 0.05$) and averaged 159% of requirements compared with 102% in CON. However, EBAL during the first week postpartum was lower in OVE (83% vs. 89% of requirements). After parturition the concentration of ceruloplasmin, creatinine, bilirubin and reactive oxygen metabolites (ROM) was greater (Diet × Time; $P < 0.05$) in OVE. Around calving the expression of ER and oxidative stress indicator genes XBP1, PERK, GRP94 and HSP40 was lower in OVE than CON but TRB3, HSPA1A, HSPA1B and CREB3L3 had greater (Diet × Time; $P < 0.05$) expression in OVE. Expression postpartum of the inflammatory genes NFKB1, RELA, CHUK, MYD88, TNF, SAA3, and PTX3 increased (Diet × Time; $P < 0.05$) in OVE. Genes associated with cell growth (mTOR, RPTOR, AKT3, TP53) also had greater (Diet × Time; $P < 0.05$) expression in OVE after parturition. Overall, results indicated that negative EBAL induced by prepartal OVE was associated with hepatic pro-inflammatory and pro-stress upregulation.

Key Words: transition cow, nutrition, transcriptomics

Production, Management and the Environment: Diet and Forage I

235 Effect of dried distillers grains with solubles on nitrogen emissions from soil-applied beef manure. J. Roth* and W. Powers, *Michigan State University, East Lansing.*

Dried distillers grains with solubles (DDGs) is an important feed in cattle diets but may affect emissions of ammonia (NH_3) and nitrous oxide (N_2O), an important greenhouse gas. The objective of this study was to determine the effect of feeding steers diets containing DDGs on NH_3 and N_2O emissions following manure application to soil. Angus steers (n = 4; initial BW = 414 kg) were fed diets containing 20% DDGs (12.2% crude protein) or 40% DDGs (16.6% crude protein) for 23 d. During the last 2 d, steers were housed in metabolism crates for a manure collection period. Steers were fed twice daily (0600 and 1800) during the collection period. Twice daily urine and feces were collected, separately, and mixed by treatment. Manure N content was determined (6.7% and 9.3% N for the 20% and 40% manures). Manure was stored frozen until the land application phase began. Thawed manure (570 g) was surface applied to 25 cm-deep soil over a sand base in 208-L tubs (6 replicates per treatment). Continuous NH_3 and N_2O headspace concentrations were measured for 26 d and daily emissions calculated. Data were analyzed using mixed model procedures. Average daily concentration of NH_3 (ppm) and average daily NH_3 emission (mg/d) were lower as a result of feeding the 20% treatment (6.4 versus 12.0 ppm ($P < 0.01$; SEM = 0.35); 52.4 versus 99.1 mg/d ($P < 0.01$; SEM = 3.14), for 20% and 40% tubs, respectively). Manure N-adjusted average daily NH_3 emission was less from tubs where the 20% manure was applied (13.4 versus 15.1 mg NH_3/g manure N; $P = 0.02$; SEM = 0.52). Average daily N_2O concentration (ppm) and average daily N_2O emission (mg/d) were lower from the 20% treatment (0.80 versus 0.92 ppm ($P < 0.01$; SEM = 0.02); 2.50 versus 5.25 mg/d ($P < 0.01$; SEM = 0.48) for 20% and 40% tubs, respectively). Manure N-adjusted average daily N_2O emission was not different between treatments (0.72 mg N_2O/g manure N; $P = 0.28$; SEM = 0.11) suggesting that differences in manure N content explained differences in N_2O emissions. Overall, feeding increased dietary protein resulting from high DDGs diets increases both NH_3 and N_2O emissions when manure is land applied.

Key Words: air emission, beef, dried distillers grains

236 Effects of PN Beef supplements and exogenous growth promotants on feedlot performance and carcass characteristics. K. J. Phelps*[1], K. A. Miller[1], C. L. Van Bibber-Krueger[1], C. A. Alvarado-Gilis[1], A. K. Sexten[1], J. S. Jennings[2], J. M. Gonzalez[1], and J. S. Drouillard[1], *[1]Kansas State University, Manhattan, [2]Alltech Inc., Nicholasville, KY.*

The experimental objective was to evaluate feedlot performance and carcass traits of beef steers fed alternative diets. Beef steers (initial BW 383 kg ± 30; 64 pens; 8 steers/pen) were used in a randomized complete block design with a 2 × 2 factorial treatment arrangement. For factor 1 (feed amendments), diets that combined inorganic trace mineral supplement, vitamins A and E, Rumensin, and Tylan (C) were compared with diets with PN Beef supplement (PN; Alltech, Inc.). PN treatments were fed a basal diet with PN Beef Receiver from d 1–20, and PN Beef Finisher from d 21 to harvest. Factor 2 consisted of the presence or absence of exogenous growth promotants (+GP vs. –GP). Steers in the +GP treatments were implanted with Component E–S, reimplanted with Component TE–S, and fed 400 mg/steer daily of ractopamine–HCl (Elanco Animal Health) for 28 d before harvest. The basal diet consisted of steam-flaked corn, wet corn gluten feed, wheat straw, and supplement. Steers were fed once daily ad libitum in partially covered, concrete-surfaced pens for 175 d then shipped to a commercial abattoir for harvest. Final BW, HCW, incidence of liver abscesses, marbling score, LM area, 12th rib fat thickness, and KPH were measured. There were no interactions between GP and feed amendments for performance or carcass traits ($P > 0.10$). Gain efficiency, DMI, ADG, HCW, and carcass traits were not different for C and PN ($P > 0.05$), but liver abscess incidence was greater for PN than for C (19.0 vs. 12.6%; $P < 0.05$). Gain, efficiency, and DMI were greater for +GP compared with –GP ($P < 0.05$). HCW were 432 and 376 kg for +GP and –GP, respectively ($P < 0.01$). Percentages of USDA Select were not affected by GP, but fewer carcasses were classified as premium Choice or Prime with +GP compared with –GP (42.8 vs. 58.4%; $P < 0.01$). Implants and β agonists increased carcass mass, but also decreased carcass quality grade. Inorganic trace elements, vitamins A and E, and in-feed antimicrobials were effectively replaced with PN Beef supplements, yielding comparable feedlot performance and carcass quality.

Key Words: growth promotant, antimicrobial, liver abscess

237 Effect of dietary nitrate supplementation on dairy cattle enteric methane and nitrous oxide emissions. Q. Wang[1], C. J. Neumeier*[1], G. Getachew[2], D. H. Putnam[2], A. R. Castillo[3], and F. M. Mitloehner[1], *[1]Department of Animal Science, University of California, Davis, Davis, [2]Department of Plant Science, University of California, Davis, Davis, [3]University of California Cooperative Extension, Merced.*

Nitrate acts as alternative hydrogen sink in the rumen to inhibit methanogenesis and therefore ruminal methane production. However, under anaerobic conditions, such as in the rumen, nitrate might be reduced to nitrous oxide, which may offset the greenhouse gas reduction benefit of nitrate feeding on methane mitigation. The present study investigated the effects of varying concentrations of nitrate supplementation (1, 2, and 3% nitrate ion on a dry matter basis) versus isonitrogenous concentrations of urea on enteric greenhouse gas emissions with an in vitro gas production system. Gas samples were collected from the in vitro systems at 2, 4, 6, 8, and 12 h incubation times and analyzed for carbon dioxide, methane, and nitrous oxide concentrations. Liquid samples were collected at 0, 3, 6, and 12 h incubation times and analyzed for nitrate, nitrite, and ammonium concentrations. All data was analyzed using the Proc Mixed Model in SAS. Nitrate vs. urea treatments at 2 and 3% decreased ($P < 0.001$) methane production during the early (0 to 8 h) and overall (0 to 12 h) incubation periods. Nitrous oxide production was observed only in the nitrate treatments. Nitrate feeding at 3% decreased ruminal methane by 3.2 mg/g dry matter feed and produced 0.018 mg nitrous oxide/g dry matter feed, respectively, equivalent to a decrease of 61.8 mg carbon dioxide equivalents/g dry matter feed. To maximize the inhibitory effect of nitrate on enteric methane production, nitrate would have to be supplemented at least 3 times daily. This study indicates that nitrate supplementation may be an effective strategy to mitigate enteric greenhouse gas emissions. Further research is necessary to evaluate methane and nitrous oxide emissions in vivo with nitrate supplementation.

Key Words: greenhouse gas, hydrogen sink, methanogenesis

238 Effect of dietary protein concentration on utilization of dairy manure nitrogen for plant growth, leachate nitrate-N losses, and ammonia emissions from lysimeters. C. Lee[1], G. W. Feyereisen[2], A. N. Hristov*[1], C. J. Dell[3], J. P. Kaye[4], and D. B. Beegle[4], *[1]Department of Animal Sciences, The Pennsylvania State University, University Park, [2]USDA-ARS-SWMRU, St. Paul, MN, [3]USDA-ARS-PSWMRU, University Park, PA, [4]Department of Crop and Soil Sciences, The Pennsylvania State University, University Park.*

Animal diet can have a significant effect on manure composition and nutrient losses during storage and following application to soil. This lysimeter experiment was designed to investigate the effects of dietary protein concentration on nitrate-N (NO_3-N) and ammonia (NH_3) losses from dairy manure applied to soil and manure N use for plant growth. Lactating dairy cows were fed diets with 16.7 (HighCP) or 14.8% (LowCP) crude protein content. Feces and urine were labeled with ^{15}N by ruminal pulse-doses of $^{15}NH_4Cl$. Unlabeled and ^{15}N-labeled feces and urine were used to produce manure for a study with 21 lysimeters (Hagerstown silt loam; fine, mixed, mesic Typic Hapludalf) in a greenhouse. Manure application rate was 277 kg N/ha. NH_3 emissions were measured at 3, 8, 23, 28, 54, and 100 h after manure application. Manure was incorporated into the soil and a leaching event was simulated. Spring barley was planted (387 plants/m^2) 7 d after the leaching event and harvested at senescence, 86 d after planting. There was no difference in whole-crop barley dry matter and N yields ($P = 0.11$ and 0.41, respectively) between LowCP and HighCP manures. The leachate NO_3-N concentration was also not different ($P = 0.08$) between manures, but urinary N had a greater ($P < 0.001$) contribution to NO_3-N than did fecal N. NH_3 emission rates were on average about 100% greater ($P < 0.001$) for HighCP vs. LowCP manures. Delta ^{15}N of NH_3-N was markedly greater ($P < 0.05$) for manures containing ^{15}N-labeled urine compared with manure with ^{15}N-labeled feces. In this study, similar plant yields and NO_3-N leaching losses were obtained by fertilizing with manures from cows fed low- vs. high-protein diets (deficient or adequate in metabolizable protein supply, respectively). Nitrogen from HighCP urine had the highest recovery rate in whole barley plants, barley kernels, and leachate NO_3-N. Applied at equal N soil application rates, HighCP manure resulted in markedly greater NH_3 emissions than LowCP manure with urine N being the primary source of the emitted NH_3.

Key Words: dietary protein, ammonia emission, nitrate leaching

239 Effect of abomasal ferrous lactate infusion on phosphorus digestion and absorption in lactating dairy cows. X. Feng*, K. F. Knowlton, A. D. Dietrich, and S. Duncan, *Virginia Polytechnic Institute and State University, Blacksburg.*

The objective of this study was to evaluate the effect of ferrous lactate infusion on phosphorus (P) digestion and absorption from the intestinal tract of lactating dairy cows. Four ruminally cannulated lactating cows were used in a 4 × 4 Latin square with 14 d in each period. Cows were fed a TMR diet containing 0.39% P, providing 100% of the cows' calculated P requirement. On d 8 to d 14 of each period, each cow was infused daily with 0, 200, 500, or 1250 mg Fe in the form of ferrous lactate solution (ferrous lactate in 1 L double distilled water) into the abomasum. Treatments were calculated to approximate 0, 2, 5, or 12.5 mg Fe/L in drinking water assuming cows drinking 100 L water per day. Total fecal collection was conducted in the last 4 d of each period and fecal samples were analyzed for total P and inorganic phosphorus (Pi) using the molybdovanadate yellow method and blue method, respectively. The phytate P content of feed and fecal samples was determined with high performance ion chromatography (HPIC). Milk samples were collected from d 11 to d 14 and coccygeal venous blood samples were collected in the last 2 d of each period. All data were analyzed using PROC GLIMMIX in SAS 9.2 and polynomial contrasts were used to evaluate linear and quadratic effects of treatment. Dry matter intake was not affected by treatment ($P > 0.05$) but the digestibility of dry matter, NDF, and nitrogen decreased linearly with increasing ferrous lactate infusion ($P < 0.01$; 68.5% to 67.0%, 38.3% to 36.2% and 66.4% to 64.1%). Milk yield, content of milk protein, lactose, and SNF, and SCC were unaffected by treatment ($P > 0.05$). A quadratic effect on milk fat percent was observed ($P = 0.04$) with the lowest milk fat at 500mg Fe/d infusion. Treatment effects on intake and digestibility of total P, Pi, and phytate P were not observed ($P > 0.05$). In the short-term, water iron up to 12.5 mg/L did not affect production or P status of lactating cows.

Key Words: dairy cow, ferrous lactate, phosphorus digestion and absorption

240 Effects of supplemented chromium propionate on milk performance and disease occurrence status in transition cows. C. Wang*[1,3], K. Wang[1], Z. Y. Duan[2], Y. Lao[2], D. M. Wang[1], and J. X. Liu[1], *[1]Institute of Dairy Science, Zhejiang University, Hangzhou, China, [2]Kemin Industries (Zhuhai) Co. Ltd., Zhuhai, China, [3]Zhejiang Agriculture & Forestry University, Lin'an, China.*

The objective of the study was to investigate the effects of supplemented chromium propionate on milk performance, blood parameters and disease occurrence status in transition cows. Seventy-five cows were blocked based on previous milk production, parity, estimated calving date and body weight, and were randomly assigned to one of 5 treatments and supplemented with 0, 25, 50, 100 and 150 g chromium propionate (KemTRACE Chromium Propionate 0.4% Dry containing 0.4% chromium) per ton of concentrate. The experiment lasted from one month before calving to 2 mo after calving. The Cr source was supplemented throughout the whole experiment. Milk yields were recorded and milk compositions were analyzed for 2 consecutive days every 10 d. Blood parameters and the content of chromium in milk, urine and feces were analyzed before trial, one week before calving, one week after calving, one month after calving and 2 mo after calving. All data except for disease occurrence status were analyzed by Mixed procedure of SAS. Disease occurrence status data were analyzed for treatment effects using the FREQ procedure of SAS. Milk yield increased as the dosage of supplemented chromium increased ($P = 0.02$) and then leveled off at a level higher than 50 g/ton. Supplementation of chromium decreased the disease rates and plasma NEFA of cows ($P = 0.05$) during the transition period. Chromium level in milk did not change in all treatments ($P > 0.05$), and the chromium in blood and urine did not increase ($P > 0.05$) at levels lower than 50 g/ton, indicating that chromium propionate can be safely fed to dairy cows at lower dosages. In conclusion, supplementation of chromium propionate at 50 g/ton can increase milk yield and is beneficial to dairy cow's health in transition period.

Key Words: chromium propionate, milk performance, health status

241 Transfer of dietary aflatoxin B1 to milk aflatoxin M1 and effect of adding absorbent on the transfer and lactation performance of dairy cows. J. L. Xiong*[1], Y. M. Wang[2], Y. Li[1,3], and J. X. Liu[1], *[1]Institute of Dairy Science, Zhejiang University, Hangzhou, China, [2]Novus International Trading (Shanghai) Co., Ltd., Shanghai, China, [3]Department of Animal Science, Zhoukou Vocational and Technical College, Zhoukou, China.*

The objectives of the study were to investigate the transfer rate of aflatoxin from feed to milk and to evaluate the efficacy of adsorbent in

reducing aflatoxin M1 (AFM1) in milk of dairy cows fed different doses of aflatoxin B1 (AFB1). Twenty-four Holstein cows in late lactation (271 ± 29 DIM, 21.6 ± 3.1 kg milk/d) were blocked by DIM, body weight, and milk yield in a 2 × 3 crossover design. Cows were added with aflatoxin B1 at 0, 20 or 40 μg/kg DM, with or without adsorbent (Solis Mos, Novus International Inc.), respectively. The experiment consisted of 2 consecutive periods with AFB1 challenging for 7 d and clearing for 5 d each period. In the second period cows were switched to different Solis Mos treatments without changing AFB1 level. Variables of data were analyzed using the mixed procedure of SAS. Dry matter intake, milk yield, contents of milk protein and milk fat, and somatic cell count were not affected by either AFB1 dosage or Solis Mos. Cows fed aflatoxin B1 at a level of 20 or 40 μg/kg excreted significantly higher AFM1 ($P < 0.01$) in milk than the 0 μg/kgDM, irrespective of Solis Mos, with significant difference between 20 and 40 μg/kg-added treatments ($P < 0.01$). Solis Mos numerically reduced the excretion of AFM1 ($P > 0.05$). Amount of AFB1 added to the diet and addition of Solis Mos did not have influence on the rate at which dietary AFB1 was transferred to AFM1 in milk. It is inferred that addition of Solis Mos and AFB1 in the diet has no effect on lactation performance of cows, while the milk AFM1 concentration linearly increased with the adding level of dietary AFB1 but was not influenced by the addition of Solis Mos.

Key Words: aflatoxin, adsorbent, transfer

242 Effect of stocking density in the prepartum period on health and productive parameters of Jersey cows. A. Dresch*[1], P. Silva[2], H. Hooper[1], C. Spies[1], P. Lau[1], K. Lobeck[2], K. Machado[1], M. Endres[2], and R. Chebel[1], *[1]Department of Veterinary Population Medicine, University of Minnesota, St Paul, [2]Department of Animal Science, University of Minnesota, St Paul.*

Objectives were to evaluate the effect of different stocking densities during the prepartum period on incidence of diseases and milk yield of Jersey cows. Within each replicate (n = 4), 2 pens were assigned to 80% stocking density (80D, n = 38) and 2 pens were assigned to 100% stocking density (100D, n = 48). Nulliparous and parous animals were housed separately pre and postpartum. Animals were scored for body condition and locomotion at enrollment, within 1 d postpartum (DIM), and at 35 and 56 DIM. Cows were examined within 1 DIM for retained placenta; 4, 7, 10, and 14 DIM for metritis; and, 35 DIM for endometritis. Data regarding displacement of abomasum, mastitis, and culling were recorded up to 60 DIM. Cows were milked thrice daily. Data regarding energy-corrected milk yield in the first month postpartum is reported. Pen was considered the experimental unit (n = 8/treatment). Dichotomous data were analyzed by logistic regression using the GLIMMIX procedure and continuous data were analyzed by ANOVA using the MIXED procedure for repeated measures. Pen was included as the random effect. Treatment was nested within pen and replicate and cows were nested within treatment. Stocking densities were 74.0 and 94.3% (±0.3) of headlocks and 80.7 and 102.8% (±0.4) of stalls for 80D and 100D, respectively. There was no effect of treatment on incidence of stillbirth (80D = 3.9 vs. 100D = 3.4%; $P = 0.50$), retained placenta (80D = 4.4 vs. 100D = 7.4%; $P = 0.13$), and endometritis (80D = 7.4 vs. 100D = 7.1%; $P = 0.65$). There was a tendency ($P = 0.10$) for incidence of metritis to be greater for 80D (21.5%) than 100D (13.9%). Treatment did not affect percentages of cows with locomotion score >2 at 35 ($P = 0.94$) and 56 ($P = 0.77$) DIM. Body condition score was not affected by treatment (80D = 2.97 ± 0.02 vs. 100D = 2.97 ± 0.01; $P = 0.91$). Percentage of cows removed from the herd within 60 DIM (80D = 4.4 vs. 100D = 3.0%; $P = 0.42$) and yield of energy corrected milk (80D = 27.56 ± 1.52 vs. 100D = 27.98 ± 1.50 kg/d; $P = 0.85$) were not affected by treatment. In conclusion, reducing stocking density did not improve health and productive parameters and unexpectedly tended to increase incidence of metritis.

Key Words: stocking density, prepartum, health

243 Supranutritional doses of selenium and vitamin E reduce the negative effects of heat stress in sheep by reducing systemic and respiratory oxidative stress. S. S. Chauhan*[1,2], P. Celi[3,2], B. J. Leury[2], F. Liu[2], and F. R. Dunshea[2], *[1]Department of Animal Husbandry, Himachal Pradesh, Shimla (HP), India, [2]Melbourne School of Land and Environment, The University of Melbourne, Parkville, VIC, Australia, [3]Faculty of Veterinary Science, University of Sydney, Narellan, NSW, Australia.*

The aim of the study was to elucidate the role of supranutritional dietary doses of selenium and vitamin E to ameliorate the effect of heat stress (HS) either individually or synergistically by reducing oxidative stress in sheep. Thirty-two Merino × Poll Dorset ewes were housed in one of 2 climatic chambers maintained at either thermoneutral (TN) (18- 21°C and 40–50% relative humidity (RH)) or HS (28–40°C and 30–40% RH) conditions. Sheep were allocated in 2 × 2 factorial design to different levels of selenium (0.24 (LS) and 1.20 (HS) mg Se (as SelPlex) kg^{-1} DM) and vitamin E (10 (LV) and 100 (HV) I.U. of vitamin E kg^{-1} DM). Respiration rate and rectal temperature were recorded at 0900, 1300 and 1700 h each day and blood samples were collected on d 1 and 7. Data were analyzed by multivariate linear mixed models using Genstat 14th edition. Average respiration rate (169 v. 78 breaths/min) and rectal temperature (40.10 v. 39.47°C) were increased ($P < 0.001$) during HS, particularly at 1700 h. Although there were no overall effects of vitamin E on physiological parameters, there were interactions ($P < 0.001$) between vitamin E and temperature such that vitamin E decreased respiration rate (157 vs. 182 breaths/min) and rectal temperature (40.26 vs. 40.54°C) during HS but not TN conditions. Se decreased respiration rate (165 vs. 174 breaths /min) during HS but not TN. Plasma reactive oxygen metabolites concentration were reduced by 20% ($P < 0.05$), while biological antioxidant potential was increased by 10% ($P < 0.05$) in sheep on the HSHV diet compared to those that received the LSLV diet. The ratio of daily water intake to feed intake was reduced by 22 % ($P < 0.05$) in sheep fed the HSHV diet compared to those fed the LSLV diet. Exhaled breath condensate hydrogen peroxide concentration was reduced by 40% ($P < 0.05$) in sheep fed the HSHV diet compared to sheep fed the LSLV diet. These data suggest that the negative effects of heat stress can be ameliorated by supranutritional doses of selenium and vitamin E through improved redox homeostasis

Key Words: heat stress, oxidative stress, sheep

244 Effect of rice bran and legume inclusion in a straw diet on intake, digestibility, nitrogen retention, digesta kinetics and methane production of beef cattle. M. Pen*, D. B. Savage, J. V. Nolan, and R. S. Hegarty, *School of Environmental and Rural Science, University of New England, Armidale, NSW, Australia.*

The effect on production of supplementing a straw diet with legume forage or rice bran was evaluated in beef steers. Twelve Brangus-cross, rumen-fistulated steers (671 ± 40 kg) were allocated randomly to 3 treatments (n = 4): straw only (S), 75% straw + 25% alfalfa (SA), 82% straw + 18% rice bran (SRB) on DM basis and were adapted to diets for 17 d, followed by 18 d of experimentation. Wheaten straw (DM 88.9%, CP 6%, crude fat < 1%), alfalfa (DM 86.2%, CP 15.8%, crude fat 1.3%) and rice bran pellet (DM 91%, CP 15.3%, crude fat 17.2%) were offered ad libitum each day at 10:00H and 17:00H. Fecal DM excretion and kinetics of particulate and liquid phases of digesta were determined from fecal marker patterns after dosing with Cr-mordanted-NDF and Co-EDTA. The purine derivatives:creatinine in 'spot' urine samples enabled prediction of daily microbial crude protein production (MCP). The data were analyzed by the General Linear Model procedure using SPSS 17.0. Inclusion of alfalfa or rice bran with straw increased DM intake by 19% and 15% ($P < 0.01$) and N intake by 83% and 67% ($P < 0.001$). DM digestibility did not differ between treatments (53.5%). The effective rumen degradation rate of straw in situ (rumen dilution rate 0.02/h) was lowest ($P < 0.001$) in SRB; i.e., 21.6%, cf. 32% (SA) and 29% (S). Rumen ammonia-N concentrations (mg/L) were 55 (SA), 36 (SRB) and19 (S) ($P < 0.05$). MCP (g/d) for SA (184) was higher ($P < 0.05$) than for SRB (90) and S (97). N retention for S (20 g/d) was increased ($P < 0.01$) by SA (122%) and SRB (149%). Methane yield (L/kg DMI) in respiration chambers, estimated over two 24-h periods, differed between treatments ($P < 0.05$), i.e., 23.1 (SA), 15.6 (SRB), 27.7 (S). The lowest yield (SRB-fed cattle) was associated with the highest crude fat intake ($P < 0.001$) and these cattle had the lowest total VFA concentration ($P < 0.01$), acetate:propionate ($P < 0.01$) and protozoa numbers ($P < 0.001$) in rumen fluid. The study indicates that inclusion of rice bran or alfalfa can markedly improve production in beef cattle given low-digestibility straw diets.

Key Words: rice bran, alfalfa, enteric methane emission

245 In vitro gas production and DM digestibility of two malt barley varieties sown with different seeding and N fertilization rates in seven sites across Canada. S. Ding*[1,2], M. Oba[2], M. L. Swift[3], W. Z. Yang[1], and T. A. McAllister[1], *[1]Lethbridge Research Centre, Lethbridge, AB, Canada, [2]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, [3]Alberta Agriculture and Rural Development, Lacombe, AB, Canada.*

Chemical composition of malt barley grain varies with seeding rate (SR), N fertilizer application rate (NR) and growing environment. However, few studies have documented the effects of these agronomic factors on the fermentability in the rumen. An in vitro study was conducted to examine the effects of SR and NR on gas production (GP) and DM disappearance (DMD) of malt barley grain using batch culture. Two malt barley varieties, Copeland (CL) and Metcalfe (MC), seeded at rates of 200 or 400 plants/m^2 with NR of 0, 30, 60, 90 and 120 kg/ha, respectively, were harvested and collected in 2007 from 7 sites across Canada. Total 560 samples (i.e., 7 sites × 2 varieties × 2 SR × 5 NR × 4 samples) were ground through a 6-mm screen and fermentability was assessed by measuring in vitro GP and DMD after 24 h of incubation. Across the 7 sites, the CP content (% DM) of malt barley linearly ($P < 0.01$) increased from 8.7 to 15%, whereas the starch content (% DM) linearly ($P < 0.01$) reduced from 66 to 57% with increasing NR. However, there were only 4 sites in which the effects of SR on the contents of CP and starch were significant ($P < 0.01$). Increasing NR linearly ($P < 0.01$) reduced DMD of CL from 2 sites and reduced DMD of MC from one site with no effects for other sites. There was only one site where SR decreased ($P < 0.01$) DMD of CL by 11%, but increased ($P < 0.01$) DMD of MC by 17%. At SR of 400, high NR (120 kg/ha) decreased ($P < 0.03$) GP of CL from 2 sites by 12 −17% compared with control, whist reduced ($P < 0.01$) GP of MC from one site by 38%. The results indicated that NR effectively changed CP, starch content of malt barley and ruminal degradation. Further, the differences in GP and DMD were site-dependent, suggesting a potential effect of growing environment on the nutritive value of malt barley.

Key Words: DM digestion, gas production, malt barley

246 Biomass yield and nutritive value assessment of *Chloris gayana* grown in a tropical region. S. Uwituze*[1], O. Twajamahoro[1], G. Uwimana[2], and M. Mutimura[2], *[1]National University of Rwanda, Butare, Rwanda, [2]Rwanda Agriculture Board, Kigali, Rwanda.*

The present study evaluated suitability of *Chloris gayana* (CG; also known as Rhodes grass) for pasture production in terms of biomass yield and nutritive value. The experiment was a complete randomized design with 3 treatments and 3 replicates. Treatments consisted of 3 cutting stages: at 80 d after planting (First cut), at 70 d after the first cut (Second cut), and at 150 d after planting (Late cut). There were 3 plots per treatment. The herbage was cut manually with a sickle to 5 cm above ground when CG achieved 50% flowering. Subsamples were used for proximate analysis. In vitro fermentation medium consisted of 1:2 ruminal fluid: McDougall's buffer and each sample (0.2 g, DM basis) was put in a gas syringe. There were 3 replicates per treatment. Syringes containing samples with 30 mL of fermentation medium and 2 blanks were incubated in a water bath at 39°C for 72 h. Readings of gas volumes were recorded every 2 h. Gas accumulated within 24 h of incubation was used to compute kinetic coefficients of fermentation using PROC Nonlinear Model of SAS. Biomass yield for the late cut (1.88 ton DM/ha) was greater ($P < 0.01$) than that obtained during the first (0.79 ton DM/ha) or second (0.71 ton DM/ha) cuts. The first cut of CG yielded biomass similar ($P = 0.68$) to that obtained during the second cut. Concentrations (DM basis) of ash (10.1%), CP (8.7%), P (0.4%), N (1.4%) decreased as CG matured from 80 d to 150 d (9.0, 6.9, 0.3, 1.1) % for ash, CP, P and N, respectively. There was an interaction between incubation time and cutting stage ($P < 0.01$). The first cut of CG yielded more gas throughout the 72-h incubation period than the second and late cuts, but the second and late cuts produced similar gas over time ($P > 0.05$). First cut had the greatest ($P < 0.05$) degradation rate but the shortest ($P < 0.05$) in vitro retention time compared with the second and late cuts, respectively. The current study recommends CG for farmers of tropical region due to its good biomass yield and nutritional quality. It is also recommended to harvest CG for the first time at 80 d after planting to benefit from its best nutritive value.

Key Words: biomass yield, *Chloris gayana*

247 Dietary exposure to ergot alkaloids decreases contractility of bovine mesenteric vasculature. A. M. Egert*[1], D. H. Kim[1], D. L. Harmon[1], and J. L. Klotz[2], *[1]University of Kentucky, Lexington, [2]USDA-ARS, FAPRU, Lexington, KY.*

Ergot alkaloids are hypothesized to cause vasoconstriction in the midgut, and prior exposure may affect vasoactivity of these compounds. Objectives were to profile vasoactivity of ergot alkaloids in mesenteric artery and vein and determine if previous exposure to endophyte-infected tall fescue affected vasoactivity of ergonovine (ERN), ergocryptine (ERP), ergotamine (ERT), ergocristine (ERS), ergocornine (ERO), ergovaline (EXT), lysergic acid (LSA), and 5-hydroxytryptamine (5HT). Ruminally cannulated Angus steers (n = 12; BW = 547 ± 31 kg) were paired by weight and randomly assigned to 6 blocks. Steers were ruminally dosed daily with 1 kg of either endophyte-infected (E+; 4.45 ppm ergovaline) or endophyte-free (E-) tall fescue seed for 21 d before slaughter. Branches of mesenteric artery (MA) and vein (MV) supporting the distal jejunum were collected after slaughter, placed in a modified Krebs-Henseleit buffer on ice, cleaned of fat and connective tissue, and sectioned into 2-mm segments. Vessels were equilibrated to 1.0 g tension for 90 min in a multi-myograph chamber with 5 mL of Krebs-Henseleit buffer and constant oxygenation (95% O_2/5% CO_2; pH = 7.4; 37°C). Final working concentrations of alkaloids ranged from 5×10^{-10} to 1×10^{-6} M for EXT and 5×10^{-9} to 1×10^{-4} M for all other agonists. Contractile response was normalized to a maximum KCl response. Data were analyzed using PROC MIXED of SAS for effects of seed treatment, agonist concentration, and the interaction. There were seed × concentration interactions ($P < 0.01$) for ERP, ERT, ERS, ERO, EXT, ERN, and 5HT in MA indicating that E- steers had a greater contractile response than E+ steers. Steers receiving E- had a greater MV contractile response to ERP, ERN, and 5HT ($P < 0.01$) and tended to for EXT ($P = 0.09$). No response was evident for ERN, ERP, ERS, LSA, and 5HT in MA and ERN, LSA, and 5HT in MV of E+ steers. These data show that steers exposed to E+ had diminished contractility in small intestinal vasculature and suggests initial exposure to ergot alkaloids has potential to alter nutrient absorption from the midgut, but the response may be transient.

Key Words: ergot alkaloid, mesenteric artery and vein, tall fescue

248 Steam-explored rice straw produced in an industrial-scale reactor as a feed ingredient for lactating dairy cow. Y. J. Su[1], G. L. Liu*[1,2], X. K. Zhang[1], C. G. Zhang[1], and G. Yang[1], *[1]State Key Laboratory of Dairy Biotechnology, Shanghai Bright Holstan Co. Ltd., Shanghai, China, [2]Shanghai Dairy Breeding Center Co. Ltd., Shanghai, China.*

Rice straw is an important roughage resource for ruminants in many rice-producing countries. In this study, Steam-explored rice straw (SERS) was produced by the proprietary process in an industrial-scale reactor. To evaluate the value of SERS as a feed ingredient for lactating dairy cow, production parameters and milk composition were determined in a feeding trial with 50 Chinese Holstein cows (DIM = 82 ± 10.0 d; BW = 538 ± 54.9 kg) in a completely randomized design involving 2 diets and 60-d periods. One diet was a conventional dairy ration that contained corn silage, alfalfa hay, Chinese leymus and commercial concentrate. The other diet contained these same feed ingredients and added SERS at 2% of ration dry matter. These 2 diets were formula to be similar net energy of lactation (1.7 Mcal/kg), neutral detergent fiber (32.4%) and crude protein (17.2%) levels. There were no difference in average DMI (23.5 versus 23.6 kg/d, $P = 0.832$) and milk yield (38.6 versus 38.8 kg/d, $P = 0.899$) for cows fed the 2 diets. Compared with the conventional ration, the diet that contained SERS did not affect ($P > 0.05$) the percentage of milk protein, fat and lactose. These results indicated that SERS produced in an industrial-scale reactor may be useful as a feed ingredient for lactating dairy cows in China.

Key Words: dairy cow, rice straw, steam

249 Volatile fatty acids accumulated in rumen contributed to the low dietary physically effective NDF induced subacute ruminal acidosis. F. Li, J. Yao*, Z. Li, S. Li, and K. Liu, *College of Animal Science and Technology, Northwest A&F University, Yangling, Shaanxi, China.*

The objective of this experiment was to characterize the relationship among rumen fermentation variables, microorganisms and dietary peNDF content that eliminating the confounding effects of dissimilar DMI. Ten multiparous Xinong Sannen dairy goats with 4 fitted with ruminal cannula were divided into 2 groups. Goats in each group were assigned into 1 of the 2 dietary treatments (Long alfalfa, LA or Short alfalfa, SA) according to a paired 2 × 2 crossover design with 2 periods. The $peNDF_{8.0mm}$ content of alfalfa hay was 42.1 and 14.5% for LA or SA group, respectively. Each period, goats in LA group were fed 1 d ahead of SA group and orts alfalfa of each goat was recorded before the morning feeding. The amount of alfalfa supplied to the goats in SA group was equal to the corresponding LA goats. Each period consisted of a 21-d adaptation period, followed by a 9-d sample period. Three species cellulolytic microorganisms relative abundance were measured by RT-qPCR. Rumen pH and chewing time were continuous monitored for 24 h. Milk production, composition and DMI have no different between LA and SA group. Duration time that pH below 5.80 in SA group was longer than LA group (5.08 vs. 1.65 h). Reducing dietary peNDF increased rumen total VFA (114.6 vs. 95.1 mM) and decreased chewing time (511 vs. 723 min/d), but did not affect the ratios of acetate, propionate and butyrate. Relative abundance of *Fibrobacter succinogenes* and *Ruminococcus flavefaciens* were increased with reducing dietary peNDF, but did not changed the *Ruminococcus albus*. In summary, reduced dietary peNDF induced subacute ruminal acidosis and the low rumen pH was contributed to the high rumen VFA concentration which was correlated with the amount of cellulolytic microorganisms.

Key Words: peNDF, rumen fermentation, subacute ruminal acidosis

250 Visceral chemical composition and cellularity of beef cows grazing different herbage allowances of native pastures. A. Casal, A. L. Astessiano*, A. I. Trujillo, and M. Carriquiry, *Facultad de Agronomia, UdelaR, Montevideo, Uruguay.*

Associations between food intake and mass and composition of various organs of the gastrointestinal tract (GIT) and liver in the short term were reported previously in ruminants. To study the long-term of 2 forage allowances of native pastures on mass and composition on GIT organs and liver in beef cows of different genetic groups, adult cows (n = 32) in a factorial arrangement of herbage allowances throughout the year (2.5 vs. 4 kg DM/kg BW; LO vs. HI) and cow genotype (purebred: Angus and Hereford vs. F1 crossbred; PB vs. CR) were used in a complete randomized block design. Cows were maintained in the herbage allowance treatment since May 2007 and gestated and lactated one calf every year from 2007 to 2009. At the end of the third year, cows were slaughter at 190 ± 15 d postpartum and GIT viscera and liver samples were collected to measure concentration of protein, lipid, DNA and RNA. Data were analyzed using a mixed model and means were considered to differ when $P < 0.05$. Expressed on an empty body weigh basis, PB cows tended ($P = 0.07$) to present a greater relative mass of the

stomach complex than CR cows. Protein content of the abomasum and omasum was greater in HI-PB than LO-PB and intermediate in CR (HI and LO) cows. The lipid content of the reticulum-rumen and abomasum tended to be less ($P < 0.09$) in HI than LO cows. Large intestine DNA tended ($P = 0.07$) to be lower in HI than LO cows. The protein:DNA ratio of the large intestine was greater in HI-CR than LO-CR cows but did not differ between HI-PB and LO-PB cows. Although hepatic DNA concentration did not differ among cow groups, the protein:DNA ratio was lower in HI-CR than LO-CR cows but did not differ between HI-PB and LO-PB cows that presented intermediate values. Small intestine RNA concentration and RNA:protein ratios were greater in LO-CR than other 3 cow groups. Hepatic RNA and RNA:protein was greater in HI-CR than HI-PB, being intermediate in LO (CR and PB) cows. These results suggested that CR cows showed greater plasticity to adapt their visceral mass and composition to sparse environments.

Key Words: cattle, rangeland, viscera

251 Substitution of polymer coated urea for soybean meal on growth performance and blood parameters in feedlot lambs fed corn stalks. A. Chegeni*[1,2], Y. L. Li[1], C. G. Jiang[1], and Q. Y. Diao[1], *[1]Feed Research Institute, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Lorestan Agricultural and Natural Resources Research Center, Khorramabad, Lorestan, Iran.*

The objective of this experiment was to evaluate the effects of replacing different levels of soybean meal by Optigen II (Alltech Inc. Nicholasville, KY) as polymer coated urea (PCU) on feed intake, growth performance and blood parameters of feedlot lambs. Sixty 4 thin-tailed Han × Dorper crossbreed lambs were blocked by BW (27 ± 3.3 kg) and allocated in a randomized complete block design to 4 treatments. Each treatment had 4 pens with 4 lambs per pen. The treatments were control (PCU0), PCU33, PCU66, and PCU100 with 0, 33%, 66%, and 100% substitution rate of soybean meal nitrogen by Optigen II (DM basis), respectively. Four isonitrogenous(CP = 13.5%) and isocaloric (ME = 1.95 Mcal/kg) dietary treatments contained 60% concentrate and 40% corn stalk (DM basis) and were offered ad libitum as TMR to ensure approximately 5% ort. Lambs were fed 56 d after 14 d adaptations twice daily in 2 equal portions at 0700 and 1900 h. Data were analyzed as a RCBD using the GLM procedure of SAS (pen was as the experimental unit). Substitution of Optigen for 33% and 66% soybean meal nitrogen had no effect on DMI, but PCU100 significantly ($P = 0.04$) decreased DMI. There was no difference for ADG between PCU33 and CON, however, by increasing percent of Optigen II in the diet, ADG significantly decreased ($P < 0.01$). As a result, gain to feed ratio (G/F) was not influenced when 33% soybean meal nitrogen was replaced by Optigen, but G/F decreased ($P = 0.02$) in PCU66 and PCU100 compared with CON. Blood urea nitrogen tended to linearly increase ($P = 0.09$) with increasing Optigen percent in the diet. Substitution of Optigen for 33% and 66% soybean meal nitrogen had no effect on plasma total protein, but it was lowest ($P = 0.02$) in PCU100. The results showed that soybean meal could be partly replaced by Optigen in the diet of feedlot lambs. Substitution of Optigen for 33% soybean meal nitrogen had no negative effect on growth performance or blood parameters in feedlot lambs fed 40% corn stalk.

Key Words: feedlot lambs, growth performance, polymer-coated urea

252 Effect of conservation and maturity of primary growth grass/clover on chewing activity and fecal particle size in heifers. A. S. Koch*[1], P. Nørgaard[1], and M. R. Weisbjerg[2], *[1]Dept. of Veterinary Clinical and Animal Science, University of Copenhagen, Copenhagen, Denmark, [2]Dept. of Animal Science, Aarhus University, Foulum, Denmark.*

The study evaluated structural effectiveness of NDF from of spring harvest grass/clover forages of primary growth by assessing chewing activity and feces particles > 1.0 mm in heifers. Two batches of mixed ryegrass, red and white clover harvested in 2009 on May 9 and 25 were conserved as either silage or hay. The forages early silage (ES) and hay (EH), and late silage (LS) and hay (LH) had DM contents of 45, 84, 25 and 83%, and NDF contents of 32, 44, 42 and 50% of DM, respectively. Forages were fed as sole feed to 4 Jersey heifers of 435 ± 30 kg BW in a 4 × 4 Latin square experiment. Feeding level was 90% of individual ad libitum intake, divided in 2 daily meals at 0800 and 1530 h. Jaw movements oscillations (JMO) were recorded for 96 h continuously using Hall sensor fitted chewing halters. Jaw movements (JM) were identified from JMO, clustered into cycles and periods of rumination and eating and summarized into min per day. Feces were sampled 3 times daily and machine washed in nylon bags of 0.01 mm pore size. Feces particulate matter was freeze-dried and divided into small (0–1.0 mm) and large (>1.0 mm) particle fractions by dry sieving. Data was analyzed by the MIXED procedure in SAS with period, conservation, harvest time, and conservation × harvest time as fixed effects and heifer as random. Daily intake of ES, EH, LS, and LH was 8.7, 9.4, 7.2, and 7.2 kg DM and 2.7, 4.1, 3.0, and 3.6 kg NDF respectively. Early compared with late harvest caused similar NDF intake and time spent eating, but smaller mean rumination per kg NDF intake ($P = 0.002$). Hay compared with silage caused greater NDF intake ($P < 0.001$), and less mean time spent eating ($P = 0.02$) and ruminating ($P = 0.004$) in min/kg NDF intake. Feeding silage compared with hay resulted in a greater proportion of washed fecal particle DM < 1.0 mm, while harvest time hardly affected fecal particle size. Results indicate that NDF from late cut forages and silage stimulated rumination more effectively, and that heifers retain large forage particles in the rumen better with silage compared with hay.

Key Words: chewing activity, fecal particle size, grass/clover

253 Effect of weaning age and milk feeding level on pre and post weaning growth performance of Sahiwal calves. S. A. Bhatti*[1], A. T. Cheema[1], G. Akbar[2], P. C. Wynn[3], M. Sarwar[1], and H. M. Warriach[3], *[1]Institute of Animal Nutrition and Feed Technology, University of Agriculture, Faisalabad, Pakistan, [2]Livestock Production Research Institute, Bahadurnagar, Okara, Pakistan, [3]EH Graham Centre (NSW Industry and Investment and Charles Sturt University), Wagga Wagga, Australia.*

Our objective was to evaluate pre and post weaning growth of Sahiwal calves weaned either at 8 or 12 weeks (WK) and offered milk at 10 or 15% of body weight (BW) to weaning. Forty-eight Sahiwal day-old calves born within 45 d were randomly allocated to 4 groups of 12 equalized for sex. Calves in 2 groups were offered milk either at 10 (M10) or 15% (M15) of BW up to d 28 adjusted weekly. The calculated milk intake at d35 was reduced to zero by d 56 (WK8). Calves in the other 2 groups were offered milk as for groups 1 and 2 but were weaned at d 84 (WK12) by reducing the milk for BW at d 70 to zero. Calves were offered a concentrate ration (21% CP and 80% TDN) from d 28 to 112 (16 weeks of age; WK16). Fed and fasted (12h) blood was taken fortnightly from wk 3. Data were analyzed using mixed procedures (SAS) in a 2 × 2 factorial design with weaning age and milk feeding level as the 2 factors. The weaning combination of WK8/M10 produced a significantly smaller calf at the least cost per kg live weight. By contrast the WK12/M15 calves were heavier, but more costly. The significant differences in fed and fasted blood glucose at WK9 showed that the calves weaned at WK12 remained in the pre-ruminant state longer

than those weaned at WK8. By WK13 both groups showed a similar glucoregulatory response. Thus early-weaning or restricted milk feeding are likely to accelerate rumen development. Offering milk at 15% of BW and weaning at 8 weeks provided the best compromise to minimize feeding cost, but maintain a growth performance commensurate with early puberty.

Table 1. Live weights, growth rates, production cost and blood glucose (mg/dL) of calves offered milk 10% or 15% (M10 or M15) of BW and weaned at WK8 or WK12

	WK8		WK12		
Parameter	M10	M15	M10	M15	SE
Live weight WK16 (kg)	60.2[a]	70.7[b]	72.0[b]	88.3[c]	20
Daily live weight gain (g/d)	350[a]	432[b]	450[b]	544[c]	2.2
Cost/kg live weight (PKR[1])	188[a]	232[b]	249[b]	313[c]	11
Fed blood glucose WK9	86.7[c]	87.3[c]	120.7[b]	135.2[a]	6.0
Fasted blood glucose WK9	80.1[c]	79.2[c]	98.2[b]	108.8[a]	4.2
Fed blood glucose WK13	77.7	79.1	74.8	75.8	6.0
Fasted blood glucose WK13	86.9	89.6	90.1	88.9	4.2

[a–c]Different superscripts denote significance at $P < 0.05$.
[1]1 US$ = PKR 97.

Key Words: Sahiwal calves, weaning regimen

254 Investigating the nutritive value of Mexican sunflower leaves for ruminant animals. A. H. Ekeocha*[1] and A. O. Akinsoyinu[2], *[1]Ondo State University of Science and Technology, Okitipupa, Ondo, Nigeria, [2]University of Ibadan, Ibadan, Oyo, Nigeria.*

An experiment was conducted to determine the proximate composition of Mexican sunflower leaves (MSL). Proximate composition of MSL was determined according to AOAC (1990). The MSL (g/100g DM) contained CP 16.3; CF 21.8; EE 2.8, ash 14.7; and GE 1.9 kcal/g. The CP content was 16.3% and this was high when compared with tropical grass species, which seldom exceed a CP level of 15% and whose protein content is satisfactory for animal production for only about 4 mo of the year. It compares favorably with that of cassava leaf meal (16.67%), and far exceeds the minimum protein requirement (10–12%) for ruminants. The CF level of 21.8% for MSL is low compared with that of tropical grass species which may be as high as 45–50% at more matured stages of growth. It is comparable to the CF level of *Amaranthus* spp. (17.01%), Siam leaf meal (16.0%), Cassava leaf meal (15.63%), deep litter manure (16.60%) and guava leaf (16.10%). %). The ether extract content was low (2.81%). This value was lower than the values of 5.61% reported for *Vernonia amygdalina* leaf and far lower than the value of 8.14% reported for Siam weed. The total ash content 14.68% was high and this was comparable to the ash content of *Vernonia amygdalina* leaf (13.86%) but higher than the value of 8.28% reported for *Acacia albida* used as a browse plant for sheep in the semi-arid region of Nigeria and higher than the value of 11.00% reported for Leucaena to feed Yankassa sheep and 11.54% reported for Siam weed leaf meal but commensurable with the value reported for cassava leaves which has an ash content of 16.07%. The gross energy (GE) value was 1900kcal/kg. This is lower than the GE value of Groundnut cake (2600kcal/kg) and *Vernonia amygdalina* leaf (2720 kcal/kg). The Nitrogen Free Extract level of 44.38% for MSL was comparable to that of Siam leaf meal (44.40%) used to feed West African Dwarf Sheep but lower than the value of 33.85% reported for *Vernonia amygdalina* leaf. On the whole, gross chemical analysis indicates that MSL contained appreciable level of nutrients that could be utilized in the diets of ruminants.

Key Words: Mexican sunflower leaves, nutritive value, sheep

812 Evaluation of a high forage total mixed ration in mid- to late-lactation dairy cows D. Gadeken*, C. Hulstein, D. P. Casper, K. Kalscheur, and J. Anderson. *Dairy Science Department, South Dakota State University, Brookings.*

Dairy producers have been asking how much forage could be included in the ration so that a lactating dairy cow can consume sufficient nutrients to support similar milk production. The production of high quality forages having high DM and NDF digestibility are needed to evaluate this feeding scenario. Twenty mid- to late-lactation lactating Holstein dairy cows were blocked on parity (10 primiparous and 10 multiparous), milk production (range 33.9 to 56.6; mean = 41.5 kg/d), and DIM (range 140 to 287; mean = 225 d) and randomly assigned within blocks to 1 of 2 rations based on ration forage concentration. Forages were 60% 2012 first-cutting alfalfa haylage and 40% 2012 corn silage blended on a DM basis and then fed at either 60% (Low Forage, LF) or 80% (High Forage, HF) of the ration DM. Experimental design was a randomized completed block design with 4 continuous weeks for data collection preceded by a 1 week covariate data collection period in which all cows were fed the LF ration. Cows were milked 3x/d and milk weights recorded at each milking and milk samples were collected at each milking once weekly for analysis of milk composition. Rations were similar in CP (16.4%), starch (20.1%), ADF (21.8%), and NDF (34.1%) concentrations. The use of a covariate was highly significant ($P < 0.01$). Milk production was reduced ($P < 0.01$) by feeding the HF diet compared to cows fed the LF (28.1 and 24.1 kg/d for LF and HF, respectively), while milk fat (3.98 and 3.96%), milk protein (3.17 and 3.11%), milk lactose (4.81 and 4.77%), and milk solids-not-fat (8.87 and 8.77%) percentages were similar ($P > 0.10$) for cows fed both rations. The forage quality and digestibility in this study was not adequate to support the milk production of mid- to late-lactation dairy cows. The digestibility of DM (DMD = 75.7%) and NDF (NDFd = 55.7%) for the alfalfa haylage was above average but, the corn silage quality was average (DMD = 72.9, NDFd = 52.3%, and starch = 32.1%) in this study. In this study, the forage quality and digestibility when fed at high rates did not support similar milk production in mid- to late-lactation dairy cows.

Key Words: forage, lactation, dairy cow

816 Use of pelleted sericea lespedeza (*Lespedeza cuneata*) for natural control of coccidiosis in weaned goats. T. H. Terrill*[1], D. S. Kommuru[1], S. Desai[1], J. E. Miller[2], J. M. Burke[3], and J. A. Mosjidis[4], *[1]Fort Valley State University, Fort Valley, GA, [2]Louisiana State University, Baton Rouge, [3]USDA/ARS, Booneville, AR, [4]Auburn University, Auburn, AL.*

Coccidiosis can be a devastating disease in goats, particularly for young, recently-weaned animals, causing diarrhea and even death. Feeding dried sericea lespedeza (SL; *Lespedeza cuneata*) to young goats has been reported to reduce the effects of internal parasites, but there have been no reports of the effects of feeding this forage on *Eimeria* spp. in goats. A confinement feeding study was completed on 24 recently weaned intact Kiko-cross bucks to determine effects of SL pellets on an established *Eimeria* infection. The bucks were assigned to 1 of 2 treatment groups based upon *Eimeria* oocysts per gram (OPG) of feces (n = 12/treatment group, 2 animals/pen), and then fed 1 of 2 pelleted rations ad libitum; 90% SL leaf meal pellet or a 14% crude protein commercial pellet. Fecal samples were taken from individual animals every 7 d for 28 d to determine OPG and gastrointestinal nematode eggs per gram (EPG), and blood samples to determine packed cell volume (PCV). After 7 d, the SL pellet diet reduced ($P < 0.05$) OPG and EPG in goats by 96.9 and 78.7%, respectively, compared with animals fed the control diet. The OPG and EPG remained lower ($P < 0.05$) in treatment than control animals until the end of the trial. There was no effect of diet on PCV values throughout the experiment. Dried, pelleted SL has excellent potential as a natural anticoccidial feed for weaned goats.

Key Words: coccidiosis, goats, sericea lespedeza

817 Sericea lespedeza as an aid in the control of *Eimeria* spp. in lambs. M. Acharya*[1], J. Burke[1], J. Miller[1], T. Terrill[1], and J. Mosjidis[1], *[1]University of Arkansas, Fayetteville, [2]USDA, Agricultural Research Service, Booneville, AR, [3]Louisiana State University, Baton Rouge, [4]Fort Valley State University, Fort Valley, GA, [5]Auburn University, Auburn, AL.*

Coccidia, a diarrhea causing protozoan parasite, is a significant health and production challenge for sheep during times of stress. Typical treatment involves the administration of sulfa drugs and amprolium, a thiamine antagonist. This research examines the effect of sericea lespedeza (SL) for control of coccidiosis in lambs. In Exp. 1, naturally infected lambs (n = 76; 23 ± 1 kg) weaned at 102.7 ± 1.4 d of age were randomly assigned to groups receiving 2% BW/d of either alfalfa pellets (n = 38, control) or SL (n = 38, treatment) with or without amprolium added to drinking water. Fecal oocyst count (FOC), fecal egg count (FEC), and fecal score (FS; 1 = solid pellets; 5 = slurry) were determined from the day of weaning to 21 d post-weaning in 7 d intervals. In Exp. 2, naturally infected lambs (n = 72; 20 ± 1 kg) were randomly assigned to groups. They were fed either control creep feed (n = 40, 16% CP) or SL pellets (n = 32, 14% CP) 30 d before weaning. Intake of SL was increased from 100 g/lamb/d (before weaning) to 454 g/lamb/d (after weaning). Lambs were weaned at 103.6 ± 0.9 d of age and moved to semi-confinement. The FEC, FOC, packed cell volume (PCV), FS, and dag score (soiling around rear of lamb; DS; 1 = no soiling; 5 = heavy soiling) were determined 14 d before weaning and in 7 d intervals from weaning until 21 d post weaning. A mixed model was used for data analysis. To determine treatment differences, chi-squared analysis was used. In Exp. 1, dietary group showed similar FOC, but in amprolium treated lambs FOC decreased ($P < 0.001$). Higher fecal score in control compared with SL lambs ($P = 0.05$) indicated signs of coccidiosis. In Exp 2, pre-weaning FOC was similar but decreased in post-weaning SL lambs and remained lower ($P = 0.004$). Post-weaning coccidiosis treatment was required for 33% of control ($P < 0.001$) but not in SL lambs. Dag ($P = 0.01$) and FS ($P = 0.001$) were similar pre-weaning, but lower at weaning and thereafter in SL-fed lambs. The use of SL was effective in prevention and control of coccidiosis in lambs.

Key Words: coccidia, lambs, sericea lespedeza

818 The relationship of OPP infection to performance and TMEM154 genotype in a Midwestern sheep flock. T. W. Murphy*[1] and T. A. Taylor[1], and D. L. Thomas[1], *[1]Department of Animal Sciences, University of Wisconsin-Madison, Madison, [2]Research Animal Resources Center, University of Wisconsin-Madison, Madison.*

Ovine progressive pneumonia (OPP) is an incurable, degenerative, viral disease of sheep affecting the respiratory and nervous systems in an escalating fashion over an animal's lifetime. Objectives of the study were to determine (1) effect of OPP status (POS or NEG) on the performance of Hampshire (H; n = 72) and Polypay (P; n = 58) ewes and their lambs, and (2) relationship between TMEM154 genotype and OPP status of the ewes. Data were from the UW-Madison flock at the Arlington Ag Research Station and consisted of 314 ewe and 425 lamb records. The flock is intensively managed with most ewes lambing in winter and a few ewes lambing in fall. Incidence of POS ewes was 58.3% and 43.1% among H and P ewes, respectively. The statistical model for analysis of ewe fertility, litter size, and weight of lamb weaned per ewe exposed included year, breed, OPP status, and age at lambing nested within year as fixed effects, and service sire and ewe as random effects. 70-d lamb weaning weight was analyzed similarly but with the addition of fixed effects of lamb birth type, sex, and the breed x birth type interaction. There were no differences ($P \geq 0.24$) between POS and NEG ewes for any of the traits. The ewes were enrolled in the National Sheep Improvement Program (NSIP), and EBV's for traits and indexes were available for each ewe. Within breed analyses considering only OPP status revealed no significant differences ($P > 0.14$) between POS and NEG ewes for the NSIP values. Frequencies of TMEM154 haplotypes across both breeds were 0.77, 0.13, 0.04, and 0.06 for haplotypes 1, 2, 3, and 4, respectively. Within and across breeds, ewes with 1 or 2 copies of haplotype 2 or 3 had a higher ($P \leq 0.024$) incidence of OPP than ewes of diplotype 1,1. Our results agree with some previous studies that have shown no effect of OPP infection on ewe performance, which suggests that intensive management from lambing to weaning may minimize negative effects of OPP infection. In agreement with very recent studies on genetic susceptibility to OPP, producers wishing to decrease genetic susceptibility to OPP infection should select 1,1 TMEM154 diplotype animals.

Key Words: sheep, ovine progressive pneumonia, TMEM154

819 Effect of feeding a pelletized diet containing 21% ground pumpkin seeds on BW, fecal egg count, and blood hematocrit in Katahdin cross lambs. E. N. Escobar, J. Rodriguez*, A. N. Gideon, V. Purnell-Cropper, and H. Taylor, *University of Maryland Eastern Shore, Princess Anne, MD.*

This investigation was conducted to evaluate the effect of a diet containing ground pumpkin (*Cucurbita* sp.) seeds (PS) on *Haemonchus contortus* infection in lambs. Katahdin cross female and wether lambs (n = 20, 4 to 6-mo old), with average BW = 22.6 ± 0.91 kg, were used. Following a 2-wk adjustment period, the lambs were randomly allocated to individual pens (1.9 × 2.3 m) with slotted floors and unrestricted access to fresh water. Individual feed intake was adjusted up to 4% BW to minimize orts and recorded daily. The lambs were dewormed with albendazole (Valbazen, 10 mg/kg) and moxidectin (Cydectin, 0.2 mg/kg). After a 21-d dewormer withdrawal period, all lambs were orally inoculated 3 times, every other day, with a larval inoculum containing 1,450 L3 *H. contortus*. After the experimental inoculation, a pelletized commercial 15% crude protein diet was fed as the control (CTRL, n = 10). The treatment (TRT) feed was formulated with similar ingredients as the CTRL diet plus 21% ground PS, and it was calculated to be similar in protein and energy content and fed to 10 lambs. To minimize feedstuff selection ground PS were incorporated into the pelletized mixture. The experimental diets were fed for 9 consecutive week. Weekly the lambs were weighed, and fecal (rectal) and blood (jugular venipuncture) samples were collected. A modified McMaster technique was used to determine fecal egg count (FEC, eggs per gram, epg), and hematocrit (% PCV) was determined in whole blood. The data were analyzed as repeated measures using the SAS statistical package. FEC+100 was natural log-transformed to stabilize variance. After 9 wk, overall BW of the Katahdin lambs was similar ($P > 0.05$) in CTRL lambs (25.85 kg) and the TRT lambs (24.11 kg). The only significant difference ($P < 0.05$) in BW was between weeks, as expected. After 9 wk, there was no significant difference ($P > 0.05$) between the CTRL and TRT groups on % PCV or FEC (31.02 vs. 31.58 and 380.8 epg vs. 502.3 epg, respectively). Ground PS incorporated into pelletized feed at a rate of 21% failed to affect *H. contortus* burden in lambs as expressed in FEC and PCV.

Key Words: ground pumpkin seed, *Haemonchus contortus*, lamb

820 Effect of ground pumpkin seeds (*Cucurbita* sp.) fed in a pelletized diet on BW, fecal egg counts, and blood hematocrit in experimentally *Haemonchus contortus* infected meat goat kids. E. N. Escobar*, J. Rodriguez, A. N. Gideon, V. Purnell-Cropper, and H. Taylor, *University of Maryland Eastern Shore, Princess Anne, MD.*

This investigation was conducted to evaluate the effect of ground pumpkin (*Cucurbita* sp.) seeds (PS) on *Haemonchus contortus* infections in meat goat kids. Sixteen 6- to 8-mo-old females and castrated male goat kids, average BW 20.8 ± 1.4 kg, were used. After a 2-wk adjustment period, the kids were randomly allocated to individual pens (1.9 × 2.3 m) with slotted floors and ad libitum access to water. Individual feed intake was adjusted up to 4% BW to minimize orts and recorded daily. The kids were dewormed with albendazole Valbazen (10mg/kg) and Cydectin (0.2mg/kg). After a 21-d dewormer withdrawal period, all goat kids were orally inoculated 3×, every other day, with a larval inoculum containing 1,450 L3 *H. contortus*. Then, a pelletized commercial 15% CP diet was fed as the control (CTRL) feed to 8 kids. The treatment feed (TRT) was formulated with similar ingredients as the CTRL diet plus 21% PS, calculated to be similar in protein and energy content and it was fed to 8 kids. To minimize kid feedstuff selection PS were ground and incorporated into the pelletized mixture. The experimental diets were fed for 8 consecutive weeks. Weekly, the kids were weighed (BW), and fecal (rectal) and blood (jugular venipuncture) samples were collected. A modified McMaster Technique was used to determine fecal egg count (FEC, eggs per gram, epg), and hematocrit (% PCV) was determined in whole blood. The SAS statistical package was used for data analysis. FEC+100 was natural log-transformed to stabilize variance and the data analyzed. After feeding 8 wk, overall BW was similar in CTRL (20.53 kg) and TRT (20.74 kg) fed kids ($P > 0.05$). The only significant difference ($P < 0.05$) in BW was between wk, as expected. The mean FEC was similar ($P > 0.05$) between CTRL (473.2 epg) and TRT (478.5 epg) groups of kids. The values for % PCV were 26.07% and 27.30% for the CTRL and TRT kids, respectively ($P > 0.05$). Ground PS fed at a level of 21% incorporated into a pelletized diet failed to affect *H. contortus* burdens in goat kids expressed as FEC and %PCV.

Key Words: goat kids, *Haemonchus contortus*, pumpkin seeds

821 Safety and efficacy of low-dose, subacute exposure of mature ewes to sodium chlorate. J. B. Taylor*[1], R. S. Dungan[2], and D. J. Smith[3], *[1]USDA, ARS, US Sheep Experiment Station, Dubois, ID, [2]USDA, ARS, Northwest Irrigation and Soils Research Laboratory, Kimberly, ID, [3]USDA, ARS, Biosciences Research Laboratory, Fargo, ND.*

The objective was to determine the safety and efficacy of low-dose, subacute exposure of mature ewes to $NaClO_3$ in the drinking water. Twenty-five ewes (BW = 62.5 ± 7.3 kg) were placed indoors in individual pens with ad libitum access to water and feed. After 7 d of adaptation, ewes were assigned randomly to 1 of 5 treatments: 0 (control), 30, 60, 90, or 120 mg $NaClO_3 \cdot kg\ BW^{-1} \cdot d^{-1}$. Treatments were delivered in the drinking water for 5 d (i.e., 120 h). Endpoints of subclinical toxicity were daily water intake, whole-blood methemoglobin percentage, and packed-cell-volume (PCV). Efficacy of treatments was based on fecal *Escherichia coli* concentrations. Based on water intakes and BW, actual daily $NaClO_3$ exposures were 0 and 28, 56, 80, and 110 ± 2 mg $kg\ BW^{-1}$ for control and 30-, 60-, 90-, and 120-mg treatments, respectively. Such doses neither induced methemoglobin formation (0.310, 0.304, 0.382, 0.334, and 0.300 ± 0.053%, respectively) nor altered PCV (42.5, 44.2, 43.8, 41.4, and 42.9 ± 1.9%, respectively). Ewes that consumed ≈110 mg $NaClO_3 \cdot kg\ BW^{-1} \cdot d^{-1}$ drank ≈14% less ($P < 0.05$) total water on d 2 than did other treatment groups. By d 5, the comparative reduction in voluntary water intake was nearly 30% less, which was accompanied with a reduction in feed intake. This response indicated that subacute exposure to ≥110 mg $NaClO_3 \cdot kg\ BW^{-1} \cdot d^{-1}$ may not be safe for mature ewes. Consumption of $NaClO_3$ for 5 d reduced fecal *E. coli* in a dose-dependent fashion ($P < 0.08$). Using unlike letters (a, b, and c) to indicate differences ($P < 0.10$) in fecal *E. coli* concentrations, the result of treatment contrasts for ewes consuming 0, 28, 56, 80, and 110 mg $NaClO_3 \cdot kg\ BW^{-1} \cdot d^{-1}$ were a, a, b, bc, c, respectively. These data suggested that subacute exposure to ≤28 mg $NaClO_3 \cdot kg\ BW^{-1} \cdot d^{-1}$ was not efficacious, with respect to fecal *E. coli*. At 22 d after treatments stopped, fecal *E. coli* in all $NaClO_3$-treated ewes were similar to control ewes, which indicated that the effect of $NaClO_3$ is rapidly reversible following subacute exposure. In summary, daily consumption of 56 to 80 mg $NaClO_3 \cdot kg\ BW^{-1}$ for 5 d was safe for targeted, short-term reduction of fecal *E. coli* in mature ewes.

Key Words: chlorate, diarrhea, *E. coli*

822 Cyclical and mild heat stress does not reduce dry matter intake but decreases average daily gain in Afshari lambs. E. Mahjoubi*[1], L. H. Baumgard[2], H. Amanlou[1], H. R. Mirzaei[1], N. Aghaziarati[1], M. H. Yazdi[1], G. R. Noori[1], and M. G. Khan[1], *[1]Zanjan University, Zanjan, Iran, [2]Iowa State University, Ames.*

Decreased DMI during heat stress (HS) does not fully account for decreased performance in dairy cows but does appear to completely

explain reduced growth in calves and pigs. To investigate the effect of heat stress on DMI and growth of Afshari lambs, 32 male lambs (38.1 ± 5.1 kg) were used in a completely randomized design in 2 periods (16 lambs per treatment). In period 1 (P1) all 32 lambs were housed in thermoneutral (TN) conditions [25.6 ± 2.6°C and a temperature-humidity index (THI) of 72 ± 2.6] and fed at libitum for 8 d. In P2, which lasted 9 d, 16 lambs were subjected to HS (29 to 43°C and a THI of more than 83 at least 14 h/d), the other 16 lambs were maintained in TN, but they consumed the same amount of feed (pair-fed, PFTN) as the HS lambs. During each period DMI and water intake were measured daily. Respiration rate, rectal temperature and skin temperature at the shoulder, rump, and front and rear leg were recorded at 0700 and 1400 h daily. All data were statistically analyzed using the PROC MIXED procedure of SAS to test differences between environments and periods. Water intake increased ($P < 0.05$) during P2 in both HS and TN lambs (88 and 35%, respectively). HS increased the 0700 and 1400 h temperature at the shoulder (3 and 10.6%), rump (2.7 and 12.7%), rear (3 and 13%), and front leg (3 and 13%) and respiratory rates (72 and 124%; $P < 0.001$, 0700 and 1400 h, respectfully) but only the 1400 h rectal temperature increased ($P < 0.01$; 0.62°C) in HS lambs. Interestingly, HS did not decrease DMI but average daily gain was reduced (36%; $P < 0.01$) compared with the PFTN lambs. These results imply that the direct effects of heat (not mediated by reduced DMI) are responsible for a portion of reduced sheep growth.

Key Words: Afshari lamb, heat stress, growth rate

823 The relationship between metatarsal and metacarpal condyle length and claw size in sheep—A postmortem study. S. Azarpajouh*[1], M. Mehdizadeh[2], and A. Mohamadnia[3], *[1]University of Missouri-Columbia, Columbia, [2]Shahrekord University, Shahrekord, Iran, [3]Ferdowsi University, Mashad, Iran.*

Understanding the hoof growth pattern in sheep could provide valuable information for proper hoof trimming to create appropriate weight bearing surfaces. The objective of this study was to determine whether differences in hoof growth result from the anatomic condition of distal condyles of the metacarpal and metatarsal bones in sheep. Fore and hind limbs of twenty 2-yr-old (average wt 27 kg) untrimmed pastured Afshari ewes were collected after slaughter. The following distances of the metacarpal and metatarsal bones were measured in mm: L1 = lateral end of the bone to the lateral border of the physis; L2 = lateral end of the bone to the abaxial border of the lateral condyle; X1 = lateral border of the physis to the abaxial end of the lateral condyle; X2 = the physis to the distal end of the condylar ridge; X3 = the axial aspect of physis to the axial end of the lateral condyle; D1 = lateral end of the bone to the medial border of the physis; D2 = lateral end of the bone to the abaxial border of the medial condyle. Analogous measurements were taken on the medial surfaces. Toe length, toe height, heel height, and sole length were also measured on the claws. Similar measurements between right and left legs were averaged and medial and lateral surfaces of each bone and medial and lateral claws on each limb were compared using a paired *t*-test. All the measurements in metacarpal bone were greater on the medial surface and the differences were significant ($P < 0.05$), except for X2 and X3. In metatarsal bone L1, X1 and X3 were greater on the medial surface but L2, X2, D1 and D2 were greater in the lateral surface and the differences were significant in X2 and D2. In forelimbs, toe length and toe height were greater in the lateral claws, but heel height and sole length were greater in the medial claws. In hind limbs, all the measurements except toe height were greater in the lateral claws. In conclusion, there is no relationship between metacarpal and metatarsal condyle length and the size of the corresponding claws, and there is no significant difference between claws in sheep. Therefore, beginning hoof trimming from a special claw is not necessary.

Key Words: hoof anatomy, hoof trimming, sheep

824 Doe fitness traits among four meat goat breeds in a reconstituted herd on humid, subtropical pasture. R. Browning Jr.*[1], J. Groves[1], M. L. Leite-Browning[2], L. Moore[1], and M. Byars Jr.[1], *[1]Tennessee State University, Nashville, [2]Alabama A&M University, Huntsville.*

This 2-yr study evaluated does brought together to rebuild the TSU research herd after natural disaster. Straightbred does (n = 253) were of the Boer (B), Kiko (K), Myotonic (M), and Spanish (S) breeds. The average doe age was about 4 yr for each breed. Does were mated each fall to produce purebred and F_1 kids. Herd management follows a low-input model to assess doe fitness. Does grazed on mixed-species pastures year-round at 9.5 head/ha supplemented with orchardgrass hay. Does had ad libitum access to 16% CP molasses tubs during winter. Does were dewormed once per year as a group at kidding and as individuals upon signs of endoparasitism. Does were sampled for fecal egg counts and pack cell volumes several times over the 2-yr study period to further assess internal parasitism. The proportional rates of does showing signs of endoparasitism once or multiple times annually were affected by breed ($P < 0.01$). Boer had higher ($P < 0.01$) annual treatment rates (78 ± 6%) than K, M, and S (41, 38, and 32 ± 8%, respectively); the other 3 breeds did not differ. Boer had higher ($P \leq 0.02$) multiple treatment rates per year (37 ± 15%) than K, M, and S (10, 15, and 6 ± 6%, respectively); the other 3 breeds did not differ. Fecal egg counts and packed cell volume were affected ($P < 0.01$) by breed, lactational status, and sample month. Boer had higher ($P \leq 0.03$) egg counts (1547 eggs/g feces) than K, M, and S (996, 723, and 890 eggs/g, respectively); the other 3 breeds not differing. Boer had lower ($P < 0.01$) hematocrits (14.5 ± 1.2%) than K, M, and S (19.5, 20.3, and 21.5 ± 1%, respectively); K and S also differed ($P = 0.01$). The proportion of does weaning kids per doe exposed and doe exit rates were affected by breed ($P < 0.01$). Weaning rates were higher ($P < 0.01$) for K (53 ± 13%) and S (54 ± 13%) than for B (7 ± 4%) and M (19 ± 9%). Annual doe exits due to illness or reproductive failure differed ($P \leq 0.03$) among all the breeds (B = 71 ± 6%; K = 18 ± 4%; M = 46 ± 7%; S = 17 ± 4%), except between Kiko and Spanish. Significant genetic variability was observed among doe breeds for fitness under the prevailing management conditions.

Key Words: breed, fitness, goat

825 Modeling the body composition of growing Santa Inês ewe lambs. L. F. L. Cavalcanti*[2,1], I. Borges[2], V. L. Silva[2], and L. O. Tedeschi[1], *[1]Texas A&M University, College Station, [2]Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil.*

The most common breed of sheep in Brazil is the Sanat Inês. It is characterized by animals of small frame score and high capacity for storing energy in the form of fat deposits, mainly into the abdominal cavity. Therefore, the use of empirical equations based on body condition score to predict body composition (i.e., fat) may not be accurate. The objective of this study was to evaluate the Von Bertalanffy nonlinear equation [$Y = A \times (1\text{-}B \times e^{-k \times EBW})^3$; in which Y is the measured variable (kg), A is the asymptote (kg), B is a constant related to the intercept (kg), and k is the growth rate (1/kg)] to predict body composition of Santa Inês ewe lambs. Fifty 5 female lambs with initial live BW of 14 to 23 kg were confined and fed *Cynodon* spp. hay, corn meal, soybean meal, and mineral diet formulated to contain 2.3 Mcal/kg of ME, 22.5% CP, and

34.6% of NDF. The animals were divided into 2 groups in pairs and the first animal was fed at ad libitum regimen while the second animal received about 70% of the ad libitum animal DMI. Both animals were slaughtered when the ad libitum animal reached 20, 30, or 40 kg of BW (6 per BW). The body components were analyzed for ether extract (EE) and CP. The Von Bertalanffy nonlinear function was fitted using the CP% and EE% on the empty BW (EBW, kg, DM basis). The coefficients obtained to estimate CP were: A = 22.82 ± 4.6%, B = - 0.63 ± 0.07%, k = 0.07 ± 0.03 1/kg with a residual standard error (RSE) of 3.83%. For the EE, the coefficients were: A = 64.76 ± 3.7%, B = 1.36 ± 0.53%, k = 0.14 ± 0.03 1/kg with a RSE = 6.46%. When the predicted values of each model was linearly regressed on the respective observations, both had intercept = 0 and slope = 1 ($P < 0.001$). The mean bias (MB), Pearson correlation coefficient (r), and bias correction (Cb) for the CP% were, −0.0002, 0.8637, and 0.9893, respectively; and for the EE% these statistics were 0.0071, 0.8827, 0.9927. The observed increase in EE percentage and decrease in CP relative to BW as the EBW increased was in agreement with the literature for growth of mammals. The Von Bertalanffy nonlinear equation can satisfactorily predict the body composition of Santa Inês ewe lambs.

Key Words: evaluation, growth, Von Bertalanffy

826 Time limits of postmortem cell survival in goat ear skin stored at room temperature. M. Singh*, X. Ma, G. Kannan, and E. Amoah, *Fort Valley State University, Fort Valley, GA.*

Cloning of animals from somatic cells has been achieved in almost all livestock species in recent years. This technology has great potential for reviving endangered species, preserving lost genetics due to accidental death, and/or expanding use of superior quality animals. For a successful cloning experiment, integrity of nuclear DNA of the somatic donor cells is a pre-requirement. Any damage to DNA will lead to developmental defects in cloned offspring. In many instances, animals may be dead for days, leading to decomposition of cellular structures and ultimately damage to nuclear DNA. One way of ensuring nuclear integrity is by in vitro culture of cells to be used as nuclear donors. The goal of this study, therefore, was to determine the maximum time limit within which live cells can be obtained from animal tissues after their death. To achieve this goal, whole ears of 3 healthy Spanish goats of 2–3 yr old were collected from a slaughter facility and stored in the laboratory at 25–26°C. After 0, 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20 d of storage, 2- to 3-mm^2 skin pieces (n = 30) were excised from ear skin for each time interval and cultured in DMEM media supplemented with 10% FBS, 50 units/mL of penicillin, and 50 μg/mL of streptomycin in 6 (60 mm) dishes. The outgrowth of fibroblast-like cells around the explants (>50 cells) was recorded after 10–12 d of culture. All explants exhibited growth of cells up to 8 d postmortem (dpm), 66.6% exhibited growth in 10-dpm, but none of the explants exhibited growth beyond 10 dpm. Secondary cultures were established from primary outgrowth of 0- and 10-dpm cultures from one of the goats and a growth-curve was generated using a 24-well microtiter plate format at passage 3 level. Although the primary cells from 10-dpm cultures took a longer time to reach the comparative confluence level of 0-dpm, the growth-curves generated from passage 3 cell populations of these cultures were not significantly different, and showed similar cell morphology. These results suggest that live cells can be cultured from dead animals up to 10 d after their death, with comparable growth profile to that of fresh tissues.

Key Words: cell survival, goat skin, postmortem

827 Validation of the role of chromium in reducing body fat by determining the expression of multiple transcripts involved in fatty acid biosynthesis in domestic goat. M. Sadeghi and M. J. Najafpanah*, *University of Tehran, Tehran, Iran.*

Understanding relationships between metabolic health and diet is one of the main goals of biochemistry researchers. Chromium is required for the normal role of insulin in the use of carbohydrate, protein and fat. In this study, we examined the expression of 7 genes related to lipid metabolism in 4 tissues (liver, visceral fat, subcutaneous fat and longissimus lumborum muscle) in Mahabadi kids after feeding. Twenty-four, 4–5 mo old male kids were individually penned for 90 d feeding period. Treatments included levels of 0.5, 1, and 1.5 mg/d of Cr^{3+} plus standard control diet and a standard control diet lacking Cr^{3+}. On d 90, the kids were slaughtered and tissue samples were collected. Total RNA was extracted and real-time PCR was performed using HSP-90 as a housekeeping gene. In the following table, the status of gene expression is shown. The results showed that except for SCD gene, lipid biosynthesis has increased significantly in all lipogenic tissues ($P < 0.05$). The beneficial role of SCD gene is to convert saturated into unsaturated fatty acids. In agreement with a previous study, this experiment suggests that the decrease in body fat synthesis can be explained by the decrease in gene expression.

Table 1.

Gene name	Liver	Visceral fat	Subcutaneous fat	LL muscle
Stearoyl CoA desaturase (SCD)	↑	↑	↑	↑
Fatty-acid-binding protein (FABP)	↓	↓	↓	↓
Lipoprotein lipase (LPL)	↓	↓	↓	NS
Fatty acid synthase (FASN)	↓	↓	↓	NS
Leptin (LEP)	NS	↓	↓	↓
Hormone-sensitive lipase (HSL)	NS	↓	↓	↓
Diacylglycerol acyltransferase (DGAT1)	↓	↓	↓	↓

Key Words: lipogenic tissue, metabolic health, multiple transcripts

Undergraduate Student Competition: ADSA-SAD Undergraduate Competition: Original Research

255 Leptospirosis and erythrocyte patterns: An exploration through nonlinear dynamics. C. A. Comyn*[1], S. P. Washburn[1], and V. Cortese[2], [1]*North Carolina State University Department of Animal Science, Raleigh,* [2]*Zoetis, Cattle-Equine Immunology and Biologics, Simpsonville, KY.*

Leptospirosis, a bacterial disease of worldwide distribution and significance, hays long had a correlation to erythrocytes, platelet counts, and hemoglobin levels in various mammalian species. However, documentation of these phenomena has been rare in cattle. Using the principles of physiological nonlinear dynamics, the study objective was to compare erythrocyte fluctuation patterns in healthy cattle versus patterns in cattle testing positive for *Leptospira* spp. with the expectation that cows testing positive for *Leptospira* spp. would have fewer fluctuations from the linear trend. Experimental and control groups were established by testing cattle for *Leptospira* spp. using urine samples followed by real-time PCR to identify bacterial isolates in the urine. Nine visibly healthy Holstein cows from one dairy herd in Virginia were used in this study; 4 tested positive for *Leptospira* spp., and 5 tested negative for *Leptospira* spp. Blood samples were collected at 24-h intervals for 12 d. The blood samples were submitted for complete blood counts at the Antech Diagnostic Laboratory in Manakin, VA. Mean red blood cell (RBC) counts were similar for the 2 groups of cows across the 12-d period. A linear trend line for RBC counts was calculated for each cow and then average fluctuation from the linear trend was calculated using the mathematical technique of detrended fluctuation analysis (DFA). Cattle testing positive for *Leptospira* spp. had numerically lower fluctuation in RBC counts compared with cattle testing negative for *Leptospira* spp., but the difference was not significant (0.29 ± 0.045 vs. 0.45 ± 0.115; $P = 0.26$). It should be noted that the group observed was relatively small; with a larger study group, results may have been more significant. Further, because animals observed in this study were asymptomatic, it may be possible that cattle experiencing an acute infection would maintain a lower DFA value for RBC counts. However, more research will need to be done to corroborate this.

Key Words: leptospirosis, nonlinear dynamics

256 Effect of milk feeding frequency and weaning age on growth and intake of dairy calves. S. A. McCullough*[1], T. S. Dennis[1], S. E. Fraley[1], B. Houin[2], and T. D. Nennich[1], [1]*Purdue University, West Lafayette, IN,* [2]*Homestead Dairy, Plymouth, IN.*

The objective of this study was to determine the effects of milk feeding frequency and weaning age on growth, intake, and feed efficiency of dairy calves on a commercial dairy. In this randomized complete block design with a 3 × 2 factorial arrangement of treatments, 162 Holstein heifers (BW = 40.5 ± 5.18 kg) were blocked in groups of 6 by birth date and hutch type. Heifers were assigned to either 2 (2×), 3 (3×), or 4 (4×) times per day milk feeding and either 7 (7WK) or 9 wk (9WK) weaning times. Calves were fed whole milk and allowed ad libitum access to starter. Calves received the same amount of milk per treatment at 3.8 L/d of milk for 14 d, 6.7 L/d from d 15 to 21, and 7.6 L/d from d 22 to 1 wk before weaning when calves were reduced to 3.8 L of milk once per day. Calves were weighed at birth and measured every 2 wk for weight, hip and withers height, heart girth circumference (HGC), and hip width. Data were analyzed as repeated measures using the Proc Mixed procedure of SAS. There were no interactions between feeding frequency and weaning age. Body weight at wk 10 was the greatest for 4× with calves weighing 95.6, 93.5, and 91.4 kg for 4×, 3×, and 2×, respectively ($P < 0.001$). Average daily gain (ADG) was greater ($P < 0.01$) for 4× calves than 2× calves with 3× being intermediate (0.79, 0.73, and 0.76 kg/d, respectively). At wk 10, calves fed 4× were taller at the hip ($P < 0.008$) and withers ($P < 0.01$) than 2×. The HGC was greater ($P < 0.01$) for 4× and 3× calves than for 2× (93.2, 92.8, and 91.9 cm, respectively). Starter intakes were similar for milk treatment, but calves weaned at 7WK had greater starter intake ($P < 0.01$) from 6 to 8 wk of age than 9WK. Calves weaned at 9WK were heavier at the end of the study than those weaned at 7WK (95.0 and 92.0 kg, respectively; $P < 0.001$), and overall ADG was greater for 9WK calves at 0.78 kg/d as compared with 0.74 kg/d for 7WK ($P < 0.02$). Calves weaned at 9WK had greater HGC ($P < 0.05$) and hip widths ($P < 0.001$), and were taller at the hip ($P < 0.001$) at the end of the study. Feeding calves milk 4 times per day improved calf growth as compared with feeding milk 2 times per day.

Key Words: dairy calf, milk, weaning

257 Characterization of quarter milking pulsation and take-off in a conventional milking parlor. S. M. Smith*, J. M. Bewley, K. J. McQuerry, and C. L. Wood, *University of Kentucky, Lexington.*

Overmilking may increase teat end hyperkeratosis and contribute to mastitis incidence. The objectives of this study were (1) to characterize the frequency of individual quarter milking using the Milpro P4C (Milkline, Gariga di Podenzano, Italy) and to describe the anatomical features that contribute to uneven milkout. The Milpro P4C system stops milking individual quarters using an individual quarter pulsation milking system with 4 independent pulsation channels per cluster instead of 2. The study was conducted at the University of Kentucky Coldstream Dairy during January 2013. The exact times when the partial take-off feature was employed were collected recorded by the milking system. Udder and teat characteristics were scored subjectively 3 times to create composite scores. Teat length and udder tilt were scored using the Holstein Association Linear Scoring System. Teat shape was scored according to the system described by Hickman (1985). Teat end shape was scored using the system described by Seykora and McDaniel (1985). Teat end callosity was scored according to Mein (2001). Milk weights were collected from the Milkline System. Cow demographic data (DIM and parity) were collected from PCDart. The partial takeoff procedure was not recorded for 5 of the 8 milking units due to equipment error or failure. For the 3 milking units functioning properly, the partial takeoff feature of the milking system was employed in 55% of 1263 valid milkings. The LOGISTIC procedure of SAS (Cary, NC) was used to develop a model to predict the likelihood of uneven milkout. Udder tilt, teat shape, teat end shape, and teat callosity were significant predictors of uneven milkout ($P < 0.05$) while milk yield (kg) was not ($P = 0.14$). These results demonstrate that a quarter based pulsation system may be beneficial for cows with varying udder and teat shapes. The partial takeoff feature was employed in over half of valid milkings indicating potential improved milkout and reduced risk of overmilking with this type of milking system.

Key Words: quarter milking, udder trait, pulsation

258 Variation in milk production within dairy herds. S. K. Finney*, M. L. Eastridge, W. P. Weiss, and N. R. St-Pierre, *The Ohio State University, Columbus.*

Understanding the variation of milk yield on dairy farms may assist dairy farmers in improving profitability. This study was conducted to determine the variation among farms with different levels of rolling herd average (RHA) for annual milk yield. Data from Dairy Herd Improvement were collected yearly from 2003 through 2011. The data included yearly RHA for milk, fat, and protein for each herd in Ohio and the annual production of milk, fat, and protein by individual cows having completed a lactation within the respective year for each herd. Dairy farms having at least 50 cows of either Holstein or Jersey were used, and individual cows must have completed a lactation of over 290 d in milk. Cows either above or below 3 standard deviations from the average milk yield for a herd were eliminated. The individual cow data were analyzed with SAS to calculate the herd average and standard deviation (SD) for yields of milk, fat, and protein. These data were then merged with the RHA data by herd. Quartiles within each year were determined using PROC Univariate within SAS and were then used to classify herds into categories for yields of milk, fat, and protein. For Holstein herds, the SD within each quartile RHA class was (low to high RHA milk) 1515, 1594, 1676, and 1801 kg and coefficients of variation (CV) were 17.5, 16.6, 16.1, and 15.0%, respectively. The SD for Jersey herds was 1060, 1239, 1262, and 1378 kg and CV of 17.4, 17.5, 16.6, and 16.7%, respectively. Variation within herds increased ($P < 0.01$) as the RHA increased, but the CV decreased ($P < 0.01$). Variation in milk yield within herds also was affected by year. Further analysis of this variation may provide evidence for recommendations to minimize the variation of milk yield on dairy farms.

Key Words: RHA milk, milk yield variation, yield variation within herd

259 Choosing appropriate temperature-humidity indices to predict the incidence of heat stress in lactating dairy cattle by analyzing local weather data for central Iowa. E. Hodges*, P. J. Berger, and G. Takle, *Iowa State University, Ames.*

Heat stress is known to cause a depression in milk yield and reduce reproductive success in dairy cattle. Few areas in the United States have been evaluated to compare temperature-humidity index (THI) values to milk yield and reproductive success. The objective of this research was to determine if weather conditions in central Iowa could be expected to cause heat stress in dairy cattle. Hourly weather data was obtained over a period of 5 years (2008–2011) from 2 local weather stations. The data were used to calculate hourly, daily, and monthly values for 7 temperature-humidity indices (THI) previously applied in dairy cattle. Each THI was a different weighted function of temperature and humidity. Six additional indices were calculated to incorporate wind speed and solar radiation. These indices had previously been applied in beef cattle feedlot settings. THI values from other states were matched against those in central Iowa, with the incorporation of wind speed and solar radiation. The former have been ignored in comparison of indices with regard to dairy cattle. The incorporation of wind speed and solar radiation relationships from beef feedlot trials in Nebraska matched an existing THI formula established from Georgia work. The onset of heat stress in beef cattle was established by visual observation. The onset of heat stress in dairy cattle was established by analysis of reproduction and lactation data. This research confirmed the existence of heat waves in the summer months with sufficient magnitude to facilitate the discovery of depressed milk yield and reproductive success.

Key Words: temperature-humidity indices, solar radiation, wind speed

260 Correlations among nutritional status of the dairy cow during early gestation and subsequent growth and cardiac measurements of her offspring. D. K. Hardin*, B. E. Voelz, H. M. Kerr, K. A. Barton, C. O. Lemley, and J. E. Larson, *Mississippi State University, Mississippi State.*

The potential of calves to become productive cows may be related to characteristics of growth and cardiac function early in life. The objective of this experiment was to determine whether nutritional status of the dam, as determined by concentrations of glucose and β-hydroxybutyrate (BHBA) and milk production during early gestation, was correlated with measurements of the calf at birth and at 1 mo of age. From parturition until 90 d pregnant, blood samples were collected every 14 d in Holstein cows. Plasma was later assayed for concentrations of glucose and BHBA. Calves (n = 26) born from these cows were measured for blood pressure, heart girth, hip and wither height as well as carotid artery hemodynamics measured via Doppler ultrasonography (pulsitility index (PI), resistance index (RI), and vessel diameter). Mean arterial pressure (MAP), pulse pressure (PP), and blood flow (BF) were then calculated. The CORR procedures of SAS were used to analyze data; means (±SD) are presented. In calves at birth, mean milk production of dams during early gestation (89.2 ± 18.3 kg) was positively correlated ($P < 0.05$) with heart girth (77.0 ± 4.3 cm). As expected, length of gestation was also positively correlated with heart girth of calves at birth ($P < 0.05$) and at 1 mo of age ($P < 0.01$). There tended to be a positive correlation between mean concentration of glucose in dams ($P = 0.07$; 3.48 ± 0.6 mmol/L) and MAP in calves at birth (80.1 ± 8.8 mmHg) and a negative correlation between mean concentration of BHBA in dams ($P = 0.06$; 905.3 ± 505.2 μmol/L) and PP in calves at birth (42.8 ± 7.0 mmHg). Mean concentration of glucose in dams was positively ($P < 0.05$) correlated with wither height in calves at 1 mo of age. Length of gestation was negatively ($P < 0.01$) correlated with RI in calves at 1 mo of age. Milk production in the dam was positively correlated ($P < 0.10$) with hip and wither height, and PI but negatively correlated with MAP in 1 mo old calves. These correlations lead to speculation that early gestational environment may affect growth and hemodynamic parameters in young calves.

Key Words: cattle, dairy, Doppler

261 High moisture corn increased hepatic gene expression for anapleurotic and gluconeogenic enzymes compared with dry corn for Holstein cows in the postpartum period. C. M. Ylioja*, R. J. Rockwell, and M. S. Allen, *Michigan State University, East Lansing.*

Holstein cows (n = 48) were used in a randomized block design experiment to determine hepatic gene expression responses to dietary starch source in the postpartum period (PP). Treatments were dry corn (DC) or high moisture corn (HMC) fed from parturition until 28 ± 3 d PP. HMC increased milk yield 3.4 kg/d compared with DC (42.6 vs. 39.2 kg/d, $P = 0.02$), but did not affect 3.5% fat-corrected milk (FCM, $P = 0.11$) or dry matter intake (DMI, $P = 0.52$) during the treatment period. Sustained effects of treatment were detected when cows were offered a common diet from 29 ± 3 d to 84 ± 3 d PP; HMC increased DMI and FCM compared with DC but effects diminished over time (interaction $P < 0.03$). HMC increased plasma glucagon concentration over time during the treatment period compared with DC both before ($P = 0.001$) and after ($P = 0.04$) feeding. Liver tissue obtained by biopsy at 7 ± 3d prepartum and 14 ± 3d PP was analyzed by qRT-PCR for relative mRNA abundance of genes related to metabolism. HMC allowed increased anapleurosis compared with DC by increasing gene expression for pyruvate carboxylase (1.44 fold, $P = 0.01$), propionyl CoA synthetase (1.19 fold, $P = 0.05$), propionyl-CoA carboxylase α (1.16 fold, P

= 0.05), and increasing expression for methylmalonyl CoA epimerase more over time (pre- vs. postpartum) for HMC than DC (1.30 vs. 1.03 fold, $P = 0.03$). Gene expression for carnitine palmitoyl transferase 1α tended ($P = 0.11$) to decrease more over time for HMC (0.77 fold) than DC, which was relatively unchanged (0.97 fold). HMC also increased expression for citrate synthase compared with DC (1.15 fold, $P = 0.07$). Expression for phosphoenolpyruvate carboxykinase (PCK1) was not affected by treatment ($P > 0.15$) but HMC increased glyceraldehyde 3-phosphate dehydrogenase (1.13 fold, $P = 0.02$), and tended to increase glucose 6-phosphatase (1.17 fold, $P = 0.10$), consistent with increased gluconeogenesis. Effects of treatment on plasma glucagon concentration and hepatic gene expression are consistent with increased milk yield for HMC compared with DC.

Key Words: starch fermentability, glucagon, gene expression

262 The association of telomere length and body weight in lactating Holsteins. I. W. Haagen*, C. D. Dechow, and D. E. Brown, *Penn State University, University Park.*

Telomeres are a repetitive TTAGGG DNA sequence on the end of chromosomes that protect the integrity of the chromosome and are reported to become shorter following cell division. The objective of this study was to evaluate the association between telomere length and body weight (BW) in lactating Holstein dairy cows. A total of 132 cows with 273 BW observations from 11 commercial herds and 88 cows with 46,020 observations from the Penn State Dairy Research Center herd were used in this study. BW in commercial herds was estimated using heart girth circumference measurements taken up to 4 times per lactation from 2008 to 2009. BW is electronically recorded daily at the Penn State Dairy Research Center as cows exit the milking parlor and BW from lactations 1 to 3 were considered. DNA was extracted from whole blood and telomere length estimated with quantitative PCR by comparing relative expression of a 79 base pair telomere product to a 144 base pair reference gene product. Cows ranged in age from 22 mo to 121 mo at the time of blood collection. Cows were stratified into high (TH) and low telomere (TL) length groups of equal size. BW was evaluated separately for commercial herd cows and PSU cows with a model that included effects of telomere group, lactation, stage of lactation, contemporary group, and the random effect of cow. Telomere group had a significant association with BW ($P < 0.05$) in both the commercial and PSU populations. The least-squares-means (LSM) estimate of BW in commercial herd TH was 737.5 kg compared with 685.9 kg in TL. The TH at PSU had a LSM estimate of 661.6 kg, whereas cows in TL had a LSM estimate of 639.6 kg. The results of this study suggest that a positive association may exist between telomere length and BW. However, telomere length was available at different ages. A controlled study with telomere length determined at the same age for all cows is required to more fully describe the relationship between telomere length and BW.

Key Words: telomere, body weight

263 The effects of corn silage inclusion in pre-weaned calf diets. S. Retz*[1], S. I. Kehoe[1], K. McFarland[2], and G. Suen[2], *[1]University of Wisconsin-River Falls, River Falls, [2]University of Wisconsin-Madison, Madison.*

Dairy calves should receive feed that will stimulate rumen development and allow for healthy growth. However, calf grain starters can be expensive and some farmers feed corn silage instead. Corn silage may not provide enough rumen stimulation and energy substrate for healthy papillae development. The objective of this trial was to assess the effects of starter feed on calves over the course of their developmental cycle by quantifying rumen morphology. Thirty 6 heifer calves and 9 bull calves were reared in blocks of 15 at the US Dairy Forage Research farm where they were individually housed in hutches. All treatments were fed pasteurized milk with either all calf starter (C; 18% crude protein), 40% corn silage and 60% calf starter (CC), or all corn silage (CS). Nine bull calves, one from each treatment during each block, were slaughtered at 8 wk of age. Rumens were collected and 3 samples from 4 areas within the rumen were taken; left side caudal dorsal sac (LB), right side caudal dorsal sac (RB), right side cranial ventral sac (RD) and left side cranial ventral sac (LD). Twelve papillae per sample were randomly measured for length and width. The Mixed procedure of SAS (2010) was used with block as a random effect to analyze for treatment differences. No significant differences were found for papillae length for region LB (8.1 ± 1.5, 3.9 ± 1.9, and 6.4 ± 1.5 for treatments C, CC, and CS, respectively) and RB (10.2 ± 3.2, 4.4 ± 2.4, and 7.9 ± 2.4 for treatments C, CC, and CS, respectively). There were significant differences between treatments for regions LD (11.7 ± 1.2, 5.3 ± 1.2, and 10.1 ± 1.2 for treatments C, CC, and CS, respectively) and RB (8.7 ± 1.1, 2.8 ± 1.1, and 5.7 ± 1.1 for treatments C, CC, and CS, respectively). There were no significant differences between treatments for papillae width. This data indicates that corn silage added to calf starter may not result in as much rumen development for some areas of the rumen as calf starter or only corn silage. Data collected for calf health and growth parameters is currently being analyzed.

Key Words: calf, corn silage, rumen development

Teaching/Undergraduate and Graduate Education: Learning Styles and Student Success

264 Developing critical academic and social connections for incoming students prior to the first day of classes using a combination of innovative programs . H. D. Tyler* and J. A. Sterle, *Iowa State University, Ames.*

At-risk college students are most successful if they develop early connections to the faculty and other students in their major. Accordingly, 3 strategies were developed to create meaningful connections to our program. First, a computer program was developed to survey students during Freshman Orientation on their interests and career goals and assign faculty academic advisers based on common interests. These students were able to connect with their adviser before coming to campus for classes; an added benefit is that these matched advisors are more able to provide appropriate career mentoring, having more contacts with the industry of interest for that particular student for finding relevant internships and jobs. Although students can re-enter the program and switch advisors at any time in their program, less than 5% actually do so. Second, the peer mentor program in our department was greatly expanded to allow selected, trained upperclassmen to mentor small groups of 6–10 new students during their first semester of college. All new students within a peer mentor group have the same faculty advisor; often, the peer mentor also shares the same advisor. Mentor groups meet at least once a week during their first semester in addition to taking relevant industry trips together. Lastly, Facebook groups were created for each cohort of potential incoming students 6 mo before their college entry date. This allowed them to establish relationships with other students and create a social network before the first day of school. Over 200 students were members of the group formed for incoming students in 2012. The types of posts evolved from the time the group was formed; initially, students shared information about themselves. After they signed up for classes, they sought information about our program, and finally after they arrived at Iowa State, they used the site to plan social activities and coordinate classes with their peers. Investing time and resources into the new student experience is crucial for developing successful relationships that are vital to student success.

265 Learning style preferences of animal science undergraduates. C. Mortensen* and A. Thoron, *University of Florida, Gainesville.*

Studies have linked higher student achievement when instructed in learning environments that match their learning styles. We administered 2 learning style instruments to investigate the learning style preferences of undergraduate students in the Department of Animal Sciences at the University of Florida. The Group Embedded Figures Test (GEFT) segregates students into either field-dependent or field-independent learning styles. The Gregorc Style Delineator (GSD) measures student's natural predispositions for learning along 4 bipolar continuous mind qualities: Concrete-Sequential (CS), Abstract-Sequential (AS), Abstract-Random (AR), and Concrete-Random (AR). Student scores were evaluated based on sex and their specific degree option: Food Animal Industry, Equine Industry, and Animal Biology (pre-veterinary medicine). Results of the GEFT indicated Animal Biology students had a higher preference for a field-independent learning style (mean score 14.0 ± 0.36) compared with Equine Industry (13.0 ± 0.79; $P = 0.10$) and Food Animal Industry (12.5 ± 1.04; $P \leq 0.05$) students. Male students (14.8 ± 0.64; n = 26) had a higher preference ($P = 0.06$) for a field-independent learning style compared with female students (13.4 ± 0.36; n = 129). Overall, 63% of animal science students preferred a field-independent compared with 19% field dependent learning style, 18% remained neutral. Students with a field-independent learning style are described as being more analytical, find it easier solving problems, likely to favor learning activities that require individual effort, and are less receptive to social reinforcement. Field-dependent learners perceive globally, have a more difficult time solving problems, are more attuned to their social environment and tend to favor a spectator approach to learning. No differences were found among degree options or sex in GSD scoring. Overall, students scored higher in CS (48%) compared with AS (15%), AR (15%) or CR (21%) learning styles. The CS learner is described as relating to the concrete world with hands-on experiences, prefer structure and wants explicit and clear directions. Activities that accommodate CS learners are checklists, worksheets, demonstrations, outlines and diagrams.

Key Words: learning style

266 Motivation for undergraduate students to participate in an equine study abroad course. C. Brady*[1], J. Peters[2], M. Voigt[1], and M. Russell[2], *[1]Department of Youth Development and Agricultural Education, Purdue University, West Lafayette, IN, [2]Department of Animal Sciences, Purdue University, West Lafayette, IN.*

The purpose of this study was to assess what motivated students to participate in a short-term equine study abroad course. The survey instrument was adapted from an instrument validated for assessing motivation to participate in voluntary career development events. The adapted instrument was reviewed by an expert panel for content validity, and a post-hoc Cronbach's α coefficient of 0.943 demonstrated an excellent level of internal validity. The survey was administered following the Dillman Tailored Design Method to 22 students in fall 2012, after their participation in the study abroad course in spring 2012. Twenty-two 5-point Likert scale questions were used to measure self-efficacy and 4 motivation factors; attainment (significance of doing task well), cost (negative aspects of task), intrinsic (individual satisfaction in task) and utility (relationship of task to future goals). Sixteen students completed the survey, 15 females and 1 male. Cost motivation (4.43 ± 0.61) had the highest mean score, followed by self-efficacy (4.33 ± 0.53), intrinsic (3.99 ± 0.53), utility (3.94 ± 0.36) and attainment (3.45 ± 1.08). Means were compared using a paired sample *t*-test. Using a value of ($P < 0.05$) cost motivation was greater than all other factors. Self-efficacy was greater than either attainment or utility. Intrinsic motivation was only different from cost motivation, and there was not difference between attainment and utility motivation. There has been a perception that intrinsic motivation, was a primary motivator, but in this set of students, that supposition was not supported. It is important to note that cost motivation were time and effort costs and did not include any items about material cost to participate. This study indicates that time cost is a primary student motivator, and short-term study abroad courses may be a path to involvement of more students in a study abroad experience.

Key Words: study abroad, student motivation

267 Student perceptions of sustainable and organic agriculture. L. Unruh Snyder*[1], T. Durham[2], A. Davis[4], and T. Irani[3], *[1]North Carolina State University, Raleigh, [2]Florida Gulf Coast, Fort Myers, [3]University of Florida, Gainesville, [4]Purdue University, West Lafayette, IN.*

Eighty-four students at 3 different universities were recruited for a survey that assessed their knowledge, attitudes, and opinions on the prospects of incorporating more curriculum on organic and sustainable agriculture. Respondents were enrolled in 1 of 4 agricultural courses or one biology class among the 3 universities. Subjects were asked to self-report basic demographic information and address a series of open-ended short answer questions developed by the investigators, including questions centered on the concepts of organic and sustainable agriculture. Students provided a range of words for the themes to define organic and sustainable agriculture. Overall, student responses demonstrated many different variations of organics. However, definitions of sustainable agriculture were more ambiguous. A prevailing view did not emerge from the data, with 13% reporting "do not know." Within the cohort, students' qualitative responses speculated that organic agriculture will increase in the future (40%), and 11% of students felt that it would decrease. With the remaining students perspectives speculating that organic agriculture will not change (4%) or will remain a minority in agriculture (11%). Nine percent of the students were unsure about whether organic agriculture would change at all and the remaining 25% not responding to the question at all. If a university was to implement a teaching plan that incorporates organic agriculture to a greater extent, students indicate they would prefer "hands-on" techniques (51%) and field work situations as the primary methods of learning. Traditional methods of discussion and lecturing were cited 4% and 7%, respectively. When asked about the utility of field trips as learning modality, 15% of the student responses agreed with this prompt. However, 68 students responded "no," 14 said "yes," and 3 did not respond. Those who volunteered a reason overwhelmingly cited "lack of time." Although the results indicated a lack of direct participatory interest, the results of this survey denoted a role for organic and sustainable agriculture in the curriculum.

Key Words: perceptions, organic, sustainable

268 Student engagement in learning anytime/anywhere: Enhancing learning with technology in the animal sciences. J. M. Osborne*, B. A. Wenner, T. A. Evans, M. C. Chakerian, R. W. Flood, M. R. Hendrick, and H. N. Zerby, *The Ohio State University, Columbus.*

Many courses in the OSU Department of Animal Sciences occur in a traditional setting with students attending lecture in person at scheduled times. Conversion from quarters to semesters and an institutional directive to align educational experiences with student needs prompted consideration of alternative forms of instruction. Instructors of the large enrollment (100+) writing course "Animals in Society" chose the Hybrid-Flexible (Hy-Flex) Instructional Model, which allowed students to attend twice-weekly lectures in-person or synchronously online. Lecture content was integrated in learning activities during weekly in-person recitation sections (25–30 students). Technologies to implement the Hy-Flex model for lectures were selected to permit students to vary mode of attendance on a daily basis and review lectures anytime-anywhere. The technologies were expected to support a robust learning community and provide student-instructor interaction. Adobe Connect was the internet platform for lecture delivery and recording. Students responded to questions using Poll Everywhere software, which also provided a back-channel for student questions regardless of attendance mode. Small online discussion groups used the OSU course management system. In autumn 2012, 94 students consented to participate in a research study. Online attendance increased from 20 to 40% to 60–70% by the end of the term, with 49% of students attending more than 75% of lectures online. Eighty-four percent of students agreed that technology helped them actively participate in the course; 17% thought that technology hindered their interaction with the instructor. A slight majority (56%) agreed that instructional technology helped create a sense of community among students. There was no correlation between mode of attendance and overall grade or grade on writing assignments that required knowledge of lecture content. Results suggest that online attendance did not cause reduced understanding of course concepts and that technology can be used to support student engagement with course content and develop a learning community within a large enrollment course.

Key Words: technology, online, anytime/anywhere learning

269 Predicting the quality of an undergraduate animal science course using the IDEA survey. M. J. Anderson, K. J. Stutts, M. M. Beverly, and S. F. Kelley*, *Sam Houston State University, Huntsville, TX.*

The Individual Development and Educational Assessment (IDEA) survey is a mechanism that uses student feedback to assess and improve teaching, learning, and the higher education process. The IDEA survey contains questions pertaining to course objectives, teaching methods and styles, and a description of the course with the goal of determining the quality of the instructor and overall course. The objective of this study was to determine which of the survey questions were most important when predicting the quality of the course in undergraduate animal science courses. A step-wise regression analysis was performed on data from 238 courses spanning a 6-year period. Thirty-five of the 43 questions on the survey were included in the analysis. Eight questions were not included in the analysis because they involved students' preconceptions that could not be affected by the instructor during the course. This analysis indicated that only 6 of the 35 questions entered into the model were significant. These 6 questions had an r^2 of 0.7056 compared with an r^2 of 0.7443 for all 35 questions. The analysis indicated that these questions account for the majority of variation within the model. The top 3 questions with positive relationships toward predicting the quality of the course were: 1) the instructor demonstrated the importance and significance of the subject matter, 2) students made progress on gaining factual knowledge, 3) the instructor explained course material clearly and concisely. Conversely, a question pertaining to the instructor encouraging students to use multiple resources for research purposes had a negative relationship toward predicting the quality of the course. This indicated that students believed this area was not a valuable skill in animal science courses. In conclusion, an animal science instructor can improve the quality of their course by displaying the importance the subject matter and clearly presenting the course material to expand the students' knowledge of that subject.

Key Words: IDEA, undergraduate teaching, animal science

270 The role of trace minerals in feed stability and swine production. M. D. Lindemann*, *University of Kentucky, Lexington.*

Trace minerals (Cu, Fe, Mn, Zn, I, and Se) must be supplemented to diets of swine of all ages to meet their physiologic need for a variety of body purposes such as energy metabolism, connective tissue growth, bone formation, inflammatory response, immune function, and structural or catalytic involvement with a host of enzymes. The collective effect of these metabolic and physiologic impacts can result in changes in the rate and efficiency of whole animal growth and production. While minimum concentrations of these nutrients are established for growth, relatively less research is available that would establish supplementation needs to optimize the metabolic responses. Additionally, while there is some research that helps to establish the whole animal toxicity levels for the nutrients, there is relatively less research related to the effect of supplementation rates between those of the supposed requirement for growth and the presumed toxicity level on factors related to metabolic efficiency. In addition to the direct effect of absorbed minerals on metabolism, because of the prooxidant nature of Cu, Fe, Mn, and Zn, the supplementation level has the potential to interact with time, temperature, and moisture to affect the stability of various constituents of the feed. The constituents that are potentially affected most by prooxidants are vitamins, fats, and exogenous enzymes. Historic research has demonstrated that all of these can be affected by the level of supplemental trace minerals. The trace mineral affecting stability the most has varied among studies. Additionally, because oxidation is a chemical phenomenon, it would be assumed that the reactivity of the individual minerals should be a function of its chemical properties (e.g., rate and extent of dissociation) and that assumption has been demonstrated to be valid in comparisons of the forms of the minerals that are available to the feed industry (various inorganic forms as well as organic forms). Decisions about trace mineral supplementation should, in many situations then, also involve consideration of the source of minerals and their effect on feed stability relative to its consequent effect on animal wellbeing.

Key Words: trace mineral, feed stability

271 Exploring cellular trace mineral metabolism in bovine and porcine tissues. R. S. Fry*[1], J. W. Spears[2], M. S. Ashwell[2], and S. L. Hansen[3], *[1]Provimi North America, Brookville, OH, [2]North Carolina State University, Raleigh, [3]Iowa State University, Ames.*

The objective of this presentation is to provide an overview of the metabolic pathways responsible for copper (Cu), iron (Fe), and zinc (Zn) metabolism in mammalian tissues. Rodents and cell lines have been utilized for more than a decade to determine the role and necessity of these cellular mechanisms. These data have provided a foundation for scientists to build upon, and we have conducted numerous trials characterizing gene products responsible for Cu and Fe metabolism in bovine and porcine tissues. Copper transporter 1 is essential for Cu uptake. Mice with intestinal deleted Ctr1 are characterized by high mortality rates and reduced survivability, and liver Cu and cuproenzyme synthesis is markedly reduced in mice with hepatic Ctr1 deletion. Antioxidant 1 (ATOX1) is one of several vital Cu chaperones that prevent Cu deficiency and toxicity. Copper is delivered to Cu-dependent ATPases via ATOX1. While both are present in the intestine and liver, ATP7A is essential for Cu utilization from the enterocyte for synthesis of cuproenzymes, and ATP7B is required for biliary Cu excretion and incorporation of Cu into ceruloplasmin, a Cu-dependent ferroxidase. Divalent metal transporter 1 is responsible for Fe acquisition in the small intestine and liver. Manganese can also be transported via DMT1 and possibly a small portion of Cu. Ferroportin (FPN) is responsible for Fe export from the enterocyte and is regulated by hepcidin, a small peptide hormone that is produced by the liver and secreted into plasma to promote internalization and degradation of FPN in response to increases in body Fe stores. Proteins responsible for Zn absorption are categorized into 2 families. The family of ZnT transporters is responsible for Zn utilization and these transporters may also play a role in sequestering Zn in intracellular compartments. The ZIP family of transporters is responsible for Zn acquisition, especially ZIP4, which is essential for intestinal Zn uptake. Further characterization of these molecular mechanisms will broaden our knowledge of trace mineral metabolism in animal nutrition.

Key Words: copper, iron, zinc

272 Relative bioavailability, immune function, and antimicrobial effects of trace minerals. K. C. Klasing* and V. J. Iseri, *University of California, Davis.*

There are many nutritional and non-nutritional effects of nutrients that are added to feeds to optimize animal performance and health. A subset of nutritionally required lipids, vitamins and trace minerals possess bioactivities that function across a range of mechanisms including substrates or co-factors for key metabolic processes (nutritional effects), regulators of pathways and cellular decisions, and direct activities on the viability of potential pathogens along the mucosa of the GI track (pharmacological or non-nutritional effects). Among trace minerals, iron, zinc, and copper have been shown to possess this range of activities. Investigations of bioactive nutrients must consider each of these mechanisms to understand their net impact on the health and productivity of animals. For example, copper is required at relatively low levels as a co-factor for a variety of enzymes; each of which has a different priority for this cofactor. Studies examining the ability of dietary copper to fulfill its role as a cofactor should focus on those enzymes that have a low priority, such as lysyl oxidase in tendons, and not on enzymes that have a higher priority or can switch to other divalent cations, such as superoxide dismutase in immune cells. Copper also has direct anti-microbial effects on intestinal microflora and these actions occur at levels that are an order of magnitude higher than needed as a cofactor for lysyl oxidase. Studies on the anti-microbial actions of copper should focus on the dietary fraction that remains in the lumen of the distal intestines and is available to influence the microbial milieu rather than the fraction that is absorbed and used as a cofactor for enzymes. At intermediate concentrations, copper influences regulatory decision made by T-helper lymphocytes and macrophages. Thus, bioavailability/bioefficacy is context dependent and the specific function (nutritional versus regulatory versus anti-microbial) needs to be considered when comparing nutrient sources.

Key Words: copper, requirement, immunity

273 Practical applications of trace minerals in dairy cattle. T. R. Overton* and T. Yasui, *Cornell University, Ithaca, NY.*

Trace minerals have critical roles in immune function, oxidative metabolism, and energy metabolism in ruminants. To date, the primary trace elements of interest in diets for dairy cattle have included zinc (Zn), copper (Cu), manganese (Mn), and selenium (Se), although

data also support potentially important roles of chromium (Cr), cobalt (Co), and iron (Fe) in diets. Trace minerals such as Zn, Cu, Mn, and Se have classically and essentially defined roles as components of key antioxidant enzymes and proteins. Available evidence suggests that these trace minerals can modulate aspects of oxidative metabolism and immune function through these roles; recent work has demonstrated that source of Zn, Cu, and Mn fed to dairy cattle during the transition period and early lactation can modulate both aspects of oxidative metabolism and production. Chromium has been shown to have roles in both immune function and energy metabolism of cattle; dairy cows fed Cr during the transition period and early lactation have evidence of improved immune function, increased milk production, and decreased subclinical endometritis. Limited research has been conducted with focus on Co and Fe nutrition; some data do support roles of Co in cow productivity during early lactation. At the farm level, one factor that complicates trace mineral nutrition is the existence of a large number of antagonisms affecting bioavailability of individual trace minerals, thus determining the optimum level and source of trace minerals at the farm level continues to be a challenge. Collectively, increasing evidence supports a role for trace mineral nutrition in modulating production, health, and reproduction in cattle. Furthermore, opportunities for specific modulation of aspects of health, milk production, and reproduction through supplementation strategies for diets of transition dairy cows are attractive because of the known dynamics of energy metabolism, immune function, and oxidative metabolism during this timeframe.

Key Words: trace mineral, oxidative metabolism, immune function

Dairy Foods: Chemistry and Processing II

W1 Microfiltration and ultrafiltration process to produce micellar casein concentrate and milk protein concentrates with 80% protein content. P. Salunke, C. Marella*, and L. E. Metzger, *Dairy Science Department, Midwest Dairy Foods Research Center, South Dakota State University, Brookings.*

Milk protein concentrates (MPC) are used in applications that require dairy ingredients with higher level of protein relative to total solids (TS). MPC is essentially skim milk (SM) powder with reduced level of lactose. MPC has same ratio of casein to serum protein (SP) as found in SM. In some applications, protein ingredients with a reduced level of SP content may be preferred. The objective of the present research was to compare microfiltration (MF) and ultrafiltration (UF) processes for production of MCC and MPC with 80% protein relative to TS. 227 L of pasteurized SM was subjected to MF using 0.5-μm spiral-wound polyvinylede fluoride membrane. During the process, diafiltration (DF) water was added at 6 intervals, totaling to 100% of feed volume. In another process, 227 L of pasteurized SM from the same lot was subjected to UF using 10 kDa polyethersulfone membranes. During the process, DF water was added at 4 different intervals, totaling to a final addition of 40%. Both the processes used a volume reduction of 5. There were significant ($P <$ 0.05) differences in all of the compositional parameters except fat and casein for the MF retentate (MFR) and UF retentate (UFR). UFR had a higher total nitrogen (TN), TS, lactose, ash and calcium content as compared with MFR. This affected the TN/TS ratio found in both the retentates, MFR had a ratio of 81.7 and UFR had a ratio of 77.18. The differences in membrane pore sizes, operating pressures and level of DF used all contributed to the differences in final TN/TS ratio obtained. Capillary gel electrophoresis analysis of individual protein fractions present in the UFR and MFR showed that UFR has β-lactaglobulin to α-lactalbumin (α-LA) ratio of 2.57, which is close to the ratio found in SM. The MFR has a ratio of 3.57 indicating preferential transmission for α-LA by the MF membrane. The results from this study show that MF and UF processes could be used for production of MCC and MPC with similar TN/TS ratio with careful selection of operating parameters.

Key Words: MPC or MCC, micro- and ultrafiltration, capillary gel electrophoresis

W2 Understanding shear-induced aggregation in partially crystalline oil-in-water emulsions. G. Fuller*[1,2], T. Considine[1], M. Golding[2], L. Matia-Merino[2], and A. MacGibbon[1], *[1]Fonterra Co-operative Group Limited, Palmerston North, New Zealand, [2]Massey University, Palmerston North, New Zealand.*

Fat globules in food products such as cream are prone to irreversible aggregation due to the presence of both solid and liquid fat in the dispersed phase and weak interfacial films. This can lead to undesirable changes in both texture and functionality. Despite the need to understand and control this process, many questions still remain because the factors affecting aggregation are numerous and often interdependent. To study the aggregation process, 35% fat emulsions with different solid fat content (SFC) stabilized by 2% sodium caseinate were studied under shear (cone-and-plate geometry) at 5°C over 6 d. SFC was varied by combining hydrogenated palm kernel oil and canola oil. To study the effect of different interfacial film compositions, Tween 20 (0.5. 1.5 and 2.5% by wt) was added after homogenization. The results showed that emulsions containing 0.5% Tween 20 had distinctly different aggregation behavior compared with those with ≥ 1.5% Tween 20 regardless of solid fat content and the applied shear rate. At 0.5% Tween 20, aggregation time increased with increasing SFC whereas at ≥ 1.5% Tween 20, aggregation time decreased with increasing SFC. This behavior was likely due to a transition from a mixed protein-surfactant interface at 0.5% Tween 20 to a surfactant dominated interface at ≥ 1.5% Tween 20. By revealing how small changes in surfactant concentration significantly influence shear-induced aggregation behavior in oil-in-water emulsions with different SFC, these results will aid in the development of food products with improved shelf-life and stability.

Key Words: emulsion, shear-induced aggregation, partial coalescence

W3 Effect of Maillard-induced glycosylation on the molecular configuration of whey protein and its solubility and thermal stability for beverage applications. Q. Wang* and B. Ismail, *University of Minnesota, St Paul.*

Whey proteins are reasonably soluble in acidic beverages; however, thermal processing and prolonged storage can result in protein aggregation and subsequent deterioration of quality. Consequently, whey protein acidic beverages available on the market have a short shelf life and contain at most 4% protein, which is below the minimum percentage (4.2%) required by the FDA to claim a "high protein beverage." The objective was to determine the solubility, thermal stability, nutritional quality, and structural changes of partially glycosylated whey protein (PGWP). Maillard-induced glycosylation conditions were optimized to promote glycosylation of whey protein, while minimizing browning and maintaining nutritional quality. Solubility and thermal stability of PGWP and WPI were compared over a wide range of pH, protein concentrations, and heating temperatures and times. Differential scanning calorimetry and SDS-PAGE were employed to monitor onset of denaturation and polymerization, respectively. Samples were analyzed by surface-enhanced Raman spectroscopy and by matrix-assisted laser desorption ionization-time of flight mass spectrometry to determine secondary and tertiary structural changes and glycosylation sites, respectively. Compared with WPI, PGWP maintained higher solubility and thermal stability at protein concentrations greater than 4.2%, over a wide range of pH, including the pH around the isoelectric point (pI) of whey protein. The enhanced solubility and thermal stability was attributed to structural rigidity, unique glycosylation sites and resistance to denaturation. The nutritional quality was maintained and advanced stages of Maillard reaction were not detected. Our findings demonstrated the possibility of using PGWP in the production of high protein acidic beverages (>4.2% protein) and provided information that is essential to understand the structure/function relationship upon Maillard-induced glycosylation of whey proteins.

Key Words: whey protein, glycosylation, solubility

W4 Development of a multiclass method for determination of 38 veterinary drugs in milk by ultra-high-performance liquid chromatography-tandem mass spectrometry. R. W. Han[1,3], N. Zheng[1,2], J. Q. Wang*[1,2], Z. N. Yu[3], X. M. Xu[1,2], Y. P. Zhen[1,2], X. Y. Qu[1,2], and L. C. Huang[1,2], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Ministry of Agriculture–Milk and Dairy Product Inspection Center (Beijing), Beijing, China, [3]College of Food Science and Engineering, Qingdao Agricultural University, Qingdao, Shandong, China.*

A simple, selective and rapid multi-residue method was developed to determine 38 veterinary drugs simultaneously in milk by ultra-high-performance liquid chromatography-tandem mass spectrometry (UPLC-MS/MS). The selected veterinary drugs include 14 β-lactams, 8 quinolones, 8 sulfonamides, 5 tetracyclines, and 3 macrolides. The analytes were extracted by water-acetonitrile (1:3), and then purified using Oasis HLB cartridge. The elution with water-acetonitrile (8:1) was injected into the UPLC-MS/MS system on a Waters UPLC C_{18} column in gradient mode. Multiple reaction monitoring (MRM) experiments in the positive ionization mode were performed to achieve data acquisition under MS/MS. Results showed good accuracy and repeatability. Average recoveries for different veterinary drugs in milk were 67.9–117.5% for β-lactams, 79.3–117.7% for quinolones, 71.3–106.1% for sulfonamides, 76–115.5% for tetracyclines and 78.2~106.1% for macrolides. The coefficients of variation (C.V.) of the recoveries were less than 15% for intraday and interday precisions. The limits of quantification (LOQs) for β-lactams, quinolones, sulfonamides, tetracyclines and macrolides were 0.3–10 ng/mL, 0.03–0.6 ng/mL, 0.03–0.3 ng/mL, 0.6 ng/mL and 0.03–0.6 ng/mL, respectively. Finally, the method was applied to 25 raw milk samples and traces of some veterinary drugs under allowable levels were detected, such as flumequine, sulfapyridine, sulfamethoxazole and lincomycin.

Key Words: veterinary drugs, milk, UPLC-MS/MS

W5 A UPLC-MS/MS method to simultaneous determine aflatoxin M1, ochratoxin A, zearalenone and α-zearalenol in milk. L. C. Huang[1,3], N. Zheng[1,2], J. Q. Wang*[1,2], J. B. Cheng[1,3], R. W. Han[1,2], X. M. Xu[1,2], and S. L. Li[1,2], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Ministry of Agriculture–Milk and Dairy Product Inspection Center (Beijing), Beijing, China, [3]College of Animal Science and Technology, Anhui Agricultural University, Hefei, China.*

Our objective was to develop an ultra-high-performance liquid chromatography triple-quadrupole spectrometry (UPLC-MS/MS, TQ-S, waters, USA) method to simultaneously determine aflatoxin M1, ochratoxin A, zearalenone and α-zearalenol in milk. The analytes were extracted by acetonitrile, and purified by solid phase extraction (SPE) using Oasis HLB cartridge, and then injected into the UPLC-MS/MS system. The mycotoxins were separated by UPLC BEH C_{18} column in gradient mode and determined in multiple reaction monitoring mode under positive- and negative-mode electrospray ionization. The optimized conditions of purification were SPE pH 5.0, eluting solution of 100% methanol, SPE flow rate of 1.5 mL/min and washing water of 2 mL. The matrix effects of 3 milk matrices, including raw milk, liquid milk and milk powder, were evaluated by the signal suppression-enhancement and compensated by external matrix-matched calibration. Correlation coefficients (r^2) of external matrix-matched calibration curves were higher than 0.996 in their respective linear ranges (0.01–1.00 μg/kg). The LOD and LOQ ranges of 4 mycotoxins selected were 0.001–0.005 μg/kg and 0.003–0.015 μg/kg, respectively. The method validation in 3 matrices at low (0.025 μg/kg) and high (0.5 μg/kg) spiked levels obtained reasonable recoveries (87.0–109%) and repeatability (CV < 10%). Intra- and inter-day tests at levels of 0.025 μg/kg also got satisfactory recoveries (23.1–25.4 μg/kg) and RSDs (7.4–9.9%). Finally, the method was successfully applied to milk samples, and traces of 4 mycotoxins were detected. The results demonstrated that the proposed method was sensitive, reliable and robust. Therefore, the developed method was suitable for the simultaneous determination of 4 mycotoxins in milk and could be performed for their routine analysis in mycotoxin study and survey.

Key Words: mycotoxin, milk, UPLC-MS/MS

W6 Comparison of amino acid composition of milk from different species. J. X. Zhang[2,3], J. Q. Wang*[1,2], D. P. Bu[2], J. H. Yang[2], L. Ma[2], and J. T. Chen[2], *[1]Agronomy College of Heilongjiang August First Land Reclamation University, Heilongjiang, China, [2]Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [3]Xinjiang Agricultural University, Urumqi, China.*

The objective of this study was to investigate variation of milk amino acids composition of different dairy animals. Milk samples from cows, goats, yaks and buffalos (n = 20 for each species) were obtained from different farms, and transported to the laboratory as packed for analysis. Amino acids were extracted by hydrolyzed with 7.8 mol/L HCl for 24 h, and concentrations of amino acids were determined by Hitachi L-8900 high speed amino acid analyzer. Data was processed by Excel and analyzed by SAS 9.0 and PCA with The Unscrambler 9.8 procedure. Results showed that concentrations of all tested amino acids were different among the cow, yak, buffalo and goat ($P < 0.01$). Concentration of total AA was found to be yak > buffalo > goat > cow (11024.49, 8271.16, 6325.35, 5688.38). According to Ser (118.60, 171.55, 234.44), Thr (119.39, 181.45, 230.47), Val (203.83, 287.27, 376.91) and Tyr (107.62, 132.26, 172.70) profiles base of the PCA scores and loading plots, cow, buffalo, and yak milk were grouped together, whereas goat milk (the 4 amino acids were 170.45, 176.08, 254.19, 128.09) was in a second group. Buffalo and yak milk showed higher Pro (483.01, 613.23) and Ile (263.96, 321.50) concentrations compared with the cow (Pro 132.50, Ile 230.16) samples, whereas yak (518.21) milk was characterized by a higher concentration of Lys compared with the milk from buffalo (368.53). It was concluded that the 4 specials showed distinct amino acids profiles.

Key Words: milk, species, amino acid

W7 Determination of milk composition using near-infrared transflectance spectrum. L. Ma[1,2], J. Q. Wang*[1], D. P. Bu[1], J. H. Yang[1], J. X. Zhang[1], and J. T. Chen[1], *[1]Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Inner Mongolia Agricultural University, Huhhot, Inner Mongolia, China.*

Near-infrared transmission/reflection spectrum has been used in food and agricultural products test extensively. The objective of this study was to investigate main components in milk using near-infrared transflectance spectrum. Milk samples (n = 150) were collected from one dairy farm, and protein (3.70 ± 0.24%), fat (4.56 ± 0.69%), lactose (5.02 ± 0.14%), total solids (14.09 ± 0.79%) and non-fat solids (9.74 ± 0.27%) in milk were measured by MilkoScan FT 120. Milk transflective spectra ranged from 400 to 2500 nm were collected using NIRS DS2500, with sample 2 mm thick. Data was exported to the Unscrambler 9.8 (CAMO, Oslo, Norway) for multivariable analysis. The same samples were employed for calibration and full cross validation. Regression model of spectroscopy was constructed via partial least squares. The loading plots showed that middle and long wavelength (1300–2500 nm) spectroscopy contributed much to milk components model. Satisfied results of calibration and prediction were obtained in this study, for high determination coefficients (R^2) of calibration and validation for protein, fat, lactose, total solids and non-fat solids above 0.90. Root mean square error (RMSE) of validation suggested better prediction accuracy for milk protein, lactose, and nonfat solids, which were less

than that of fat and total solids. Excellent ratio of prediction to deviation (RPD) value was observed for protein, while RPD for fat, lactose, total solids and non-fat solids were acceptable. It was concluded that near infrared transflectance spectrum would be capable of in milk composition determination.

Table 1. Parameters of milk composition model

			Calibration			Validation			
Milk composition	Pre-treatment	PC	Predicted Y vs. measured X	RMSE	R^2	Predicted Y vs. measured X	RMSE	R^2	RPD
Protein	No	9	Y =0.969x +0.114	0.036	0.98	Y=0.960x +0.148	0.045	0.97	4.97
Fat	No	6	Y =0.916x +0.383	0.177	0.93	Y=0.910x +0.410	0.197	0.92	3.06
Lactose	MSC	12	Y =0.928x +0.362	0.029	0.96	Y=0.911x +0.448	0.042	0.91	3.15
Total solids	SNV	5	Y =0.922x +1.093	0.219	0.92	Y=0.915x +1.188	0.234	0.91	3.41
Nonfat solids	SNV	11	Y =0.940x +0.569	0.067	0.94	Y=0.927x +0.695	0.077	0.92	3.54

Key Words: near-infrared transflectance spectrum, milk composition

W8 Evolution of milk calcium content during the year. C. Hurtaud*[1], M. Johan[1], S. Leurent[2], Y. Gallard[2], and L. Delaby[1], *[1]INRA-Agrocampus Ouest UMR 1348 PEGASE, Saint-Gilles, France, [2]INRA Domaine du Pin-au-Haras, Exmes, France.*

Calcium content is regarded as being relatively stable in cows' milk during lactation. However, results from commercial herds, have suggested that changes in milk calcium (Ca) content can occur. The objective of this experiment was to compare the characteristics of milk (especially milk Ca content) based on low input grass based systems compared with corn silage based systems, across 2 breeds of dairy cows (Holstein, HO vs. Normande, NO).The experiment took place on the INRA experimental farm of Le Pin-au-Haras. Sixty dairy cows were observed from calving to drying off. Two feeding systems were compared. The Intensive system (IS) was designed to maximize individual performance, with a high energy diet (in winter, corn silage with 30% concentrate; in spring, summer and autumn periods, pasture with 4 kg/d of concentrate supplemented with corn silage from July). The Grass system (GS) was designed to decrease inputs (in winter, conserved grass with no concentrate; in spring, summer and autumn, pasture with no concentrate). The experimental design was a continuous design. No significant interaction was detected between feeding system and breed for milk yield and composition. During the whole year, GS treatment reduced milk yield (−5 kg/d), with no significant effect on protein and total Ca contents. The NO cows produced less milk, but with higher protein and total Ca contents. During winter, GS treatment reduced milk yield, protein and total Ca contents. Milk Ca content decreased from January to June and rapidly increased after July irrespective of breed. During May and June, HO milk had a Ca concentration below the French limit of 1.2 g/L of the European health allegation of milk for consumption. There was a significant effect of stage of lactation and month on Ca content. Month included numerous significant factors such as maximum daily temperature, day length and radiance duration. This study clearly showed that both cow genotype and lactation stage affects milk Ca content. However, the lactation stage did not explain all the seasonal variations of milk calcium content observed in this trial.

Key Words: milk, dairy cow, calcium

W9 Quantitative analysis of supercritical carbon dioxide (sc-CO_2) treated β-lactoglobulin tryptic peptides. C. Kembel* and R. Jimenez-Flores, *California Polytechnic State University, San Luis Obispo.*

Whey protein is an abundant source of biologically active peptides that have a diverse set of functional properties. One limitation in the production of novel peptides is the native folding of the proteins secondary and tertiary structure. β-Lactoglobulin is a barreled protein with a hydrophobic core capable of binding other proteins. Due to its abundance in whey, it represents an important source of bioactive peptides. We present a method with the potential for the production of novel bioactive peptides from whey. Supercritical CO_2 is known to change protein conformation due to its hydrophobic properties, high diffusion coefficient, low viscosity, and low surface tension. Because β-Lactoglobulin contains a large hydrophobic core where binding sites are present, sc-CO_2 treatment is likely to expose these hydrophobic sequences. These sequences are normally confined to the interior of the protein away from enzymatic attack under normal conditions. Therefore upon exposure to sc-CO_2, these sequences were shown to be more susceptible to trypsin hydrolysis. This method increases the potential for the production of novel peptides. Minor changes in the temperature of the sc-CO_2 treatment induced subsequent conformational changes resulting in different peptides. Variable conditions (pH, temperature, and pressure) sc-CO_2 was shown to yield unique fingerprints by SDS-PAGE. Capillary electrophoresis was then used to discern the peptide profiles of the sc-CO_2 treated peptides as well as native peptides. Distinct differences in peptide profiles were noted. Subsequent analyses will include HPLC-MS to determine peptide sequences and quantity differences in peptide treatments.

Key Words: supercritical CO_2, whey protein, bioactive peptide

W10 AFM imaging and analysis of phospholipid monolayers. J. Cuthbert*[1], S. Gallier[2], D. Gragson[1], and R. Jimenez-Flores[1], *[1]California Polytechnic State University, San Luis Obispo, [2]Massey University, Palmerston North, New Zealand.*

Membrane structure analysis in biological systems is fundamental for understanding its relationship with function. Membrane analyses still relies on observations of the physical phenomena of its components in model systems. Dairy foods are complex systems that incorporate parts of colloidal properties with emulsions. The emulsion in a dairy system is unique due to the presence of the milk fat globule membrane (MFGM). This membrane is composed of phospholipids and proteins, and it has an important biological function in the initial stages of mammals' lives, and in humans it has an important nutritional role throughout their life. In our work to elucidate the structure/function relationship of the MFGM, we are exploring some structural aspects of its phospholipids. Therefore, in this work we present how the properties of the phospholipid/protein monolayers found in milk fat globules were investigated using atomic force microscopy (AFM) in a model system with phospholipids extracted from raw milk and either β-casein or β-lactoglobulin. Slides of the phospholipid and phospholipid-casein monolayer films were prepared as models from a Langmuir trough. The aim was to determine if the monolayers would form liquid-ordered domains or alternatives. Our observations indicate that this technique distinguishes liquid ordered domains in AC contact mode. In this mode, the cantilever oscillates above the surface. It is gentle enough to image phospholipid monolayers without damage. When the tip approaches the surface, the sample's intermolecular and electrostatic forces change the cantilever's amplitude and phase angle. As the cantilever is affected by surface forces, a piezoelectric scanner adjusts its height. The monolayer

domains were best observed in the height and phase traces where the ridges were salient. Because the monolayer domains were more elastic than the surrounding surface, they can be observed in the phase trace. A typical monolayer region was approximately 2 nm high and showed a change of 4° in the phase trace. We conclude that the AFM is a good technique to measure changes in monolayers that could happen during digestion of lipids.

Key Words: atomic force microscopy, milk fat globule membrane, monolayer

W11 Correlation between solubility and solubility index of high protein milk protein concentrates. H. Patel*[1], P. Salunke[1], and J. Amamcharla[2], *[1]Dairy Science Department, South Dakota State University, Brookings, [2]Animal Sciences and Industry, Kansas State University, Manhattan.*

Solubility of high protein ingredients such as milk protein concentrate (MPC) is an important primary property. Measuring the solubility of MPC is a lengthy and tedious process. Developing a simple, quick, and reliable procedure can save time and efforts. Solubility Index (SI) is a well-established method for the determination of solubility of milk powders. The SI is a good indicator of insoluble constituents of milk powders. However, no reports are available in the literature indicating the use of SI for predicting solubility of MPC. The objective of present study was to find out whether correlations exist between SI and percent solubility of MPC80 under a wide range of reconstitution conditions. Five representative samples of MPC80 with a similar protein (81–82%), lactose and mineral contents were obtained from different countries. Solutions (5% w/w) were prepared by reconstituting MPC at 4 different temperatures (20, 40, 50 and 60°C). During reconstitution, aliquots from each of this solution were withdrawn at different time intervals (2, 10, 20, 30, 45 and 60 min). A total of 120 samples were analyzed in this way. The SI of these samples was determined using a centrifugation method at 700g for 10 min). Percent solubility was determined by the standard gravimetric method. The data were analyzed using PROC REG available in SAS and the correlation coefficient (r^2) between percent solubility and SI was obtained. The results of the present study indicated that there was a strong correlation between the solubility and SI measured at different time and temperature of reconstitution. As the temperature and time of reconstitution increased, there was a significant ($P < 0.05$) increase in the solubility. Consequently, there was a significant ($P < 0.05$) decrease in SI. The r^2 value of 0.94 for different reconstitution temperatures and that of 0.81 for different reconstitution time indicated that SI can be used as a quick and routine method in place of the traditional solubility method for characterizing the solubility of MPCs as it is simple, fast, reliable, and easy to perform.

Key Words: milk protein concentrate (MPC), solubility, solubility index (SI)

W12 Phospholipids from milk help cancer prevention in skin cell culture. L.-A. Nguyen*[1], L. H. Laiho[1], and R. Jiménez-Flores[2], *[1]California Polytechnic State University, Biomedical Engineering Department, San Luis Obispo, [2]Dairy Products Technology Center, San Luis Obispo.*

Milk phospholipids (MPL) have a unique composition due to their biological role of engulfing the milk fat globules as milk is synthesized. This unique combination of MPL has been studied and found to have diverse biological activities or functions. In this study we focused on measuring the protective effect of milk phospholipids on skin cell culture after exposure to UV light. This model system has been used as means to identify skin cancer preventing agents. Our study focused on evaluating the expression of a UV-induced DNA damage marker, cyclin-dependent kinase inhibitor, p21WAF1/CIP1. Our previous work had shown some preliminary histology and MTT tissue viability results, which suggested that MPL act upon skin cells in a protective manner against UV (UV) radiation. Western Blots were used to quantify p21 expression in human keratinocytes in 4 categories of samples: No-UV, UV, UV+MPL, MPL and in HeLa (p21 positive control). In the No-UV samples, cells were not irradiated by UV light. Treatment consisted on exposure to a UV dosage of 10 mJ/cm^2. After UV treatment, the same amount of protein from each sample (determined by BCA assay) was loaded into a 4–12% Bis-Tris SDS-PAGE gel, run under denaturing, non-reducing conditions then blotted and treated with antibodies for the quantitative detection of p21 proteins. Finally, intensities of p21 protein bands were analyzed. Under non-reducing conditions, 3 p21 proteins covalently bonded with each other showed up as 63 KDa molecules on the PVDF membrane. The UV and HeLa samples showed a 2.28 fold, and 1.23 fold increase in p21 expression, respectively, compared with the No-UV samples control. The MPL samples showed a 0.948 fold decrease in p21 compared with the No-UV samples, and the UV+MPL samples showed only a 1.13 fold increase in p21. Less p21 expression in the UV+MPL samples compared with the UV samples suggested that less DNA damage occurred in the samples that were treated with MPL. Conclusion: Milk Phospholipids reduced UV-induced DNA damage in human keratinocytes through incorporation in cell media and could potentially be incorporated as a chemopreventive agent.

Key Words: milk phospholipid, cancer, UV

W13 Reduction of aflatoxin M_1 content during manufacture and storage of Egyptian Domiati cheese. M. Motawee*, *National Organization for Drug Control and Research, Cairo, Egypt.*

Elevated levels of aflatoxin M_1 (AFM_1) in milk and milk products is considered to pose certain hygienic risks for human health. The maximum level of AFM_1 allowable in Egyptian milk is 50 ng/L and while a previous study found the majority of milk was below this level, some milk contained up to 250 ng/L. Domiati cheese is the most popular soft white pickled cheese in Egypt and accounts for 75% of the cheese produced and consumed in Egypt. During manufacture of Domiati cheese from 5% to 14% of salt is added to the milk depending on the season and cheese ripening temperature. The aim was to determine what proportion of initial AFM_1 in milk is retained after manufacture into Domiati cheese and remains during 90 d storage. Milk was inoculated with 1µg/kg AFM_1 then pasteurized at 63°C for 30 min and made into Domiati cheese using salt additions of 6%, 8% and 10% (wt/wt). Cheese making was performed on 3 separate occasions. The AFM_1 levels in milk, cheese and whey were determined using an ELISA test kit. Pasteurization of milk caused ≤ 10% loss of AFM_1. About 60%, 58%, and 56% of total AFM_1 remained in cheese curd made using 6%, 8% and 10% salt respectively, with the residual being lost in the whey. After 2 wk storage at 20°C, all of the cheeses had a 17% reduction in AFM_1 compared with their levels after manufacture. With continued storage through 90 d the losses of AFM_1 were significantly different ($P < 0.05$) with reduction in AFM_1 or 20.5%, 21.4%, 22.0% for cheeses made using 6%, 8% and 10% salt respectively. Thus, including pasteurization of milk, conversion of milk into Domiati cheese and its subsequent storage period for 3 mo produced an overall 32% reduction of AFM_1. In conclusion, as well as avoiding contamination of milk with AFM_1 there is a lower health risk to the population from the presence of AFM_1 in

milk when the milk is pasteurized and converted into Domiati cheese that is then stored for the customary 3 mo.

Key Words: aflatoxin, Domiati cheese, storage

W14 Limited glycerolysis and transesterification reactions to change the fatty acid composition and crystallization properties of butterfat. D. Sanchez-Macias[2,1], A. Laubscher*[1], and R. Jimenez-Flores[1], *[1]California Polytechnic State University, San Luis Obispo, [2]Agroindustrial Engineering Department, Universidad Nacional del Chimborazo. Riobamba, Ecuador.*

Saturated fatty acids in butterfat have been regarded as a nutritional disadvantage in some dairy products. Several different strategies have been tried and tested for the modification of the fatty acid composition of bovine milk. The nature of the rumen forces the cow to produce saturated fatty acids, and bypass techniques have limited results. Enzymatic modification of milk fat has also limits in efficiency since enzymes work only in an aqueous media and therefore only in the interface of emulsions. Fractionation of butterfat based on differential crystallization had in the past some limited success, but no clear difference was obtained by removing crystals formed at relative high temperatures, where saturated fatty acids were assumed to be present in higher concentration. We approached this strategy, by attempting a chemical rearrangement of fatty acids in the triglycerides of milk fat by a limited glycerolysis and transesterification, in which glycerol was used as an intermediary for rearrangement of fatty acids, and limited amounts of oleic acid were added. Glycerolysis and transesterification took place in the same vessels with minimal amount of alcoholic KOH as catalyzer and a temperature of 200°C for 2 h. Resulting combinations of triglycerides from this reaction showed significantly different fatty acid distribution; Control butterfat heated without any catalyzer served as control and reference. The major differences were observed when comparing the crystals separately from the remaining oil fraction. Even in the group without oleic acid, the crystals showed fatty acids increase in 16:0 and 18:0 of 17 and 45% respectively; changes of fatty acid composition on the other tested fractions was even more pronounced. The crystal fractions were drastically different in morphology and color in the treated samples compared with controls. We conclude that there is some technological potential in partial chemical glycerolysis and transesterification to modify the composition of butterfat fractions

Key Words: fatty acid, butterfat, glycerolysis transesterification

W15 The effects of microfluidization on the particle size distribution of liposomal aggregates between whey buttermilk and commercial sweet buttermilk. T. Nguyen* and R. Jimenez-Flores, *California Polytechnic State University, San Luis Obispo.*

Milk-derived ingredients from the production of cheese and butter can be used as vehicles for nutrients. One of the advantages of ingredients from milk that contain milk fat globule components such as phospholipids is that they form emulsions with fat, or liposomes when treated with high shear. Our objective in this work was to measure the effect of shear on regular buttermilk and whey buttermilk. The effects of microfluidization at 2000 psi on the particle size distribution of liposomal aggregates between whey buttermilk and commercial sweet buttermilk at pH 4.6 and 6.8 were compared with whey protein isolate. At pH 4.6, the average aggregate size increased in sweet buttermilk after every one of 3 passes total through the microfluidizer. There was a slight decrease in the average aggregate size of whey buttermilk after the first pass and an increase in the average size for the second and third passes. Similarly, a slight decrease was seen in the average particle size of whey protein isolate after the first 2 passes and an increase in the average size after the third pass. The aggregate size distribution of whey buttermilk resembled that of whey protein isolate at pH 6.8. There was an alternate decrease and increase in the average aggregate size after each pass. In contrast, a slight decrease in average particle size was seen in sweet buttermilk after the first 2 passes and an increase in size after the final pass at pH 6.8. At pH 4.6, whey protein isolate and both buttermilks had a greater number of small particles after microfluidization. In contrast, at pH 6.8, each dairy product had a greater number of larger particles. This could be due to hydrophobic interactions between the aggregates. This study suggests that microfluidization at various pH affects the size distribution of whey buttermilk aggregates or liposome particles so that size can be manipulated and therefore can be utilized as a novel ingredient and in the processing of dairy foods to deliver nutrition.

Key Words: phospholipid, microfluidization, nutrition delivery

W16 Fast and easy screening of whey protein types using a novel portable infrared spectroscopy. T. Wang* and L. Rodriguez-Saona, *The Ohio State University, Columbus.*

Whey proteins are attractive ingredients to the food industry because of their high nutritional value and wide functionality. Whey protein powders are available from different suppliers using various processing methods and conditions, resulting in variability in their macromolecular structure, components levels and thus having an effect on their functionality. There are 3 major types of whey protein including whey protein isolates (WPI), whey protein concentrates (WPC) and whey protein hydrolysates (WPH) providing diverse functionality to food applications. Our objective was to develop a simple and rapid method to differentiate whey protein types by combining a portable infrared spectrometer and pattern recognition analysis. Whey protein powders including WPI (n = 23), WPC (n = 8) and WPH (n = 14) from different suppliers were evaluated. A portable infrared spectroscopy (Cary 630, Agilent Technologies) was used for spectra collection by pressing the whey protein onto an ATR-IR diamond crystal with a pressure clamp. Spectra were analyzed by soft independent modeling of class analogy (SIMCA) for powder classification. SIMCA model showed a strong ability to differentiate whey protein types by forming tight clusters far from each other (interclass distances > 3). Major band responsible for separation was associated with carboxylic acid side chain in amino acids present in whey proteins. Portable IR units enable to quickly assess the quality of the incoming raw material allowing for timely corrective measures during manufacture. Portable systems are simple to use and require minimal or no sample preparation, thus reducing assay time and helping to streamline the analytical procedure so that it is more applicable for field-based screening and higher sample throughput.

Key Words: whey protein, infrared spectroscopy, pattern recognition analysis

W17 Effect of transglutaminase treatment on the functionality of MPC and MCC: Functional properties. P. Salunke*, C. Marella, and L. E. Metzger, *Dairy Science Department, Midwest Dairy Foods Research Center, South Dakota State University, Brookings.*

Milk protein concentrate (MPC) and micellar casein concentrate (MCC) are products manufactured using ultra- and micro-filtration

respectively. Functional properties such as alcohol stability (AS), heat stability (HS), solubility and solubility index (SI) are affected by presence or absence of constituents in MPC and MCC particularly, casein, whey proteins, lactose, and minerals. However, MPC and MCC alone are unable to deliver critical functional properties required in certain products such as high heat stable products, emulsions, and processed cheese products. The use of cross-linking enzymes such as transglutaminase (TGase) has the potential to modify the physical properties of MPC or MCC and may improve their functional properties. The objective of this study was to determine the effect of TGase treatment of MPC and MCC retentates on the functionality of MPC and MCC. Three lots of MCC and MPC retentate were produced using 3 different lots of pasteurized skim milk. Each replicate of retentate was divided into 3 equal portions. One portion of the retentate was treated with TGase at 0.3 units/g of protein, one portion was treated with TGase at 3.0 units/g of protein and one had no TGase addition. All the retentates were incubated for 25 min at 50°C, heat treated at 72°C for 10 min, cooled to 4°C and then spray dried. Various functional properties including AS, HS, solubility and SI at room temperature (RT) and hot water were tested using 5% protein solution of MCC and MPC. MPC samples had significantly ($P \leq 0.05$) higher AS, HS, solubility and significantly ($P \leq 0.05$) lower SI as compared with respective MCC treatments. TGase treatment significantly ($P \leq 0.05$) increased the AS, HS, SI, and significantly ($P \leq 0.05$) decreased the solubility. The study demonstrates that TGase treatment was found to significantly ($P \leq 0.05$) affect and modifythe functionality of MCC and MPC. These TGase treated ingredients can be used in products where whey protein have detrimental effect including high heat stable products, emulsions or processed cheese products.

Key Words: transglutaminase, MPC or MCC, functional properties

W18 Effect of transglutaminase treatment on the functionality of MPC and MCC: Yogurt formulation. P. Salunke*, C. Marella, and L. E. Metzger, *Dairy Science Department, Midwest Dairy Foods Research Center, South Dakota State University, Brookings.*

Milk protein concentrate (MPC) can be used in yogurt formulations to increase the protein content of yogurt. In contrast micellar casein concentrate (MCC) produced using microfiltration has a reduced level of whey protein and has not been utilized in yogurt. The use of transglutaminase (TGase) has the potential to modify the physical properties of MPC or MCC and may improve its functionality in yogurt. The objective of this study was to determine the effect of TGase treatment of MPC and MCC retentates on the functionality of MPC and MCC when they are used in yogurt formulation. Three lots of MCC and MPC retentate were produced using 3 different lots of pasteurized skim milk. Each replicate of retentate was divided into 3 equal portions. One portion of the retentate was treated with TGase at 0.3 units/g of protein, one portion was treated with TGase at 3.0 units/g of protein and one had no TGase addition. All the retentates were incubated for 25 min at 50°C, heat treated at 72°C for 10 min, cooled to 4°C and then spray dried. Each MCC and MPC was then used in a yogurt formulation that was standardized to 8.5% MSNF and 5.75% protein using deproteinized whey powder and distilled water. In each formulation, the MPC or MCC utilized contributed 5% protein. All the ingredients were mixed and were subjected to heat treatment in the rapid visco analyzer (RVA) at constant speed of 150 rpm using a profile where it was heated from 45°C to 93°C over a period of 10 min, held for 6 min at 93°C, and cooled to 45°C in 10 min. After cooling to 45°C, the sample was acidified using glucono-δ-Lactone and mixed thoroughly at 500 rpm for 1 min, incubated at 45°C in water bath for 2.5 h and subsequently stored at 4°C overnight. The yogurt manufactured using MPC had significantly ($P \leq 0.05$) higher RVA-viscosity, water holding capacity (WHC) and syneresis as compared with the MCC samples. In the MCC yogurt samples there was significant ($P \leq 0.05$) decrease in RVA-viscosity, WHC and syneresis as enzyme level increased. TGase treatment was found to significantly ($P \leq 0.05$) affect the functionality of MCC and MPC in yogurt formulations.

Key Words: transglutaminase, MPC or MCC, yogurt functionality

W19 Adiponectin concentrations in cow milk during induced negative energy balance. S. P. Singh*[1], S. Häussler[1], J. J. Gross[2], R. M. Bruckmaier[2], and H. Sauerwein[1], *[1]Institute of Animal Science, Physiology and Hygiene Group, University of Bonn, [2]Veterinary Physiology, Vetsuisse Faculty University of Bern.*

Induced negative energy balance (NEB) in dairy cows decreased milk protein concentration. Fat mobilization during NEB may affect the concentrations of the adipokine adiponectin (Aq) in blood but also in milk. We therefore aimed to investigate the effect of a deliberately induced NEB on Aq concentrations in these body fluids. Multiparous Holstein cows (n = 21) were allocated to either a control (C, n = 10) or restriction (R, n = 11) group after 12 wk of lactation. Feeding in the preceding period and in the C group was according to the recommendations of Society of Nutrition Physiology. In R, an energy deficit was induced of at least 30% of the calculated requirements. Skim milk samples from 2 consecutive milkings each in wk 2, 12 and 17 of lactation (wk 17 = 2nd wk of R or C feeding) and plasma samples from these times were used. Milk protein content was assessed by infrared analyzer and Aq was measured by ELISA (Mielenz et al., 2013, Domest. Anim. Endocrinol.). The intra- and interassay variations were 4.5% and 11.9%. The limit of detection was 0.03 ng/mL. Assay accuracy was determined by linearity of serial samples dilutions. Milk Aq (μg/mL and ng/mg milk protein) were calculated and data (means ± SEM) were analyzed by Mixed Model (SPSS). Milk Aq concentrations (μg/mL) were higher in wk 2 than in wk 12 of lactation (0.88 ± 0.05 vs. 0.47 ± 0.03; $P < 0.001$). Numerically less Aq was observed in milk of R compared with C cows (0.43 ± 0.03 vs. 0.56 ± 0.06; $P > 0.05$); plasma Aq was not different between R and C. Across all animals in wk 12 and 17, milk Aq was correlated with plasma Aq (r = 0.342; $P = 0.026$). Blood Aq during this period was about 70 fold higher than in milk (35.02 ± 1.15 vs. 0.48 ± 0.02). When expressed as per mg of milk protein, Aq concentrations in wk 2 were also higher (1.7 fold) than in wk 12 ($P < 0.001$), and R animals had slightly lower concentrations (−15%, $P > 0.05$) than C cows. Our results indicate a significant decline in milk Aq both per volume and per mg milk protein as lactation advances. The lack of differences between the R and C group indicates that an induced NEB at this stage of lactation does neither affect Aq secretion nor transfer from blood to milk.

Key Words: adiponectin, milk, feed restriction

W20 Effect of transglutaminase treatment on the functionality of MPC and MCC: Imitation mozzarella cheese manufactured in twin screw cooker. P. Salunke*, C. Marella, and L. E. Metzger, *Dairy Science Department, Midwest Dairy Research Center, South Dakota State University, Brookings.*

A critical parameter in dairy based imitation mozzarella cheese (IMC) is the amount of intact casein provided by dairy ingredients in the formulation. From a functionality perspective, rennet casein is the preferred ingredient to provide intact casein in a formulation. However, the use of transglutaminase (TGase) has the potential to modify the physical properties of MPC or MCC and may improve its functionality in IMCs. The objective of this study was to determine the effect of TGase treatment of MPC and MCC retentates on the functionality of MPC and MCC when they are used in IMCs. Three lots of MCC and MPC retentate were produced using 3 different lots of pasteurized skim milk. Each replicate of retentate was divided into 3 equal portions. One portion of the retentate was treated with TGase at 0.3 units/g of protein, one portion was treated with TGase at 3.0 units/g of protein and one had no TGase addition. All the retentates were incubated for 25 min at 50°C, heat treated at 72°C for 10 min, cooled to 10°C and then spray dried. Each MCC and MPC was then used in IMC formulation that was standardized to 21% fat, 1% salt, 48% moisture, and 20% protein. In each formulation, the MPC or MCC utilized contributed all the protein. A preblend of all the ingredients (except lactic acid) was prepared (4.0 kg) in the Blentech twin-screw cooker by mixing at 50 rpm for 20 min at 20°C. The temperature of the preblend was then increased to 74°C over 5 min and held for an additional 4 min maintaining the auger speed of 120 rpm. The IMC formulation using either MCC or MPC treated with the highest TGase level did not form an emulsion. The IMC made from MCC treatments had significantly ($P \leq 0.05$) higher TPA-hardness and stretchability on pizza as compared with their respective MPC treatments. The IMC made from TGase treated MCC and MPC had significantly ($P \leq 0.05$) lower melt area, and significantly ($P \leq 0.05$) higher transition temperature and stretchability as compared with their respective controls. The study demonstrates that TGase treatment modifies the functionality of MCC and MPC in IMC applications.

Key Words: transglutaminase, MPC or MCC, IMC functionality

Ruminant Nutrition:
Fats, Fatty Acids, Oils, and Glycerin Supplementation I

W21 Investigation of microbial diversity in the feces of cattle fed different diets. M. Kim*[1], J. Kim[2], L. Kuehn[1], J. Bono[1], E. Berry[1], N. Kalchayanand[1], H. Freetly[1], A. Benson[2], and J. Wells[1], *[1]USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, [2]University of Nebraska, Lincoln.*

Understanding of the bovine fecal microbiome could contribute to solving issues regarding animal production, cattle health and food safety. The objective of this study was to examine the influence of diet on the fecal microbiome in feedlot cattle. The next-generation pyrosequencing technology was used to investigate fecal microbiomes of 426 cattle fed one of 3 diets: finishing diet (83% dry-rolled corn, 13% corn silage, 4% supplement), late growing diet (66% dry-rolled corn, 26% corn silage, 8% supplement), and early growing diet (70% corn silage and 30% alfalfa haylage). A total of 2,149,008 16S rRNA gene sequences were obtained from 333 cattle with at least 2,000 sequence reads and classified into taxa using the RDP classifier. One-way ANOVA followed by Tukey's test was used to compare the mean abundance of a taxon among the 3 diet groups. *Firmicutes* was the first predominant phylum and accounted for more than 50% of total sequences in all 3 diet groups. *Bacteroidetes* was the second predominant phylum in the finishing and the late growing diet groups, while TM7 was the second predominant phylum in the early growing diet group. The genera *Fecalibacterium*, *Anaerovibrio*, *Prevotella*, *Parabacteroides* and *Pantoea* were significantly more abundant ($P < 0.0001$) in the late growing diet group than in other 2 groups, while the genera *Oscillibacter*, *Turicibacter*, *Coprococcus*, *Clostridium*, *Blautia*, *Lactobacillus* and *Subdoligranulum* were significantly more abundant ($P < 0.0001$) in the finishing diet group than other 2 groups. The abundance of the genera *Sporacetigenium*, *Anaerovorax*, *Propionibacterium* and *Akkermansia* was significantly higher ($P < 0.0001$) in the early growing diet than other 2 diet groups. A principal coordinates analysis of the unweighted UniFrac showed that bovine fecal microbiomes were separated based on diets. The present study indicates that diet has an effect on the fecal microbiome of cattle, particularly between cattle fed forage-rich and grain-rich diets. USDA is an equal opportunity provider and employer.

Key Words: 16S rRNA, microbiome, pyrosequencing

W22 Reproductive performance of beef heifers supplemented with saturated or unsaturated rumen bypass fat. N. M. Long*[1], T. A. Burns[1], S. K. Duckett[1], and D. W. Schafer[2], *[1]Department of Animal and Veterinary Science, Clemson University, Clemson, SC, [2]Department of Animal Science, University of Arizona, Tucson.*

Research on fat feeding to influence reproduction has shifted to feeding fat before and after breeding. Heifers (n = 118) were blocked by age, breed, and BW and pen fed alfalfa hay (4.5 kg/head/d). Heifers were individually fed an isocaloric supplement that contained 90% beet pulp and 10% molasses at 1.0 kg (C) or either 0.5 kg of the C with 0.2 kg of StratG (SG) or EnerGII (EG) fed 5 d/wk. Heifers received treatments for 3 wk before 7 d controlled intravaginal drug release (CIDR) synchronization followed by visual estrus detection. Blood samples were collected 3 times 4 d apart before CIDR insertion. Heifers were AI 12 h after estrus was detected and remained on treatment supplementation regimen for 28 d after CIDR removal. A blood sample was collected at the end of treatment. Pregnancy was determined d 30 post AI via transrectal ultrasonography. Serum progesterone (P4) and leptin were measured by RIA and serum triglycerides and cholesterol was measured by colorimetric procedures. Serum fatty acid (FA) profiles were measured by GLC. Serum lipids and hormones were analyzed using the MIXED model of SAS and binary reproductive data was analyzed using the GLIMMIX procedure. Heifers BW gain during supplementation was similar ($P = 0.35$) between treatment groups (32 ± 2 kg). Percent of heifers cycling (P4 > 0.75 ng/mg in any samples) tended to be less ($P = 0.08$) for SG heifers compared with the other treatments (36 vs 55 and 56%, SG, C and EG). Rates of estrus after PGF2α were similar ($P = 0.19$) between treatments (53, 69, and 77%, C, SG and EQ). AI pregnancy rates of heifers detected in estrus were similar ($P = 0.35$) between treatments (81, 77, and 63%, C, SG and EQ). Serum total and specific FA, cholesterol and triglycerides were different ($P < 0.05$) between treatments at d 21 and 56. Serum leptin was increased ($P < 0.05$) in both SG and EG at d 21 compared with C heifers. At d 56 of treatment, SG had greater ($P < 0.05$) plasma leptin compared with EG with C heifers having further reduced serum leptin concentration. Feeding rumen protected FA led to no changes in reproduction, but changed circulating lipid composition and leptin with differences between fat types.

Key Words: fats, heifer, serum fatty acid

W23 Effect of crude glycerin on carcass and meat characteristics of Nellore bulls. E. H. C. B. van Cleef[1], J. M. B. Ezequiel[2], A. P. D`Aurea[2], J. B. D. Sancanari[2], D. A. V. Silva[2], F. B. O. Scarpino[2], and R. M. P. Pardo*[3], *[1]Kansas State University, Manhattan, [2]São Paulo State University, Jaboticabal, São Paulo, Brazil, [3]Sucre University, Sincelejo, Colombia.*

A study was conducted to determine the effect of crude glycerin on carcass and meat characteristics of Nellore bulls. Thirty animals (277.7 ± 23.8 kg BW) were fed experimental diets for 82 d. Treatments consisted of a control diet containing 30% corn silage, 35% corn grain, 19.2% soybean hulls, 14.6% sunflower meal, and 1.2% supplement, and diets containing 7.5, 15, 22.5 or 30% glycerin (dry matter basis). Crude glycerin replaced corn grain and soybean hulls. Bulls were stratified in a randomized block design, by initial BW, and assigned randomly to 30 individual pens. Over a period of 21 d, bulls were transitioned from diets containing 20% concentrate to their respective 70% concentrate diets, using 4 step-up diets. Cattle were harvested on d 103, carcass data was collected 24 h post chill, and meat was sampled from the 12th rib. Data were analyzed using the MIXED procedure of SAS, with the animal considered as the experimental unit. Contrasts were used to determine the linear and quadratic effects of glycerin, and 0% glycerin × glycerin treatments. HCW (223.6 ± 7.6 kg), DP (53.4 ± 0.6%) LM (64.3 ± 3.3 cm^2), BF (3.8 ± 0.8 mm), carcass pH (6.1 ± 0.1), and commercial cuts weights were not affected ($P > 0.05$) by the addition of crude glycerin to the diets. The estimated body fat was 2.85% greater ($P \leq 0.05$) for treatments with glycerin. There were no difference on meat color (L* = 32.6 ± 2.2; a* = 12.3 ± 0.8; b* = 3.2 ± 0.6), shear force (4.4 ± 0.5 kgf/cm^2), cooking loss (32.4 ± 2.2%), and water-holding capacity (74.4 ± 2.1%), however, the cholesterol content of meat was decreased ($P \leq 0.05$) from 36.8 mg/g (control) to 27.0 mg/g (30% glycerin). Feeding up to 30% crude glycerin to Nellore bulls can increase meat quality, decreasing cholesterol content without depreciating carcass characteristics.

Key Words: biodiesel, carcass, feedlot cattle

W24 Effect of essential oils, monensin, and tylosin on performance and carcass characteristics of finishing heifers. J. S. Schutz*[1], M. L. Hubbert[1], C. J. Redding[1], J. D. Caballero[2], P. J. Guiroy[3], and C. A. Loest[2], *[1]Clayton Livestock Research Center, New Mexico State University, Clayton, [2]Animal and Range Sciences, New Mexico State University, Las Cruces, [3]Cargill Incorporated, Minneapolis, MN.*

Public perception regarding antimicrobial drug use in animal diets has increased investigations of alternative natural plant extracts to modify ruminal fermentation and potentially improve efficiency of feed utilization. This study evaluated the effects of plant extract products containing essential oils (EO) on performance and carcass traits of feedlot heifers fed diets with or without monensin and tylosin. Crossbred yearling heifers (n = 662; initial BW = 324 ± 3 kg) were assigned to 36 pens (18 or 19 heifers/pen) in a randomized complete block design (blocked by BW). Six treatments, in a 2 × 3 factorial arrangement, were finishing diets with (MED) or without (NON-MED) added monensin (300 mg/d) plus tylosin (90 mg/d), and top-dressed with a pellet (230 g/d) containing either plant extract-A (EOA; 300 mg/d active product), plant extract-B (EOB; 250 mg/d active product), or no EO (CON). Statistical analysis used the mixed procedure of SAS and orthogonal contrasts. Antimicrobial drug × EO interactions were not significant ($P > 0.15$). Heifers fed MED diets had similar ($P = 0.21$) ADG (1.48 vs. 1.46 ± 0.02 kg/d), lower ($P < 0.01$) DMI (8.11 vs. 8.29 ± 0.11 kg/d), and greater ($P < 0.01$) G:F ratio (0.183 vs. 0.176 ± 0.001) than heifers fed NON-MED diets during 134 (3 blocks) and 135 (3 blocks) DOF. Carcasses of heifers fed MED diets had lower ($P = 0.04$) marbling scores, and tended to have greater ($P = 0.14$) LM area than those fed NON-MED diets. Heifers receiving EOA and EOB had a tendency for lower ($P = 0.11$) carcass-adjusted ADG, a tendency for greater ($P = 0.12$) DMI from d 0 to 84 (and numerically greater DMI overall), and lower ($P = 0.07$) G:F ratio than those receiving CON. Heifers given EOA had a tendency for more ($P = 0.11$) carcasses to grade choice or better than those receiving CON (51.6% vs. 43.6%). Results indicated that the essential oils evaluated in this study were not as effective as monensin and tylosin for improving feed efficiency. Supplementing feedlot finishing diets with EOA could possibly improve quality grade.

Key Words: essential oil, antimicrobial, beef cattle

W25 Traditional and novel feed additives for beef cattle. F. G. Ribeiro*[1,2], C. C. Coutinho[1,2], D. C. Rivaroli[1,3], A. Cominotte[1,4], E. Rodrigues[1], A. M. Jorge[1], E. A. Filgueiras[5,2], and R. D. Sainz[6,7], *[1]Universidade Estadual de São Paulo, Botucatu, SP, Brazil, [2]CAPES - Coordenação de Aperfeiçoamento de Pessoal de Nível Superior, Brasília, DF, Brazil, [3]CNPq - Conselho Nacional de Desenvolvimento Científico e Tecnológico, Brasília, DF, Brazil, [4]FAPESP - Fundação de Amparo à Pesquisa do Estado de São Paulo, São Paulo, SP, Brazil, [5]Universidade Federal de Goiás, Goiânia, GO, Brazil, [6]Embrapa, Goiânia, GO, Brazil, [7]University of California, Davis.*

Four diets were fed to 64 crossbred heifers (predominantly Angus and Red Angus) for 28 d (adaptation) plus 95 d (experimental). Treatments consisted of: C, Control diet; B, Control diet plus a probiotic + prebiotic premix (Bioformula, 2 g/day); M, Control diet plus Rumensin (120 mg monensin/day);BM, Control diet plus a combination of these 2 additives (Biofórmula + Rumensin). The concentrate:forage of the diet was 25:75 on a dry matter basis. Animals were weighed individually every 28 d after 12 h feed withdrawal. Feed offered was monitored daily, and feed refusals collected and weighed every 2 d. All animal care procedures were conducted according to the regulations of the Brazilian National Council on Control of Animal Experimentation (CONCEA). Performance variables were analyzed using the GLM procedure of Minitab (Minitab, Inc., State College, PA, USA). Body weight data were analyzed by analysis of covariance, with treatment as a main effect, and days on feed as a covariate, with animal nested within treatment included as a random effect to correct for auto-correlation of repeated measures in the same animal. Individual feed intakes were estimated using the methodology of Perry and Fox (1997; J. Anim. Sci. 75:300–307). Estimated feed intakes were similar among treatments (9.91, 9.90, 9.83 and 9.81 kg/day for C, B, M and BM, respectively; $P > 0.10$). However, ADG were greater in animals fed diets containing feed additives relative to controls (1.280, 1.322, 1.319 and 1.397 kg/day for C, B, M and BM, respectively; $P = 0.054$. Likewise, these feed additives improved feed efficiency relative to controls (0.129, 0.134, 0.139 and 0.143 for C, B, M and BM, respectively; $P < 0.001$). We conclude that supplementation with probiotics and prebiotics has potential to improve the performance of beef cattle, and that these effects are additive with those obtained using ionophores.

Key Words: probiotic, ionophore, feedlot

W26 Effect of essential oils (Next Enhance 300) on fermentation characteristics of rumen microbiota in continuous culture. N. F. Johnson*[1], M.C. Westerhold[1], M. S. Kerley[1], W. J. Sexten[1], and T. J. Wistuba[2], *[1]University of Missouri, Columbia, [2]Novus International Inc., St. Charles, MO.*

Antibiotics and ionophores are used to improve feed efficiency by modifying rumen fermentation. Public concern with antibiotic use has increased interest in alternative modifiers. Essential oils are naturally occurring volatile plant compounds reported to improve ruminant N and/or energy utilization via rumen modification. Next Enhance 300 (NE, Novus International Inc.) is a combination of garlic (diallyl disulfide) and cinnamon (cinnamaldehyde) extracts which have demonstrated the ability to modify rumen fermentation. The objective of this experiment was to evaluate fermentation characteristics of rumen microbiota in continuous culture as NE inclusion increased. Treatment levels of 0, 15, 30, 60, 120, and 240 mg/kg DM were added to a corn (60.3%) and DDG (24.3%) diet. Two continuous culture fermentation runs were conducted using dairy cow rumen fluid inoculum. Fermenters were acclimated for 4 d followed by 3 d collections. Fermenter pH was measured and sampled at 0, 4, 8, and 12 h post feeding with daily effluent collection. Run was treated as a block with the experiment analyzed statistically as a randomized complete block. NE did not affect ($P > 0.59$) microbial efficiency, ammonia, pH, or VFA concentrations. Increasing NE inclusion quadratically increased ($P < 0.05$) OM and CP digestibility. Microbial nitrogen flow responded quadratically, but was not significant ($P = 0.29$). Inclusion of NE at 30 and 60 mg/kg DM resulted in maximal OM and CP digestibility. Based on these results, it was concluded that Next Enhance 300 could affect ruminal fermentation of low fiber corn based diets by increasing digestibility and microbial protein flow from the rumen. The next step will be to determine the mechanism by which NE results in greater fermentation activity.

Key Words: essential oil, feed efficiency, rumen fermentation

W27 Supplementation of rumen-protected PUFA in corn-fed beef steers. C. M. Warner*, S. L. Archibeque, T. E. Engle, J. J. Wagner, D. R. Woerner, I. N. Roman-Muniz, and H. Han, *Colorado State University, Fort Collins.*

Rumen bypass fat is commonly added to increase energy intake in dairy cattle. The objective of this study is to examine the addition of rumen bypass fat during finishing period on performance and carcass charac-

teristics in grain fed steers. This study was conducted as a completely randomized block design with 126 cross-bred steer calves (initial BW 529.5kg ± 10.7) randomly assigned to pens with 9 steers/pen (n = 7 pens / treatment). Each pen was randomly assigned to one of 2 treatment groups; the rumen bypass fat treatment (BF) and the control diet (CON). The diets were formulated to be isonitrogenous and isocaloric. Animals were fed twice daily at 110% of the previous daily ad libitum intake. Feed bunks were cleaned and orts were collected weekly. DM content was analyzed and diet samples were collected weekly for proximate analysis. Feedlot performance and carcass characteristics were assessed. Steers fed the CON diet had a greater level of performance for most of the parameters measured. The CON treatment had greater DMI (10.14 kg vs. 8.77 kg; $P < 0.02$) and tended to have greater ADG (1.699 kg vs. 1.469 kg; $P < 0.09$). Hot carcass weight was not significantly different between treatments ($P < 0.19$). Marbling score ($P < 0.04$) and quality grade ($P < 0.02$) were greater for steers fed the CON diet than those fed BF. The L. dorsi area tended to be greater ($P < 0.10$) in steers fed CON (87.60 cm^2) than those fed BF (84.88 cm^2). Gain:feed was slightly increased for the BF treatment group, but was not significant ($P < 0.74$). These data suggest that rumen bypass fat can be added to finishing diets without significant reduction in final body weight, although there may be modest reductions in marbling and quality scores. More research is needed to elucidate the potential mechanism for these reductions.

Key Words: bypass fat, fatty acid composition, PUFA

W28 Effects of extracts of cashew nut shell and castor oil on in vitro ruminal fermentation, gas production kinetics, and methane production. C. T. Marino[2], M. J. Ruiz-Moreno[1], T. M. Schulmeister[1], F. M. Ciriaco*[1], D. D. Henry[1], V. R. G. Mercadante[1], G. C. Lamb[1], and N. DiLorenzo[1], *[1]North Florida Research and Education Center, University of Florida, Marianna, [2]Universidade de São Paulo, FMVZ, Pirassununga, Brazil.*

Extracts of cashew nut shell oil contain anacardic acid, cardol and cardanol, which have been reported to have antimicrobial and antioxidant activity. Ricinoleic acid, one of the fatty acids from castor oil has been reported to have antimicrobial activity similar to that of ionophores. The objective with this study was to evaluate the effects of a mixture of extracts (EX) of cashew nut shell oil and castor oil on in vitro ruminal fermentation parameters, gas production kinetics and methane production. Two incubation substrates (80% concentrate and 100% forage) and 4 doses of EX (0, 40, 80 and 120 mg/L of fermentation fluid) were tested in a randomized complete block design with a 2 × 4 factorial arrangement of treatments. Incubations were conducted for 24 h in 3 d (replicates) with duplicate bottles each day and a 2:1 ratio of buffer:ruminal fluid. Total gas produced was collected in gas sampling bags and analyzed for methane and H_2S concentration. No effect ($P > 0.10$) of EX dose or diet x EX dose interaction was observed for any of the variables. Total gas production and fractional rate of gas production was greater ($P < 0.01$) for concentrate vs. forage substrate. Concentrate substrate had greater ($P < 0.01$) IVDMD (62.0 vs. 56.8%) and methane production (1.91 vs. 1.30 mmol) than forage. Concentration of NH_3-N in the incubation fluid was greater (7.0 vs. 5.2 m*M*; $P < 0.01$) in forage vs. concentrate substrate, likely as a result of N concentration in the incubation substrate. In conclusion, adding up to 120 mg/L of a mixture of extracts from cashew nut shell and castor oil did not affect in vitro ruminal fermentation or methane production in forage- or concentrate-based incubation substrates.

Key Words: fermentation, cashew nut, castor oil

W29 Production performance parameters of early lactation dairy cows fed a diet supplemented with Megalac or a fatty acid prill containing high levels of palmitic acid. E. Block*[1], L. Kung[2], and C. Merrill[2], *[1]Arm & Hammer Animal Nutrition, Princeton, NJ, [2]University of Delaware, Newark.*

Megalac (Church & Dwight Co. Inc., Princeton, NJ) calcium salts of fatty acids (palmitate 45%; oleate 37%; linoleate 6%; stearate < 3%; other fatty acids < 10%) was compared with a high palmitic acid fatty acid prill (Guarantee-palmitate (min) 80%; stearate 4–7%; oleate 8–12%; other fatty acids <5.5%), in an early lactation feeding trial for 10 wk. Thirty multiparous cows (average of 45 DIM) were randomly assigned to 1 of 2 rations identical except for supplemental fat. Fat sources were supplemented on an equal fatty acid basis and were 1.2% of total DM added fatty acids. Daily milk weights and DMI were averaged by week. Milk components were assessed twice weekly, and these were averaged by week. All cows were placed on a common diet for one week before initiation of the trial. All data except body weight was analyzed using a GLM, with treatments as fixed effects, cows as the experimental unit (fixed) and replicated by weeks (random). Because there were no differences in pre-trial performance ($P > 0.05$) between the 2 groups of cows, covariate analysis was not used. Body weights were analyzed as one way ANOVA. Results are provided in the table that follows. Milk and milk component yields were greater with Megalac than with palmitic fatty acid prill. Feed efficiency was also higher with Megalac. Although cows fed palmitic fatty acid prill gained more weight than cows provided with Megalac, weight changes were variable and failed to reach significance. Based on results we conclude that different fatty acids have different digestibilities, absorption and/or differing biological effects post absorption.

Table 1. Daily production parameters and body weight (BW) change over 10 wk for cows fed Megalac or a high palmitic acid fatty acid prill

Variable	Megalac	Palmitic prill	SEM	$P > F$
DMI, kg	28.08	27.89	0.189	0.496
Milk, kg	45.53	42.26	0.435	<0.001
Fat, kg	1.95	1.74	0.026	<0.001
Protein, kg	1.35	1.26	0.013	<0.001
Lactose, kg	2.14	1.98	0.022	<0.001
Solids, kg	5.82	5.37	0.061	<0.001
3.5% FCM, kg	51.32	46.61	0.573	<0.001
FCM/DMI	1.84	1.68	0.020	<0.001
ECM/DMI	1.77	1.62	0.018	<0.001
BW change, kg	24.3	37.3	6.35	0.317

Key Words: fat supplementation of cows, Megalac, palmitic acid

W30 Effect of feeding milk fat rich in conjugated linoleic acid on immune response in BALB/c mice. D. P. Bu, R. C. Zhang, and J. Q. Wang*, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Conjugated linoleic acid (CLA) has been shown to have immunoenhancing properties in mice. We examined the influence of milk fat enriched with CLA on the immune response of BALB/c mice. Seventy 2 BALB/c mice (female 36, 6 mo, BW 18–22g) were housed in 12 cages (n = 6) at constant temperature (22 ± 2°C) and were fed with a normal diets ad libitum, free access to water. Mice were infused either 0.4 mL of saline solution (CK), normal milk fat (P), milk fat enriched with CLA (CLA, contains c9t11CLA of 2.77mg/g fat from cows supplemented with sunflower oil), Immunosuppression induced by cyclophosphamide (Cy), Cy plus normal milk fat

(CyP) or Cy plus milk fat enriched with CLA (CyCLA) through syringe. Mice in CK, P, CLA also received 0.3 mL intraperitoneal saline solution injection while mice in Cy CyFAT, CyFLA received intraperitoneal injection of 0.3 mL cyclophosphamide solution (30 mg/kg BW) every 5 d. Body weight of each mouse was recorded weekly. After 35 d feeding, all mice were killed by cervical dislocation. Spleen and thymus were removed and weighed. The abdomen splenocytes lymphocyte transformation test was conducted by MTT assay to concanavalin A (Con A) (10 mg/L). Compared with CK, weight of spleen and thymus in P and CLA increased ($P < 0.05$). However, mice induced with cyclophosphamide decreased spleen and thymus weight ($P < 0.05$). Ratios of spleen and thymus weight to body weight were not different among treatments. Mice infused with milk fat had greater lymphocyte transformation in response to Con A ($P < 0.05$) than those in control. ConA index were 1.56^{c}, $.98^{b}$, 2.71^{a} in CK, P, CLA and 1.30^{c}, 1.70^{b}, 2.06^{a} in Cy, CyP, CyCLA, respectively. Our results suggest that milk fat enriched with CLA improves some immune responses.

Key Words: milk fat, CLA, immune response

W31 Does supplementing essential fatty acids in the late gestation and the preweaning periods influence future productivity of Holstein heifers? M. Garcia*, L. F. Greco, W. W. Thatcher, J. E. P. Santos, and C. R. Staples, *University of Florida, Gainesville.*

Information on the effect of feeding of long-chain fatty acids (LCFA) on future offspring productivity is lacking. Holstein cows (n = 96) were fed (1) no fat supplement (control; 2.3% dietary fat), (2) hydrogenated LCFA (SFA, Energy Booster 100, Milk Specialties, Eden Prairie, MN; 1.7% of dietary DM), or (3) Ca salts of LCFA containing essential LCFA (EFA; Megalac-R, Arm and Hammer Animal Nutrition, Princeton, NJ; 2.0% of dietary DM) from dry-off to calving. Heifers (n = 56) born from these cows were fed a milk replacer (MR) of low linoleic acid (LLA. 0.56% LA, DM basis) or high LA (HLA, 1.78% LA, DM basis) during the first 60 d of life. A single grain mix was offered between 31 and 60 d of life. Performance of replacement heifers that went on to complete at least 290 DIM (n = 33) was evaluated. Diets did not affect culling rate. Body weight at birth was not influenced by dam diet but ADG for the first 60 d of life was greater for heifers born from dams fed SFA vs. EFA (0.45, 0.48, and 0.42 kg/d for heifers born from control, SFA-, and EFA-fed dams, respectively). Sixty-day intake of LA averaged 6.2 and 12.1 g/d for LLA and HLA heifers, respectively. Type of MR did not influence ADG (0.45 vs. 0.45 kg/d) during the first 60 d of life. After weaning and during the first lactation, heifers were fed diets formulated to meet nutritional requirements. Heifers born from dams supplemented with either fat source (control vs. (SFA + EFA)), tended to have a greater number of AI at first conception (2.6 vs. 1.7, $P = 0.06$) and were older at first calving (24.2 vs. 22.9 mo, $P = 0.02$). Heifers born from dams fed fat prepartum produced more ($P = 0.02$) mature equivalent milk during their first lactation (10,605 ± [CS1] 458, 11,745 ± 486, and 12,559 ± 568 kg for heifers born from control (n = 13), SFA- (n = 11), and EFA-fed dams (n = 9), respectively). Heifers fed HLA MR did not produce more milk than those fed LLA MR (12,011 ± 423 vs. 11,262 ± 403 kg). Fat supplementation during the last 2 mo of pregnancy can "program" calves in utero to produce more milk during their first lactation.
[CS1]Special key strokes

Key Words: heifer, fatty acid, fetal programming

W32 Performance and health responses of dairy calves offered different milk replacer allowances. A. Bach*[1,2], M. Terré[2], and A. Pinto[2], *[1]ICREA, Institut de Recerca i Estudis Avançats, Barcelona, Spain, [2]Department of Ruminant Production, IRTA, Caldes de Montbui, Spain.*

Eighty female Holstein calves (12 ± 4 d old and 41.7 ± 4.3 kg of BW) were blocked by age and assigned to either a maximum of 6 L/d daily milk replacer (MR) allowance (LMR) or a 8 L/d (HMR). Calves were kept individually until 52 d of age and then moved into pens forming groups of 10. Al calves had ad libitum access to a mash starter feed (20.4% CP, 18.5% NDF). Calves in the LMR group received 6 L of MR/d in 3 separate doses whereas calves in the HMR received 8 L of MR/d also distributed in 3 separate feedings. At 52 d of age, calves were moved to pens and pre-weaned by offering 2 L of the same MR/calf twice daily in a trough until the age of 59 d, when MR was further reduced to a single dose of 2 L until the age of 73 d when all calves were weaned. Individual starter feed and MR consumption was recorded on a daily basis until 52 d of age, and on a group-basis until weaning time. Body weight was measured at the beginning of the study and at 52 (pre-weaning), 73 (weaning), 110, 160, and 228 d of age. Data from entrance until pre-weaning were analyzed using an ANOVA (n = 40). The data from pre-weaning to completion of study were analyzed using a 2-level mixed-effects model that accounted for the dependence of calves within pen (n = 4). Solid feed consumption was greater ($P < 0.01$) in LMR (821 ± 42.1 g/d) than in HMR calves (462 ± 42.1 g/d) between 42 and 52 d of age (pre-weaning). Solid feed consumption increased, and LMR showed a more ($P < 0.001$) marked increase than HMR calves. However, HMR calves grew faster ($P < 0.05$) than LMR calves (805 vs. 703 ± 30.7 g/d, respectively) until pre-weaning time, but from pre-weaning to weaning, LMR calves grew more ($P < 0.05$) than HMR calves (977 vs. 857 ± 30.7 g/d, respectively). No differences in feed efficiency and incidence of disease were observed between treatments. It is concluded that before pre-weaning, HMR calves grow more than LMR calves, but between pre-weaning and weaning, LMR grow more than HMR calves overcoming the difference in BW at pre-weaning. As a result, there are no differences in BW at weaning and at 228 d of life and no differences in incidence of disease.

Key Words: efficiency, intake, starter

W33 Consequences of essential oils (cinnamaldehyde and garlic oil) on rumen fermentation and performance of lactating dairy cattle. M. Blanch*[1], A. Viso[1], and A. Bach[2,3], *[1]Novus International Inc., St Charles, MO, [2]ICREA, Barcelona, Spain, [3]Department of Ruminant Production, IRTA, Caldes de Montbui, Spain.*

The objective of this study was to determine the effect of Next Enhance 300 (NE300; cinnamaldehyde and garlic oil encapsulated product) on rumen fermentation and milk production of dairy cows. Sixteen lactating dairy cows (8 rumen-cannulated) participated in a switch-back design with three 4-wk periods and 2 treatments: control (unsupplemented) and NE300 (300 mg NE300/cow/d). Cows were housed in 2 different pens (blocked for parity, DIM, and level of milk production) and received the same TMR diet (16.0% CP, 31.4% NDF). Individual milk production and feed intake were collected throughout the study. All cows were sampled for milk components (fat, protein, lactose, urea, and SCC) on d 0, d 7, d 14, d 21, d 27, and d 28. Cannulated animals were used to collect rumen fluid to determine VFA and ammonia-N concentrations and monitor rumen pH using indwelling pH probes for 3 consecutive days within period. On d 28, rumen samples were collected at 0, 2, 4, 6, and 8 h after the morning feeding. In addition, cows were blood-sampled to determine glucose and insulin concentrations on d 0, d 7, d 14, d 21, and d 28 at 4 h after the morning feeding. Data were analyzed using a mixed-effects model with time entering the model as a repeated measure using each cow within period and treatment as subject. Period and sequence had no effect on any dependent variable measured. In terms of milk yield, there was a significant triple interaction ($P < 0.05$) between treatment, parity, and days on treatment; basically, after 15 d on treatment, multiparous cows

on NE300 produced more milk (approximately 3 kg/d) than multiparous cows on control. Overall feed efficiency was numerically greater (P = 0.11) in NE300 than in control cows (1.46 and 1.33, respectively). In general, blood and rumen parameters were not affected by treatments. Results of this study indicate that NE300 could be an alternative to increase milk yield and feed efficiency in lactating dairy cows.

Key Words: essential oil, dairy cow

W34 Milk fatty acid profile in dairy cows fed with fatty acids unsaturated sources. R. V. Barletta*[1], J. E. Freitas Jr.[1], M. D. S. Oliveira[2], R. Gardinal[1], V. G. C. Lacuna[1], V. P. Bettero[2], B. C. Benevento[1], B. C. Venturelli[1], E. Ferreira de Jesus[2], G. D. Calomeni[1], J. R. Gandra[1], and F. P. Rennó[1], *[1]University of São Paulo, São Paulo, SP, Brazil, [2]University Jlio de Mesquita, Jaboticabal, SP, Brazil.*

The aim of this study was to evaluate the milk fatty acid profile in dairy cows supplemented with unsaturated fatty acids sources. Eight Holstein cows in the mid lactation (80 ± 20 d in milk; mean SD) cannulated in the rumen and abomasums (580 ± 20 kg of weight; mean ± SD) with milk yield of 25 kg/d were assigned randomly into two 4 × 4 Latin squares, fed the following diets: (1) control (C); (2) refined soybean oil (SO) (inclusion of 3% in the total dry matter); (3) whole soybean raw (WS) (inclusion of 16% in the total dry matter); and (4) calcium salts of unsaturated fatty acids (CSFA) (inclusion of 3% in the total dry matter). Milk yield and the dry matter intake were measured daily throughout the experimental period. The milk samples used for evaluating fatty acids profile were obtained at the 16th day of each experimental period, each sample coming from the 2 daily milkings, and were quantified by gas chromatography (Shimadzu GC 2010). Data were analyzed using PROC MIXED of SAS 9.1 according with the orthogonal contrasts (C vs. SO + WS + CSFA), (SO vs. WS + CSFA) and (WS vs. CSFA). No effect of sources of fat in the diets on fatty acid concentrations of short, medium and long chain, varying the carbon number of 6 to 18, total C18 saturated, fully unsaturated C18, and total of saturated and unsaturated (P < 0.05). The concentrations of the isomers C18: 1 *trans*-11 (vaccenic acid), CLA *cis*-9,*trans*-11 CLA and *trans*-10,*cis*-12 were not altered by the experimental diets. No effect was observed in the fat sources used in this study on the profile of fatty acids in milk.

Key Words: linoleic acid, abomasum, whole soybean

W35 Incorporation of n-6 and n-3 fatty acids into plasma lipid fractions of lactating cows: acute effect of abomasal infusions of linoleic and linolenic acids. L. C. Nagengast*, C. L. Preseault, J. C. Ploetz, C. M. Klein, and A. L. Lock, *Michigan State University, East Lansing.*

The effect of abomasal infusions of linoleic (18:2) and linolenic (18:3) acids on the concentration of n-6 and n-3 fatty acids (FA) in plasma lipid fractions over a 24-h period were evaluated in a repeated measures design. Six rumen-fistulated Holstein cows (252 ± 33 DIM and 44 ± 6 kg milk/d) were randomly assigned to 1 of 2 FA treatments. Treatments were abomasal infusions (67 g/d of total FA) of (1) n-6 FA blend (N6) providing 43 g/d 18:2 and 8 g/d of 18:3; or (2) n-3 FA blend (N3) providing 43 g/d 18:3 and 8 g/d 18:2. FA were provided by infusion at 6 h intervals over 24 h. Blood samples were collected on d −2, d −1, and 0 h before the first infusion and 1, 3, 6, 12, and 24 h after initiation of infusions. FA concentration of plasma phospholipids (PL), cholesterol esters (CE), triglycerides (TG), and NEFA was determined. Data were analyzed using PROC MIXED in SAS with hour as the repeated measure. Total FA in each fraction was not altered by treatment. There were marked differences in the FA composition of the individual plasma fractions and in the distribution of n-6 and n-3 FA among fractions. N3 increased the concentration of 18:3 and total n-3 FA in TG, NEFA, and PL (P < 0.01). In TG and NEFA the concentration of 18:3 was highest at 3 h with a 126 and 76% increase compared with N6, respectively (P < 0.001). In PL, 18:3 concentrations started to increase at 3 h, and continued to increase to 24 h when it was 175% higher compared with N6 (P < 0.001). There was a trend for N3 to increase the concentration of 18:3 in CE (P = 0.08), which was 23% higher compared with N6 at 24 h (P < 0.001). Treatment did not affect the concentration of 18:2 or total n-6 FA in TG, NEFA, or CE (P > 0.20), with a trend for N6 to slightly increase the concentration of 18:2 in PL (P = 0.09). Results demonstrate that within 24 h of abomasally infusing 18:3 the concentration of n-3 FA in plasma TG, NEFA, and PL was increased; however, no such increases were observed for n-6 FA in these fractions with 18:2 infusion over a 24-h timeframe.

Key Words: dairy cow, plasma lipid, polyunsaturated fatty acid

W36 Performance, intestinal modulation and blood parameters of calves supplemented with an essential oils blend. F. H. R. Santos[1,2], M. R. Paula*[1,4], D. Lezier[1,3], J. T. Silva[1,3], G. Santos[1,3], and C. M. M. Bittar[1,3], *[1]ESALQ/USP, Piracicaba, Sao Paulo, Brazil, [2]Fapesp, Sao Paulo, Sao Paulo, Brazil, [3]CNPq, Brasilia, DF, Brazil, [4]Capes, Brasilia, DF, Brazil.*

The objective was to evaluate the use of an essential oils blend (EO) via milk-replacer or starter concentrate, with regard to improvements in overall performance and occurrence of diarrhea, as well as intestinal microbiota and blood parameters of calves until 10 weeks of age. The blend of essential oils (Activio Grasp) consisted of cinnamon essential oil, rosemary, oregano and pepper extract. Twenty-seven calves from 1 to 4 d of age were distributed in a randomized block in the following treatments: Control = No EO; MR = 400 mg/kg of EO in milk replacer; and MRS = 200 mg/kg of EO in milk replacer and 200 mg/kg of EO in concentrate starter. Animals were individually housed, received 6 L of milk-replacer/d (20:16; Sprayfo Violeta, Sloten do Brasil Ltda) in 2 meals, and had water and starter concentrate (18% CP; 80% TDN) free-choice. Fecal scores and starter intake were evaluated daily. From the second week until the 10th week of life blood parameters were determined from weekly drawn blood samples. Fecal samples were collected weekly for enterobacteria enumeration. Treatments comparisons, as well as, orthogonal contrast (control vs. MR+MRS) show that feeding EO in milk replacer or starter concentrate did not affect (P > 0.05) performance, blood parameters or intestinal modulation (Table 1).

Table 1. Performance, fecal score and blood parameters of calves supplemented with EO

	Treatment[1]				P <	
	C	MR	MRS	EPM	T	C vs. OE
Starter intake, g/d	589.10	545.70	450.93	55.9	0.205	0.235
Live weight, kg	50.68	43.32	46.61	1.5	0.179	0.185
Daily gain, g	395.5	398.1	378.3	36.1	0.908	0.873
Fecal score	1.8	1.7	1.8	0.09	0.527	0.443
Hematocrit, %	20.2	19.9	21.0	0.62	0.395	0.450
Total protein, g/dL	7.45	6.79	6.90	0.40	0.442	0.362
Glucose, mg/dL	107.21	107.21	102.93	6.06	0.883	0.747
BHBA, mmol/L	0.14	0.14	0.19	0.02	0.925	0.739
Enterobacteria, log cfu/g feces	4.5	4.5	4.3	0.24	0.652	0.873

[1]C = control; MR = 400 mg/kg of EO in milk replacer; MRS = 200 mg/kg of EO in milk replacer and 200 mg/kg of EO in concentrate starter; T = treatment effect; C vs. OE = orthogonal contrast control vs. MR+MRS.

Key Words: diarrhea, enterobacteria, hematocrit

W37 Glycerol to improve alfalfa utilization: Effects on in vitro gas production and microbial protein synthesis. Á. R. Alfonso Ávila*[1,2], É. Charbonneau[2], C. Lafrenière[1], and R. Berthiaume[3], *[1]Agriculture and Agri-Food Canada, Sherbrooke, Qc, Canada, [2]Département des Sciences Animales, Université Laval, Québec, Qc, Canada, [3]Valacta, Ste-Anne-de-Bellevue, Qc, Canada.*

The increased production of biodiesel in recent years has renewed the interest for the use of glycerol as an energy source in livestock diets. However, when it comes to assessing glycerol in association with forages, data are scarce. The objective of this project is to determine if interactions between glycerol and forages do exist. A 2 × 3 factorial design which consisted of 2 non-structural carbohydrate (NSC) concentrations in alfalfa (high [HNSC] or low [LNSC]) and 3 glycerol treatments (control, 15% crude glycerol [CG] and 15% pure glycerol [PG]), plus one additional treatment (AT: LNSC with 5% sucrose + 5% starch) were evaluated. Five pre-planned contrasts were tested using the 7 treatments: 1) HNSC vs. LNSC alfalfa; 2) with vs. without glycerol; 3) interaction alfalfa and glycerol; 4) CG vs. PG and 5) AT vs. HNSC. Last contrast verified if the addition of exogenous sugars to LNSC had the same effects as feeding HNSC alfalfa. Using in vitro 24-h batch culture with rumen fluid, incubations were performed in triplicates and measured gas production each 10 min for a total of 24 h, whereas ammonia, pH, volatile fatty acids, microbial N (MN) and microbial mass (MM), in vitro DM and NDF, and in vitro true digestibility (IVTD) were determined after 24 h. Statistical differences were declared at $P \leq 0.05$. A decrease in the acetate:propionate ratio was observed with HNSC in comparison to LNSC (2.87 vs. 3.27) and with the addition of glycerol vs. no glycerol (2.78 vs. 3.65). No interaction was observed between alfalfa type and glycerol. Glycerol had no effect on IVTD. Reductions in MM (185.5 vs. 240.5 mg/g DM) and MN production (16.8 vs. 25.8 mg/g of OM apparently digested) were observed with CG in comparison to PG. Also CG tended to produce more CH_4 after 24 h, which agrees with the larger acetic acid production found for CG in comparison to PG. The AT had lower microbial protein synthesis and propionic acid production in relation to HNSC. Although no effect was observed for the degradation and metabolism of alfalfa when using glycerol, results clearly show that the rumen does not respond as well to the addition of CG vs. PG.

Key Words: forage, glycerol

W38 Effect of feeding reduced fat dried distillers grains with solubles on lactation performance of Holstein cows. E. Castillo-Lopez*[1], K. M. Algya[1], T. J. Klopfenstein[1], D. Hostetler[1], K. Karges[2], S. C. Fernando[1], and P. J. Kononoff[1], *[1]University of Nebraska-Lincoln, Lincoln, [2]Dakota Gold Research Association, Sioux Falls, SD.*

The objective of this experiment was to evaluate the effect of feeding reduced fat dried distillers grains with solubles (RFDG) on milk production and milk composition. Twelve multiparous lactating Holstein cows (mean and SD, 89 ± 11 DIM and 674 ± 68.2 kg BW) were randomly assigned in 4 × 4 Latin squares over 21-d periods. Treatments (DM basis) were (1) CONTROL, 0% RFDG; (2) 10% RFDG; (3) 20% RFDG; and (4) 30% RFDG. Cows were milked twice daily at 0730 and 1930 h. Milk production was recorded daily and milk samples were collected during the AM and PM milkings of d 19, 20 and 21 of each period for analysis of milk components. Cows were fed once daily at 0930 to allow for approximately 5% refusals and were allowed access to feed at all times except during milking. Total DMI increased linearly ($P < 0.01$) with the inclusion of RFDG, with estimates of 25.0, 23.8, 25.9 and 27.9 ± 1.38 kg/d for CONTROL, 10, 20 and 30% RFDG, respectively. Milk yield was not affected ($P = 0.78$) by increasing levels of RFDG and averaged 34.0 ± 1.29 kg/d. The percent of milk protein tended ($P = 0.07$) to increase with RFDG inclusion with estimates of 3.08, 3.18, 3.15, and 3.19 ± 0.06% for CONTROL, 10, 20 and 30% RFDG treatments, respectively. The yield of milk protein, however, was similar ($P = 0.23$) across treatments with an average of 1.05 ± 0.04 kg/d. The percent ($P = 0.66$) and the yield ($P = 0.53$) of milk fat were not affected by treatment and averaged 3.66 ± 0.09% and 1.24 ± 0.05 kg/d across treatments, respectively. Results of this experiment indicate that dairy rations can be formulated to include up to 30% RFDG while maintaining lactation performance, demonstrating that RFDG is an effective alternative energy and protein feed source for the dairy industry.

Key Words: by-product, dairy, lactation

W39 Use of crude glycerin for dairy cows. M. I. Marcondes*[1], T. R. Pereira[1], M. Valverde da Silva[2], T. E. da Silva[1], A. S. Trece[1], and W. L. Cardoso[1], *[1]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil, [2]Master Alimentos LTDA, Rio Pomba, Minas Gerais, Brazil.*

The current concern about global warming, and the increasing share of biodiesel in the global energy matrix have increased interest in cultivation and processing of oil seeds. Therefore, this study aimed to evaluate the inclusion of crude glycerin replacing corn grain for medium-low production dairy cows. Twelve Holstein cows were distributed into three 4 × 4 Latin squares, according to milk production. Animals were fed 70% corn silage in dry matter basis, plus concentrate. Corn was replaced in the concentrate by a mixture of crude glycerin and a protein corn co-product called Mazoferm, in the proportion of 0, 33, 66, and 100% in dry matter basis, and those represented inclusions of 0, 4, 8, and 12% of crude glycerin in the diets (%DM). Dry matter and nutrient intake were evaluated, as well as their digestibilities. Milk production and composition were also evaluated. The statistical analysis were carried out using proc MIXED (SAS) with 10% of probability for type I error. The inclusion of glycerin did not affected ($P > 0.10$) DM, NDF and TDN intakes. DM and NDF digestibilities were also not affected by glycerin inclusion ($P > 0.10$). Intake and digestibility of crude protein (CP) have decreased linearly ($P < 0.10$). Ether extract and non-fiber carbohydrate intake have increased linearly ($P < 0.10$). Milk production (MP) and MP corrected for 4% fat (PL4G) were not affected by diets ($P > 0.10$). There was also no significant diet effect ($P > 0.10$) on milk composition (fat, protein, lactose, total solids and somatic cell score). Serum levels (HDL, LDL, VLDL, triglycerides, and glucose) have not been affected significantly by glycerin in the diet ($P > 0.10$), apart from total cholesterol, which decreased linearly with the increasing inclusion of crude glycerin ($P = 0.091$). Crude glycerin can totally replace corn grain ground in diets for cows producing 15 kg of milk.

Key Words: digestibility, intake, milk

W40 Performance, digestion, milk fatty acids, and plasma amino acids in response to the supplementation of methionine and plant extracts to dairy cows. G. G. S. Salvati[1], N. N. Morais Junior[1], F. C. F. Lopes[3], R. A. N. Pereira[2], and M. N. Pereira*[1], *[1]Universidade Federal de Lavras, Lavras, MG, Brazil, [2]Empresa de Pesquisa Agropecuária de Minas Gerais, Lavras, MG, Brazil, [3]Empresa Brasileira de Pesquisa Agropecuária, Juiz de Fora, MG, Brazil.*

Rumen microbial yield and PUN were reduced when 2-hydroxy-4-methylthio butanoic acid isopropyl ester (HMBi, MetaSmart, Adisseo) was added to 15.8% CP, soybean based diets. A mixture of cardol, cardanol (phenolic from the cashew nutshell) and ricinoleic acid (C18:1 c9 hydroxylated at C12 from castor oil) (Essential, Oligobasics) may

affect rumen fermentation. The response of lactating cows to HMBi (35g/d), associated to Essential (10g/d), was evaluated. Twenty-eight Holsteins (211 ± 103 DIM) were fed a common diet for 14d and then a treatment for 29d, in a covariate adjusted randomized block design. Response was evaluated on the last 7d. Treatments were a 2x2 factorial arrangement of the 2 factors, orally dosed to each cow twice per day. Diets had 17% soybean meal, 5.8% raw soybeans, and 18.3% CP. Milk yield did not differ (30.5kg/d, $P > 0.64$), similarly to solids yield, DMI, and total tract digestibility ($P > 0.25$). Milk protein was increased from 3.25% to 3.35% by HMBi ($P = 0.03$). Methionine and histidine as a % of plasma amino acids were increased by HMBi without Essential ($P < 0.04$ for interaction) and Essential decreased isoleucine ($P = 0.03$). Essential without HMBi reduced C15:0 anteiso as a % of milk FA ($P = 0.05$ for interaction) and as a % of odd and branched chain FA (OBCFA) ($P = 0.03$ for interaction). Essential decreased C17:0 iso as a % of FA ($P = 0.02$) and the summations of C15:0 iso + C17:0 iso ($P < 0.01$) and of C15:0 anteiso + C17:0 anteiso ($P = 0.02$). HMBi also reduced C15:0 iso + C17:0 iso as a % of FA ($P = 0.04$). Although OBCFA profile of milk fat indicated a depression in rumen microbes synthesis in response to both HMBi and Essential, the daily excretion of urinary allantoin was similar ($P > 0.70$). HMBi reduced the mean PUN along the day from 18.2 to 15.6mg/dL ($P = 0.03$), markedly at sampling times 0, 1, 2, 3, and 6 h post-feeding, and ruminal ammonia content 12 h post-feeding ($P < 0.01$). HMBi increased milk protein content and decreased PUN, while plant extracts did not induce detectable animal response.

Key Words: essential oil, methionine, odd- and branched-chain fatty acids

W41 Sources of rumen protected fat supplementation on milk yield and composition and ruminal parameters of dairy cows grazing a tropical pasture. F. Batistel*[1], J. De Souza[1], K. C. Welter[2], M. M.V. Silva[1], A. V. Pires[1], V. N. Gouvea[2], D. F. A. Costa[1], and F. A. P. Santos[1], *[1]University of São Paulo, Piracicaba, SP, Brazil, [2]University of São Paulo, Pirassununga, SP, Brazil.*

The objective of this experiment was to investigate the effects of supplementation of lactating cows grazing a tropical pasture with diets containing calcium salts of palm oil (CSPO) or calcium salts of soybean oil (CSSO) on ruminal fermentation and milk production . Five rumen-cannulated cows (90 ± 12 DIM) were used in a 5x5 Latin square and subjected to the following treatments: a) control (no fat); b) 400 g CSPO cow^{-1} d^{-1}; c) 700 g CSPO cow^{-1} d^{-1}; d) 400 g CSSO cow^{-1} d^{-1}; and e) 700 g CSSO cow^{-1} d^{-1}. Treatment periods were 24 d in length. Cows grazed paddocks of *Pennisetum purpureum* and received 8 kg cow^{-1} d^{-1} (DM) of concentrate twice daily. Milk yield was measured every 2 d and milk composition was analyzed every 6 d. Rumen fluid samples were collected on d 22 at 0, 1, 2, 4, 6, 8, 12, 18 and 24 h after feeding concentrate in the morning and analyzed for pH and VFA. Data were analyzed as repeated measures using a mixed model with animal and period as random effects. Both levels of CSPO increased milk yield (17.7 kg d^{-1}). The use of 700 g CSSO decreased milk production (15.9 kg d^{-1}) compared with control and 400 g CSSO (16.7 and 17.1 kg d^{-1}, respectively). Fat supplementation did not affect milk protein, milk casein and milk lactose concentrations. The CSSO reduced milk fat concentration and yield. Addition of 700 g d^{-1} of CSSO decreased milk fat yield at 22% in comparison to control (0.48 vs. 0.62 kg d^{-1}). Both CSPO levels increased milk fat, protein and lactose yield when compared with control and CSSO. Ruminal pH was not affected by fat supplementation. Acetate and butyrate concentrations were higher for 400 g CSPO than 700 g CSSO (70.5 vs. 65.9 mmol ml^{-1} and 13.1 vs. 12.6 mmol ml^{-1}). In addition, valerate and isobutyrate were higher for 400 g CSPO than for 400 g and 700 g of CSSO (1.35 vs. 1.04; 0.98 and 1.30 vs. 1.04; 1.06 mmol ml^{-1}). The decreased concentration of branched-chain fatty acids suggests that microbial growth was affected negatively by CSSO supplementation. Dairy cows grazing tropical pasture supplemented with fat can have an increased milk yield depending of level and source of fat.

Key Words: palm oil, soybean oil, milk

W42 Effect of a live-yeast-based product on colostrum quality and milk yield in first month of lactation on a private dairy farm. C. Julien*[1,2], A. Fernandez[3], and J. P. Marden[3], *[1]INRA, UMR1289 TANDEM, Tissus Animaux Nutrition Digestion Ecosystème et Métabolisme, Castanet-Tolosan, France, [2]Université de Toulouse, INPT ENSAT, INP-ENVT, UMR1289 TANDEM, Castanet-Tolosan, France, [3]Lesaffre Feed Additives, Marcq-en-Baroeul, France.*

The objectives were to (i) evaluate the effect of a live-yeast-based product supplementation during dry period of dairy cows on colostrum quality and milk yield (ii) test the on-farm use of Brix refractometers (Optical-OBR and Digital-DBR) instead of colostrometer (CLM). Fifty Holstein dairy cows of a private farm (Sepx, France) were involved in the trial: 16 cows calving between December 2011 and February 2012 were used as control (CTRL) and the next 34 cows calving between March and September 2012 (YST) received 15 g/d of a mix of live yeast and yeast wall cells (Lesaffre Feed Additives, France) from dry to the calving. Two samples of colostrum were taken at first milking: one was measured within 1h of collection with both CLM and OBR by the farmer. The other sample was frozen for subsequent measurement by DBR (MA871, Milwaukee, WI) taken as reference. Data were analyzed using R.14.1 software with a linear model including the effects of rank of lactation, DIM at first control and treatment. Optical Brix measured on fresh colostrums on-farm and digital Brix measured on thawed colostrums were highly correlated ($R^2 = 0.89$, $P < 0.001$, n = 44). It showed clearly that on-farm measurement with OBR on fresh colostrums is as accurate as lab measurement with DBR on frozen colostrums. On the contrary, IgG content evaluated with CLM and DBR presented a correlation of $R^2 = 0.47$ ($P < 0.001$, n = 44) highlighting a less accurate on-farm assessment of colostrum quality perhaps due to the temperature non-sensitivity of CLM. Supplementation of dry dairy cows with live-yeast-based product did not alter colostrum quality. However, it tended to improved milk yield ($P = 0.13$) and protein yield ($P = 0.096$) measured at first control in the first month of lactation: +15% and +13%, respectively. To conclude, supplementation of cows during dry period with the live-yeast-based product seems not to alter colostrum quality but tended to improve milk and protein yields in first month of lactation. Also, colostrum quality can be easily and more accurately assessed by dairy farmers on-farm by means of a Brix refractometer than by a colostrometer.

Key Words: dairy cow, colostrum, live yeast

W43 Sugar cane silage additive for high production dairy cows. B. T. C. Silveira, M. I. Marcondes, K. G. Ribeiro*, O. G. Pereira, M. G. F. Teixeira, and L. L. Cardoso, *Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil.*

Sugar cane silage production process can be an alternative to reduce handling costs in dairy production systems. The objective was to evaluate sugar cane silage for Holstein high production cows. The experiment was carried out at UEPE-GL ranch, at Universidade Federal de Viçosa, Viçosa-MG, Brazil. The treatments were corn silage (CS), with roughage:concentrate relationship of 60:40 in dry matter (DM); and 4 diets based on sugar cane(SC), with roughage: concentrate relationship of 40:60 in DM, as it follows: Sugar cane silage (SCS), Sugar cane silage with *Lactobacillus buchneri*, and sugar cane silage with *Lactobacillus plantarum* plus *Pediococcus pentosaceus* (SCSLP). Fifteen Holstein cows were divided into 3 blocks by milk production (25, 30, 35 kg/d), and they were evaluated during 5 periods of 15 d. Animals were assigned in completely randomized block design in scheme of repeated measures. Diets were isonitrogenous and isoenergetic, and dry matter intake was daily regulated. Milk production was daily recorded in 2 milking, and at the end of each period milk was sampled to analyze milk fat, protein, lactose and total dry extract. Treatment affect milk production with SCS having the lowest production (23.69 kg/d) compared with other treatments ($P = 0.001$). SC is usually a low quality forage, with low fiber digestibility and reduced proportion of soluble carbohydrates, that possibly decreased energy availability for milk production. Sugar cane supplementation improved material quality and allowed similar performance with CS and SCIN. There was no effect of roughage over 4% fat corrected milk production and milk fat, lactose, total dry extract ($P > 0.05$). Milk protein reduced when SCSLP was used ($P = 0.019$), with no acceptable explanation to these results. SCS can replace SCIN or CS for high production cows when additives are used. Supported by CNPQ/FAPEMIG/INCT-CA/FUNARBE

Key Words: *Lactobacillus buchneri*, *Lactobacillus plantarum*, *Pediococcus pentosaceus*

W44 Effects of evaporative cooling prepartum and vitamin E supplementation on performance of Holstein cows during summer in Florida. G. C. Gomes*[1], J. E. Zuniga[1], L. F. Greco[1], L. D. P. Sinedino[1], E. S. Ribeiro[1], N. Martinez[1], R. S. Bisinotto[1], F. S. Lima[1], E. Karakaya[1], M. A. Engstrom[2], J. E. P. Santos[1], and C. R. Staples[1], *[1]University of Florida, Gainesville, [2]DSM, Belvidere, NJ.*

The objective was to evaluate vitamin E (VitE) supplementation above NRC recommendations to cows managed in cooled (C) or noncooled (NC) environments prepartum on performance. Holstein cows (n = 70) were blocked by parity, milk yield, and body weight, and assigned randomly to 1 of 4 treatments arranged in a 2 × 2 factorial starting at 4 wk prepartum. Cows were housed until parturition in either a sand-bedded free-stall barn equipped with fans and sprinklers (C) or in an open lot provided with shade only (NC). After calving, cows were housed together in free-stall facility equipped with fans and sprinklers. All-rac-α-tocopherol (DSM, Belvidere, NJ) was top dressed daily at 1000 IU prepartum and 500 IU postpartum for moderate VitE (M) or 3000 IU prepartum and 2000 IU postpartum for high VitE (H) resulting in treatments: CH, CM, NCH, and NCM. The study lasted from 4 wk pre- to 15 wk postpartum. Measurements included intake of DM, yields of milk and milk components, body weight, respiration rate, and 4 times hourly measurement of vaginal temperatures for 7 d. Data were analyzed by ANOVA for repeated measures with the PROC MIXED of SAS. During prepartum, temperature and humidity index (THI) averaged 74.8 ± 4.9, and cows were exposed to THI > 70 during 85% of the day. Cooling prepartum reduced body temperature by 0.38°C in the afternoon. Results are in Table. Providing evaporative cooling during the last 4 wk of gestation improved lactational performance of dairy cows. Supplementation with VitE above NRC recommendations increased fat and protein concentration of milk, but did not influence yields of milk and milk components.

Table 1. Evaporative cooling (EC) and vitamin E (VitE) for periparturient dairy cows

	Treatment					*P*-value		
Item	NCM	NCH	CM	CH	SEM	EC	VitE	EC × VitE
DMI, kg/d								
Prepartum	9.2	8.7	10.1	10.4	0.3	0.01	0.72	0.24
Postpartum	21.9	21.9	21.4	21.4	0.6	0.41	0.93	0.95
Milk, kg/d	31.7	30.4	33.2	34.5	1.1	0.01	0.98	0.25
ECM, kg/d	31.3	30.5	33.4	35.6	1.1	0.01	0.52	0.18
Fat, %	3.55	3.64	3.69	3.88	0.05	0.01	0.01	0.31
Protein, %	2.97	3.01	2.94	3.04	0.02	0.88	0.01	0.30
FCM/DMI	1.57	1.48	1.69	1.77	0.07	0.01	0.94	0.21
Respiration rate, breaths/min	67	71	42	44	3	0.01	0.33	0.73

Key Words: dairy cow, heat stress, vitamin E

W45 Macromineral maintenance requirements for Holstein young calves. J. P. P. Rodrigues*[1], J. C. M. Lima[1], M. I. Marcondes[1], M. Campos[2], F. S. Machado[2], A. S. Trece[1], M. M. D. Castro[1], B. P. Moreira[1], and P. G. Castro[1], *[1]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil, [2]Embrapa Gado de Leite, Juiz de Fora, Minas Gerais, Brazil.*

The aim was to determine the calcium (Ca), phosphorus (P), magnesium (Mg), sodium (Na) and potassium (K) retention efficiency and maintenance requirements of Holstein calves from birth to 87 d of age. The comparative slaughter method was used. Fourty-2 male Holstein calves were utilized (3 d of age, 35.56 ± 5.86 kg). Thirty 2 calves were randomized in 4 diets (2; 4; 6; 8 kg of raw milk), with starter (20% CP; 80% TDN; 0.57% Ca; 0.46% P; 0.08% Na; 0.38% K; 0.34% Mg) ad libitum. Each treatment had 8 replications: 4 slaughtered at 57d and 4 slaughtered at 87d. Those animals with 58d were fed Coast-cross hay plus starter ad libitum after weaning. Dry matter intake was registered daily. After slaughtering, the digestive tract was cleaned and empty body weight (EBW) was obtained. Each animal was separated into carcass (CC) and non-carcass components (NCC; head, legs, tail, leather, blood, organs, viscera), both milled using a cutter and sampled after homogenization. The relationship between body weight (BW) and EBW was 0.886. The reference group was used to estimate initial EBW composition. The mineral composition from milk, starter, hay, CC and NCC was performed by inductively coupled plasma mass spectroscopy (ICP-OES). The retained minerals (RM; mg/kg EBW/d) were regressed on mineral intake (MI; mg/kg EBW/d), according to the model: RM = β_0 + β_1*MI. All parameters were tested using the mixed procedure (SAS 9.2). The β_0 values found were −103.41 (P = 0.0147); −13.52 (P = 0.2999); −0.829 (P = 0.7241); −5.595 (P = 0.1382); −0.738 (P = 0.2381) for Ca, P, Na, K and Mg, respectively. These values can be used as the maintenance requirements (mg/kg EBW/d), being the mineral loss when intake as equal to zero. The β_1 values were 0.804 (P = 0.0087); 0.419 (P = 0.0005); 0.216 (P = 0.0009); 0.119 (P = 0.0047); 0.0455 (P = 0.0025) for Ca, P, Na, K and Mg, respectively. Significance of all β_1 parameters suggests that the models use accurate minerals retention efficiency. Highest β_1 for Ca and P may be correlated with the high skeletal growth. The requirements for maintenance (mg/kg EBW/d) can be calculated as the module of β_0. Supported by CNPq/FAPEMIG/INCT CA/FUNARBE/CAPES/EMBRAPA.

Key Words: calcium, calf, phosphorus

W46 In vitro study on the effects of sodium-calcium malate and live yeast on ruminal fermentation and methane production. J. Alcañiz*[1], A. Ortiz[1], M. D. Carro[3], M. J. Ranilla[2], and J. J. Mallo[1], *[1]NOREL S.A., Madrid, Spain, [2]Universidad de León, León, Spain, [3]Universidad Politécnica de Madrid, Madrid, Spain.*

The objective of this study was to analyze the effects of sodium-calcium malate (MS), live yeast (LY) and their combination on in vitro ruminal fermentation and methane production (MP). A system of batch cultures of mixed ruminal microorganisms (BCRM) was used. Experimental treatments were control (no additives), sodium-calcium malate (MS), Live yeast (LY) and combination of both (MSLY). Bottles (120 mL) including 300 mg of a diet (40% forage: 60% concentrate) and 30 mL of a mix solution 1:4 of rumen fluid and buffer solution described by Goering and Van Soest (1970) were used for the incubation. Additives were added at dose of 9 mg MS/BCMR and 1.5 mg LY/BCMR. Bottles were incubated at 39°C for 16 h. At the end of the incubation period, total gas production was measured in each bottle using a pressure transducer and a calibrated syringe. A gas sample was removed from each bottle and stored in a hemoguard vacutainer before analysis for methane by gas chromatography. Bottles were uncapped, the pH was measured immediately, and samples were taken for volatile fatty acids, lactate and ammonia-N analyses. Incubations were replicated 4 times to allow statistical analysis. Data were analyzed using Proc Mixed of SAS. No differences were found between treatments on acetic, butyric, lactic, valeric acid (VA) and MP. PH was similar for all treatments. MS increased propionate (PR) compared with control (319 vs. 287 mmol, $P < 0.01$), reduced VA production (17.3 vs. 19.5, $P < 0.01$) and acetic:propionic ratio (A:P) (2.85 vs. 3.13, $P < 0.05$). LY reduced VA production compared with control (17.1 vs. 19.5, $P < 0.001$). MSLY increased PR (329 vs. 289, $P < 0.001$) isobutiric (17.5 vs. 12.3, $P < 0.001$), isovaleric acid (22.1 vs. 19.8, $P < 0.01$) and total production of volatile fatty acids (1570 vs. 1449, $P < 0.05$) compared with control. MSLY increased also the total ammonia production (229 vs. 202, $P < 0.001$) and reduced gas production (2851 vs. 2923, $P < 0.01$). With this experiment we concluded that combination of additives was the most effective treatment affecting a higher number of parameters. LY only affected VA and MS was the most effective treatment to reduce A:P ratio.

Key Words: malate, live yeast

W47 Yeast supplementation of lactating dairy cows during summer. G. G. S. Salvati[1], N. N. Morais Junior[1], F. F. Cardoso[1], A. C. S. Melo[1], M. Aronovich[3], R. A. N. Pereira[2], and M. N. Pereira*[1], *[1]Universidade Federal de Lavras, Lavras, MG, Brazil, [2]Empresa de Pesquisa Agropecuária de Minas Gerais, Lavras, MG, Brazil, [3]Empresa de Pesquisa Agropecuária do Estado do Rio de Janeiro, Niterói, RJ, Brazil.*

Dairy cows subjected to heat stress have reduced feed intake and increased reliance on glucose, making feeding strategies capable of improving diet digestibility plausible for improving post rumen nutrient flow and performance. The effect of yeast on digestion and performance of lactating cows during the warm summer months of southeast Brazil was evaluated. Cows were individually fed in tie stalls, THI was above 68 for 75.6% of the time. Twenty-eight Holsteins (207 ± 87 DIM) received a standardization diet for 14 d and then a treatment for 70 d, in a covariate adjusted randomized block design with repeated measures over time. Treatments were: Yeast (*Saccharomyces cerevisiae*, strain NCYC 996; Procreatin7, Lesaffre) or Control. Capsules of 10 g were orally dosed to each cow daily, equivalent to 25 × 10^{10} cfu of live cells and 5 × 10^{10} cfu of dead cells. The diet contained corn silage (37.7%), Tifton (7.1%), raw soybeans (4.1%), soybean meal (16.5%), corn (20.7%), citrus pulp (11.9%), 18.3% CP, 37.5% NDF,

and 26.7% starch. Yeast increased the yield of milk (26.7 vs. 25.4kg/d, $P = 0.03$) and solids, especially lactose ($P = 0.03$). Response in milk yield was consistent over time and started on d 5. The daily intake of digestible OM, total tract digestibility of nutrients, urinary allantoin excretion, ruminal pH and protozoa content, chewing pattern along the day, and DMI did not respond to Yeast ($P > 0.21$). There was a trend for increased plasma glucose on Yeast (62.9 vs. 57.3mg/dL, $P = 0.09$), coupled to lowered respiratory frequency (48 vs. 56 breaths/min, $P = 0.02$), at similar rectal temperature ($P > 0.51$). On d 71 to 73, citrus pulp was abruptly replaced by the same amount of corn to induce acidosis. The increased load of starch increased DMI from 7AM to 1PM, and jugular blood pCO_2, HCO_3^-, and base excess, and decreased blood pH ($P < 0.01$). Yeast increased blood pH from 7.32 to 7.34 ($P = 0.02$). Yeast supplementation improved milk yield of cows under heat stress, the mechanism apparently involved regulation of body homeothermia and glucose availability to the mammary gland, but not diet digestibility.

Key Words: *Saccharomyces cerevisiae*, probiotic, yeast

W48 Strategies to modify the biohydrogenation pathways of polyunsaturated fatty acids in the rumen. A. Siurana[1], A. Ferret[1], M. Rodriguez[1], V. Fievez[2], D. Bravo[3], and S. Calsamiglia*[1], *[1]Autonomous University of Barcelona, Spain, [2]Ghent University, Ghent, Belgium, [3]Pancosma, Geneva, Switzerland.*

Two experiments were conducted to determine the effects of lipases and essential oils on rumen fermentation and apparent biohydrogenation of linoleic (LA) and linolenic (LNA) acids. In experiment 1, a 50:50 forage:concentrate diet containing linseed oil (8.3% of DM) was incubated in a batch culture of rumen fluid at 2 pH levels (6.4 and 5.6) in 2 replicated periods. Treatments were: control; lipase 1 and 2 (0.4 and 4 μL/g DM); a lipase inhibitor (0.4 and 2 mg/g DM); Oxy-propyl-thiosulfate (PTSO) (60 and 120 mg/L); Eugenol (EUG) (150 and 500 mL/L) and Cinnamaldehyde (CIN) (150 and 500 mL/L). Samples were collected to analyze ammonia-N, volatile fatty acids (VFA) and the fatty acid (FA) profile. In experiment 2, 8 continuous culture fermenters (1,320 mL) were used in 3 replicated periods (5 d of adaptation and 3 d of sampling). Fermenters were fed 95 g/d of DM of a 60:40 forage:concentrate diet containing 5% DM of linseed oil. Treatments were control, lipase 1 (4 μL/L), PTSO (90 mg/L) and CIN (250 mg/L), and 2 pH levels (6.4 and 5.6). During the last 3 d of each period, samples were taken to analyze VFA, ammonia-N and the FA profile. Lipase 1 increased the apparent biohydrogenation of LNA and reduced the efficiency of intermediary steps of biohydrogenation of LA and LNA in experiment 1, but these results were not observed in experiment 2. The PTSO inhibited the apparent biohydrogenation of LA and LNA and decreased total VFA concentrations. The low pH inhibited the biohydrogenation of LA, increased the t10 C18:1, and decreased total VFA concentrations. Results indicated that effects of lipase 1 observed in the batch culture were not observed in long-term dual flow continuous culture fermentations. Reducing the pH inhibited the ruminal fermentation and increased the alternative pathway of ruminal biohydrogenation. The PTSO modified the pathways of fatty acid biohydrogenation, but the magnitude of the effect was pH-dependent.

Key Words: polyunsaturated fatty acid biohydrogenation, lipase, essential oil

W49 Effect of rumen-protected choline top-dressed during the transition period on milk yield and composition in Holstein dairy cows on two commercial dairies. M. C. Amundson*[1], P. D. Carvalho[1], R. W. Bender[1], R. R. Grummer[1,2], R. D. Shaver[1], and P. M. Fricke[1], *[1]University of Wisconsin-Madison, Madison, [2]Balchem Corporation, New Hampton, NY.*

Pregnant Holstein cows and heifers on 2 commercial farms were blocked by parity and randomly assigned to 2 treatments. Cows (n = 925) in the first treatment were supplemented rumen-protected choline (RPC; Reashure, Balchem Corp., New Hampton, NY) during the transition period, whereas cows (n = 952) in the second treatment were not supplemented (control; CON). All cows were housed together in transition pens, and RPC cows were individually top-dressed 60 g/d RPC while restrained in feedline headlocks from 21 d before to 21 d after calving. Daily milk yield collected by the parlor system and downloaded as a weekly average which was analyzed for the first 14 wk of lactation within parity using PROC MIXED of SAS with treatment, farm, week, and all 2- and 3-way interactions as fixed effects and cow within treatment within farm as a random effect. Milk yield did not differ between RPC vs. CON cows in first (30.5 vs. 30.7, n = 990) or second (41.4 vs. 41.4, n = 440) lactation, whereas third and greater lactation RPC cows tended ($P = 0.06$) to have greater milk yield than CON cows (45.5 vs. 44.3, n = 515). Data from DHI records for monthly milk testing including milk yield, fat, protein, and SCC were analyzed using PROC MIXED of SAS with treatment, lactation, farm, DIM, month, and treatment by lactation, and treatment by farm interactions as fixed effects and cow within treatment within farm within lactation as a random effect. Milk yield did not differ between RPC vs. CON cows in first (30.9 vs. 31.1 kg/d, n = 963) or second (39.2 vs. 39.6 kg/d, n = 427) lactation, whereas third and greater lactation RPC cows had greater ($P < 0.05$) milk yield than CON cows (43.0 vs. 41.4 kg/d, n = 487). Milk fat and protein did not differ between RPC and CON cows (3.78% vs. 3.81% and 3.05% vs. 3.06%, respectively; n = 1,877), whereas RPC cows had a lower ($P = 0.02$) linear SCC compared with CON cows (4.0 vs. 4.1; n = 1,877). We conclude that supplementing RPC during the transition period did not affect milk components but increased milk yield for older cows during and beyond the postfresh supplementation period.

Key Words: choline, milk component, milk yield

W50 Effects of a commercial feed additive on production losses during acute heat stress conditions in Holstein dairy cows. K. A. Davison*[1], R. O. Rodrigues[1], J. A. Davidson[2], N. M. Barkley[1], A. L. Kenny[1], E. C. Adkins[1], and M. R. Waldron[1], *[1]University of Missouri, Columbia, [2]Purina Animal Nutrition Center, Gray Summit, MO.*

The objective of this study was to assess the effects of a commercial carbohydrate-based feed additive on dry matter intake (DMI), milk yield, milk composition, and plasma metabolites during an acute period of heat stress. Forty-eight mid-lactation Holstein dairy cows were blocked according to milk yield, days in milk, and parity and then randomly assigned to one of 2 dietary treatments within block. Treatments were calculated to provide 100g (as fed) daily of either sucrose (control; CTL) or a commercial feed additive (Rally, Purina Animal Nutrition, Shoreview, MN; RAL) administered as part of the total mixed ration (TMR). Cows were individually fed the TMR in 2 daily allotments for a total of 39d; 27.25 ± 0.3 d during thermoneutral (TN) conditions, followed by 11.75 ± 0.3 d during heat stress (HS) conditions (daily cyclical temperatures ranging from 23.8°C to 30.2°C, temperature-humidity index of 69.2 to 75.5) in temperature-controlled environmental chambers. Daily DMI was determined using feed issue and refusal records. Milk yield was recorded daily and milk components were assessed weekly. Blood was sampled twice weekly and analyzed for concentrations of plasma glucose, β-hydroxybutyrate, and nonesterified fatty acids (NEFA). All variables were analyzed using the SAS mixed model ANOVA procedure with repeated measures. There was no significant treatment difference during the TN period for any

of the variables measured. During HS, RAL cows displayed increased DMI (treatment by time, $P < 0.05$) and milk yield (treatment by time, $P = 0.05$) relative to CTL cows. Milk fat percentage tended to decrease to a greater extent in cows fed RAL (treatment by time, $P < 0.07$), but milk fat yield was not different between treatments ($P > 0.20$). Plasma NEFA concentrations of RAL cows were lower (treatment, $P < 0.03$) than those of CTL cows during HS. Feeding RAL before and during a period of acute cyclical HS increased DMI and milk yield, and appeared to favor improved energy balance of mid-lactation dairy cows during HS.

Key Words: Rally, heat stress, dairy

W51 Effect of dietary and metabolizable protein in early lactation on the lactational performance and metabolism of dairy cows. H. M. Dann*[1], P. Ji[1], K. W. Cotanch[1], H. M. Gauthier[1], M. P. Carter[1], S. Y. Morrison[1], J. Darrah[1], Y. Koba[2], and R. J. Grant[1], *[1]William H. Miner Agricultural Research Institute, Chazy, NY, [2]ZEN-NOH National Federation of Agricultural Cooperative Associations, Tokyo, Japan.*

Multiparous Holstein cows (n = 84) were used to evaluate the effect of crude protein (CP) and metabolizable protein (MP) in corn silage-based diets fed during the fresh and early lactation periods on performance and blood metabolites. Treatments were (1) a low-protein diet (L; 15.3% CP, 35.6% NDR, 24.2% starch) for 1 to 91 d in milk (DIM; LL), (2) a high-protein diet (H; 17.0% CP, 33.3% NDR, 24.6% starch) for 1 to 21 DIM and a L diet for 22 to 91 DIM (HL), and (3) a H diet for 1 to 21 DIM and a moderate-protein diet (M; 16.2% CP, 34.4% NDR, 24.5% starch) for 22 to 91 DIM (HM). Diets contained 40% corn silage, 12% haylage, and 48% concentrates. The MP supply at 19.1 kg dry matter intake (DMI) was estimated (NDS v3) to be 1798, 1895, and 1999 g/d for L, M, and H, respectively. Cows were housed in sand bedded freestalls, fed in a Calan Broadbent feeding system, and milked 3× daily. Dry matter intake and milk yield were measured daily. Milk composition was measured weekly starting at wk 2. Serum was collected at 1, 3, 5, 7 10, 13, 16, and 19 DIM and analyzed for blood urea N (BUN) and nonesterified fatty acids (NEFA). After 21 DIM, serum was collected weekly and analyzed for BUN. Data were analyzed as a completely randomized design by ANOVA with the MIXED procedure of SAS using treatment and time as fixed factors and cow within treatment as a random factor. Through the first 91 DIM, treatment did not affect DMI, milk yield, fat content, or protein content. As expected, protein intake and concentrations of milk urea N (MUN) and BUN were highest for HM. Serum NEFA was not affected by treatment (549 ± 36 μEq/L; $P = 0.99$). Milk N efficiency was higher for LL than HM. Diets containing lower crude protein can be fed successfully to cows in early lactation as long as the metabolizable protein supply is adequate.

Table 1.

Item	LL	HL	HM	SE
DMI, kg/d	26.2	26.2	26.5	0.4
CP intake, kg/d	3.9[b]	4.0[b]	4.4[a]	0.1
Milk, kg/d	51.2	50.2	52.4	1.2
Fat, %	3.51	3.58	3.58	0.09
True protein, %	2.82	2.86	2.89	0.04
MUN, mg/dL	8.3[b]	9.0[b]	11.8[a]	0.2
BUN, mg/dL	8[c]	10[b]	12[a]	<1
SCM/DMI	1.90	1.91	1.98	0.04
Milk N efficiency, %	39.8[a]	38.6[ab]	36.9[b]	0.5

[abc]$P \leq 0.05$.

Key Words: cow, early lactation, metabolizable protein

W52 Influence of an antioxidant supplementation on production and health status of dairy cows. J. McNamara[1], S. Shields*[1], and E. von Hemiendahl[2], *[1]Washington State University, Pullman, [2]Lohmann Animal Health GmbH, Cuxhaven, Germany.*

Vitamin E allows for optimum immune and inflammatory state of dairy cattle, however, it can be a significant cost. Antioxidants scavenge the reactive oxygen species in feed and may be able to spare vitamin E to supply higher amounts to the cow for the endogenous radical defense system. Therefore, our objective was to test the effect of inclusion of Loxidan in a dairy ration to reduce the effective amount of vitamin E necessary to maintain production and health of lactating dairy cattle. The study was a randomized complete block, and cows were individually fed a TMR ad libitum to requirements from 14 to 84 d postpartum. Twenty cows each were allotted to 3 treatments; a control ration to supply 1000 IU per cow per d of vitamin E; the same ration with 150 mg/kg diet of antioxidant blend (Loxidan, Lohmann Animal Health, Cuxhaven, Germany); or a ration to supply 3000 IU per cow per d Vitamin E. There was no effect of treatment on DMI in any parity group. Milk production was the same in multiparous cows on all treatments (35.0 ± 1.2 (SEM) kg/d); however, in 1st lactation animals milk production was greatest ($P < 0.01$) in animals on the high vitamin E, least on lower vitamin E and intermediate on Loxidan. Serum vitamin E was similar between control and Loxidan, and higher on the higher vitamin E treatment. There were no effects on milk composition, body weight or serum glucose, NEFA, or BHBA. A serum indicator of stress, advanced oxidation protein products (AOPP), was lower in animals fed the Loxidan-supplemented or higher vitamin E diet compared with controls, especially in multiparous animals (Treatment × DIM × parity $P < 0.05$). The SCC of these cows was low (58,000) and there was no treatment effect; but there was a treatment × parity interaction ($P < 0.001$) in that SCC in control 2nd lactation animals was 112,000 and in Loxidan treatment 8,000; high vitamin E was 24,000. The results indicate that a lower inclusion rate of vitamin E can be fed if the diet is additionally protected with antioxidants to achieve similar results to a higher rate of vitamin E feeding, and in 1st parity animals a slight increase in milk production.

Key Words: vitamin E, antioxidant, Loxidan

W53 Verifying consistent bioavailability values in rumen-protected lysine. M. R. Culbertson*[1], M. J. Poss[1], F. D. Valdez[1], and D. A. Sapienza[2], *[1]Kemin Industries Inc., Des Moines, IA, [2]Sapienza Analytica LLC, Slater, IA.*

To characterize and predict the release rate and pattern of a rumen-protected amino acid (LysiPEARL, Kemin Industries, Des Moines, IA), an analytical test method was developed and validated. This dissolution test method, adopted from the United States Pharmacopeia (USP), can be used to ensure consistent product performance by characterizing batch-to-batch manufacturing uniformity and corroborate reliable intestinal digestibility of lysine through in vitro bioavailability model correlation. In validating this time release method linearity, repeatability, and accuracy were demonstrated. The use of conductivity as a test method for quantitating lysine dissolution was assessed and accepted in both multifactorial ANOVA ($P > 0.05$) and fit factor ($f_1 \leq 5$ and $f_2 \geq 50 \leq 100$) analyses, as well as by comparing samples using a validated orthogonal test method, high-performance liquid chromatography (HPLC). The method was challenged to detect changes in product resulting in significant dissolution differences in both PEARL size distribution ($P < 0.01$) and coating ($P < 0.01$). Three batches of rumen-protected lysine were manufactured and then characterized by both dissolution and rumen

in vitro by-pass kinetic modeling. The kinetic modeling, based on a combination of rumen degradation and intestinal release information, offered lysine release results consistent with the laboratory validated dissolution method in all product batches cross-examined in this study with an $r^2 = 0.94$. The laboratory dissolution method is an accurate tool to evaluate manufacturing conditions and ensure reproducible intestinal bioavailability when balancing rations with rumen-protected amino acids.

Key Words: bioavailability, dissolution, rumen-protected lysine

W54 Effect of supplying limiting amino acids in diets with reduced CP on milk and protein yield. M. A. C. Danes*[1], G. A. Broderick[1], and C. Parys[2], *[1]University of Wisconsin, Madison, [2]Evonik Industries AG, Hanau, Germany.*

Supplying limiting essential amino acids (EAA) to dairy cows may allow reducing dietary CP without loss of milk and protein yield, thereby increasing N efficiency. This strategy was evaluated by infusing limiting EAA into the abomasum of cows fed diets with reduced CP concentration. Ten Holstein cows were blocked by DIM into 2 5x5 Latin squares with 5 treatments: (1) positive control (16% CP), formulated to meet metabolizable protein (MP) requirements; 14.9% CP with (2) or without (3) EAA infusion; or 13.5% CP diet with (4) or without (5) EAA infusion. All diets contained alfalfa silage, corn silage, high moisture corn, canola meal, soybean meal and soybean hulls. The EAA solutions were prepared according to AminoCow to provide all limiting EAA in each treatment. Data from the last 4 d of each 14-d period were analyzed using Proc Mixed of SAS. Contrasts and LSM are reported in the table. Cows yielded on average 10 kg less milk than expected, making the 14.9% CP diet not MP limiting according to AminoCow, which may explain why no effect was detected on that diet (contrast 3). The 13.5% CP diet did not differ from the positive control (contrast 2) but the predicted balance of EAA indicated that methionine, lysine and histidine were limiting. Infusion of EAA on this diet overcame the deficiency, which increased ECM and tended to increase milk and protein yield (contrast 4). The NRC (2001) model underestimated MP-allowable milk by, respectively, 2.5, 4.2 and 8.2 kg for the 16, 14.9 and 13.5% CP diets. The number of cows used limited statistical power. However, results suggested that the lowest CP diet with supplemental EAA infusion was the best treatment, indicating the advantage of balancing dairy rations for amino acids.

Table 1.

	Treatment					Contrasts[1]			
Variable	16% CP	14.9% CP + EAA	14.9% CP	13.5% CP + EAA	13.5% CP	1	2	3	4
DMI, kg/d	23.2	22.6	23.7	23.8	23.0	NS	NS	NS	NS
Milk, kg/d	35.6	34.5	35.7	36.7	34.6	NS	NS	NS	<0.10
ECM, kg/d	34.5	33.4	34.9	37.1	33.8	NS	NS	NS	<0.05
Fat, kg/d	1.24	1.19	1.27	1.38	1.22	NS	NS	NS	<0.05
Protein, kg/d	1.00	0.98	1.00	1.05	0.98	NS	NS	NS	<0.10
MUN, mg/dL	12.4	10.5	11.4	9.0	8.9	<0.1	<0.01	NS	NS
EUN (%)	26.3	28.8	27.5	32.1	30.8	NS	<0.01	NS	NS

[1]Contrasts: 1 = 16 vs. 14.9; 2 = 16 vs. 13.5; 3 = 14.9 vs. 14.9 + EAA; 4 = 13.5 vs. 13.5 + EAA.

Key Words: amino acid, nitrogen

W55 Baseline bovine plasma concentrations of free amino acids during lactation. T. A. Burnett*[1], A. M. L. Madureira[1], G. Wu[2], J. R. Thompson[1], and R. L. A. Cerri[1], *[1]University of British Columbia, Vancouver, BC, Canada, [2]Texas A&M University, College Station.*

Amino acids play nutritional and regulatory roles in lactation. At present, little is known about changes in their concentrations in the plasma of lactating cows during the entire lactation period. This study was conducted to fill in this gap of knowledge. Eighty-nine lactating Holstein (40 primiparous and 49 multiparous) cows were used throughout the first 9 mo of lactation. Cows were maintained in free stall barns and fed a TMR diet (CP = 17.8%, MP = 48.3g/DM) twice a day through the entire experiment, this ration was maintained for a minimum of 200 d in lactation. Information on health episodes, reproductive status, age of gestation and milk production was recorded. Blood samples were collected using sodium-heparin vacutainers on 9 different days in milk 0, 3, 7, 15, 30, 60, 90, 180 and 270. Samples were taken in 9 cohorts consisting of different cows at the same stage of lactation. Plasma was analyzed quantitatively for 24 amino acids using HPLC methods involving derivatization with o-phthaldialdehyde. Data were analyzed by ANOVA for repeated measures using Proc MIXED of SAS. GLN, THR, CIT, β-ALA, TAU, ALA, and ORN were not affected by days in milk, milk production or reproductive status ($P > 0.10$). There was an effect of days of lactation on concentrations of ASP, ARG, TYP, TRP, MET, VAL, PHE, ILE, PRO and LYS in plasma ($P < 0.01$). Correlations between free amino acids and days of lactation were all negative ($r^2 = 0.09$ to 0.20; $P < 0.01$) with a major decrease in free amino acids occurring between d 60 and 90 of lactation. Changes in ASN, SER, and GLY depended on both days of lactation ($P < 0.01$) and yield of milk production ($P < 0.01$), but no interactions were found. There were negative correlations ($r^2 = 0.10$ to 0.17; $P < 0.05$) between age of gestation and the following amino acids: TAU, TYR, MET, and PHE. In conclusion, concentrations of specific amino acids in plasma decreased after 60 d in milk, independent of milk production. Stage of gestation also affected the concentrations of TAU, TYR, MET, and PHE. Taken together, these results suggest a basis to develop possible new strategies for improving health, lactation and reproduction of cows.

Key Words: amino acid, dairy cattle, reproduction

W56 An evaluation of amino acid utilization in lactating dairy cows consuming DDGS and different levels of fat. H. A. Paz* and P. J. Kononoff, *University of Nebraska-Lincoln, Lincoln.*

Eight multiparous Holstein cows were used in a replicated 4 × 4 Latin square to determine the lactation response and AA utilization when dairy cows were fed either conventional (12% fat) or low-fat (6.6% fat) distillers dried grains with solubles (DDGS). Dietary treatments were 1) Control (CON), no DDGS, 2) 29% conventional DDGS (DG), 3) 29% low-fat DDGS (LF), and 4) 29% low-fat DDGS plus rumen inert fat (LF+RIF). Diets were formulated to be isonitrogenous (18.5% CP) but not isocaloric. Net energy of lactation was estimated to be 1.59, 1.61, and 1.68 Mcal/kg of DM for the LF, CON and LF+RIF, and DG diets, respectively. Periods lasted 21 d with the last 3 d for data collection. Compared with cows fed the CON diet, cows fed diets with DDGS had a greater ($P = 0.03$) DMI (22.7 vs. 26.6 ± 1.14 kg/d) and similar ($P = 0.26$) milk yield (31.8 ± 3.0 kg/d). Milk protein percentage was greater in cows fed diets with DDGS ($P = 0.01$) compared with those fed the CON diet (3.22 vs. 3.09 ± 0.08%) and milk fat percentage was lower ($P = 0.01$) in cows fed the DG diet compared with those fed the other diets (3.14 vs. 3.74 ± 0.18%). Arterial concentration of Lys was similar (11.7 ± 0.96 μg/mL; $P = 0.83$) across diets and concentrations of Leu (38.8 ± 2.62; $P < 0.01$), Met (3.77 ± 0.21 μg/mL; $P < 0.01$), and

Phe (10.9 ± 0.49; $P = 0.03$) increased in diets with DDGS compared with the CON diet (27.9 ± 2.62, 2.96 ± 0.21, and 9.61 ± 0.49 µg/mL, respectively). Arteriovenous differences of essential AA were similar ($P \geq 0.19$) across diets. Extraction efficiencies of Lys and Met did not differ across diets and averaged 59.8 ± 4.84% ($P = 0.54$) and 57.3 ± 0.36% ($P = 0.36$), respectively. For cows fed the CON diet, Met was ranked as the first limiting AA followed by Lys and the opposite was observed for cows fed diets with DDGS. Across diets, Arg was the third limiting AA. Low-fat DDGS can be included at high levels without negative effects on milk yield and milk fat percentage. Despite the fact that diets containing DDGS resulted in a lower supply of lysine, physiological indicators of lysine utilization were not affected.

Key Words: dairy cow, distillers dried grains with solubles, extraction efficiencies

W57 Estimation of the metabolizable methionine contribution of four rumen-protected products using the AUC methodology. L. Faivre[1], Y. Mercier[1], E. Devillard[1], and B. K. Sloan*[2], *[1]Adisseo France, Commentry, France, [2]Adisseo North and Central America, Alpharetta, GA.*

Methionine is one of the most limiting amino acids (AA) for milk protein synthesis and is critical achieving a well-balanced ration for AA. Because the required dietary metabolizable methionine (MMet) concentrations cannot be reached by using conventional feedstuffs, various rumen protected methionine (RPM) sources have been developed. To be effectively used, these RPM sources need to be well characterized for their real contribution of MMet. The aim of the present study was to measure the MMet contribution of 4 RPM products MetaSmart (Adisseo, France), AminoShure-M (Balchem, USA), Pro-Met (Bioscreen, Italy) or a prototype product (Adisseo, France), using the Area Under the Curve (AUC) methodology described by Graulet et al. (2005). Eight nonlactating rumen cannulated Holstein cows fed 75% hay and 25% concentrate were used in a replicated incomplete Latin Square design with 4 periods of one week. They received a spot dose of 50g equivalent methionine via the rumen cannula. Blood samples for methionine concentration assessment were obtained from 8 h before and until 72 h after the spot dose. The AUCs were used to estimate the percentage of MMet. An ANOVA with repeated measures was performed using PROC MIXED of SAS/ STAT software (SAS 9.1.3; SAS Institute Inc., Cary, NC). The proportion of methionine reaching the blood stream was calculated at 54.1 ± 5.9% for MetaSmart, which was consistent with previous data (52.3 ± 3.4%, Graulet et al., 2005). AminoShure-M was statistically lower ($P < 0.001$) than Metasmart and evaluated at 42.4 ± 6.5%. Pro-Met measured at 12.2 ± 4.7% was also significantly lower than AminoShure-M. As for the bioavailability of the prototype product, it was not statistically different from MetaSmart bioavailability and was calculated at 57.4 ± 4.3%. This study suggests that MMet contribution of different RPM can be very variable, and products need to be characterized by approved methodologies to determine their real MMet contribution for an optimal usage.

Key Words: metabolizable methionine, rumen-protected amino-acids, area under the curve

W58 A controlled on farm evaluation of methionine for lactating dairy cows. N. N. Morais Junior[1], G. G. S. Salvati[1], R. C. Oliveira[1], R. A. N. Pereira[2], and M. N. Pereira*[1], *[1]Universidade Federal de Lavras, Lavras, MG, Brazil, [2]Empresa de Pesquisa Agropecuária de Minas Gerais, Lavras, MG, Brazil.*

Controlled on farm trials allows for large number of experimental units. We evaluated the response to the isopropyl ester of 2-hydroxy-4-(methylthio) butanoic acid (HMBi, MetaSmart, Adisseo). Cows were paired blocked and randomly assigned to 2 pens of primiparous and 2 of multiparous, in free stalls. The final data set had 234 Holsteins (215 ± 105 DIM at d 26), 96 primiparous and 138 multiparous. Within parity, a pen received HMBi (30g/d) added to a Control diet. Soybean meal and heated soybeans were the major protein sources. HMBi was manually mixed to the first daily feed delivery by 4 researchers housed at the farm along the experiment. The same batch of TMR was fed to all pens. Cows were fed and milked 3x/d. Milk yield on 3 consecutive days was used for blocking and as covariate in the statistical model. Treatments were offered for 28d and response was evaluated on d 24 to 28. Diets were sampled at each feeding in 5 locations of the feed bunk. Composite TMR samples were frozen. Feed refusals were measured, sampled and frozen. Data was analyzed with Mixed as a randomized block design and intake data used pen as replicate and sampling day as repeated measures over time. The CP of the consumed diet was 17.1% of DM ($P = 0.71$), orts 5.3% of offered ($P = 0.64$), and DMI 19.3 kg/d ($P = 0.59$). Cows had similar BCS and girth perimeter ($P > 0.21$). Milk yield before treatment allocation was 34.6 kg/d ($P = 0.95$) and 34.7 on d 24 to 28 ($P = 0.83$). HMBi increased protein yield (1.096 vs.1.049 kg/d, $P = 0.05$) and content (3.18 vs. 3.07%, $P = 0.03$). PUN was reduced by HMBi (13.9 vs.15.6 mg/dL, $P = 0.02$), but MUN did not respond (15.7 vs.16.4 mg/dL, $P = 0.20$). The urinary allantoin to creatinine ratio was increased by HMBi ($P = 0.03$). HMBi increase the plasma content of 11 amino acids at $P < 0.01$, 2 at $P < 0.07$, and cysteine ($P = 0.60$) and lysine ($P = 0.18$) had non-statistical increases. The total of plasma amino acids was increased by 10.4% of Control ($P < 0.01$), methionine increased by 30.8% ($P < 0.01$), and the increase in other amino acids ranged from 4.4 to 19.2%. HMBi decreased PUN, and increased microbial yield, plasma amino acids, and milk protein yield and content.

Key Words: amino acid, methionine, protein

W59 Forages fertilized with selenium as a way to supplement lactating dairy cows. R. Seboussi*[1], G. F. Tremblay[2], P. Y. Chouinard[1], Y. Chorfi[3], G. Bélanger[2], Y. Couture[3], V. Ouellet[1], and E. Charbonneau[1], *[1]Université Laval, Québec, QC, Canada, [2]Agriculture and Agri-Food Canada, Québec, QC, Canada, [3]Université de Montréal, St-Hyacinthe, QC, Canada.*

Fertilization with Se improves the forage Se concentration, but no data on its impact on lactating cows are available. This study aimed to determine the effect of forages fertilized with Se on the performance of lactating dairy cows. A high Se grass and legume silages (1.5 ppm Se) were produced by fertilizing one fourth of forage fields with 2.5 kg/ha of Selcote Ultra (1% Se wt/wt). The low Se silages (0.06 ppm) were harvested from the remaining area. Thirty-three mid- to late-lactation primiparous Holstein cows were used in an unbalanced randomized block design. Each block of cows entered the experiment when enough animals with similar DIM were available and an average 77-d period of Se-depletion was performed. Cows were then randomly assigned for 42 d to one of the 4 experimental TMR fed ad libitum with diets based as follows: CTRL = low Se silages; ISe = low Se silages supplemented with inorganic Se (sodium selenite); OSe = low Se silages supplemented with organic Se (Sel-Plex); FSe = high Se silages. Pre-planned contrasts were tested: (1) CTRL vs. Se-supplemented diets; (2) ISe vs. OSe and FSe; (3) OSe vs. FSe. The CTRL diet (0.12 ppm) had a lower ($P < 0.001$) Se concentration than ISe (0.70 ppm), OSe (0.79 ppm) and FSe (0.80 ppm) diets, which did not differ statistically in Se concentration. No treatment effects were observed on DMI, milk yield, ECM, FCM and

milk fat and lactose concentrations. Cows fed the ISe diet had lower (P = 0.01) milk protein concentration (3.44%) than cows fed OSe (3.58%) and FSe (3.51%) diets but their milk protein yields were similar. Higher SCC were observed for cows fed CTRL than Se supplemented diet (P = 0.05) but the form of Se supplement had no significant effect. Blood glutathione peroxidase was similar between treatments. Apparent Se digestibility was similar in cows fed CTRL (42.5% of intake) and Se-supplemented diets but it was lower (P = 0.04) in cows fed the ISe diet (38.6%) than OSe (42.2%) and FSe (49.8%) diets. Apparent Se digestibility tended (P = 0.07) to be greater in cows fed the FSe than the OSe diet. Forages fertilized with Se are therefore an effective way to provide adequate levels of dietary Se to dairy cows.

Key Words: lactating cow, selenium, forage

W60 Effect of feeding various dosages of *Saccharomyces cerevisiae* fermentation product on serum markers of the innate and adaptive immune system of multiparous dairy cows. C. M. Shriver-Munsch[1], E. M. Zaworski[1], A. N. Fadden[1], W. K. Sanchez[2], I. Yoon[2], and G. Bobe*[1,3], *[1]Oregon State University, Corvallis, [2]Diamond V Mills, Cedar Rapids, IA, [3]Linus Pauling Institute, Corvallis, OR.*

We previously documented that feeding 56 or 112 g/d of *Saccharomyces cerevisiae* fermentation product (SCFP; Original XP) to transition dairy cows resulted in lower somatic cell counts in milk and lower incidence of clinical mastitis. The objective of this study was to examine how feeding SCFP may improve mammary gland health in transition dairy cows on a commercial dairy farm. Multiparous Holstein cows were given individually a supplement containing either 0 (control: n = 14), 56 (n = 15), or 112 g (n = 13) of SCFP daily during morning lock-up as a top dressing to their total mixed ration. The supplement consisted of 0, 56, or 112 g of XP mixed with 84 g of molasses and 168, 112, or 56 g of corn meal, respectively. Supplement feeding began 28 d before predicted calving date (at least 14 d prepartum) and ended 28 d postpartum. Blood samples were collected weekly and more often around calving to measure serum concentrations of markers of innate (haptoglobin and serum amyloid A) and adaptive immunity (IgG, IgM, and IgA). Feeding SCFP (112 or 56 versus 0 g/d) tended to decrease serum concentrations of serum amyloid A in the last week before calving (13.9 versus 23.4 mg/L; P = 0.06) and increased it in the first week after calving (180 versus 82 mg/L; P = 0.02). Doubling feeding rates of SCFP (112 versus 56 g/d) decreased serum haptoglobin concentrations prepartum (3.4 versus 4.5 mg/L; P = 0.03). Feeding SCFP (112 or 56 versus 0 g/d) tended to decrease serum concentrations of IgM (2.38 ± 0.17 g/L versus 2.93 ± 0.25 g/L; P = 0.07). Our results suggest that feeding *Saccharomyces cerevisiae* fermentation product may alter immune function during the transition period.

Key Words: acute phase protein, immunoglobulin, yeast culture

W61 Effect of feeding various dosages of *Saccharomyces cerevisiae* fermentation product on serum concentrations of macrominerals of multiparous dairy cows. A. N. Fadden[1], E. M. Zaworski[1], C. M. Shriver-Munsch[1], W. K. Sanchez[2], I. Yoon[2], and G. Bobe*[1,3], *[1]Oregon State University, Corvallis, [2]Diamond V Mills, Cedar Rapids, IA, [3]Linus Pauling Institute, Corvallis, OR.*

Feeding 56 g/d of *Saccharomyces cerevisiae* fermentation product (SCFP; Original XP) to transition dairy cows has been reported to promote feed consumption around calving. We hypothesized that greater feed intake may be reflected in improved macromineral status. To test this hypothesis, multiparous Holstein cows were given individually a supplement containing either 0 (control: n = 14), 56 (n = 15), or 112 g (n = 13) of SCFP daily during morning lock-up as a top dressing to their total mixed ration. The supplement consisted of 0, 56, or 112 g of XP mixed with 84 g of molasses and 168, 112, or 56 g of corn meal, respectively. Supplement feeding began 28 d before predicted calving date (at least 14 d prepartum) and ended 28 d postpartum. Blood samples were collected at days −21, −14, −7, −3, −1, −1, 0, 1, 3, 7, 14, 21, and 28 postpartum to measure serum concentrations of calcium, magnesium, and phosphorus. Feeding SCFP (112 or 56 vs. 0 g/d) increased serum concentrations of phosphorus during the supplementation period (6.43 ± 0.11 mg/dL vs. 6.09 ± 0.14 mg/dL; P = 0.03) and calcium in the 48 h around calving (8.26 ± 0.19 mg/dL vs. 7.88 ± 0.18 mg/dL; P = 0.04). Whereas, feeding SCFP (112 or 56 versus 0 g/d) decreased serum concentrations of magnesium (2.49 ± 0.04 mg/dL versus 2.65 ± 0.05 mg/dL; P = 0.005) without reaching levels that may influence feed intake. Doubling feeding rates of SCFP (112 versus 56 g/d) did not significantly alter serum concentrations of calcium, magnesium, and phosphorus (P > 0.10). Our results suggest that feeding *Saccharomyces cerevisiae* fermentation product may be beneficial during the transition period to support the macromineral status of dairy cows.

Key Words: dairy, macromineral, yeast culture

W62 Effect of feeding various dosages of *Saccharomyces cerevisiae* fermentation product on serum indicators of feed intake of multiparous dairy cows. E. M. Zaworski[1], A. N. Fadden[1], C. M. Shriver-Munsch[1], W. K. Sanchez[2], I. Yoon[2], and G. Bobe*[1,3], *[1]Oregon State University, Corvallis, [2]Diamond V Mills, Cedar Rapids, IA, [3]Linus Pauling Institute, Corvallis, OR.*

We previously documented that feeding 56 or 112 g/d of *Saccharomyces cerevisiae* fermentation product (SCFP; Original XP) to transition dairy cows improved SCFP consumption on the day of calving. The objective of this study was to examine how feeding SCFP may improve feed consumption in transition dairy cows. On a commercial farm, multiparous Holstein cows were given individually a supplement containing either 0 (control: n = 14), 56 (n = 15), or 112 g (n = 13) of SCFP daily during morning lock-up as a top dressing to their total mixed ration. The supplement consisted of 0, 56, or 112 g of XP mixed with 84 g of molasses and 168, 112, or 56 g of corn meal, respectively. Supplement feeding began 28 d before predicted calving date (at least 14 d prepartum) and ended 28 d postpartum. Blood samples were collected at days −7, −3, −1, −1, 0, 1, 3, and 7 postpartum to measure serum concentrations of markers of stress (cortisol), inflammation (haptoglobin and serum amyloid A), hunger (visfatin), and energy status (insulin, glucose, BHBA, and NEFA). Feeding SCFP (112 or 56 versus 0 g/d) decreased serum concentrations of cortisol (1.2 vs. 1.9 µg/L; P = 0.007). Feeding SCFP tended to decrease serum concentrations of serum amyloid A before calving (12.6 vs. 20.8 mg/L; P = 0.09) and increased it after calving (162 vs. 75 mg/L; P = 0.04). Doubling feeding rates of SCFP (112 vs. 56 g/d) tended to decrease serum haptoglobin concentrations (7.8 vs. 11.2 mg/L; P = 0.09). No significant effects at $P \leq 0.10$ were observed for serum concentrations of visfatin, insulin, glucose, BHBA, and NEFA. Our results suggest that feeding *Saccharomyces cerevisiae* fermentation product may improve feed intake around calving in part by decreasing cortisol secretion.

Key Words: cortisol, feed intake, yeast culture

W63 Effect of applying a bacterial inoculant to corn silage on the performance of lactating dairy cows. O. C. M. Queiroz[1], F. C. Basso[2], R. Daetz[1], A. Schlaefli[1], J. J. Romero[1], J. H. Shin[1], F. H. Kamada[2], U. Carneiro[2], and A. T. Adesogan*[1], *[1]Department of Animal*

Sciences, IFAS University of Florida, Gainesville, [2]Department of Animal Sciences, UNESP, Jaboticabal, Sao Paulo, Brazil.

The objective was to determine the effect of applying a bacterial inoculant to corn silage on the performance of dairy cows. Corn silage was harvested at 35% DM, treated with or without 150,000 cfu/g of fresh forage of an inoculant containing *Lactococcus lactis* SR 3.54, *Lactobacillus plantarum* CHCC6072, and *Enterococcus faecium* M74 (Chr. Hansen, Denmark) and ensiled in 2 3.7-m wide plastic bags for 186 d. Sixty lactating dairy cows (20 ± 4 DIM) were blocked by parity and milk production and randomly assigned to treatments. Cows were fed a common diet for a 10-d covariate period followed by a 90-d experimental period when a TMR consisting of 35% corn silage, 11% alfalfa hay and 54% of a concentrate was fed. Milk production and DMI of individual cows were recorded daily. Milk and feed ingredients were sampled weekly and chemically characterized. Cows were dosed with chromic oxide for 10 d and fecal samples were collected in the last 5 d to estimate in vivo apparent digestibility. The data was analyzed as a randomized complete block design and the statistical model included treatment, time (repeated), parity, and the interactions. Compared with cows fed silage without inoculant, cows fed inoculated silage had greater yields of milk (38.4 vs. 37.4 kg/d; SEM = 0.23), FCM (38.2 vs. 37.3 kg/d; SEM = 0.22), fat (1.33 vs. 1.30 kg/d; SEM = 0.01) and lactose (1.91 vs. 1.82 kg/d; SEM = 0.01) and greater FCM:DMI ratio (1.72 vs. 1.54 kg/d; SEM = 0.02). Daily DMI (23.2 vs. 25.3 kg/d; SEM = 0.14) and concentrations of milk fat (3.43 vs.3.48%; SEM = 0.01) and protein (2.82 vs. 2.93%; SEM = 0.005) were lower in cows fed the inoculated silage versus the no inoculated silage diet. However, DM (70.7 vs. 71.6%; SEM = 0.92) and NDF digestibility (56.9 vs. 58.6%; SEM = 1.1) were unaffected by treatment. In conclusion, applying the inoculant to corn silage increased milk production and efficiency of feed utilization by lactating dairy cows.

Key Words: silage inoculant, milk yield, *Lactococcus*

W64 Use of virginiamycin and rumen-protect fat, and its association in the diet of crossbred dairy cows grazing tropical pastures. R. C. Silva[1], B. Pessim[3], L. A. Souza[3], J. A. Alves Neto[1], J. M. B. Benatti*[1], A. D. Moreira[1], A. F. Campos[1], P. H. Gonçalves[3], R. D. Signoretti[2], and G. R. Siqueira[2], *[1]Universidade Estadual Paulista – FCAV, Jaboticabal, São Paulo, Brazil, [2]Agencia Paulista de Tecnologia dos Agronegócios - Alta Mogiana, Colina, Sâo Paulo, Brazil, [3]Centro Universitário de Barretos, Barretos, São Paulo, Brazil.*

The study aimed to evaluate virginiamycin (VM), rumen-protected fat (RPF) and its association in the production of dairy cows supplemented and maintained on pasture under rotational stocking Tanzania. A total of 16 crossbred Holstein × Zebu cows (predominantly 3/4 grade of Holstein blood), average live weight of 500 kg, with production at the beginning of the experiment 20 kg / day were distributed in 4 4 × 4 Latin square. The experimental area was 24 paddocks with 1.750 m^2 (total of 4.2 ha) formed with *Panicum maximum* 'Tanzania', irrigated and managed grazing system in flash. The supplement was made up of citrus pulp (79.8 g/kg), soybean hulls (21.7 g/kg), corn germ (256.5 g/kg), peanut meal (30.2 g/kg) refinazil (114.0 g/kg), corn (430.0 g/kg) and mineral core doped Factor Premium (Premix, Patrocinio Paulista-SP) (67.8 g/kg). Treatments consisted of control; VM (35 mg/kg of concentrate) RPF protected fat soybean oil (1% DM of concentrate) and VM (35 mg/kg of concentrate) associated with RPF (1% DM of concentrate), the experimental unit was the animal. The variables were analyzed using the SAS software (version 9.0) using the PROC MIXED considering significant difference $P < 0.10$. There was no interaction for any of the variables ($P > 0.10$). The inclusion of RPF did not affect milk production ($P = 0.155$), with an average of 17.17 kg/d, the VM has increased from 16.92 to 17.42 kg/d ($P = 0.087$). In milk yield corrected for 4% of fat, the use VM increased milk production at 0.66 kg/d ($P = 0.034$) and RPF decreased by inclusion of 0.75 kg/d ($P = 0.017$). The inclusion of RPF decreased ($P < 0.10$) percentages of total solids, lactose and nonfat dry extract and did not alter the percentages of fat, protein and milk urea nitrogen. The VM reduced the protein ($P = 0.098$) and did not alter the other characteristics of milk. The virginiamycin supplementation in dairy cows grazing grass Tanzania increases milk production while maintaining quality. The use of RPF reduced milk production correct for 4% of fat.

Key Words: fodder, milk additive, supplement

W65 Influence of an antioxidant supplementation on adipose and liver transcriptome in early lactation dairy cattle. J. McNamara*[1], S. Shields[1], J. Thomson[2], and E. von Heimendahl[3], *[1]Washington State University, Pullman, [2]Montana State University, Bozeman, [3]Lohmann Animal Health GmbH, Cuxhaven, Germany.*

Vitamin E supplementation to dairy cattle can support a stronger immune and inflammatory system, but is expensive and can itself be oxidized. Antioxidants scavenge the reactive oxygen species in feed and could spare vitamin E in the ration. Therefore, greater amounts of vitamin E are absorbed and are available for the endogenous radical defense system. Our objective was to test the effect of inclusion of an antioxidant added to the feed to reduce the vitamin E necessary to maintain production and health of lactating dairy cattle. In addition we were interested to know if vitamin E could alter the expression of key immune or inflammatory functional genes in adipose and liver. The study was a randomized complete block, and cows were fed a TMR ad libitum to requirements from 14 to 84 d postpartum. Twenty cows each were allotted to 3 treatments; a control ration containing 1000 IU/kg vitamin E; the same ration with 150 mg antioxidant (Loxidan, Lohmann Animal Health, Cuxhaven) per kg DM or a ration with 3000 IU/kg vitamin E. Adipose and liver samples were taken at 7 and 28 DIM, RNA was prepared and samples were analyzed on the Affymetrix Bovine gene array chip, with the data analyzed using Genesifter by Geospiza. Plasma Vitamin E was higher ($P < 0.01$) in higher vitamin E compared with control with or without Loxidan. In primiparous animals, milk production was highest ($P < 0.01$) in animals on the high vitamin E, intermediate on low vitamin E with Loxidan and lowest on control. In the adipose transcriptome showed 27 genes improving response to stress that increased in animals fed Loxidan; in the liver 18 genes controlling antioxidant activity increased in animals fed Loxidan ($P < 0.05$ for all). Higher vitamin E feeding showed 5 genes controlling immune processes increased compared with control. The advanced oxidation protein products were lower ($P < 0.05$) in higher vitamin E or Loxidan-Low vitamin E compared with controls. A lower inclusion rate of vitamin E can be fed if the diet is additionally protected with antioxidants to maintain production and may improve immune and inflammatory status.

Key Words: vitamin E, lactation, antioxidant

W66 Effect of *Saccharomyces cerevisiae* live cells on milk yield and digestibility of buffalo cows. F. Masucci[1], G. De Rosa[1], CMA Barone[1], P. Parente[1], ML Varricchio[1], A. Di Francia[1], and E. Chevaux*[2], *[1]Università di Napoli Federico II, Dipartimento di Agraria, Portici (NA), Italy, [2]Lallemand SAS, Blagnac, France.*

The effects of *Saccharomyces cerevisiae* strain CNCM I-1077 dietary supplementation were examined in lactating buffalo cows. On a farm

in Caserta province, 44 buffalo cows were divided into Control and Saccharomyces groups balanced for age (on average, 52.7 ± 2.1 mo), days in milk (120 ± 64 d) and milk production (9.2 ± 1.37 kg/head/d). The groups were fed the same total mixed ration (TMR) that was supplemented, in Saccharomyces group, with 50 g/day of yeast supplement (Levucell SC), corresponding to 10×10^9 cfu/day live cells. The experimental period lasted 16 weeks. At the beginning and at the end of this period, each cow was weighted and scored for BCS. Every 2 weeks milk yield of each cow was measured and sampled; DMI was also evaluated on pen basis. At the end of experimental period, total tract in vivo digestibility was evaluated by using acid insoluble ash as indigestible marker. Milk traits and estimated mozzarella cheese yield were analyzed by a linear mixed model for repeated measures including the effects of diet, time and the interaction diet*time. The effect of diet on DMI, BCS and digestibility coefficients were analyzed by one-way ANOVA. No differences ($P > 0.05$) were found between the dietary groups for live weight (663.0 vs. 689.6 kg, respectively for Control and Saccharomyces group, SEM 11.8) and BCS (6.33 vs. 6.11 SEM 0.39). Saccharomyces supplemented cows presented higher ($P < 0.05$) TMR-DMI (16.1 vs. 16.5 kg/d, SEM 0.11) and milk yield (7.6 vs. 8.3 kg/head/d, SEM 0.251). Although milk fat (9.10 vs. 9.64%, SEM 0.254) and milk protein (5.39 vs. 5.34%, SEM 0.10) were not influenced by the treatment ($P > 0.05$), Saccharomyces group had greater ($P < 0.01$) estimated mozzarella yield (2.17 vs. 2.45 kg/d SEM 0.075). Total tract in vivo digestibility coefficients of dry matter, organic matter, crude protein and NDF were significantly higher in Saccharomyces compared with Control group. Overall, live yeast supplementation to lactating buffaloes significantly increased milk production, without decreasing milk quality, live weight and BCS.

Key Words: buffalo cow, live yeast, milk production

W67 Effects of arginine concentration on the in vitro expression of casein and mTOR pathway related genes in mammary epithelial cells from dairy cattle. M. Z. Wang[1,2], B. L. Xu[1], D. P. Bu[2], J. Q. Wang[2], and J. J. Loor*[3], *[1]Yangzhou University, Yangzhou, China, [2]State Key Laboratory of Animal Nutrition, Beijing, China, [3]University of Illinois, Urbana.*

Arginine is a conditionally-essential amino acid that is taken up by bovine mammary gland in excess of its output in milk. In this study we evaluated the effects of arginine level on the expression of casein and signaling pathway-related genes in mammary epithelial cells. The treatments (applied for 24 h) were designed to be devoid of Arg 0X (control; 0.00 mg/L), resemble the profile of Arg in casein (Arg 1X; 278.00 mg/L), be deficient, Arg 0.25X; 69.50 mg/L) and Arg 0.5X (139.00 mg/L), or be in excess of the amount in casein, Arg 2X (556.00 mg/L), Arg 4X (1,112 mg/L), and Arg 8X (2,224 mg/L). Cultures were run in triplicate for each treatment. An ANOVA with Arg level as fixed effect and replicate as random effect was used for statistical analysis. Treatment means were separated using Fisher's least significant difference pair-wise comparisons. The expression of CSN1S, CSN3 and mTOR in the experimental groups was higher than those of the control group ($P < 0.05$). Except for Arg 0.25X and Arg 8X ($P > 0.05$), the expression of CSN1S2, CSN2 and JAK2 in other experimental groups was higher ($P < 0.05$) than those in the control group. Except for Arg 8X ($P > 0.05$), the expression of STAT5 in the other experimental groups was higher than those of the control group ($P < 0.05$). It was also observed that, except for Arg 0.5X, S6K expression was higher in other experimental groups than the control group ($P < 0.05$). In contrast, except for Arg 0.25X, the other experimental groups resulted in lower 4EBP1 expression than the control group ($P < 0.05$). Among groups, the expression of CSN1S1, CSN1S2, CSN2, CSN3, JAK2, STAT5, mTOR and S6K gene was highest with Arg 2X ($P < 0.05$); the reverse was true for 4EBP1 gene, with the lowest expression in this group ($P < 0.05$). Taken together, arginine appears to play an important role in the transcriptional regulation of casein genes and mTOR related genes in bovine mammary epithelial cells.

Key Words: mammary, milk protein, nutrition

W68 Essential amino acid signal on translation regulation pathways in mammary tissue. S. I. Arriola Apelo*[1], L. M. Singer[1], X. Lin[2], and M. D. Hanigan[1], *[1]Department of Dairy Science, Virginia Polytechnic Institute and State University, Blacksburg, [2]Animal Science and Technology College, Shandong Agriculture University, Shandong Province, China.*

Signaling pathways regulate rate of protein translation in the mammary gland. The quantitative effects of Ile, Leu, Met, and Thr on mammalian target of rapamycin (mTOR) and eukaryotic initiation factor (eIF) 2 pathways were studied with a central composite design consisting of 4 central runs, 2 axial runs per AA, and a complete 2^4 factorial. The central run was set to 35% of the concentration of Dulbecco's Modified Eagle Medium (DMEM) for each of the above AA. Axial runs were set to 0 and 100% of DMEM. Factorial runs were set at 20 and 50% of DMEM. Mammary tissue slices (0.12 ± 0.02 g) from 5 lactating dairy cows were incubated 4 h at 37°C in 5 mL of treatment media enriched with [$^2H_5$] Phe. Western immunoblotting was performed to identify total and site-specific phosphorylated mTOR (Ser2448), eukaryotic elongation factor (eEF) 2 (Thr56), ribosomal protein (rp) S6 (Ser235/236), and eIF2a (Ser51). The statistical model included individual AA linear and quadratic effects and one-way interactions as fixed continuous effects, and cow as a random effect. Neither linear and quadratic amino acid effects nor interactions among them were significant for eIF2a (Ser51) phosphorylation. In the mTOR pathway, AA did not affect mTOR phosphorylation. However, phosphorylation of eIF2 and mTOR were negatively correlated (−0.28, $P < 0.001$) as expected. Downstream of mTOR, Leu ($P = 0.027$) inhibited eEF2 phosphorylation, which is known to stimulate translation elongation. The effect of Leu tended to be affected by concentrations of Ile (Leu*Ile, $P = 0.058$) and Thr (Leu*Thr, $P = 0.093$). Phosphorylation of mTOR was negatively correlated with that of eEF2 (0.31, $P < 0.001$). Interestingly, rpS6 phosphorylation was linearly affected by concentrations of Ile (Ile, $P = 0.013$), but not of Leu, and this response was affected by Thr (Ile*Thr, $P = 0.007$). Phosphorylation of rpS6 and eEF2 were negatively correlated (0.38, $P < 0.001$), and the former tended to be correlated with mTOR phosphorylation (0.15, $P < 0.086$). These results are in agreement with previous ones where independent effects of Leu and Ile on translation regulation were observed.

Key Words: essential AA, mTOR pathway, protein translation

W69 Effects of two different ruminant methionine technologies on milk and milk component production across a range of metabolizable methionine adequacy. R. S. Ordway*[1], C. G. Schwab[2,3], B. K. Sloan[4], and N. L. Whitehouse[2], *[1]Balchem Corporation, New Hampton, NY, [2]University of New Hampshire, Durham, [3]Schwab Consulting LLC, Boscobel, WI, [4]Adisseo North and Central America, Alpharetta, GA.*

Methionine is often considered the first limiting AA in dairy cow diets and providing more metabolizable Met (MP-Met) in diets in the form of ruminant Met products may have positive consequences on lactational performance and the efficiency of utilization of metabolizable protein

(MP). Ruminant Met products can only be used effectively in ration formulation if they are well characterized in terms of the quantity of MP-Met they provide per unit of product and it is reasonable to assume that diets adequate in MP-Met would not elicit a milk or milk component response to additional MP-Met. Forty multiparous lactating Holstein dairy cows were used in a replicated randomized complete block split plot 5 × 5 Latin square design with a 2 × 2 × 5 factorial arrangement of treatments. The main effects were (1) 2 levels of dietary Met adequacy [Limiting (L) or Adequate (A)]; (2) 2 forms of dietary Met (encapsulated DL-Met, Smartamine M (S), or the dry isopropyl ester of the Met analog, MetaSmart (M); and (3) 5 incremental levels (0, 3, 6, 9, or 12 g/d) of supplementary estimated MP-Met. The basal diets were formulated to meet NRC (2001) requirements for energy and nutrients and were identical except for predicted Met in MP (L: 1.81% and A: 2.31%). The Lys to Met ratios in MP for the L and A diets were 3.73:1 and 2.94:1, respectively. Smartamine M was used to make the basal diet adequate in MP-Met and significance was declared at $P < 0.05$. There were no differences in DM intake, milk fat yield, or milk urea N across treatments. There was a linear decrease in milk yield, protein yield, and lactose yield and a linear increase in fat concentration for AS. There was a linear increase in milk protein concentration for both LS and LM and a linear increase in milk protein yield for LM only. The results of this research indicate that the Met status of the basal diet and the source of supplemental dietary Met affect the response in milk and milk component production differently and also provide evidence that Met analogs are metabolized differently than DL-Met.

Key Words: methionine, methionine analogue, amino acids

W70 Performance and health of Holstein dairy calves fed Peptide Powder 80 or hydrolyzed wheat protein as alternative protein sources in milk replacers. H. Chester-Jones*[1], D. Dean[2], D. Ziegler[1], K. Halpin[2], M. Raeth-Knight[3], and D. Carlson[4], *[1]University of Minnesota Southern Research and Outreach Center, Waseca, [2]International Ingredient Corporation, St. Louis, MO, [3]University of Minnesota, St. Paul, [4]Milk Products, Chilton, WI.*

One-hundred twelve (2–4 d old) individually fed Holstein heifer calves (39.7 ± 0.7 kg) were randomly assigned to 1 of 4 treatments in January, 2012 to evaluate pre- (d 1 to 42) and post-weaning (d 43 to 56) calf performance and health when partially replacing milk protein in milk replacers (MR) with Peptide Powder 80 or hydrolyzed wheat protein. Peptide Powder 80 (International Ingredient Corp., St. Louis, MO) is a novel protein source designed for MR made up of hydrolyzed vegetable proteins and yeast (80% CP, % DM). All calves were fed a non-medicated 20% protein:20% fat MR at 0.284 kg in 1.99 L water (12.5% solids) 2× daily for the first 35 d and 1× daily from d 36 to weaning at d 42. Calf starter (CS; 18% CP, as-fed) and water were offered free choice d 1 to 56. Day 1 to 14, 1:1 neomycin:oxytetracycline was added to the MR solution to provide 22 mg/kg BW/d. Lysine and total sulfur amino acid concentrations in MR were balanced across all treatments with the use of synthetic AA. Treatments (TRT) were (1) Control all milk MR; (2) MR with 33% of the CP replaced by hydrolyzed wheat protein; (3) MR with 33% of the CP replaced by Peptide Powder 80; and (4) MR with 33% of the CP replaced by Peptide Powder 80 and additional Thr and Trp to be equivalent to TRT 1. There were no pre- or post-weaning ADG, CS, DMI and hip height (HH) differences ($P > 0.05$). Overall 56 d total BW gain, CSI, DMI and HH gain averaged 36.9 kg, 47.2 kg, 68.4 kg and 10.25 cm, respectively. Gain:feed (d 1 to 56) was higher ($P < 0.05$) for calves on TRT 2 (0.56) vs. those fed TRT 3 and 4 (0.53), but G:F did not differ between TRT 1 calves (0.54) and calves fed TRT 3 or 4. There were no TRT differences in scouring d and treatment costs. Under the conditions of this study, partially replacing milk protein in MR with Peptide Powder 80 or hydrolyzed wheat protein resulted in similar calf performance.

Key Words: Holstein calves, milk replacer protein sources, performance

W71 Effects of feeding LysiPEARL and rumen-protected lysine sources on plasma lysine concentration in lactating dairy cows. W. D. Weich*[1], K. F. Kalscheur[1], F. R. Valdez[2], and C. A. Macgregor Jr.[3], *[1]South Dakota State University, Brookings, [2]Kemin Industries, Inc., Des Moines, IA [3]Soy Best, West Point, NE.*

A common method to balance for metabolizable protein lysine in lactating dairy cows is to feed commercial sources of rumen-protected (RP) lysine. The objective of these experiments was to evaluate the effects of feeding a source of RP-lysine on plasma lysine. In the first experiment, 40 Holstein cows were fed a common diet randomly assigned to one of 5 topdress treatments: (1) Control, (2) Lysine HCl, (3) Aminoshure-L (Balchem Inc., New Hampton, NY), (4) LysiPEARL (Kemin Industries Inc., Des Moines, IA), and (5) USA Lysine (Kemin Industries Inc.). Each lysine treatment provided 150 g/h/d of lysine HCl and were blended into 900 g of ground corn and fed so treatments were consumed before availability of the daily TMR. Jugular blood samples were taken at 2 h intervals starting at feeding and analyzed for plasma amino acid (AA) concentration. Responses of plasma lysine concentrations compared with control were summed for each plasma collection to demonstrate overall change. Cows fed LysiPEARL (171 mg/dL) and USA LYSINE (256 mg/dL) had greater ($P < 0.10$) lysine concentrations, while cows fed Aminoshure-L (40 mg/dL) and Lysine HCl (86 mg/dL) were not different ($P > 0.10$) from cows fed Control. In the second experiment, LysiPEARL was added to fresh soy gums which were then added to mechanical extracted soybean meal (MES) (Soy Best; West Point, NE). Eight Holstein dairy cows were randomly assigned to one of 2 treatments. The first treatment diet contained 2.27 kg MES fortified with LysiPEARL (TRT), while the second treatment contained 2.27 kg MES without the LysiPEARL addition (CON). Diets were fed for 8 d and jugular blood samples were collected at 0.5 h before feeding and at 2 h intervals for 20 h on d −1 and d 8. Plasma AA data were summarized and expressed as a change from baseline determined on d −1. Plasma lysine for cows fed TRT (33.3 mg/dL) was greater ($P < 0.10$) compared with cows fed CON (21.4 mg/dL). In conclusion, results demonstrate LysiPEARL products are effective in increasing plasma lysine concentration when fed alone or when inserted into gums and combined with MES.

Key Words: rumen-protected lysine, mechanical extracted soybean meal

W72 Impact of fiber and monensin in texturized calf starters when fed in the nursery phase on calf health and performance in both the nursery and grower phases. D. Ziegler*[1], B. Ziegler[2], H. Chester-Jones[1], D. Schimek[2], and M. Raeth-Knight[3], *[1]University of Minnesota Southern Research and Outreach Center, Waseca, [2]Hubbard Feeds Inc., Mankato, MN, [3]University of Minnesota, St. Paul.*

One-hundred four (2–4 d old) individually fed Holstein heifer calves (41.2 ± 0.72 kg BW) were randomly assigned in a 2 × 2 factorial design to evaluate calf performance and health when fed texturized calf starters (CS) with varying fiber levels with and without monensin (M).The effect of the nursery diets on later calf performance were observed in group pens (7 heifers/pen) when fed a common diet from 9 to 25 wk of age. All nursery calves were fed a non- medicated 20% protein:20% fat milk replacer (MR) 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. Calf starter (CS; 18% CP, as-fed) and water were fed free choice d 1 to 56. Day 1 to 14, 1:1 neomycin:oxytetracycline was added to the MR solution to provide 22 mg/kg BW/d. Treatments were 1), Lower fiber (LF) CS with 0 mg/kg M; 2), LF CS with 49.5 mg/kg M; 3), Higher fiber(HF) CS with 0 mg/kg M and 4), HF CS with 49.5 mg/kg M. LF CS avg. 8.5% ADF and 16.4% NDF. HF CS avg 12.3% ADF and 18.3% NDF. Over 56 d in the nursery phase, calves fed CS with M had lower gains ($P = 0.007$) total CS and total DMI ($P = 0.02$) regardless of fiber level. There were no treatment health costs, gain/feed or hip height (HH) gain differences ($P > 0.05$). In the grower phase, heifers were limit-fed a common 16% CP grain mix daily (2.73 kg/heifer, d 1 to 56 and 2.27 kg/heifer, d 57 to 112) with free choice hay. There were CS × M treatment interactions ($P = 0.05$) for gain over the 112 d grower phase. There were no differences ($P > 0.05$) in HH for the grower period but CS × M interactions ($P = 0.04$) for HH were observed for the combined study periods. Under the conditions of the nursery phase, through 56 d, calves fed M had lower intakes and gains. Fiber level had no gain affects. There were indications of compensatory growth over the 112 d grower period from calves fed CS with M in the nursery phase.

Key Words: calf performance, calf starter, monensin and fiber levels

W73 Manual manipulation of calf starter for calves fed milk replacer: Effects on growth, starter intake, and weaning. N. E. Guindon, R. G. Cabral*, N. T. Antaya, N. L. Whitehouse, and P. S. Erickson, *University of New Hampshire, Durham.*

Thirty-six Holstein heifer calves were assigned at birth to 1 of 4 treatments in a 2 × 2 factorial arrangement of treatments in a randomized complete block. The objectives of this study were to determine if manually stirring calf starter resulted in increased dry matter intake (DMI), growth and improved weaning in calves fed a high protein milk replacer (HPMR). Treatments were (1) conventional MR (CMR)+ calf starter with no stirs, (2) CMR+ calf starter with stirs at 1030 and 1400 h, (3) HPMR + calf starter, and (4) HPMR + calf starter with stirs at 1030 and 1400 h. All calves had free-choice water. Milk replacer was fed twice daily. Calves were on treatment for 6 wk and weaned at wk 7 (fed MR once daily) and tracked for 1 wk until d 56. Stirs/no stirs continued until d 56. Water intake ($P < 0.001$), average daily gain (ADG) ($P < 0.0001$), DMI ($P < 0.0001$), and feed efficiency (ADG/DMI, $P < 0.01$) were increased in HPMR-fed calves compared with calves fed CMR preweaning (2.24 L/d vs. 0.97 L/d; 0.60 kg/d vs. 0.28 kg/d; 1.23 kg/d vs. 0.79 kg/d; 0.48 vs. 0.30, respectively). Calves fed HPMR had greater wither height gain ($P < 0.001$), and hip height gain ($P < 0.02$) compared with calves fed CMR preweaning (0.21 cm/d vs. 0.15 cm/d, respectively, for hip and wither height gains). Calves that had starter stirred ate less DM ($P < 0.05$) and tended to eat less starter ($P < 0.1$) compared with calves that did not have starter stirred (0.97 kg/d vs. 1.05 kg/d; 0.23 kg/d vs. 0.3 kg/d, respectively). During wk 7, calves formerly fed HPMR ate less ($P < 0.0001$) starter than calves fed CMR (0.50 vs.1.18 kg/d, respectively), but more ($P < 0.0001$) MR (1.13 kg/d vs. 0.45 kg/d). Calves that had their starter stirred tended ($P < 0.10$) to eat less starter and DM than calves that did not have their starter stirred (823 g/d vs. 979 g/d; 1.61 kg/d vs. 1.77 kg/d respectively). Postweaning, calves formally fed HPMR ate less starter ($P < 0.01$) than calves fed CMR (1.22 kg/d vs. 1.69 kg/d respectively). Manual manipulation of starter did not improve growth or DMI preweaning, weaning and postweaning phases in calves fed either HPMR or CMR.

Key Words: calf, milk replacer, starter

W74 Effect of 2-hydroxy-4-methylthio-butanoic acid (HMTBa) on ruminal fermentation, digestibility, and performance of lactating dairy cows. C. Lee[1], J. Oh*[1], A. N. Hristov[1], and G. I. Zanton[2], *[1]Department of Animal Science, The Pennsylvania State University, University Park, [2]Novus International Inc., St. Charles, MO.*

HMTBa has been shown to stimulate microbial protein production in continuous culture and also has methionine-sparing effect in vivo. The objective of this experiment was to test the effect of HMTBa on ruminal fermentation and microbial protein synthesis, nutrient digestibility and urinary N losses, and performance of dairy cows. Eight multiparous lactating Holstein dairy cows (51 DIM, SD = 3.9) were assigned to 4 treatments in a replicated 4 × 4 Latin square trial. The basal diet was formulated to meet or exceed NRC (2001) recommendations and contained corn silage, grass hay, ground corn grain, whole heated soybeans, soybean meal, canola meal, cottonseed hulls, and other minor ingredients (DM basis: 15.9% CP and 33% NDF). Treatments were 4 levels of HMTBa, fed through the mineral/vitamin premix: 0 (control), 0.05, 0.10, and 0.15% (DM basis). Each experimental period was 28 d, including 21 d for adaptation. Ruminal ammonia and microbial N were labeled through a 6-d intraruminal infusion of $^{15}NH_4Cl$. Treatment had no effect on DM intake (28.4 to 28.9 kg/d; $P \geq 0.64$), milk yield (44.6 to 45.0 kg/d; $P \geq 0.46$), and feed efficiency and milk composition ($P \geq 0.12$). Total tract apparent digestibility of nutrients was also not affected ($P \geq 0.08$) by treatment, except digestibility of CP decreased quadratically ($P = 0.01$) with HMTBa supplementation. Fecal, but not urinary, and total excreta N losses were increased ($P = 0.004$ to 0.05; quadratic responses) by HMTBa. Ruminal pH and ammonia concentration were not affected by treatment ($P \geq 0.21$). Concentrations of acetate and propionate were not affected by treatment ($P \geq 0.08$), but butyrate concentration was decreased linearly ($P = 0.03$) by HMTBa. Concentration of microbial N in reticular small and large particulate phases and whole digesta tended to be numerically increased ($P \leq 0.17$) by HMTBa. In conclusion, HMTBa had no effect on intake and performance, decreased dietary CP digestibility, and tended to increase the concentration of microbial N in reticular digesta in the conditions of this crossover trial.

Key Words: dairy cow, rumen microbial protein, 2-hydroxy-4-methylthio-butanoic acid

W75 Yeast-derived microbial protein supplementation of dairy calves. V. A. Silveira[1], K. P. Freire[1], A. V. Siqueira[1], P. A. M. Barros Junior[1], I. M. Lima[2], M. S. Zoni[3], W. Giardini[4], R. Almeida*[2], and M. N. Pereira[1], *[1]Universidade Federal de Lavras, Lavras, MG, Brazil, [2]Universidade Federal do Paraná, Curitiba, PR, Brazil, [3]Milkonsult, Castro, PR, Brazil, [4]Alltech do Brasil, Araucária, PR, Brazil.*

Yeast-derived microbial protein (YMP) is a source of high quality protein and peptides. The supplementation of YMP to dairy calves before and after the weaning phase was evaluated. Fifty-eight Holstein calves, 32 milk-fed and 26 weaned, were paired blocked within rearing stage by body weight, and were randomly assigned to YMP (Demp, Alltech) or Control for 21d. Calves were forced fed 250mL of milk or water once per day, added or not of 40g/d of YMP. Calves were group fed by automatic feeders (DeLaval calf feeder CF150X) with whole pasteurized cow milk (20L) added of milk and milk replacer powder (1kg). A calf starter concentrate was offered ad libitum to all calves, and weaned calves also had access to ryegrass hay and haylage. Body weight was obtained at 7-d intervals at 2PM, rectal temperature was measured daily at 2PM, fecal (1 = normal, 4 = watery) and activity (1 = active, 4 = recumbent) scores daily, as well as the cost of medications. Data obtained over time was analyzed with Mixed of SAS with a model containing the fixed effects of rearing stage, block within rearing stage,

treatment, interaction of treatment and rearing stage, time, and its 2 and 3 term interactions. The mean square for calf within treatment tested the treatment effect. Mean age at experimental d1 for milk-fed calves was 50.7 ± 21.9 for Control and 49.9 ± 21.7 for YMP, and for the weaned calves it was 113.0 ± 16.9 and 115.0 ± 17.8, respectively. The mean BW of milk-fed calves was 98kg and of weaned calves 163kg. The intake of fluid diet by milk-fed calves was 7.4 and 7.5L/d for Control and YMP, respectively ($P = 0.53$). There was an interaction of treatment, time and rearing stage for daily gain ($P < 0.01$). Calves during the milk-fed phase gained 1.186g/d for Control and 1.211g/d for YMP, and for the weaned phase it was 1.212g/d and 1.421g/d, respectively (SEM = 0.055). There was no detectable effect on the cost of medications ($P > 0.28$) or rectal temperature ($P > 0.35$), and treatment did not affect the frequency of fecal or activity scores ($P > 0.53$, Chi-Square). The supplementation of YMP after weaning increased the daily gain of calves raised on an accelerated early nutrition program.

Key Words: calf feeding, calf, yeast-derived microbial protein

W76 Effect of supplementing vitamin E and β-carotene to prepartum Holstein cattle on health and reproductive responses. D. Wang[1], M. Garcia*[1], R. S. Bisinotto[1], N. Martinez[1], F. S. Lima[1], L. F. Greco[1], J. H. Shin[1], A. M. M. DiCalaça[1], A. L. Ranieri[1], B. L. Artiaga[1], E. K. Ganda[1], G. C. Gomes[1], L. F. V. Becker[1], S. C. Soares[1], V. S. Rezende[1], M. A. Engstrom[2], J. E. P. Santos[1], and C. R. Staples[1], *[1]University of Florida, Gainesville, [2]DSM, Parsippany, NJ.*

Objectives were to improve health and reproductive performance of Holstein cattle by drenching antioxidants during the periparturient period. At 23 d before the expected calving date, Holsteins were blocked by parity and randomly assigned to one of 4 treatments arranged in a 2 × 2 factorial design. Factors were drenching with vitamin E (VitE; 0 or 14,000 IU/drench) and β carotene (BC; 0 or 5 g/drench). Animals were drenched at approximately d −23, −12 and 0 relative to calving. Cows were monitored daily during the first 10 DIM for rectal temperature and vaginal discharge. Cows were presynchronized with 2 injections of $PGF_{2\alpha}$ at 46 ± 3 and 60 ± 3 DIM. Cows not inseminated in estrus after the second $PGF_{2\alpha}$ injection were enrolled in a 5-d timed AI protocol starting at 72 ± 3 DIM. The occurrence of retained fetal membranes (RFM) was included in the model to analyze for metritis (MT), puerperal metritis (PMT), and fever (≥39.5°C). The incidence of RFM was 7.3% (52/708). Drenching BC to animals with RFM reduced ($P \leq 0.04$) the incidence of PMT (31.0 vs. 65.2%) and fever (41.4 vs. 69.6%). Drenching VitE tended to reduce ($P = 0.08$) the incidence of MT (24.2 vs. 27.9%) and reduced ($P \leq 0.04$) the incidence of PMT (10.6 vs. 13.5%) and fever (32.7 vs. 36.7%). However, clinical endometritis (Metricheck) at 24 DIM was not affected by treatments. Drenching primiparous cows with BC reduced ($P = 0.04$) the incidence of mastitis (64.0 vs. 52.9%) but not multiparous cows (45.3 vs. 51.0%). Number of cases of mastitis and DIM at first mastitis were not affected by treatments. Eighty percent of cows had detectable corpus luteum by 63 DIM (n = 606) using ultrasound and was unaffected by treatment. Pregnancy at 60 d post AI (palpation) to first and second AI was not affected by treatments and averaged 27.8 and 33.5% for all inseminated cows, respectively. Pregnancy at 300 DIM was 73.8% for all cows (463/627) whereas proportion of culling was 33.2% with no effect of treatments. Drenching antioxidants prepartum and at calving improved some health measures but did not influence reproductive outcomes of Holstein cows.

Key Words: cow, antioxidant, reproduction

W77 Optimal lysine and methionine concentrations for milk protein production as determined with the latest versions of Dairy NRC (2001) and AMTS-Cattle. N. L. Whitehouse*[1], C. G. Schwab[1,2], T. Tylutki[3], and B. K. Sloan[4], *[1]University of New Hampshire, Durham, [2]Schwab Consulting LLC, Boscobel, WI, [3]Integrated Solutions for Sustainable Agriculture, Cortland, NY, [4]Adisseo North and Central America, Alpharetta, GA.*

We previously reported optimal concentrations for lysine (Lys) and methionine (Met) in metabolizable protein (MP) for NRC (2001), CPM (v.3.0.10), and AMTS (v.2.1.1) (Whitehouse et al., 2009; J. Dairy Sci. Vol. 92, E-Suppl.1). The indirect dose-response approach adopted by NRC (2001) was used to generate the dose-response plots, employing the same data set as used by NRC (2001). Since then, an updated version of NRC (v.1.1.9) and v.3.3.4 of AMTS have been released and are being used. The only change made to NRC (2001) affecting predicted nutrient supply was to fix the fractional passage rate (kp) equation for dry forages. Changes in AMTS affecting nutrient supply are the following changes in the feed library of CNCPS v. 6.1: changing protein pool A1 from NPN to ammonia N, assigning soluble true protein to protein pool A2, changing the fractional digestion rates (kd) for protein pools A1 and A2, and a refinement and standardization of the chemical composition of feeds in the feed library as described by Higgs et al. (2012; Cornell Nutrition Conference Proc.). This was done to better predict MP allowable milk. The objective of this work was to use the same trial data set as used previously to estimate the requirement values for Lys and Met in MP for the updated versions of NRC (2001) and AMTS. 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 and the optimal Lys/Met ratios for both versions of each model are shown below.

Table 1.

	Original NRC	Revised NRC	AMTS v. 2.1.1	AMTS v.3.3.4
Protein content				
Lys	6.80	6.83	6.68	6.97
Met	2.29	2.28	2.40	2.53
Lys:Met ratio	2.97:1	3.00:1	2.78:1	2.75:1
Protein yield				
Lys	7.10	7.14	6.74	6.93
Met	2.52	2.37	2.31	2.34
Lys:Met ratio	2.82:1	3.01:1	2.92:1	2.96:1

Key Words: lysine requirement, methionine requirement, model

W78 Lactational and systemic response of lactating dairy cows to duodenal infusions of lysine, methionine, and branched-chain amino acids. S. C. Li*[1], D. P. Bu[2], Y. D. Zhang[2], and J. Q. Wang[2], *[1]University of Manitoba, Winnipeg, MB, Canada, [2]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Four primiparous ruminal- and duodenal-fistulated Holstein dairy cows (BW 525 ± 14 kg, DIM 176 ± 18 d) were used to investigate the effects of duodenal infusion of lysine (Lys), methionine (Met), and branched-chain amino acids (BCAA) on lactational performance and plasma metabolites. Cows were fed a basal total mixed ration containing 8% alfalfa hay, 17% grass hay, 25% corn silage, and 50% concentrate (DM basis). After 10-d adaptation to the basal ration, 4 cows were randomly assigned in a 4 × 4 Latin square design with four 8-d continuous duodenal infusions

of the following amino acid mixtures: (1) 40 g/d of Lys, 19 g/d of Met and 75 g/d of BCAA consisted of 40% leucine (Leu), 40% isoleucine (Ile) and 20% valine (LMB); (2) LMB with BCAA removed (LM); (3) LMB with Met removed (LB); and (4) LMB with Lys removed (MB). Feed and milk samples were collected in the last 4 d of AA infusion, and jugular vein blood was sampled at the last day of the infusion. Dry matter intake (18.2 kg/d), milk yield (16.98 kg/d), milk concentration of fat (4.91%), lactose (4.57%), casein protein (2.80%), and whey protein (0.95%) were not affected by treatments. No effect of the treatments was observed on plasma Lys concentration (85.8 μ*M*). Plasma Met concentration was higher in LM cows compared with that in LMB, LB, and MB cows (102.9 vs. 65.6, 79.4, and 68.9 μ*M*, respectively; $P < 0.01$). Plasma Ile and Leu concentrations were higher ($P < 0.01$) in LMB and LB cows (147.8 and 100.6, 171.2 and 113.3 μ*M*, respectively) compared with that in LM and in MB cows (115.7 and 92.0, 126.0 and 96.9 μ*M*, respectively). Valine was not affected by the treatments (167.3 μ*M*). No treatment effect on blood glucose and insulin was observed (3.82 m*M* and 0.71 ng/mL, respectively). IGF-1 in plasma tended to be lower in MB cows than that in LMB, LM and LB cows (221.6 vs. 238.2, 252.5, and 249.0 ng/mL, respectively; $P = 0.07$). The results indicated that Lys was limited AA to the basal diet used in the study as plasma Lys was not affected by all treatments, as well as a tendency of lowered IGF-1 when Lys was not infused.

Key Words: branched-chain amino acid, dairy cow, lysine

W79 Influence of combination of *Salix babylonica* extract with mineral/vitamin mixture on in vitro gas production kinetics and dry matter degradability of total mixed ration. A. Z. M. Salem*[1], M. M. Y. Elghandour[1], H. Gado[2], L. M. Camacho[3], R. Rojo[4], and J. L. Borquez[1], *[1]Facultad de Medicina Veterinaria y Zootecnia, Universidad Autonoma del Estado de Mexico, Mexico, [2]Animal Production Department, Faculty of Agriculture, Ain Shams University, Qalubia, Egypt, [3]Facultad de Medicina Veterinaria y Zootecnia, Universidad Autonoma de Guerrero, MexicoCd. Altamirano, Guerrero, Mexico, [4]CU-UAEM Temascaltepec, Universidad Autonoma del Estado de Mexico, Mexico.*

The aim of this study was to determine effects of increasing doses of the Salix babylonica extract (SB) and mineral/vitamin mixture (MV) or their combination, as additives, on in vitro gas production and some ruminal fermentation parameters of a total mixed ration of concentrate with corn silage (TMR - 50:50 on DM basis). Four levels of SB extract (0, 0.6, 1.2 and 1.8 mL/g DM) and others of MV (0, 0.5, 1.5 and 2.5 g/100 g DM). Ruminal fluid was obtained from 2 Brown Swiss cows fitted with permanent rumen cannulas fed a TMR of a 50:50 commercial concentrate and alfalfa hay ad libitum. Samples of TMR were weighed into 120 mL serum bottles with appropriate addition of SB extract and then 10 mL of particle free ruminal fluid was added to each bottle followed by 40 mL of the buffer solution and finally, MV doses were added. The GP was recorded at 2, 4, 6, 8, 10, 12, 24, 48 and 72 h of incubation. After 72 h, the incubation was stopped and the pH of the mixture was determined and filtrate used to determine dry matter degradability (DMD), partitioning factor (PF_{72}), gas yield (GY_{24}), in vitro organic matter digestibility (OMD), metabolizable energy (ME), short chain fatty acids (SCFA), and microbial protein production (MCP). Individual addition of SB extract linearly and quadratically increased ($P < 0.05$) GP during all the incubation times, while the addition of MR was linearly increased ($P < 0.05$) GP produced at 48 and 72 h of incubations. The addition of MV was only quadratically increased asymptotic GP ($P = 0.038$). The SB × MR interaction increased ($P = 0.01$) lag time and GP ($P < 0.05$) during the first 36 h of incubation. Addition of SB linearly and quadratically increased ($P < 0.05$) all fermentation parameters except DMD and rumen pH. The addition of MV had only quadratically increased ($P < 0.05$) of pH, PF_{72}, GY_{24} and MCP. Combination of SB × MV increased ($P < 0.05$) DMD, OMD, ME, PF_{72} and SCFA. Combination of *Salix babylonica* extract with mineral/vitamin mixture could be affect positively on ruminal fermentation.

Key Words: gas production, minerals/vitamin, ruminal fermentation

Ruminant Nutrition: Feeding, Ruminal Fermentation, and Efficiency of Production II

W80 Effects of different feeding frequencies on feedlot performance and carcass traits of feedlot Nellore cattle. T. V. B. Carrara*[2,3], J. Silva[2], M. C. S. Pereira[2], A. L. N. Rigueiro[2], D. H. M. Watanabe[2], D. D. Estevam[2], D. P. Silva[2], D. V. F. Vicari[2], C. A. Oliveira[2], I. C. Batista Junior[2], M. D. B. Arrigoni[1], F. T. V. Pereira[2], D. J. C. Oliveira[4], G. P. Mateus[4], D. D. Millen[2], *[1]São Paulo State University (UNESP), Botucatu, Brazil, [2]São Paulo State University (UNESP), Dracena, Brazil, [3]Supported by FAPESP, São Paulo, Brazil, [4]APTA, Andradina, São Paulo, Brazil.*

This study, conducted at the São Paulo State University feedlot, Dracena Campus, Brazil, was designed to determine the effects of different feeding frequencies on overall feedlot performance and carcass traits of Nellore cattle. The experiment was designed as a completely randomized block, replicated 12 times, in which 48 18-mo-old yearling Nellore bulls (358.2 ± 19.4 kg) were fed in individual pens for 94-d according to the following treatments: (1) feeding one time daily (1×; 0800), (2) feeding 2 times daily (2×; 0800 and 1400), (3) feeding 3 times daily (3×; 0800, 1100 and 1400), and (4) feeding 4 times daily (4×; 0800, 1100, 1400 and 1700). The adaptation program consisted of ad libitum feeding of 2 adaptation diets over period of 14-d with concentrate level increasing from 60% to 86% of diet DM. The finishing diet contained: 67.0% cracked corn grain, 14.0% sugarcane bagasse, 9.0% soybean hulls, 5.5% soybean meal, 4.0% supplement containing 30% of urea, and 0.5% limestone (DM basis). Orthogonal contrasts were used to assess linear, quadratic, and cubic relationship between feeding frequency and the dependent variable. Feeding frequency did not affect ($P > 0.10$) dressing percentage (1× = 55.0%; 2× = 54.6%; 3× = 56.1%; 4× = 55.6%), and DMI in kilos (1× = 7.75 kg; 2× = 7.95 kg; 3× = 8.44 kg; 4× = 8.10 kg) or as % of BW (1× = 1.91%; 2× = 1.98%; 3× = 2.04%; 4× = 1.97%). However, as feeding frequency increased, ADG (1× = 0.979 kg; 2× = 0.961 kg; 3× = 1.175 kg; 4× = 1.138 kg) final BW (1× = 449.8 kg; 2× = 445.4 kg; 3× = 467.4 kg; 4× = 463.6 kg), G:F ratio (1× = 0.128; 2× = 0.121; 3× = 0.141; 4× = 0.142) and HCW (1× = 246.9 kg; 2× = 243.0 kg; 3× = 263.1 kg; 4× = 258.1 kg) linearly increased ($P < 0.05$). The HCW was also affected ($P = 0.01$) cubically as feeding frequency increased. Thus, based on the results of this study, increasing feeding frequency affected feedlot performance and carcass traits of Nellore cattle. In a practical way, feeding yearling Nellore bulls 3 times daily seems to be the most feasible option, as beef prices are generally based on HCW.

Key Words: frequency, HCW, zebu

W81 Growth performance and carcass traits in Alpine male goat kids supplemented with hydroponic green fodder from wheat and corn. M. Guerrero Cervantes*[1,4], A. S. Juárez Reyes[1,4], F.G. Ríos Rincón[2,4], M. A. Cerrillo Soto[1,4], H. Bernal Barragán[3,4], and C. Angulo Montoya[3], *[1]Universidad Juárez del Estado de Durango, Durango, Durango. México, [2]Universidad Autónoma de Sinaloa, Culiacán, Sinaloa. México, [3]Universidad Autónoma de Nuevo Léon, San Nicolás de los Garza, Nuevo Léon. México, [4]Red Internacional de Nutrición y Alimentación en Rumiantes, México.*

This study was carried out to determine the effect of supplementing hydroponic green wheat (HGW; *Triticum aestivum* L.), or hydroponic green corn (HGC; *Zea mays*) on growth performance and carcass traits of Alpine male goat kids fed an oat-straw (OS) based diet. Twenty-five Alpine intact male kids (160 d of age; 20 ± 3 kg BW), were placed during 13 wk, in individual pens, assigned to 5 groups of 5 kids each, and fed with diets calculated according to the French system to balance for intestinal digestible protein (g/d), derived from nitrogen (IDPN) and from energy (IDPE). Diets were composed as follow: T1:50% OS, 35% HGW, 15% rolled corn (RC); T2:50% OS, 35% HGC, 15% cottonseed meal (CSM); T3:50% OS, 30% RS and 20% CSM; T4:50% OS, 18% HGW, 19% RS and 13% CSM; T5:50% OS, 18% HGC, 13% RS and 19% CSM. Data of daily weight gain, DMI, feed conversion and carcass traits were analyzed by ANOVA according to a completely randomized block design, using the initial BW as covariate. Orthogonal contrasts were used to compare diets with HGW and with HGC. The T2 was lower ($P \leq 0.01$) DMI (691 g/d) and feed conversion (8.7:1) was greater ($P \leq 0.05$) than in others. Intake of IDPN (60 g/d) and IDPE (61 g/d) was higher in T4 than in others. Highest ribeye area (8.5 cm^2) was registered by T5. Goat kids fed diets supplemented with HGC performed better ($P \leq 0.05$) than with HGW. In conclusion, feeding growing kids with HGC supplemented diets improved feed conversion and ribeye area and is a valuable alternative to counter high costs of concentrate feeding.

Table 1. Intake, feed conversion and carcass composition traits in Alpine male kids

	T1	T2	T3	T4	T5	SEM	P-value
Daily weight gain (g)	76	81	86	67	88	15.3	0.2051
Daily DMI (g)	798[a]	691[b]	792[a]	806[a]	791[a]	44.6	0.0001
IDPN intake (g/d)	57[ab]	45[b]	57[a]	60[a]	56[a]	4.2	0.0001
IDPE intake (g/d)	60[a]	50[b]	59[a]	61[a]	57[ab]	4.2	0.0001
Feed conversion[1]	10.6[ab]	8.7[b]	9.3[ab]	12.1[a]	9.4[ab]	1.6	0.0011
Carcass yield (%)	51	50	51	51	52	3.6	0.5967
Ribeye area (cm^2)	6.8[b]	8.2[ab]	8.2[ab]	7.1[ab]	8.5[a]	0.8	0.0025
Muscle (%)	71	71	71	72	75	2.9	0.0657
Feed cost/d ($)	0.25	0.25	0.34	0.31	0.30		

[a,b]Means with different superscript differ.
[1]Total DM intake/total weight gain.

Key Words: hydroponic green corn, hydroponic green wheat, male kid

W82 Molecular cloning and characterization of a novel cellulase with xylanase activity from a metagenomic library of goat rumen. C. Y. Fan[1], H. Q. Jiang[1], Y. H. Zhang[1], X. Z. Sun[1], and J. B. Cheng*[1,2], *[1]College of Animal Science and Technology, Anhui Agricultural University, Hefei, China, [2]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Ruminal microbiome has been as a rich source of cellulase not only for feed but also for bioenergy industry. However, this enzyme source is largely untapped because more than 85% of the ruminal microbes have not been cultivated. The objective of this study was to identify novel cellulase gene from a bacterial artificial chromosome (BAC) library and further to analyze its characteristics. BAC library was constructed using genomic DNA isolated from goat ruminal content. Screening of the clones with cellulase activity was performed on LB agar plates supplemented with 1% carboxymethyl cellulose sodium (CMC) and 12.5 mg/L chloramphenicol. The positive clones were extracted and

partially digested with Sau3AI. The 2–5kb digested DNA fragments were subcloned in pUC19 digested with *Bam*HI and introduced into *E. coli* DH5α. The gene responsible, Cel28a, contains an open reading frame consisted of 1,596 bp nucleotides that encoded 509 amino acid residues, with a typical N-terminal signal peptide of 22 amino acid residues with a molecular mass of 55 Da. A phylogenetic analysis of amino acid sequence with other cellulase enzymes suggested that cel28a belongs to glycosyl hydrolase family 5. The recombinant pET28a(+)/cel28a gene was overexpressed in *E. coli* BL21(DE3) cells to overproduce the cellulase protein with dual histidine tag at its C-terminus and N terminus. The recombinant cellulase was purified by affinity chromatography using nickel-nitrilo-triacetic acid agarise resin (Ni-NTA). The optimal substrate for cel28a to hydrolyze was CMC among CMC, oat spelt xylan, filter paper, birch wood xylan, and microcrystalline cellulose. The preference of the substrate with CMC, oat spelt xylan, and birch wood xylan indicates that cel28a is a cellulase with xylanase activity. The optimum temperature for Cel28a was 50°C, but the activity of Cel28a reduced quickly when temperature was above 60°C. The activity of Cel28a was more than 60% in the range of pH 4–6, and the optimum pH was 5.0 at 40°C using CMC and oat spelts xylan as substrate.

Key Words: cellulase, metagenome, rumen

W83 Effects of restricted versus conventional dietary adaptation over periods of 6 and 9 days on feedlot performance and carcass characteristics of Nellore cattle. A. Perdigão*[1,3], M. D. B. Arrigoni[1], D. D. Millen[2], R. S. Barducci[1], M. A. Factori[1], L. M. N. Sarti[1], M. C. S. Franzoi[1], L. C. Vieira Junior[1], M. T. Cesar[1], F. A. Ribeiro[1], D. F. Broleze[1], A. L. C. Brichi[1], and R. F. Pessin[1], *[1]São Paulo State University (UNESP), Botucatu, Brazil, [2]São Paulo State University (UNESP), Dracena, Brazil, [3]Supported by FAPESP, São Paulo, Brazil.*

This study, conducted at the São Paulo State University feedlot, Botucatu Campus, Brazil, was designed to determine effects of restricting intake of the final finishing diet (REST) as a means of dietary adaptation compared with diets increasing in concentrate (STEP) over periods of 6-d and 9-d on overall feedlot performance and carcass traits. The experiment was designed as a randomized completely block with a 2 × 2 factorial arrangement, replicated 6 times (5 bullocks/pen), in which 120 22-mo-old yearling Nellore bulls (352.03 ± 19.61 kg) were fed in 24 pens for 84-d according to the treatments: STEP for 6-d, STEP for 9-d, REST for 6-d, and REST for 9-d. The STEP program consisted of ad libitum feeding of 2 adaptation diets over periods of 6-d or 9-d with concentrate level increasing from 61 to 85% of diet DM. The REST program consisted of restricted intake of the final diet (85% concentrate) with programmed increases in feed offered until yearling bulls reached ad libitum access over periods of 6-d or 9-d. A ($P < 0.05$) protocol main effect was observed for ADG (STEP = 1.431 kg; REST = 1.332 kg), DMI (STEP = 9.26 kg, REST = 8.72 kg) and DMI as % of BW (STEP = 2.25%, REST = 2.14%). However, no ($P > 0.10$) protocol main effect was observed for G:F (STEP = 0.154, REST = 0.153), HCW (STEP = 258.5 kg, REST = 260.7 kg) and dressing percentage (STEP = 55.1%, REST = 55.1%). No ($P > 0.10$) days main effect was observed for any of the feedlot performance and carcass traits variables evaluated: ADG (6-d = 1.393 kg; 9-d = 1.370 kg), DMI (6-d = 9.03 kg; 9-d = 8.95 kg), DMI as % of BW (6-d = 2.20%; 9-d = 2.19%), G:F (6-d = 0.154; 9-d = 0.153), HCW (6-d = 262.1; 9-d = 257.0), and dressing percentage (6-d = 55.1%; 9-d = 55.1%). Animals in STEP protocol presented greater ADG because they consumed more feed, as G:F was similar when compared with animals in REST protocol. The adaptation in 6-d did not negatively affect overall feedlot performance and carcass traits of Nellore cattle.

Key Words: adaptation, feedlot, Nellore

W84 Effect of calf conditioning either before or at weaning during the dry season in northeast Mexico. R. G. Altamirano*[1], E. G. Ornelas[2,4], H. B. Barragán[2,4], R. A. Ramírez[2], and E. C. Gallegos[3], *[1]Instituo Nacional de Investigaciones Forestales, Agrícolas y Pecuarias (INIFAP), Campo Experimental Las Huastecas,, Altamira, Tamaulipas, México, [2]Universidad Autónoma de Nuevo León, Facultad de Agronomía,, General Escobedo, Nuevo León, México, [3]Universidad Nacional Autónoma de México, Fac. Medicina Veterinaria y Zootecnia,, Martínez de la Torre, Veracruz, México, [4]Red Internacional de Nutrición y Alimentación en Rumiantes, México, D.F., México.*

The effect of 3 conditioning strategies was evaluated from February through April 2012 upon 48 calves (27 females and 21 males) from a herd in Aldama, Tamaulipas. Twenty-eight days before weaning, calves with initial body weight of 121.0 kg were randomly assigned to 3 treatments: Control group (CG), without conditioning; Conditioning 28 d before weaning (CBW), and Conditioning at weaning (CAW). Conditioning consisted in application of internal and external parasite control, vitamins ADE via IM vaccination against common bacterial and viral diseases and offering a 35% CP supplement at 20 g/kg $LW^{0.75}$ per day. Body weight of 12-h fasted animals was registered and sample collected at days: −28, 0 (weaning), 28, 56 and 84. Response variables were average daily gain (ADG), internal parasite load (McMaster technique), serological immune response (IBR and BVD neutralizing antibodies testing), and incidence of clinical disease. Animals grazed pastures of Guineagrass (*Panicum maximum*), 7.1% CP and 62.8% NDF and African stargrass (*Cynodon plectostachyus*), 7.4% CP and 79.3% NDF. Data were analyzed according to a completely randomized design with 2 × 3 factorial arrangement of treatments. No interaction and sex effects ($P > 0.05$) were found. During the last 28 d before weaning, ADG of CBW calves was higher ($P < 0.05$) than the other 2 treatments (1,068 vs 411 and 409 g/d). After weaning, and up to d 84, ADG of conditioned calves was higher ($P < 0.05$) than control (614, 526 and 301 g/d, for CBW, CAW and CG, respectively). There were no differences among groups ($P > 0.05$) for nematode internal parasite load. There were more sick animals ($P < 0.05$) in the CG than in the conditioning treatments (10 vs. 3). Geometric mean (GM) of neutralizing antibodies titers showed that the serological response in vaccinated animals at d 84 was higher ($P < 0.05$) against BVDV than BoHV-1, but there was no difference ($P > 0.05$) between CBW and CAW. The CG group did not develop antibodies at d 84 against both viruses. Conditioning before or at weaning during dry season had positive effect on performance of weaned calves.

Key Words: calf, conditioning, weaning

W85 Effect of TMR particle size or rumen pH on diet and feed preference in lactating dairy cows. A. D. Kmicikewycz* and A. J. Heinrichs, *Pennsylvania State University, University Park.*

The objective of this study was to investigate effects of TMR particle size and rumen pH on diet and feed preference in lactating dairy cows. Twelve (8 ruminally cannulated) Holstein cows (91 ± 40 DIM, 695 ± 95 kg, and parity of 2.91 ± 1.16; mean ± SD) were used in a replicated 4 × 4 LSD with 4 21-d periods. Cows were assigned to squares by parity and randomly assigned to treatment. Diets contained corn silage (CS) with long (L) or short (S) particle size and were fed with 0 (L,S) or 5% (LH, SH) supplemental late cutting fine orchardgrass hay (11.7% CP, 56.0%

NDF); CS and ground corn comprised 23.2% and 11.1% of ration DM, and TMR contained 30.9% starch. Animals were housed individually, milked 2×/d, and fed 1×/d for 10% refusal rate. Each period consisted of 14 d adaptation followed by 3 d designated as baseline for feed intake. Day 17 was baseline for feed preference and rumen conditions. On d 18 DMI was restricted to 75% of baseline intake. On d 19, 4 kg (as-fed) fine ground wheat was mixed into the rumen digesta of each cow before feeding via rumen cannulas to provide a subacute rumen acidosis challenge. Data was analyzed using MIXED procedure of SAS. The rumen challenge successfully decreased rumen pH (5.39), but baseline weighted average rumen pH for all diets was very low (5.52). Average minimum rumen pH decreased from 5.06 to 4.92, and acetate, butyrate, valerate, and isobutyrate increased on challenge d. Treatments with long CS had lower DMI ($P < 0.05$) during baseline. Cows fed SH had greater DMI during challenge d compared with S, L, and LH. There was no difference in H DMI between baseline and challenge d. No differences were found for particle size selection or H preference between days for each diet. Milk yield was greatest for cows fed SH and lowest for L and LH (45.8, 44.1, 42.8 and 42.4 kg/d for SH, S, L and LH; $P < 0.05$). Milk fat, 1.49 kg/d, and protein, 1.40 kg/d, were greater ($P < 0.05$) in cows on diet SH than all other diets. Results of this study indicate prolonged low ruminal pH does not change preference for grass hay or longer forage particles.

Key Words: particle size, acidosis, ruminal pH

W86 Nutritional maintenance requirements and true absorption coefficients of calcium and phosphorus in ¾ Zebu × ¼ Holstein crossbred bulls. L. F. Prados*, S. C. Valadares Filho, A. N. Nunes, E. Detmann, D. Zanetti, D. R. Costa, S. A. Santos, L. D. S. Mariz, P. M. Amaral, L. C. Alves, and A. C. B. Menezes, *Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil.*

The objective of this study was to determine the maintenance requirements and true absorption coefficients for calcium and phosphorus in 3/4 Zebu × 1/4 Holstein crossbred bulls fed with different levels of calcium and phosphorus in diets. Eighteen 3/4 Zebu × 1/4 Holstein bulls with an initial mean body weight of 214 ± 4 kg and a mean age of 11 ± 0.2 mo were used in this study. These animals were assigned in a completely randomized design with 3 × 3 factorial arrangement. Three levels of calcium and phosphorus (low, medium and normal) and 3 periods of feedlot (56, 112 and 168 d) were tested. The 3 levels of calcium and phosphorus were low (1.8 and 2.2 g/kg), medium (3.0 and 2.4 g/kg), and normal (4.2 and 2.6 g/kg), respectively, for calcium and phosphorus in a dry matter basis. The diets were isonitrogenous (12.6%) and consisted of corn silage and concentrate (60:40) on a dry matter basis. To assess the excretions of Ca and P total fecal collection was performed for 3 d at the end of each feedlot period. Using the relationships between absorption and intake for calcium and phosphorus were obtained the daily maintenance requirements of Ca and P of 9.55 and 14.36 mg/EBW/d. Through the same regression, the true absorption coefficients of Ca and P were found to be 0.69 and 0.66, respectively. The maintenance requirement for Ca was lower than the amount recommended by the NRC (2000) (15.4 mg/BW/d). The P level recommended by the NRC (2000) is 16 mg/BW/d and is similar to the requirement value determined in this study. The true absorption coefficient for Ca was higher than the 0.55, value recommended by BR-CORTE (2010) but was similar to the value of 0.68 recommended by the ARC (1980). The absorption coefficient of P was similar to the value used by BR-CORTE (2010) (0.68). In conclusion, the maintenance requirements of Ca and P in 3/4 Zebu × 1/4 Holstein crossbred are, respectively, 9.55 and 14.36 mg/EBW/d.

Key Words: calcium, mineral requirement, phosphorus

W87 Dynamic shifts of rumen functional bacteria associated with forage types by quantitative real-time PCR. X. L. Hu, J. Q. Wang*, S. G. Zhao, J. W. Zhao, and D. P. Bu, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Ruminal microbiota is highly responsive to changes in diet and feeding regimen. This study was conducted to quantify the population of rumen dominant functional bacteria of Chinese Holstein cows fed forage based diets by real-time PCR. Forty-eight Chinese Holstein cows were blocked based on DIM and milk yield and randomly assigned to 3 treatments to evaluate the effect of the different diets on the quantity of rumen microorganism. The 3 treatments consisted of different roughage supplements which was MF (alfalfa plus corn silage, soybean meal), CSA (straw, soybean meal), CSB (straw, cottonseed and rapeseed meal). The experiment was conducted for 107 d and consisted of 2 periods. Period 1 lasted 91 d, during which cows were fed the 3 different diets (MF, CSA, CSB). Period 2 lasted 16 d and all animals were fed MF. Rumen fluid was collected by inserting a flexible plastic tube into the rumen before and after feeding on d 91 and 107. Then the rumen microbial DNA was extracted by CTAB plus bead beating DNA extraction method. Species-specific PCR primers were chosen from the literature to amplify partial 16S rDNA regions. The copy number of rumen microbiota was detected by quantitative real-time PCR. qRT-PCR analysis detected significant increases ($P < 0.05$) in the quantity (copies in per ml rumen fluid) of domain bacteria, *Prevotella bryanti*, *Ruminococcus albus*, *Selenomonas ruminantium*, and *Megasphaera elsdenii* in treatment MF than that of CSA and CSB on d 91 before feeding. And after feeding on d 91, *Prevotella brevis* and *Fibrobacter fuccinogene* in group CSA was significantly greater ($P < 0.05$) than group MF, *Ruminococcus albus* in group MF was significantly greater ($P < 0.05$) than CSA and CSB. There was not any difference on d 107 of period 2 among the 3 groups both before and after feeding. We concluded that the change of diets did produce an effect on the population of rumen functional bacteria, especially some bacteria which take part in the degradation of cellulose and protein.

Key Words: dietary change, population, rumen bacteria

W88 Effects of a corn straw or mixed forage diet on mRNA expression of genes related to glucose metabolism in the liver of dairy cows. W. Q. Li[1,2], D. P. Bu[1], J. Q. Wang*[1], X. M. Nan[1], and L. Y. Zhou[1], *[1]Institute of Animal Science, Chinese Academy of Agricultural Science, Beijing, China, [2]College of Life Science, Henan Agricultural University, Zhengzhou, China.*

Our objective was to identify the response of genes related to hepatic glucose metabolism to diets with different forage sources. Ten Chinese Holstein dairy cows in mid-lactation (DIM 100+10 d, BW 550 ± 50 kg) were randomly assigned to mixed forage diet (MF) with Chinese wildrye, alfalfa hay and corn silage as the forage source or corn straw diet (CS) with corn straw as the forage source. Diets were formulated to be isoenergetic and iso-nitrogenous. After 30-d experimental period, biopsy section of liver and blood samples were obtained at 0630h (before feeding). Expression of 28 genes coding for rate-limiting enzymes in hepatic gluconeogenesis pathway, pentose phosphate pathway, glycogen synthesis pathway, glycogen decomposition pathway, glycolysis pathway, glucose aerobic oxidation pathway, glucose transporters was detected with qRT-PCR. Statistical significance was evaluated by unpaired *t*-test analysis with SAS 9.0 software. Significance was declared at $P < 0.05$. Results showed that MF led to marked upregulation of PEPCK and G6P involved in hepatic gluconeogenesis pathway. No significant differences were observed in mRNA expression of genes involved in other glucose

metabolism pathways. Higher relative percentage mRNA abundance of G6P (22.58%), representing the important gluconeogenic enzyme and also catalyzing the last step in glycogenolysis, underscored its importance for ruminant hepatic glucose metabolism. Relative abundance of GLUT2 was the highest among hepatic glucose transporters. It was concluded that to respond to different roughage sources, genes involved in gluconeogenesis pathway and glycogen decomposition pathway had higher mRNA abundance percentage. And different roughage sources had little effect on else bovine hepatic glucose metabolism pathways and glucose transporter protein. This research paves the way for nutrient-gene interactions in dairy cows.

Key Words: diet, gluconeogenesis, glucose

W89 PCR-DGGE analysis reveals distinct diversity in the rumen bacterial community of dairy cows fed a corn straw or mixed forage diet. D. Jin, D. P. Bu*, S. G. Zhao, and J. Q. Wang, *Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Forage is an important component of diets for ruminant animals and vital in maintaining rumen function and health. The purpose of this study was to compare rumen bacterial community from cows fed different diets. Twelve healthy Chinese Holstein dairy cows fitted with rumen cannula and similar body weights were randomly assigned to 2 treatments: high forage diet (MF; forage:concentrate = 60:40) with Chinese wildrye, alfalfa hay, and corn silage as forage sources (n = 6) or low forage diet (CS; forage:concentrate = 40:60) as forage sources (n = 6). The solid and liquid fractions of rumen digesta were collected for the successive 3 d on the 13th week of the experiment. Total DNA were extracted and analyzed by denaturing gradient gel electrophoresis (DGGE) with subsequent cluster and sequence analysis. The DGGE profiles showed the quantity and optimal density of the DGGE bands in CS group were different from MF group. In addition, the DGGE-derived dendrograms showed that diet caused some changes both in liquid and solid-associated bacterial diversity. Shannon-Weiner index showed no difference ($P > 0.05$) between the 2 groups for liquid-associated bacteria, but it was lower ($P < 0.01$) in CS group than that in MF group for solid-associated bacteria. Some bands from CS group were less compared with MF group and sequences analysis of these different bands showed that diversity of *Prevotella* sp., *Acetivibrio ethanolgignens* and *Clostridium* sp. decreased in CS group. The other uncultured bacteria belonging to the phylum *Bacteroidetes*, *Firmicutes*, *Tenericutes* and *Proteobacteria* had some changes between the 2 groups. In conclusion, there is unique bacterial community and low diversity in the rumen of dairy cows fed the diet of corn straw.

Key Words: corn straw, DGGE, rumen bacteria

W90 Comparison of purine bases and nitrogen-15 for quantifying microbial protein synthesis using three marker systems and different sampling sites in cattle fed diets with sugar cane or corn silage. P. P. Rotta*[1], S. C. Valadares Filho[1], E. Detman[1], F. A. C. Villadiego[1], E. M. G. Burgos[1], A. A. G. Lobo[1], and J. A. Bendassoli[2], *[1]Universidade Federal de Vicosa, Viçosa, Brazil. [2]Universidade de Sao Paulo, Sao Paulo, Brazil.*

This study evaluated the use of 2 microbial markers [purine bases (PB) and ^{15}N] in 3 collection sites (abomasum, omasum and reticulum) and using 3 marker systems (single, double and triple) to estimate the synthesis of microbial nitrogen (MN) and the microbial protein synthesis efficiency (MPSE) in growing beef cattle. Eight ruminally and abomasally crossbred (Holstein × Zebu) bulls, with an average BW of 353 ± 36.9 kg, were used in two 4 × 4 Latin squares balanced for residual effects. The experimental diets studied were as follows: (1) 60% corn silage + 40% concentrate; (2) 40% corn silage + 60% concentrate; (3) 60% sugar cane + 40% concentrate; and (4) 40% sugar cane + 60% concentrate. Eight samples of abomasal, omasal and reticular digesta were collected in 9-h intervals for 3 d. Interactions ($P < 0.05$) were observed for MN between collection sites and microbial markers. In addition, interactions were also observed ($P < 0.05$) for the MPSE between the marker systems and the microbial markers. For PB, the greatest ($P < 0.001$) value of MN was observed for the digesta collected from the abomasum and reticulum. In contrast, for ^{15}N, the greatest ($P < 0.001$) value was observed for the digesta collected from the omasum. MN was similar ($P > 0.05$) for digesta collected from the abomasum when using both PB and ^{15}N. However, for digesta collected in the omasum, the greatest ($P < 0.001$) value was observed when ^{15}N was used. The triple marker system exhibited the greatest ($P < 0.01$) value for MN compared with the single and double marker systems. The use of ^{15}N is recommended to estimate the MN and the MPSE. In addition, the omasum is the recommended site for the collection of digesta. The triple marker system (cobalt EDTA (Co-EDTA) + ytterbium acetate (YbAc) + indigestible neutral detergent fiber (iNDF) is recommended for the above mentioned estimates.

Key Words: abomasum, omasum, reticulum

W91 Characterization of the dynamics in rumen bacterial community of cows fed three different diets using PCR-DGGE and qPCR. D. Jin[1], D. P. Bu*[1], S. G. Zhao[1], J. Q. Wang[1], and Z. T. Yu[2], *[1]Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Department of Animal Sciences, The Ohio State University, Columbus.*

Vital to the health and productivity of dairy cattle are rumen bacteria, and diet composition is the most important driver of bacterial community dynamics. This study examined bacteria communities in the rumen of dairy cows fed 3 different diets. Forty-eight Chinese Holstein dairy cows with similar days-in-milk and body weights were randomly assigned to 3 treatments mainly differing in forage source: MF diet (alfalfa hay, corn silage and soybean meal), CSA (corn straw and soybean meal) and CSB (corn straw, cottonseed and rapeseed meal). The cows were fed their assigned diet twice daily for 91 d, after which all were shifted to the MF diet. Rumen contents were collected by inserting a flexible plastic tube into the rumen and were performed at d 31, 61, 91, and 107 of the experiment before and after morning feeding. Bacterial community structure was analyzed using denaturing gradient gel electrophoresis (DGGE), with select DGGE bands being sequenced. The DGGE profiles showed clear difference among the 3 diets after feeding for 31 d, with the overall similarity being only 51%. As expected, the MF diet resulted in more unique bands than the CSA and CSB diets. The DGGE fingerprints became less difference among the 3 diets at d 61 and 91 compared with d 31, suggesting gradual adaptation of rumen bacteria to the diets. Analysis from the sequenced DGGE bands showed that genera *Vibrio*, *Prevotella*, *Brevundimonas*, and *Clostridium* were dynamic and affected by the diets. One distinct band appeared in the MF group, and sequencing of this band revealed a sequence identity being 90% identical with Vibrio sp. The qPCR quantification showed that this uncultured bacterium had a higher ($P < 0.001$) abundance in the MF group than in the other 2 groups at d 91, but it had a higher population in all 3 groups at d 107. In conclusion, different forage types changed

structure and populations of rumen bacterial community, and there was a unique bacterial community with high diversity in the rumen of dairy cows fed mixed forage.

Key Words: DGGE and qPCR, forage, rumen bacteria

W92 Heart rate and milk production of dairy cows fed with three different strategies in early lactation. D. A. Mattiauda*, P. Chilibroste, M. Carriquiry, J. P. Marchelli, and A. C. Espasandin, *Departamento de Produccion y Pasturas, Facultad de Agronomia, UdelaR, Uruguay.*

Heart rate (HR) was proposed as a good estimator of heat production in beef and dairy cows. Twenty-four Holstein multiparous cows (697 ± 30 kg BW, 3.3 ± 0.1 BCS, 3.3 ± 0.5 lactations) were used in a randomized block design to study the effect of feeding strategies (corn silage allocation) during early lactation on milk yield and HR. Cows were allocated in 3 different feeding strategies: T1) total mixed ration (TMR) offered in a dry lot pen; T2) pasture grazing offered one session (7 h) + TMR offered during the evening in a dry lot pen and T3) pasture grazing in 2 sessions (14 h) + TMR offered in the grazing paddock. All diets were formulated to offer 50 Mcal ENL and > 16.5% CP (dry matter basis). Heart rate (n = 4/treatment) (beats/min) was registered by implanted HR radiotransmitters each 15 s during 5 consecutive days at the beginning (14 ± 5 d in milk, DIM) and the end of experimental period (40 ± 5 DIM). Treatment effects were analyzed by ANOVA and LSmeans by treatment were obtained. Milk yield was greater in T1 than T2 and T3 cows (35.5, 30.1 and 29.6 ± 0.8 kg/d for T1, T2, and T3, respectively; $P < 0.001$). Heart rate at 10 DIM did not differ among treatments (93 ± 20, 110 ± 17 and 86 ± 25 beats/min for T1, T2, and T3, respectively; $P = 0.68$) but a trend ($P = 0.12$) was observed at 40 DIM being greater in T2 than T1 and T3 cows (89 ± 8, 114 ± 9 and 81 ± 11 beats/min, for T1, T2 and T3, respectively). The trend for greater HR in T2 cows was not directly associated with greater energy cost for milk production (as was greater in T1 cows) or walking activity (as was greater in T3 cows). Therefore results could suggest that T2 cows spent more energy associated to stress for feed competition (during grazing or at feed-troughs).

Key Words: dairy, feeding strategy, heart rate

W93 Assessment of in vitro fermentation characteristics of grass-legume mixed pasture forages with their different composition ratios using continuous cultures. C. T. Noviandi[1], K. Neal[1], J.-S. Eun*[1], D. R. ZoBell[1], M. D. Peel[2], and B. L. Waldron[2], *[1]Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan, [2]Forage and Range Research Laboratory, USDA-ARS, Logan, UT.*

A continuous culture experiment was performed to investigate effects of tall fescue (TF)-legume mixed pasture forages [TF-alfalfa (TF+ALF), TF-birdsfoot trefoil (TF+BFT), or TF-cicer milkvetch (TF+CMV)] with 3 different composition ratios at 25:75, 50:50, or 75:25 on a DM basis on in vitro fermentation characteristics. Nine dietary treatments were tested in a completely randomized design with a 3 (TF-legume mixtures) × 3 (TF:legume ratios) factorial arrangement (n = 3). Each culture fermentor was offered a total of 15 g DM/d in 4 equal portions at 0600, 1200, 1800, and 2400 h. Average daily culture pH ranged from 6.10 to 6.29 and was affected by TF-legume mixture and composition ratio ($P < 0.01$). Total VFA concentration averaged 51.4 mM and was not affected by treatments. While acetate concentration was similar across treatments, propionate concentration increased by the TF+CMV ($P < 0.01$). Decreasing legume proportion in the forage mixtures decreased propionate concentration ($P = 0.03$) regardless of forage types. Acetate-to-propionate ratio was higher ($P = 0.03$) with the TF+ALF compared with the TF+BFT and the TF+CMV. Ammonia-N concentration decreased ($P < 0.01$) with the TF+CMV compared with the TF+ALF, and it further decreased in cultures receiving the TF+BFT ($P < 0.01$). In addition, decrease in ammonia-N concentration ($P < 0.01$) was noticed when legume proportion in forage mixtures decreased. Offering the TF+BFT decreased methane production, whereas the methane production decreased by increasing legume proportion in all forage mixtures ($P < 0.01$). Overall results of this study indicate that TF+legume mixtures at a relatively high proportion of legume favorably shifted in vitro fermentation pathways by producing more propionate and less ammonia-N and methane. The beneficial effects with the TF+BFT may have resulted from condensed tannins in birdsfoot trefoil, while unique plant cellular structure of cicer milkvetch in the TF+CMV may contribute to the positive effects.

Key Words: continuous culture, in vitro fermentation, tall fescue-legume mixed pasture forage

W94 Cost structure and economic assessment of Spanish Assaf dairy sheep farms. M. J. Milan[1], F. Frendi[1], R. Gonzalez-Gonzalez[2], and G. Caja*[1], *[1]Ruminant Research Group (G2R), Universitat Autonoma de Barcelona, Bellaterra, Spain, [2]GEO, Benavente, Zamora, Spain.*

A total of 20 dairy sheep farms of Assaf breed, located in the Spanish Autonomous Community of Castilla y León (Provinces of León, Palencia, Valladolid and Zamora) and included in a group for receiving technical support (GEO, Gestión Empresarial de Ovino), were used to study their production cost structure during 2008 and for assessing their economic profitability. On average, farms had 89.2 ± 38.0 ha (own, 38%), 592 ± 63 ewes, yielded 185.9 ± 21.1 × 10^3 L/yr (316 ± 15 L/ewe) and were attended by 2.3 ± 0.2 annual working units (family, 64%). Total annual income was US$252.7 ± 29.9 × 10^3 coming from milk (78.6%), lamb (13.2%), culled ewes (0.5%) and other sales (0.8%, wool and manure) and completed with the European Union sheep subsidy (6.9%). Total annual costs were US$240.2 ± 24.6 × 10^3 addressed to attend feeding (62.0%), labor (18.3%), equipment maintenance and depreciation (7.6%), animal health (2.5%), financial (2.5%), energy, water and milking supplies (2.2%), milk recording (0.5%), and others costs (4.4%; assurances, shearing, association fees, etc). Mean dairy sheep farm profit per year was US$12.5 ± 7.7 × 10^3, being US$12.1 ± 10.8 per ewe, on average, and dramatically varying between US$–50.3 and 107.8 per ewe among farms. Only 60% farms were able to pay all the costs, the rest having negative exercises. Nevertheless, annual net margin was US$40.3 ± 8.5 × 10^3 on average, varying between US$0.8 and US$258.0 × 10^3 among farms. In this case, without including the opportunity costs, all farms had positive exercises. Annual cost and income (US$/ewe) functions depended on productivity (x, L/ewe) and were: $C = 207.7 + 0.653 \cdot x$ ($r^2 = 0.50$), and $I = 101.6 + 1.027 \cdot x$ ($r^2 = 0.88$), respectively, being the break-even point 284 L/ewe. Studied farms were on general of familiar type, medium-large sized, fully devoted to milk production and, most of them, economically profitable at nowadays. Flock size, milk yield and feeding costs were a key for dairy sheep farm profitability. Finally, according to the increasing trend expected for agricultural commodity prices, a proportional increase in milk price will be necessary to maintain their future profitability.

Key Words: cost, dairy sheep, profitability

W95 Effects of feeding teff hay-based diets on growth performance and ruminal fermentation profiles of growing beef steers and dairy heifers. J. E. Creech[1], J. M. Vera[2], C. T. Noviandi[2], J.-S. Eun*[2], A. J. Young[2], and D. R. ZoBell[2], *[1]Department of Plants, Soils, and Climate, Utah State University, Logan, [2]Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan.*

Teff (Erogrostis tef [Zucc.], Poaceae) is a warm-season annual grass and has attracted much interest among hay growers in the United States due to its rapid growth, palatability, and high quality and yield. The objective of this study was to assess growth performance and ruminal fermentation of growing beef steers and dairy heifers when fed teff hay-based diets. Twelve growing beef steers and 12 dairy heifers were used in a completely randomized design to test 2 dietary treatments: alfalfa hay-based TMR (AHT) and teff hay-based TMR (THT). In beef steer diets, the AHT contained 20.5% alfalfa hay and 43.0% corn silage, whereas the THT had 44.0% teff hay and 20.7% corn silage. In dairy heifer diets, the AHT contained 54.1% alfalfa hay and 24.8% corn silage, while the THT had 8.5% alfalfa hay, 42.0% teff hay, and 11.3% corn silage. All animals were placed in individual pens, and the experiment lasted 12 wk. Intake of DM increased by feeding the THT to beef steers and dairy heifers ($P = 0.01$). Dietary treatments did not affect ADG of beef steers; however, feeding the THT to dairy heifers increased ($P = 0.02$) ADG. Dietary treatments did not affect G:F in both beef steer and heifer diets. Ruminal pH averaged 6.54 or 6.51 in beef steer or dairy heifer diets, respectively, and did not differ between diets. Feeding the THT decreased total VFA concentration by beef steers and dairy heifers ($P < 0.02$). Feeding the THT to beef steers increased acetate proportion ($P = 0.02$), but the THT decreased propionate proportion ($P < 0.01$), resulting in increased acetate-to-propionate ratio due to feeding the THT ($P < 0.01$). In contrast, feeding the THT to dairy heifers tended to decrease acetate proportion ($P = 0.10$), but the THT increased propionate proportion ($P = 0.05$). Although feeding the THT decreased ruminal fermentation by beef steers and dairy heifers evidenced by decreased VFA concentration, the THT increased DMI of beef steers and dairy heifers, leading to no negative effects on growth performance. Teff can be a viable lower-cost alternative to feeding alfalfa in growing beef steers and dairy heifer diets.

Key Words: teff hay, beef steers, dairy heifers

W96 Comparison of in situ versus in vitro methods of fiber digestion at 120 and 288 hours to quantify the indigestible NDF fraction of corn silage samples. R. W. Bender*, D. E. Cook, F. Lopes, and D. K. Combs, *University of Wisconsin-Madison, Madison.*

The indigestible NDF (iNDF) as a proportion of NDF in forages is commonly calculated from the ratio: (2.4 × acid detergent lignin)/NDF. Our objective was to compare estimates of iNDF based on lignin ratio, to in vitro (IV) and in situ (IS) measurements. Thirteen corn silage samples were dried and ground through a 1-mm screen in a Wiley mill. Acid detergent lignin (ADL) was determined by NIR analysis. A 2 × 2 factorial trial was conducted, with method of iNDF analysis (IS vs. IV) and incubation time (120 vs. 288 h) as factors. Four sample replicates were utilized, and approximately 0.5 g/sample was weighed into each Ankom F57 bag (Ankom Technology, Macedon, NY; pore size = 25 μm) for all techniques. The IV-120 (37.8%) had a higher ($P < 0.01$) proportion iNDF than all other methods; IS-120 (32.1%) and IV-288 (31.2%) techniques were similar, but were both higher ($P < 0.01$) than the IS-288 technique (25.7%). Utilizing the NIR lignin values to calculate the ratio of iNDF to lignin (Table 1) yielded similar results: IV-120 had a higher ($P < 0.01$) ratio (5.9) than all other methods; IS-120 (5.0) and IV-288 (4.8) techniques were similar, but were both higher ($P < 0.01$) than the IS-288 technique (4.0). Thus, digestibility techniques at different times yielded vastly different estimates of iNDF. All techniques also yielded ratios that were higher than the commonly used ratio of 2.4 × lignin.

Table 1. In situ vs. in vitro methods of fiber digestion at 120 and 288 h to quantify iNDF

	iNDF, % of NDF		iNDF / Lignin	
	in vitro	in situ	in vitro	in situ
120 h	$37.8^{a} \pm 1.4$	$32.1^{b} \pm 1.4$	5.9^{a}	5.0^{b}
288 h	$31.2^{b} \pm 1.5$	$25.7^{c} \pm 1.2$	4.8^{b}	4.0^{c}

Key Words: indigestible NDF, fiber digestion, lignin

W97 Composition of gain and its relationship to residual feed intake and gain. M. L. Nascimento*[1], A. S. Chaves[1], R. R. Tullio[2], M. M. Alencar[2], A. N. Rosa[3], and D. P. D. Lanna[1], *[1]University of Sao Paulo, Piracicaba, SP, Brazil, [2]Embrapa Cattle Southeast, Sao Carlos, SP, Brazil, [3]Embrapa Beef Cattle, Campo Grande, MS, Brazil.*

Residual feed intake and gain (RIG), a combination between residual feed intake (RFI) and residual gain (RG), was recently proposed as a new index for genetic selection of beef cattle. The objective of this work was to examine the relationship between gain composition of Nellore steers and RIG. Data set from 3 years of study were used, totaling 363 steers. The animals were individually fed twice daily with 5% of orts, for at least 70 d (2.8 Mcal ME/kg DM; 13.5% CP). Body weight (BW) was measured at 14-d intervals and ultrasound measurements on 11–12th-rib (fat thickness and ribeye area) obtained at the start, middle and final of the experimental period. Final and initial empty BW energy were estimated by an equation for Nellore (EBW Energy = −126.73 + 10.88 × ribeye area + 70.01 × fat thickness; $R^2 = 0.73$), the retained energy was calculated by difference. To estimate the proportion of protein and fat in the gain, the composition of the fat-free dry matter was held constant. Daily gain was estimated by regression slope between BW and days on feed. Mixed models were used to obtain RFI and RG, where contemporary group (CG), based on year, animal origin and pen type was considered as random. The RIG was calculated as −1 × RFI + RG, both standardized to a variance of 1. The animals were classified as low, medium and high RIG (mean ± 0.5 SD). High and low classes were compared using mixed model, RFI class and CG were considered as fixed effects, sire as random, and initial age as covariate. DMI of high-RIG animals (efficient) was 11.5% lower and ADG was 24.2% greater compared with low-RIG animals ($P < 0.01$) without differences in final BW ($P > 0.10$). There was no relationship between RIG and fat thickness gain ($P > 0.05$), however, efficient animals had greater ribeye area gain ($P < 0.01$). The efficient animals retained 0.40 Mcal less energy/kg of gain ($P < 0.05$). Consequently, empty body gain composition was different, where efficient animals had less fat and more protein ($P < 0.05$).The phenotype selection based on RIG can select animals with lower DMI and higher ADG, whose higher efficiency can be partially explained by changes in body gain composition.

Key Words: beef cattle, fat thickness, ribeye area

W98 Estimation of bacterial protein in rumen digesta using DNA markers. C. J. R. Jenkins*, E. Castillo-Lopez, S. C. Fernando, and P. J. Kononoff, *University of Nebraska, Lincoln.*

The objective of this study was to use DNA as bacterial markers to estimate and compare the concentration of bacterial crude protein (BCP) in solid and liquid portions of rumen digesta. Using a completely randomized design, 2 multiparous, lactating Holstein cows (average DIM 14 ± 4 d, average BW 618 ± 40 kg, average DMI 23 ± 4 kg/d, average milk yield 34 ± 10 kg/d), fitted with ruminal cannulas were fed the same diet once daily at 0930 h. Every 4 h over a 24 h period, a sample of approximately 1.5 kg of rumen contents was collected from each cow and was strained through 4 layers of cheesecloth. Particle associated bacteria (PAB) was separated from the solid portion of rumen contents by adding PBS buffer and blending the mixture in a commercial blender, followed by straining through 4 layers of cheesecloth. Fluid collected after blending, as well as fluid retained from the initial straining, each underwent differential centrifugation, yielding bacterial pellets consisting of fluid associated bacteria (FAB) and PAB. DNA was then extracted from bacterial pellets and from the non-centrifuged samples of ruminal fluid and particles. The DNA from the bacterial pellets, ruminal fluid, and ruminal particle samples were subjected to real-time PCR using the TaqMan assay. Primers and a probe were designed from DNA encoding part of the 16s rRNA. The relative abundance of bacterial DNA tended to be higher ($P = 0.09$) in the solid portion (209.5 ± 26.6 mg BCP/g DM) than in the liquid portion (106.4 ± 43.6 mg BCP/g DM). Results suggest that BCP is detected in both the solid and liquid portion of rumen digesta and that it is found in higher concentrations in the solid portion.

Key Words: bacteria, marker, PCR

W99 Effect of a commercially available natural plant extract on intake and milk production of dairy cows. Y. Ying, M. Niu, A. R. Clarke, and K. J. Harvatine*, *Penn State University, University Park.*

The objective was to determine the ability of a commercially available natural plant extract (VéO Premium; Phode Laboratories, Terssac, France) to stimulate intake and its effects on milk production and feeding behavior of dairy cows. Two experiments (EXP) were conducted. First, 11 early-lactation dairy cows were used in a switchback design (EXP 1; 77 ± 15 DIM, Mean ± SD) and second 15 mid-lactation Holstein cows were utilized in a crossover design (EXP 2; 157 ± 44 DIM, Mean ± SD). Treatments were control (no supplement) or VéO fed at 4 and 4.5 g per head/d in a ground corn carrier in EXP 1 and 2, respectively. Diets were formulated to 31.5 and 31.0% NDF (EXP 1 and 2, respectively) and 17% crude protein. Treatment periods were 21 and 14 d (EXP 1 and 2, respectively) with the final 7 d used for sample and data collection. There was no effect of treatment on yield of milk, 3.5% FCM, fat, protein, or lactose in either experiment. There was also no effect of treatment on DMI or feed efficiency (FCM/DMI). Mean yield of 3.5% FCM was 53.3 and 39.9 kg/d and mean DMI was 33.0 and 27.3 kg/d across treatments for EXP 1 and 2, respectively. Additionally, there was no effect of treatment on milk FA profile in EXP 1 or average meal size or number of meals per day in EXP 2, but there was a tendency for the supplement to increase eating rate. In EXP 1, plasma insulin concentration 1 h before feeding was higher for the supplement cows compared with the control (3.36 vs. 2.13 μIU/mL; $P < 0.01$). The high level of intake in EXP 1 may have caused physical fill limitation of intake and prevented an increase in intake, however the supplement also did not increase intake in mid-lactation cows with more moderate levels of intake (EXP 2). Increased insulin before feeding may indicate a change in glucose homeostasis.

Key Words: feeding pattern, intake, plant extract

W100 Productive performance, hepatic function and nutrients utilization of dairy cows fed with *Jatropha curcas* L. seed meal treated with sodium hydroxide. A. S. Oliveira*[1], J. G. Souza[1], C. V. Araujo[1], A. Takaoka[1], D. C. Moura[3], M. C. Souza[1], E. Peron[1], J. T. Zervoudakis[3], L. S. Cabral[3], S. Mendonca[2], L. F. Moreno[1], P. H. N. Cruz[1], L. M.G. Olini[1], K. R. R. Amorim[1], F. G. Ribeiro[1], *[1]Mato Grosso Federal University, Campus Sinop, Sinop, Mato Grosso, Brazil, [2]Brazilian Agricultural Research Corporation's, Brasilia, DF, Brazil, [3]Mato Grosso Federal University, Campus Cuiaba, Cuiaba, Mato Grosso, Brazil.*

Twelve Holstein × Zebu crossbreed cows (127 ± 60 DIM, 476 ± 64 kg BW) were distributed in three 4 × 4 Latin squares, with 4 periods of 21 d (7 d of mensurations) to evaluate the effect *Jatropha curcas* L. seed meal treated with 7% of sodium hydroxide (JCM 20.0% of CP, 1.65% of ether extract, 0.16% of Na and 0.145 mg of phorbol esters (PE)/g DM) in concentrate (0, 10, 20 and 30% of DM) on performance, hepatic function and nutrients utilization. Cows were fed with pasture of *Panicum maximum* 'Mombaça' (15.0% of CP, 64.8% of NDF, DM allowance of 11.8% BW/d) and offering 4 kg/d of isonitrogen concentrates (19.8% of CP). Intake pasture was estimate using external maker fecal output (TiO_2) and indigestible NDF. Spot urine samples were obtained after milking on 20 d of each period. Data were analyzed using model mixed and applied Williams test to comparison of means for quantitative data. Alkaline treatment reduced 67.9% the PE in JCM. Pasture intake ($P = 0.965$; 8.2 kg DM/d) was not affected by JCM. Concentrate DM intake (3.51, 3.28, 2.73 and 1.80 kg/d) was not affected ($P = 0.143$) until 20% of JCM, but was reduced ($P = 0.029$) with 30% of JCM. PE intake increased with JCM level ($P = 0.001$; 0, 0.103, 0.166 and 0.163 mg/kg BW/d) but serum concentrations of aspartate aminotransaminase (91.4 IU/L; $P = 0.759$), alanine aminotransaminase (46.5 IU/L; $P = 0.29$) and gamma-glutamyltransferase (14.7 IU/L; $P = 0.628$) were not affected by JCM. OM digestibility (73.5, 70.9, 70.7 and 69.2%) of diet was reduced ($P = 0.014$) with 30% of JCM. Rumen microbial crude protein synthesis (1.32, 1.23, 1.10 and 1.01 kg/d) was reduced ($P = 0.049$) from 20% of JCM. Milk yield (11.0, 10.7, 9.5 and 9.4 kg/d) was not affected ($P = 0.607$) until 10% of JCM, but was reduced ($P < 0.001$) from 20% of JCM. Milk crude protein (3.18%; $P = 0.441$), milk fat (3.0%; $P = 0.895$), body condition score (2.9; $P = 0.279$) and milk N/intake N (18%; $P = 0.556$) were not affected by JCM. The JCM can be included in up to 10% in DM concentrate without affect productive performance, hepatic function and nutrients utilization of Holstein × Zebu crossbreed cows.

Key Words: phorbol ester

W101 Effects of heat stress and plane of nutrition on fecal composition of lactating dairy cows. J. D. Allen*[1,2], L. W. Hall[2], G. Xie[2,4], R. J. Collier[2], L. H. Baumgard[3], and R. P. Rhoads[2,4], *[1]Northwest Missouri State University, Maryville, [2]University of Arizona, Tucson, [3]Iowa State University, Ames, [4]Virginia Polytechnic Institute and State University, Blacksburg.*

The purpose of the study was to delineate the effects between heat stress (HS) and plane of nutrition on fecal nutrient composition. In 2 replications, multiparous cows (n = 12; parity = 2; 305 ± 33 DIM; 665 ± 18 kg BW) housed in climate chambers were fed a TMR consisting primarily of alfalfa hay and steam-flaked corn and subjected to 2 periods (P): (1) thermoneutral (TN) conditions (18°C, 20% humidity) with ad libitum intake for 9 d and (2) either HS conditions (cyclical temperature 31–40°C, 20% humidity: min THI = 73, max THI = 86) fed for ad libitum intake (n = 6), or pair-fed in TN conditions (PFTN, n = 6) for 9 d. Rectal temperature (Tre) and respiration rate (RR) were measured thrice daily at 0600, 1400 and 1800 h. Fecal samples were collected on d 1, 3, 5, 7, and 9 of each period for analyses of DM, NDF, ADF, CP,

ash, and starch. Data was analyzed as a complete random design, with cow as experimental unit, day as repeated measure, and each cow's P1 fecal concentration as a covariate. During P2, HS cows had a 1.8°C increase in Tre and a 3-fold increase in RR compared with PFTN cows ($P < 0.01$). Heat stress reduced ($P < 0.01$) DMI by 20% and by design PFTN cows had similar intake reductions. Milk yield was decreased 12% during HS and 8% in PFTN cows. Fecal dry matter tended ($P < 0.10$) to be higher in PFTN cows (16.6%) compared with P1 (15.8%) and HS (15.8%) cows. Fecal fiber components, NDF and ADF, were lower ($P < 0.01$) in PFTN cows (44.5 and 29.0%, respectively) compared with P1 (48.5 and 33.9%) and HS (47.1 and 32.6%) cows. Fecal starch was lower ($P < 0.05$) in HS cows (1.90%) compared with P1 (2.4%) and PFTN (2.8%) cows. There was no difference ($P > 0.10$) in fecal ash and CP. A period by day effect was seen in NDF, ADF, and starch ($P < 0.05$). Results indicate heat stress reduces fecal starch concentration, and lowered DMI reduces fecal NDF and ADF concentrations.

Key Words: dairy cow, fecal composition, heat stress

W102 Long-term performance of growing dairy heifers fed increased dietary fat from dried distillers grains. J. L. Anderson*, K. F. Kalscheur, A. D. Garcia, and D. J. Schingoethe, *South Dakota State University, Brookings.*

The objective of this study was to determine if feeding increased dietary fat from dried distillers grains with solubles (DDGS) to pre-pubertal dairy heifers influenced long-term performance. During the pre-pubertal growth phase, 33 Holstein heifers (133 ± 18 d old) were used in a 24-wk randomized complete block design with 3 treatment diets. Diets were (1) control (C) that contained 15.9% (DM basis) ground corn and 17.9% soybean products, (2) low-fat (LFDG) that contained 21.9% reduced-fat DDGS and 11.9% ground corn, and (3) high-fat (HFDG) that contained 33.8% traditional DDGS. All diets contained 39.8% grass hay, 24.8% corn silage, and 1.5% vitamins and minerals. Although diets were isonitrogenous and isocaloric, HFDG was formulated to contain 4.8% fat versus 2.8% in C and LFDG. Previous results demonstrated that growth performance was maintained, despite differences in metabolic profiles. Also, previous results indicated that heifer fed HFDG were pubertal earlier. Post-trial production data (farm and DHIA records) for each heifer was collected during the first 4 mo of lactation. Body weights, body condition scores, and frame measurements were taken 3 wk prepartum and at calving. Treatment did not affect ($P > 0.05$) age at conception or age at calving. At calving, wither height was shorter ($P = 0.03$) for heifers fed HFDG compared with other diets. For heifers fed LFDG milk production was greater (33.04, 36.40, 34.7 kg for C, LFDG, and HFDG, respectively; SEM = 1.35; $P = 0.03$) and milk protein yields tended to be greater (0.98, 1.08, and 1.03 kg; SEM = 0.043; $P = 0.06$) compared with heifers fed C. Heifers fed HFDG had similar milk production compared with C. Milk fat and energy-corrected milk yield were similar among treatments. Feeding increased dietary fat from DDGS during the pre-pubertal growth phase maintained milk production despite previous findings indicating differences in puberty. Based on these findings, producers can feed dietary fat from DDGS as a replacement for starch from corn as an energy source for pre-pubertal heifers without detriment to long-term performance.

Key Words: dairy heifer, distillers grain, long-term performance

W103 Validation and recovery rates of an indirect calorimetry headbox system used to measure heat production of cattle. A. J. Foth*[1], T. Brown-Brandl[2], H. C. Freetly[2], M. D. Hayes[2], and P. J. Kononoff[1], [1]*University of Nebraska-Lincoln, Lincoln,* [2]*USDA Meat Animal Research Center, Clay Center, NE.*

A headbox system was constructed at the University of Nebraska-Lincoln to determine heat production from dairy cattle using indirect calorimetry. The system was designed for use in a tie-stall barn to allow the animal to be comfortable and was mounted on wheels to transport between animals between sampling days. The frame was constructed out of aluminum angle iron with sides of plexiglass for other animals to remain within sight. The system continuously sampled gas produced in the headbox and directed it into foil bags, allowing for analysis of O_2, CO_2 and methane concentrations. To validate the data collected by 3 constructed units, alcohol burning lamps containing 100% ethyl alcohol were placed inside, ignited and burned for 2 h. The rate of gas flowing out of the system was recorded and samples of gas entering and exiting each of the sealed headboxes was collected into 44 L sample bags and later analyzed. The difference between gas concentrations from incoming and outgoing air, corrected to standard temperature and pressure, was calculated and the amount of O_2 consumed and CO_2 produced during the sampling time was compared with the theoretical amount of each of these gases calculated based upon the amount of alcohol burned, giving the recovery rate of each gas. Two runs were carried out on 2 separate occasions for each unit and the results can be found in Table 1. Recovery rates for O_2 and CO_2 averaged 101.3 ± 2.72% and 100.5 ± 3.59% suggesting that these units may be used to adequately estimate gas exchange and for indirect calorimetry to indirectly determine heat production.

Table 1. Means and standard deviations of 2 lamp runs on headboxes 1, 2, and 3

	Headbox 1		Headbox 2		Headbox 3	
	Mean	SD	Mean	SD	Mean	SD
Average gas flow (m^3/min)	0.94	0.01	0.97	0.01	1.03	0.03
O_2 consumed (L)	175.4	21.1	144.9	12.4	134.0	1.77
CO_2 produced (L)	116.3	11.74	95.5	4.60	89.6	4.10
Average temperature (°C)	32.5	3.95	29.8	3.43	29.0	1.90
Average dew point (°C)	16.6	4.04	13.1	3.31	13.1	1.87
O_2 recovery rate (%)	101.19	2.17	104.12	0.57	98.71	1.65
CO_2 recovery rate (%)	100.80	0.19	103.11	3.32	97.64	4.81

Key Words: indirect calorimetry, headbox, lamp run

W104 Energy requirement of Holstein calves. J. C. M. Lima[1], J. P. P. Rodrigues[1], M. I. Marcondes*[1], F. S. Machado[2], A. S. Treece[1], M. M. D. Castro[1], J. L. C. Dias[1], and T. Araújo[1], [1]*Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil,* [2]*Embrapa Gado de Leite, Juiz de Fora, Minas Gerais, Brazil.*

This study aimed to evaluate energy requirements in dairy calves. Forty-two male Holstein calves, at 3 d of age and with an average live weight of 35.56 ± 5.86 kg, were used. Ten animals were slaughtered to compose the reference group, and the remaining animals were distributed into a completely randomized design. The treatments consisted of different amounts of milk, which were: 2, 4, 6 and 8 L milk/head/d, fed twice a day, in 8 replications. The animals were fed milk until they reached 58 d. Four animals per treatment were slaughtered at 59 d, while others started to receive Coast cross hay plus starter, and they were subsequently slaughtered at 87 d. After slaughter, 2 samples were obtained for each animal, called carcass and non-carcass. The retained energy was estimated by determining energy concentration in carcass

and non-carcass samples, and diminishing by the initial body energy concentration. The HP of each animal was estimated as: $HP = \beta_0 \times e^{(\beta_1 \times MEI)}$, where MEI is metabolizable energy intake. Digestible energy intake (DEI) was obtained by controlling protein, fat and carbohydrates daily intake, which were multiplied by 5.6, 9.4, and 4.2 Mcal/kg, respectively, and by their respectively digestibilities. MEI of each animal was obtained by the equation: MEI = DEI × (0.96 × DMI + 0.88 × (1 − DMI)), where DMI is the proportion of milk intake in dry matter intake. Net (NEm) and metabolizable (MEm) energy requirements for maintenance were obtained as a function of heat production (HP) and metabolize energy intake (MEI), while net energy requirements for gain (NEg) were obtained as a function of empty body weight (EBW) and empty body gain (EBG). The NEm and MEm were respectively 85.2 and 143.4 kcal/$EBW^{0.75}$/d. The efficiency of utilization of metabolizable energy for maintenance (k_m) was 59.41%. The equation obtained for NEg and efficiency of utilization of metabolizable energy for gain (k_g) were, respectively, NEg (Mcal / d) = 0.0931 × $EBW^{0.75}$ × $EBG^{1.454}$, and 38.07%. The efficiencies of energy deposition as protein and fat were 67.69% and 60.73%, respectively. The equations suggest that net and metabolizable energy requirements for maintenance of Holstein calves exceed those commonly use in the dairy industry.

Key Words: calf, gain, maintenance

W105 Brown marmorated stink bug odor compounds do not transfer into milk in lactating dairy cattle by feeding bug-contaminated corn silage. R. L. Baldwin VI*[1], A. Zhang[2], S. W. Fultz[3], S. Abubeker[2], C. Harris[2], E. E. Connor[1], and D. L. Van Hekken[4], *[1]USDA, ARS, BFGL, Beltsville MD, [2]USDA, ARS, IIBBL, Beltsville MD, [3]University of Maryland Extension, Frederick, [4]USDA, ARS, EERC, Wyndmoor, PA.*

Brown marmorated stink bug (BMSB), *Halyomorpha halys*, is an emerging invasive species of grave concern to agriculture as a polyphagous plant pest with potential negative effects on the dairy industry. We sought to determine the risk of including BMSB contaminated silage in lactating dairy cow rations. First, 6 dairies, either highly infested (n = 3; 30 to 100 bugs per stalk) or not infested (n = 3) were sampled to assess prevalence of bug secretion compounds tridecane and E-2-decenal (odor component) in silage and milk. Second, using wild BMSB, a mini-silo dose response experiment (adding 100, 50, 25, 10, and 1 fresh crushed bugs/0.5 kg chopped corn) was conducted to assess the effect of ensiling on BMSB odor compounds. Finally, synthetic BMSB secretion compounds (10 g tridecane and 5 g E-2-decenal) were ruminally infused 2 times daily over 3 d and samples of milk, urine, and rumen fluid were collected to evaluate disposition. Samples were analyzed by solid phase microextraction (SPME) and gas chromatography-mass spectrometry (GC-MS). Milk production and feed composition were unaffected ($P > 0.05$) when BMSB contaminated silage was fed. Moreover, no E-2-decenal was detected in silage nor milk (detection threshold = 0.00125 ppm). Dose response of tridecane in mini-silo samples exhibited a linear relationship ($R^2 = 0.78$) with BMSB added; however, E-2-decenal was completely decomposed and undetectable in spiked mini-silos after ensiling. Both synthetic secretion compounds infused into rumen were undetectable in all milk and urine samples. Content of E-2-decenal was also not detectable in rumen fluid; however, tridecane was detected at 15 min post-infusion but not present thereafter. Feed intake was unaffected by infusion treatment and BMSB secretion compounds were not observed in milk. Compounds from the metathoracic gland of BMSB are not able to contaminate milk due to either the ensiling process or metabolism within the rumen. Concern over BMSB odor compounds contaminating the fluid milk supply even on highly infested farms is not warranted.

Key Words: brown marmorated stink bug, milk taint, lactating dairy cow

W106 Effects of restricted versus conventional dietary adaptation over periods of 9 and 14 days on total-tract digestibility of dry matter and starch of feedlot Nellore cattle. A. L. N. Rigueiro[2], D. H. M. Watanabe[2], M. C. S. Pereira[2], J. Silva[2], T. V. B. Carrara[1], M. C. S. Franzoi[1], R. S. Barducci[1], M. D. B. Arrigoni[1], F. Perna Junior[4], M. Caetano[3], D. P. D. Lanna[3], and D. D. Millen*[2], *[1]São Paulo State University (UNESP), Botucatu, São Paulo, Brazil, [2]São Paulo State University (UNESP), Dracena, São Paulo, Brazil, [3]University of São Paulo (USP), Piracicaba, São Paulo, Brazil, [4]University of São Paulo (USP), Pirassununga, São Paulo, Brazil.*

This study was designed to determine effects of restricting DMI of the final finishing diet (REST) as a means of dietary adaptation compared with diets increasing in concentrate (STEP) over periods of 9-d and 14-d on total-tract digestibility of DM and starch of feedlot Nellore cattle. The experiment was designed as a completely randomized block with 2 × 2 factorial arrangement, replicated 6 times (5 bullocks/pen), in which one hundred twenty 22-mo-old yearling Nellore bulls (361.3 ± 30.2 kg) were fed in 24 pens for 84 d according to the treatments: STEP for 9-d and 14-d, REST for 9-d and 14-d. Measures over time were taken on d 5, 10, 15, and 20 of experimental period. The STEP program consisted of ad libitum feeding of 3 adaptation diets over periods of 9-d or 14-d with concentrate level increasing from 55% to 85% of diet DM. The REST program consisted of restricted intake of the final diet (85% concentrate containing 55% of high moisture corn) with programmed increases in feed offered until yearling bulls reached ad libitum access over periods of 9-d and 14-d. Fecal samples were collected just before morning (0800 h) and afternoon (1500 h) meals, and a composite sample per pen in each day was made. It was observed ($P < 0.05$) an interaction between protocols, length of protocols and days for DM and starch digestibility. Yearling bulls adapted for 14-d had greater DM digestibility on the first day of the finishing period (15-d: STEP in 14-d = 79.05%, REST in 14-d = 78.05%) than those adapted for 9-d (10-d: STEP in 9-d = 68.04%, REST in 9-d = 69.39%); however, no differences ($P > 0.10$) between treatments were observed on d 15. Moreover, yearling bulls in REST for 14-d and STEP during 9-d did not present differences ($P > 0.10$) in starch digestibility over days of collection. However, yearling bulls adapted in REST for 9-d and STEP during 14-d ($P < 0.05$) only proved to be able to digest starch like those in REST for 14-d and STEP for 9-d on d 15. Thus, according to present data, yearling Nellore bulls should be adapted in 14 d, regardless of the protocol.

Key Words: adaptation, digestibility, Nellore

W107 Improvements in feed efficiency via rumen-protected amino acid supplementation limited by ration formulation software. T. R. McGill* and M. D. Hanigan, *Virginia Polytechnic Institution and State University, Blacksburg.*

To avoid nutrient limitations, MP requirements are often overestimated in the formulation of dairy cow rations. Overfeeding of N results in increased expenses for producers and increased N excretion to the environment. Thus, improvements in the efficiency of dairy cow feeding provide economic and environmental incentives. Previous improvements in feed efficiency have come via the dilution of maintenance through increased production. To achieve further improvements, it is necessary to explore approaches such as supplementation of limiting AA's in rumen protected (RP) form to diets low in MP. The goal of this study was to better illustrate the mechanism of lactation response to RPAA, and to evaluate the effect of RPAA products on milk yield. Four diets were fed to 36 multiparous Holstein dairy cows in a 4 × 4 Latin square design. Diets were (1) positive control diet with 17.1%CP (+Con), (2) negative control diet containing 15.4%CP (−Con), (3) −Con diet supplemented with 20 g/d/cow of RP methionine (RPM), and (4) −Con diet supplemented with 20 g/d/cow of RP methionine and 60 g/d/cow of RP lysine (RP M/L). Data were analyzed using the MIXED procedure in SAS 9.2. Milk yield was not significantly different between groups, suggesting that protein was not sufficiently limiting to affect production. Concentrations of MUN from cows fed –Con, RPM and RP M/L diets were significantly lower than that of cows fed +Con diet ($P < 0.0001$), suggesting improved efficiency of N metabolism in cows fed diets low in MP. The 2001 NRC formulation software was used to formulate diets. The predicted metabolizable protein balance of the –Con diet was −262 g/d, and predicted a 17.5% decrease in MP Allowable Milk compared with the +Con. This inaccuracy illustrates the need for improvement in dairy nutrition models. Model inaccuracies contribute greatly to inefficiencies in dairy cow feeding, and must be evaluated in the effort to improve dairy cow feed efficiency. Such improvements could act synergistically with RPAA supplementation to more closely match nutrient composition in feed to nutrient requirements of dairy cows.

Key Words: rumen-protected amino acid, feed efficiency, NRC

W108 The effect of a two ration feeding regimen on feed intake, milk production and composition, and plasma hormones and metabolites in dairy cows. M. Niu*, Y. Ying, P. A. Bartell, and K. J. Harvatine, *Penn State University, University Park.*

There is a circadian pattern of feed intake, milk synthesis, and plasma metabolites in dairy cows consuming a single TMR fed once a day. The object of this study was to determine if feeding multiple rations over a day that compliment theses rhythms would improve milk production. Twelve Holstein cows were used in a replicated 3 × 3 Latin square design with 21 d periods in an automated feed observation system that recorded feed weight every 10 s. Diets were control (Con; 32% NDF, 25% starch), a low forage and high fermentable starch diet (L; 28% NDF, 32% starch, 56% corn silage and 14% steamflaked corn), and a high fiber diet (H; 33.5% NDF, 22% starch, 43% corn silage and no steamflaked corn). The L and H diets were balanced to provide the same composition as the control diet when combined in a 1:3 ratio of L:H. Con was fed control diet at 0700 h, the high/low treatment (HL) was fed H at 0700 h and L at 2200 h, and the low/high (LH) treatment was fed L at 0700 h and H at 1100 h. Daily variables were analyzed by a mixed model and the contrasts were Con vs. HL and HL vs. LH. Time course data were analyzed using repeated measures and the contrasts were tested at each time point. DMI was decreased by 1.3 kg/d by HL compared with LH ($P < 0.05$). There was no difference between Con and HL for milk yield and composition, but milk fat percent was higher in HL compared with LH ($P < 0.05$, 3.61 vs. 3.44%) and HL tended to increase milk fat yield compared with LH ($P < 0.10$). Milk yield was 1.8 kg higher and fat percent was 0.38 units lower at the 0500 h milking compared with the 1700 h milking, but milk fat yield did not differ. Blood samples were collected from the tail vein at 8 times to represent the course of a day at the last 3 d of each period. There was no effect of treatment on plasma NEFA and BUN concentration, but plasma glucose was decreased 2.5 mg/dL by HL compared with Con ($P < 0.05$). Feeding HL reduced DMI and increased milk fat yield compare with the LH, but feeding multiple rations over the day had little effect on DMI or milk yield and components compared with a single TMR.

Key Words: dairy cows, milk production, multiple rations per day

W110 Developing techniques to determine the metabolizable methionine content of ruminant products. R. S. Ordway*[1], C. G. Schwab[2,3], B. K. Sloan[4], and N. L. Whitehouse[2], *[1]Balchem Corporation, New Hampton, NY, [2]University of New Hampshire, Durham, [3]Schwab Consulting LLC, Boscobel, WI, [4]Adisseo North and Central America, Alpharetta, GA.*

Several methods have been used to determine the effectiveness of ruminant Met supplements in providing metabolizable Met (MP-Met) to dairy cows. Measuring differences in the slope of changes in milk protein or plasma free Met concentrations to increasing intakes of a Met supplement are 2 of the most promising. A randomized split plot 5 × 5 Latin square using 20 lactating cows in a 2 × 2 × 5 factorial arrangement of treatments was employed using 10 d periods with the last 4 d used for milk and blood sampling. Main effects were Met adequacy of basal diet (1.8 or 2.3 MP-Met as a % of MP), Met supplement [Smartamine M (S) or dry MetaSmart (M)] and level of Met supplementation (0, 3, 6, 9 and 12 g/d MP-Met). Basal diets met NRC (2001) requirements and contained 6.8% Lys in MP. Additional S was used to achieve the high MP-Met basal diet. S and M were estimated to supply 600 and 222 g of MP-Met/kg of product, respectively. The response criteria evaluated were milk protein content (MPC), milk protein yield (MPY), plasma Met (PM) and total plasma sulfur AA (TPSAA). Three blood samples were taken from the tail vein daily at 2-h intervals after the am feeding on d 7–10 of each experimental period. Plasma samples were centrifuged, deproteinized and composited within and across days and analyzed in duplicate for AA content. For each response parameter, linear regression equations were derived for each product at each level of Met adequacy. On the limiting MP-Met basal diet, both Met supplements increased MPC 0.009 units/g MP-Met with a SE of 0.002; a precision of ± 20%. Both M and S improved MPY 9 and 6 g per g of MP-Met, respectively, with SE of >2.6 and an imprecision of >40%. For S, irrespective of level of MP-Met adequacy, both PM and TSAA increased in a linear fashion ($r^2 > 0.78$) with a precision of ± 10%; however, the predictability was poor for M ($r^2 < 0.33$). It appears PM or TPSAA are the most appropriate response parameters to use to predict the MP-Met contribution of rumen protected DL-Met sources, but they are unsuitable for products where the analog rather than DL-Met is absorbed.

Key Words: amino acid methodologies, encapsulated methionine, methionine analogue

W111 The effect of various dietary metabolizable proteins to metabolizable energy ratios on ovarian follicular activities in prepubertal Holstein heifers. H. R. Motalebei, M. Dehghan-Banadaky*, K. Rezayazdi, and H. Kohram, *Department of Animal Science, University of Tehran, Karaj, Tehran, Iran.*

The objective of the present study was to evaluate the effects of various metabolizable protein (MP) to metabolizable energy (ME) ratios on ovarian follicular dynamics in prepubertal Holstein heifers. Twenty-four Holstein heifers, weighing 217 kg, 210 ± 28 d old, were used in the trail. Heifers were randomly assigned to 3 rations of MP per day: (1) control, MP based on NRC (34.57 g), (2) 10% MP less than NRC (31.14 g), (3) 10% MP more than NRC (38 g). Metabolizable energy in all rations was based on NRC requirements (14 Mcal per day). Rations were formulated by NRC (2001) software. After 70 d of feeding, the estrous synchronization were done using 2 IM injection of PGF2α (Vetalyse, Dinoprost, Aburaihan, Iran), 11 d apart and ovarian ultrasonography (Pie medical, Falco 100, 8 MHz) was performed once daily over 10 d period from the day of estrus. The ovarian follicles were counted and classified as: class 1 (total, ≥ 2 mm), class 2 (small, 4–6 mm), class 3 (medium, 7–9 mm), class 4 (large, ≥ 10 mm) and class 5 (medium and large ≥7 mm). The results showed that there were no differences ($P > 0.05$) between rations in classes 1 to 4, but class 5 follicles were higher ($P < 0.05$) in ration 1 than rations 2 and 3. It is concluded that 10% MP less than NRC rations may had the beneficial effect on the ovarian activity in prepubertal heifers.

Table 1. The effects of various ratios of MP to ME on ovarian follicular activities (no. and class of follicles) in prepubertal heifers

	MP/ME (g/Mcal)				
No. of follicles	34.57	31.14	38	*P*-value	SEM
Class 1 (total, ≥2 mm)	13.67	13.58	14.08	NS	0.525
Class 2 (small, 4-6 mm)	9.64	8.30	9.10	NS	0.503
Class 3 (medium, 7-9 mm)	0.64	0.94	0.61	NS	0.131
Class 4 (large, ≥10 mm)	0.50	0.43	0.32	NS	0.930
Class 5 (medium and large, ≥7 mm)	1.09	1.79	0.94	0.03	0.243

Key Words: metabolizable protein, metabolizable energy, ovarian follicle

W112 Ruminal fermentation profile of cows fed diets containing dried distillers grains with solubles associated with risk factors for milk fat depression. H. A. Ramirez Ramirez* and P. J. Kononoff, *University of Nebraska-Lincoln, Lincoln.*

Four ruminally-cannulated Holstein cows, averaging (±SD) 114 ± 14 DIM and 662 ± 52 kg BW were used in a 4 × 4 Latin Square to test the effects of high dietary oil and starch as risk factors associated with milk fat depression (MFD) on ruminal fermentation when feeding of a diet containing dried distillers grains with solubles (DDGS). Formulation of the experimental diets included corn oil and ground corn to increase crude fat (CF) and starch levels. In each of the 21-d periods cows were assigned to one of 4 dietary treatments (values expressed on a DM basis): control ration containing 20% DDGS but no risk factors associated with MFD (CON; CF 5.4%, starch 20%); CON with added oil (OIL; CF 6.4%, starch 20%); CON with added starch (STARCH; CF 5.6%, starch 26%); and CON with added oil and starch (COMBO; CF 6.5%, starch 25%). There was a significant effect ($P < 0.01$) of diet on milk fat concentration (MF%) (3.19, 2.75, 2.88 and 2.21 ± 0.18% for CON, OIL, STARCH and COMBO, respectively). Ruminal pH and NH_4 were not affected by treatment (averaging 5.97 ± 0.08 and 14.5 mg/dL across treatments). Total concentration of VFA was similar for CON, OIL and STARCH (119 ± 3.64 mmol/L) whereas COMBO was lower ($P < 0.01$; 111 ± 3.64 mmol/L). Molar proportion of acetate (Ac) was affected by treatment ($P < 0.01$) being higher for CON compared with OIL, STARCH and COMBO (64.6 versus 61.9 ± 1.44 mol/100 mol). Treatment also had a significant effect ($P < 0.01$) on propionate (Pr) which was highest for COMBO, followed by OIL and STARCH; and lowest for CON (25.3, 24.5 and 22.0 ± 1.53 mol/100 mol). Concomitant with these changes Ac:Pr tended ($P = 0.12$) to decrease with the addition of risk factors (2.97, 2.64, 2.62 and 2.45 ± 0.21 for CON, OIL, STARCH and COMBO, respectively). Feeding a diet with 20% DDGS resulted in higher concentration of Ac and low Pr; by adding high levels of oil and starch to such diet these parameters were inverted resulting in a tendency to decrease Ac:Pr and reduced MF% possibly due to shifts in ruminal environment which may affect microbial metabolism and milk fat synthesis.

Key Words: ethanol by-products, ruminal pH, VFA

W113 The protein binding capacity of protein-precipitable phenolics from 10 warm-season perennial forage legumes. H. D. Naumann*[1,2], J. P. Muir[2], B. D. Lambert[2,3], A. E. Hagerman[4], and L. O. Tedeschi[1], *[1]Texas A&M University, College Station, [2]Texas A&M AgriLife Research, Stephenville, [3]Tarleton State University, Stephenville, TX, [4]Miami University, Oxford, OH.*

Condensed tannins (CT) are protein-precipitable phenolic compounds (PPP) that bind to proteins and potentially reduce ruminal protein breakdown. Ruminants consuming forages containing biologically active CT could experience an increase in ruminal-bypass protein. The objectives of this study were to determine the PPP concentration and amount of protein bound (PB) by PPP, as well as the protein binding capacity of PPP produced by warm-season perennial legumes commonly consumed by ruminants. Ten warm-season perennial legumes: *Leucaena retusa*, *Desmanthus illinoensis*, *Lespedeza stuevei*, *Mimosa strigillosa*, *Neptunia lutea*, *Desmodium paniculatum*, *Arachis glabrata*, *Lespedeza cuneata* and 2 ecotypes of *Acacia angustissima* var. *hirta* were evaluated. Protein-precipitable phenolics were determined by reacting crude plant extracts with bovine serum albumin. The amount of PB was determined by nitrogen analysis of the protein-phenolic residues. The PB to PPP ratio (PB:PPP) was used to evaluate the difference in protein binding capacity among the forage legumes surveyed. *Arachis glabrata*, included as a negative control, contained no PPP. *Desmodium paniculatum* had the greatest PPP concentration (193.9 g/kg DM; $P < 0.0001$). The greatest amounts of PB ($P < 0.0001$) were measured in *L. stuevei* and *M. strigillosa* (74.8 and 74.6 g/kg DM, respectively). The least amount of PB was demonstrated by *L. retusa*. The greatest protein binding capacities ($P < 0.05$) were demonstrated by PPP from *L. cuneata*, *D. illinoensis* and *M. strigillosa*, which had PB:PPP of 0.74, 0.67 and 0.61, respectively. Protein-precipitable phenolics from *D. paniculatum*, *L. retusa* and 2 ecotypes of *A. angustissima* demonstrated the least ($P < 0.05$) protein-binding capacities (PB:PPP = 0.17, 0.38, 0.36, and 0.31, respectively). The protein binding capacity of PPP from *L. cuneata* was more than 4 times greater than that of *D. paniculatum*, which had a PPP concentration almost 4 times greater than *L. cuneata*. Differences in protein binding capacity of PPP could translate into differences in biological value of forages consumed by ruminants, especially as it relates to ruminal escape protein.

Key Words: bypass protein, legume

W114 Ruminal degradability in vitro by sub-products of the biodiesel industry. A. L. Silva, M. I. Marcondes*, F. C. Sousa, L. S. Knupp, C. M. Velloso, C. S. Cunha, and J. P. P. Rodrigues, *Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil.*

The in vitro gas production technique is capable of simulating the ruminal environment, reflecting the rate and extent at which the components are fermented by the rumen microorganisms. The objective was to study the rumen fermentation kinetics of 18 by-products from the biodiesel industry, with potential for use for feeding ruminants, using in vitro gas production technique. The feeds studied were: cottonseed (*Gossypium* spp. L.) meal and cake; babassu (*Orbignya speciosa*) cake; canudo de pito (*Mabea fistulifera* Mart) meal; crambe (*Crambe abyssinica*) meal and cake; palm kernel (*Elaeis guineensis*) cake; sunflower (*Helianthus annuus*) meal and cake; licuri nut (*Syagrus coronata*) cake; macauba fruit (*Acrocomia aculeata*) cake; castor seed (*Ricinus communis*) meal detoxified with lime; forage radish (*Raphanus sativus*) cake; 2 jatropha (*Jatropha curcas*) cakes; 2 peanut (*Arachis hypogaea*) cakes; and soybean (Glycine max) meal. Feeds were grouped, according to the rumen fermentation kinetic parameters, in 6 different groups. It was used multivariate analysis by Ward's minimum-variance method, and adopted an R^2 of 0.8. Soybean meal was used as control treatment. Parameters evaluated were: gas production from fibrous carbohydrates (VfFC), gas production from nonfibrous carbohydrates (VfNFC), degradation rate of fibrous carbohydrates (kdFC), degradation rate of nonfibrous carbohydrates (kdNFC) and lag time (lag). The VfNFC varied from 16.72 to 200.07 mL for the macauba fruit cake and peanut cake II, respectively. While the VfFC varied from 53.09 to 242.12 mL for the palm kernel cake and macauba fruit cake, respectively. Mean kdFC values varied from 0.002 to 0.039%/h for the licuri nut cake and forage radish cake, respectively. The kdNFC for palm kernel cake and macauba fruit cake varied from 0.022 to 0.430%/h, respectively. Mean lag values varied from 0.0001 to 5.2029 h for the cottonseed cake and palm kernel cake, respectively. The sub-products forage radish cake and cottonseed, crambe and sunflower meals, contained in the group 1, showed similar quality to soybean meal. Thus, these feeds have potential to replace soybean meal in ruminant rations.

Key Words: carbohydrate, degradation rate, ruminants

W115 Urinary and blood characteristics in cattle fed low-quality tropical forage in response to infrequent nitrogen supplementation. L. M. A. Rufino*, E. Detmann, J. P. P. Rodrigues, L. H. R. Silva, S. C. Valadares Filho, M. F. Paulino, and M. O. Franco, *Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil.*

The effects of supplementation with rumen degradable protein (RDP) using 2 frequencies of supplementation on urinary and blood characteristics were evaluated in cattle fed low- quality tropical forage. Five crossbred steers, with average BW of 257 ± 18 kg, were used in a 5 × 5 Latin square design. Five treatments were evaluated: 1.control (without supplementation); 2.daily supplementation supplying 30% of the daily RDP requirements (30/D); 3.daily supplementation supplying 60% of the daily RDP requirements (60/D); 4.supplementation every 3 d supplying 30% of 3 d based requirements of RDP (30/I); and 5.supplementation every 3 d supplying 60% of 3 d based requirements of RDP (30/I). The animals were fed ad libitum with Tifton 85 hay (4.5% of crude protein). The supplement was composed of 85% casein and 15% urea: ammonium sulfate (9:1). The experimental periods lasted 24 d, being 9 d for adaptation to the treatments. The total urine collection was performed from d 16 to 18 and the excretions of urea nitrogen (UN) and 3-methylhistidine (3MH) were evaluated. Blood samples were taken from d19 to 21 via the jugular vein every 6 h (6 h, 12 h, 18 h, and 24 h) and composed on a daily basis. The concentrations of serum urea nitrogen (SUN) and plasma amino acids (PAA) were evaluated. The different collection days were considered as repeated measures. The treatments did not affect ($P > 0.10$) 3MH and PAA. The supplementation increased ($P < 0.01$) the UN and SUN. Among supplements, only a difference between amounts of RDP was detected ($P < 0.01$) for these variables, being the greatest values observed when 60% of RDP requirements were supplied. Moreover, there was a day × treatment interaction ($P < 0.01$) for both SUN and UNU. There were variations among days ($P < 0.01$) only for treatments 30/I and 60/I. In both treatments, there was an increase in SUN on d 2 of collection with return on 3rd day at concentrations similar to those observed on d 1. Infrequent nitrogen supplementation changes the nitrogen metabolism of cattle fed low-quality tropical forage.

Key Words: metabolism, nitrogen, recycling

W116 Small intestinal digestion of raw cornstarch in cattle is increased by duodenal infusion of non-essential amino acids or casein. D. W. Brake*, E. C. Titgemeyer, E. A. Bailey, and D. E. Anderson, *Kansas State University, Manhattan.*

Previous research demonstrated that small intestinal starch digestion (SISD) in cattle may be increased by postruminal infusion of casein, but reports on effects of amino acids (AA) are limited. We evaluated effects of AA on SISD in cattle. Five duodenally and ileally cannulated steers (initial BW = 259 kg) were used in a 5 × 5 Latin square with 6-d periods. All cattle were fed 4.8 kg DM/d of a soybean hull-based diet and received continuous duodenal infusions of raw cornstarch (1.5 kg/d) and Cr-EDTA in 12.6 L/d volumes. Treatments were infused duodenally and included (1) control, (2) 424 g/d casein, (3) 393 g/d AA mimicking casein (CASAA), (4) 192 g/d AA mimicking the essential AA in casein (EAA), and (5) 200 g/d AA mimicking the non-essential AA in casein (NEAA). On d 6 of each period, 6 spot samples of ileal digesta and feces were composited and subsequently analyzed. Flow of starch to the ileum tended ($P = 0.08$) to be less when cattle received casein, CASAA, or NEAA. Additionally, SISD was greatest ($P \leq 0.05$) with CASAA and least with control. When cattle were infused with EAA, SISD did not differ from control, and SISD was intermediate to control and CASAA when cattle received casein or NEAA. Flows of ethanol-soluble oligosaccharides to the ileum were greatest ($P = 0.01$) with EAA and casein, least for control and NEAA, and intermediate for CASAA. Glucose flows to the ileum averaged 61 g/d and were not affected ($P = 0.26$) by treatment. Large intestinal starch digestion tended ($P = 0.06$) to be less and starch flow to the feces was greater ($P = 0.04$) for control and NEAA than for CASAA and casein. Postruminal starch digestion was least ($P = 0.03$) for control and NEAA. Apparently, SISD in cattle receiving continuous infusion of raw cornstarch is improved by AA similar to casein, and this response was mimicked by NEAA but not EAA.

Key Words: amino acid, cattle, small intestinal starch digestion

W117 Relationships between malt characteristics and feed value of malt barley grain. S. Ding*[1,2], M. Oba[2], M. L. Swift[3], W. Z. Yang[1], and T. A. McAllister[1], *[1]Lethbridge Research Center, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [2]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, [3]Alberta Agriculture and Food, Lacombe, AB, Canada.*

Grain producers in western Canada prefer to grow malt barley over feed barley as malt barley is more economically attractive. However, less half of the malt barley produced qualifies as malt grade with the

remainder used as feed grain. Feed value of malt barley is rarely considered by grain growers and as such, there is a paucity of information available. The objective of this study was to examine the relationship of malt characteristics with chemical composition and DM digestibility (DMD). Five-hundred and 60 malt barley samples were collected across western Canada in 2007. Five malting characteristics including fine malt extract (FEXT), diastatic power (DP), α-amylase (ALPH), β-glucan (GLU) and friability (FRI) were selected due to a potential correlation to nutrient content and DMD of malt barley. Digestibility of DM was evaluated by grinding the samples through 6-mm and incubated for 24 h in batch culture. Samples were ground to 1-mm for determination of CP, NDF and starch. Correlation coefficient was analyzed using CORR procedure of SAS. FEXT (%), DP (°L), ALPH (D.U.), GLU (ppm), and FRI (%) ranged from 74 to 85, 110 to 220, 57 to 97, 51 to 580 and 34 to 110, respectively. The concentrations (% DM) of CP, starch and NDF ranged from 8.1 to 16.5, 55.6 to 67.4, and 17.2 to 21.2, respectively. Digestibility of DM (%) averaged 39.5 and ranged from 26.8 to 56.6. Protein concentration of malt barley was negatively correlated ($P < 0.01$) with FEXT ($r = -0.89$) and FRI ($r = -0.70$), but positively correlated with DP ($r = 0.63$). The starch concentration was negatively correlated ($P < 0.01$) with DP and ALPH ($r = -0.56$ and $r = -0.57$, respectively). Neither malt characteristics nor chemical composition of malt barley were correlated ($-0.24 < r < 0.28$) with DMD. These results indicate that some malt characteristics could be used as reliable criteria to select malt barley for use as feed barley. This work also demonstrates the substantial variation in chemical composition of commercially available malt barley and emphasizes the need to have an accurate and rapid means of quality assessment at the point of sale.

Key Words: batch culture, chemical composition, malt barley

W118 Investigation of dietary fiber as a potential source of trace mineral antagonism in ruminants. G. I. Zanton* and P. Fisher, *Novus International Inc., St. Charles, MO.*

Dietary fiber has been implicated as a potential antagonist against trace mineral absorption in non-ruminants at fiber concentrations significantly lower than those which would be present in ruminant diets. The magnitude of the interaction between fibrous ingredients and trace minerals has not been characterized under ruminant relevant conditions. To address this question, fibrous feedstuffs were ground through a 1 mm screen and pre-incubated in 39°C distilled water under shaking for 2 h. Insoluble material was filtered and dried for 24 h. A quantity of dried, insoluble material was weighed into 15 mL centrifuge tubes to which 10 mL of solutions containing sulfate salts of Zn or Cu were added. Tubes were shaken for 24 h at 39°C, centrifuged for 15 min at 500 × *g*, the supernatant was filtered (0.2 μm), and analyzed for mineral concentration with ICP-OES. Percent mineral bound (%MB) to fiber was determined by the difference between final and initial concentration in solution. Several experiments were conducted with wheat straw (WS) as the fiber source to evaluate %MB and the effects of: pH (3.0 and 5.5–6.5) and Zn or Cu levels (15–1000 ppm); changing WS (12.5–100 g/L) and Zn or Cu (15–1000 ppm) levels; increasing levels of Ca (0.125–25 g/L) on Zn binding; and altering both Zn and Cu levels (16–250 ppm). In addition, the effect of rumen degradation (16 h) on Zn binding was evaluated with different fibrous feeds. Under all conditions evaluated, increasing level of Zn or Cu decreased %MB to the fiber. Lower pH reduced %MB whereas increasing the level of fiber increased %MB. Increasing the level of Ca or Cu in solution decreased the binding of Zn to the fiber, whereas increasing the level of Zn did not appreciably affect the binding of Cu. Incubation of the feeds in the rumen significantly reduced the binding of Zn (78.9 vs 74.4% bound by fiber sources for $t = 0$ and 16, respectively; $P < 0.01$). Zn binding ranged from 56 to 92% for the feedstuffs evaluated with the following ranking: timothy hay < WS < alfalfa hay < wheat bran < oat bran. It is concluded that fiber can bind a significant percentage of Zn and Cu under ruminant relevant conditions.

Key Words: trace mineral, fiber, antagonisms

W119 Forage intake and digestibility by Katahdin ewes offered bermudagrass hay supplemented with apple cider vinegar. W. B. Smith*[1], E. A. Backes[1,2], J. D. Caldwell[2], K. P. Coffey[1], and A. N. Young[1], *[1]Department of Animal Science, University of Arkansas Division of Agriculture, Fayetteville, [2]Department of Agriculture and Environmental Science, Lincoln University, Jefferson City, MO.*

Currently, some small ruminant producers are supplementing with apple cider vinegar (ACV) for increased fiber digestion and feed efficiency. However, no scientific data are available to justify this practice. Our objective was to determine intake and in vivo digestibility of bermudagrass hay by ewes supplemented with different levels of ACV. Sixteen non-pregnant, nonlactating Katahdin ewes (3 to 4 yr of age; 65.9 ± 1.16 kg initial BW) were allocated randomly to 1 of 4 treatments: 0, 10, 20 or 30 mL ACV/d. Ewes were housed in individual 1.4 × 4.3 m pens fitted with rubber mats. Each ewe was offered a 100 g mixture of cracked and ground corn at approximately 1500 h daily, and the allotted level of ACV was incorporated into the mixture. Hay from large round bales of predominantly bermudagrass (72.4% NDF, 36.3% ADF) was chopped using a bedding chopper to an approximate fiber length of 2.5 cm and offered ad libitum to each ewe through a 10-d adaptation period followed by 6 d of total fecal collections. Data were analyzed using SAS PROC MIXED, where animal served as the experimental unit. Level of inclusion of ACV did not affect DM intake ($P = 0.17$), digestible DM intake ($P = 0.22$), DM digestibility ($P = 0.52$), NDF digestibility ($P = 0.23$), or ADF digestibility ($P = 0.13$). Based on these data, ACV is not a viable supplement for enhancing digestibility of bermudagrass hay at levels of inclusion up to 30 mL/d.

Key Words: apple cider vinegar, dry matter digestibility, Katahdin

W120 Evaluation of microwave irradiation effects on ruminal and postruminal degradation of guar meal. S. N. Garajeh[2,1], A. Taghizadeh*[1], N. M. Sis[2], F. P. Khajehdizaj[1], and B. B. Nobari[1], *[1]Department of Animal Science, Faculty of Agriculture, University of Tabriz, Tabriz, Eastern Aazarbaijan, Iran, [2]Department of Animal Science, Shabestar branch, Islamic Azad University, Shabestar, Iran.*

Knowledge of the extent of RUP is important in formulating diets with adequate RDP to support rumen microorganisms. When protein degradation in the rumen exceeds the microbes ability to assimilate N into microbial crude protein (MCP), excessive rumen ammonia concentrations can occur. The DM of 1 g sample of guar meal (DM 95.5%, CP 49.6%, NDF 15.1%, ADF 6.6%, EE 4.7% and OM 94.9%) in duplicate was determined and water was added to increase the moisture content of 1kg guar meal to 300 g/kg. Approximately 500 g of samples were subjected to microwave irradiation (Butane microwave BC380W) at a power of 900w for 2 and 4 min, separately. The ruminal and postruminal degradation were determined according to Gargallo et al. (2006) with 3 fistulated sheep fed diet containing 60:40 hay to commercial concentrate. Ruminal degradability of guar meal DM and CP were decreased linearly ($P < 0.0001$) as microwave irradiation time increased. Similar result was observed for postruminal degradation of guar meal CP. It seems that

microwave treatment resulted in decreasing protein solubility and led to decrease in CP degradation. When secondary and tertiary structures of a protein are unfolded, hydrophobic groups interact and reduce water binding. Moreover, hydrophobic interactions lead to aggregation followed by coagulation and precipitation, probably reducing ruminal CP degradability.

Table 1. Ruminal and postruminal degradability of DM and CP of untreated and microwave treated guar meal

	Microwave treated				Contrast	
	Untreated	2 min	4 min	SEM	Linear	Quadratic
Ruminal degradability for 12 h incubation (%)						
DM	84.8	75.4	69.8	1.09	<0.0001	0.1841
CP	79.2	73.7	59.3	1.45	<0.0001	0.0350
Postruminal degradability (%)						
DM	76.3	81.1	79.1	0.58	0.0140	0.0030
CP	95.3	90.5	93.0	0.21	0.0003	<0.0001

Key Words: microwave irradiation, guar meal, ruminal and postruminal degradation

W121 Effect of feeding a corn straw or mixed forage diet on rumen fermentation parameters and ruminal papillae morphology in dairy cows. X. X. Weng[1,2], J. Q. Wang*[1,2], D. P. Bu[1], Y. D. Zhang[1], and F. D. Li[2], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]College of Animal Science and Technology, Gansu Agricultural University, Lanzhou, China.*

Papillae protruding from the rumen wall greatly increase the surface area for absorption of nutrients, and diets play an important part for papillae development. The objective of this study was to determine the effect of dietary forage sources on rumen fermentation parameters and ruminal papillae morphology in dairy cows. Ten primiparous and rumen-cannulated Holstein dairy cows averaging 127 ± 13 d in milk (mean ± SD) were randomly assigned to mixed forage diet (MF, forage: concentrate = 60: 40) with Chinese wildrye, alfalfa hay and corn silage as the forage source or corn straw diet (CS, forage: concentrate = 40: 60) with corn straw as the forage source. Diets were formulated to be iso-energetic and iso-nitrogenous. The experiment lasted for 63 d. Samples of rumen fluid were collected via cannula every 6 h over a 72-h duration starting on d 37 of experiment period to analyze pH, ammonia and VFA concentrations. At the end of experiment, rumen papillae were biopsied from the ventral sac and observed using light and transmission electron microscope. Results showed that cows fed MF diet had higher ($P < 0.01$) ruminal acetate concentrate and ratio of acetate to propionate, and lower concentrations of ammonia-N ($P < 0.01$), propionate ($P < 0.05$), butyrate ($P < 0.01$), isobutyrate ($P < 0.01$), valerate ($P < 0.01$) and isovalerate ($P < 0.01$) than cows fed CS diet. Microscopic examination revealed a reduction ($P < 0.01$) in the width of papillae when cows fed MF diet. No significant differences ($P > 0.05$) were found for the thickness of stratum corneum, stratum granulosum, stratum spinosum, and stratum basale between dietary treatments. Biopsied papillae exhibited a decline in cellular junctions, large spaces between cells, moderate sloughing of the stratum corneum, and an accelerated migratory state in all strata below the stratum corneum in cows fed CS diet. These results suggest that increasing permeability throughout the ruminal epithelium caused by a decline of cellular junctions may be deleterious to the animal's health when cows were fed CS diet.

Key Words: forage source, morphology, ruminal papillae

W122 Effects of pistachio by-product as a replacement for alfalfa hay on milk fatty acid composition in Saanen dairy goats fed a diet containing fish oil. M. H. Ghaffari[1], A. M. Tahmasbi[1], M. Khorvash[2], A. H. Ghaffari[1], and S. Kargar*[2], *[1]Faculty of Agriculture, Excellence Center in Animal Science, Ferdowsi University of Mashhad, Mashhad, Iran, [2]Department of Animal Sciences, Faculty of Agriculture, Isfahan University of Technology, Isfahan, Iran.*

The objective of this study was to evaluate the effect of feeding pistachio by-product (PBP) as a replacement for alfalfa hay (AH) on milk fatty acid composition in Saanen dairy goats fed a diet containing fish oil. Fifteen multiparous lactating Saanen goats (on d 25 postpartum; average BW of 38.2 ± 1.2 kg) were randomly assigned to one of 3 treatments in a completely randomized design with 5 goats per treatment. Treatments consisted of feeding the following diets: 1) control (alfalfa hay), 2) 30% PBP, 3) 30% PBP + polyethylene glycol (PEG; 0.1% DM). The experiment lasted 21 d, including 16 d of treatment adaptation and 5 d of data collection. The milk fatty acid composition is presented in Table 1. Data were analyzed using the PROC MIXED procedure of SAS.The goats fed PBP (with and without PEG) had higher amounts of C16:0, and trans - C18:1 isomer in milk fat than those fed AH, while C24:0 was detected at higher concentrations in the goats fed AH ($P < 0.05$) than those of the others. Overall, different treatments did not affect saturated (SFA), mono (MUFA) and polyunsaturated fatty acid (PUFA) concentrations in milk fat. The concentrations of trans fatty acids (TFA) were higher ($P < 0.05$) for PBP and PBP-PEG than those fed AH. However, no significant differences were detected in the concentrations of short (SCFA), medium (MCFA) and long chain fatty acids (LCFA) among treatments. These findings reveal that feeding of PBP as a replacement for AH in the diet of dairy Saanen goats can modify the fatty acid profile of milk in dairy goat.

Table 1. Effect of treatments on milk FAs (g/100 g of total FA)

	Treatments				
Item	AH	PBP	PBP+PEG	SEM	*P*-value
C16:0	18.51[b]	24.08[a]	23.63[a]	0.50	0.03
C18:1 total *trans*	13.23[b]	18.76[a]	16.84[a]	0.39	0.02
SFA	58.15	56.36	54.98	3.73	0.73
MUFA	38.61	40.60	41.91	2.43	0.68
PUFA	5.54	4.28	5.25	0.51	0.37
TFA	15.61[b]	20.23[a]	19.03[a]	0.48	0.04
SCFA	17.83	15.17	14.71	0.58	0.26
MCFA	31.65	37.46	36.42	1.26	0.14
LCFA	44.11	44.98	46.31	3.26	0.89

Key Words: pistachio by-product, milk fatty acid, polyethylene glycol

W123 Effects of pistachio by-product as a replacement for alfalfa hay on ruminal fermentation, blood metabolites, and milk yield and composition in Saanen dairy goats fed a diet containing fish oil. M. H. Ghaffari[1], A. M. Tahmasbi[1], M. Khorvash[2], A. Naserian[1], and S. Kargar*[2], *[1]Faculty of Agriculture, Excellence Center in Animal Science, Ferdowsi University of Mashhad, Mashhad, Iran, [2]Department of Animal Sciences, College of Agriculture, Isfahan University of Technology, Isfahan, Iran.*

The objective of this study was to evaluate the effect of feeding pistachio by-product (PBP) as a replacement for alfalfa hay (AH) on their milk fatty acid composition in Saanen dairy goats fed a diet containing fish oil. Fifteen multiparous lactating Saanen goats (on d 25 postpartum; average BW: 38.2 ± 1.2 kg) were randomly assigned to the 3 treatment diets in a completely randomized design with 5 goats per treatment. Treatments

consisted of feeding the following diets: (1) control (alfalfa hay), (2) 30% PBP, (3) 30% PBP + polyethylene glycol (PEG, 0.1% DM). The experiment lasted 21 d, including 16 d of adaptation to the experimental diets followed by a 5-d sampling period for determining the milk yield and composition. Ruminal fluid samples were taken at 3 h after morning feeding on 20 d of the experiment. Blood samples from all the goats were obtained from the jugular vein 3 h after the morning feeding on 21 d of the experiment. Data were analyzed using the PROC MIXED procedure of SAS. The goats fed PBP had a lower ($P < 0.05$) dry matter intake (DMI) than the other treatments. There was no significant difference between the rumen pH, milk yield and composition among treatments, while rumen ammonia-N concentration was lower ($P < 0.01$) in goats fed PBP than the other treatments. There were no significant differences between treatments for blood metabolites. These findings reveal that feeding of PBP as a replacement for AH in the diet of dairy Saanen goats had no adverse effect on ruminal fermentation and blood metabolites.

Table 1. Effects of treatments on milk, rumen, and blood parameters

	Treatment				
Item	AH	PBP	PBP+PEG	SEM	*P*-value
DMI (kg/d)	1.59[a]	1.43[b]	1.61[a]	0.03	0.02
pH	6.50	6.46	6.69	0.07	0.09
Ruminal NH_3-N (mg/dL)	22.92[a]	18.26[b]	20.97[a]	0.67	0.003
Blood glucose (mg/dL)	63.8	60.0	61.0	2.05	0.39
Blood triglyceride (mg/dL)	39.2	41.3	40.0	9.44	0.98
BUN (mg/dL)	25.1	23.5	21.3	2.91	0.67
Milk yield (g/d)	1221	1218	1198	39.92	0.36
Fat (%)	2.28	2.87	3.44	0.40	0.21
Protein (%)	2.89	2.55	2.57	0.21	0.43
Lactose (%)	4.55	4.35	4.16	0.15	0.27

Key Words: pistachio by-product, polyethylene glycol, Saanen goat

W124 Effects of pistachio by-products as a replacement for alfalfa hay on rumen bacteria involved in biohydrogenation of Baluchi male sheep. M. H. Ghaffari[1], A. M. Tahmasbi[1], A. H. Ghaffari[1], A. Naserian[1], and S. Kargar*[2], *[1]Faculty of Agriculture, Excellence Center in Animal Science, Ferdowsi University of Mashhad, Mashhad, Iran, [2]Department of Animal Sciences, College of Agriculture, Isfahan University of Technology, Isfahan, Iran.*

The objective of this study was to investigate the effect of feeding pistachio by-products (PBP) as a replacement for alfalfa hay (AH) on populations of bacteria involved in rumen biohydrogenation in Baluchi sheep. Four Baluchi sheep (41 ± 1.3 kg BW) fitted with ruminal cannulas were assigned at random to 4 experimental diets in a 4 × 4 Latin square design. Treatments consisted of feeding the following diets: (1) control (0% PBP), (2) 12% PBP, (3) 24% PBP, and (4) 36% PBP. The basal diet was 36% DM alfalfa hay, 16% DM wheat straw, 20% DM barley grain, 0.3% DM sunflower oil. The experiment consisted of 4 periods. Each period lasted 20 d, comprising 16 d of adaptation to the experimental diet followed by 4 d for sampling. Bacterial populations were assessed by DNA extraction of samples of rumen liquor followed by rt-PCR analysis. All data were analyzed using the PROC MIXED procedure of SAS. Among the total ruminal bacterial community, the relative abundance of *Butyrivibrio fibrisolvens* and *Butyrivibrio proteoclasticus* were not affected by the treatments (Table 1). This finding suggests that dietary PBP at levels up to 36% DM had no effects on relative abundance of bacteria involved in rumen biohydrogenation.

Table 1. Populations of biohydrogenating bacteria[1] (percentage of total bacteria) in Baluchi male sheep fed different levels of pistachio by-product

	Pistachio by-product level					*P*-value		
Bacteria	0%	12%	24%	36%	SEM	Treatment	Linear	Quadratic
B. fibrisolvens	1.001	1.764	0.955	0.909	0.318	0.591	0.537	0.354
B. proteoclasticus	1.002	0.962	1.026	1.020	0.306	0.999	0.931	0.958

Within rows, means with different letters are significantly different ($P < 0.05$).
[1]Fold change compared to control.

Key Words: biohydrogenation, pistachio by-product, real-time PCR

W125 Effects of pistachio by-products as a replacement for alfalfa hay in the diet of sheep on ruminal fermentation. M. H. Ghaffari[1], A. M. Tahmasbi[1], M. Khorvash[2], S. A. H. Ghaffari[1], and S. Kargar*[2], *[1]Faculty of Agriculture, Excellence Center in Animal Science, Ferdowsi University of Mashhad, Mashhad, Iran, [2]Department of Animal Sciences, College of Agriculture, Isfahan University of Technology, Isfahan, Iran.*

The objective of this study was to investigate the effect of feeding pistachio by-products (PBP) as a replacement for alfalfa hay (AH) on ruminal fermentation in sheep. Four Baluchi sheep (41 ± 1.3 kg BW) were assigned at random to 4 experimental diets in a 4 × 4 Latin square design. Treatments consisted of feeding the following diets: (1) control (0% PBP), (2) 12% PBP, (3) 24% PBP, and (4) 36% PBP. The basal diet was 36% DM alfalfa hay, 16% DM wheat straw, 20% DM barley grain. The experiment consisted of 4 periods. Each period lasted 20 d, comprising 16 d of adaptation and 4 d for sampling. All data were analyzed as a 4 × 4 Latin square design using the PROC MIXED procedure of SAS. Results of ruminal fermentation parameters are presented in Table 1. Treatments had no effect on ruminal pH, while rumen ammonia-N concentration decreased linearly ($P < 0.05$) with increasing PBP levels up to 36% of DM. Reduction in the ruminal ammonia-N concentration with the feeding of PBP in the diet may have resulted from tannins (2.46% DM) bound to proteins, decreased proteolysis and subsequently lowered ammonia-N concentration in rumen fluid. Feeding of 36% PBP in the diet reduced ($P < 0.05$) total VFA and acetate concentrations, while the concentrations of propionate, butyrate and acetate to propionate ratio were similar to across all treatments. Reductions in the VFA concentration might be related to the lower microbial fermentation in presence of tannins in PBP.

Table 1. Ruminal fermentation parameters in sheep fed different levels of pistachio by-product meal (PBP)

	Treatments					*P*-value
Rumen parameter	0PBP	12PBP	24PBP	36PBP	SEM	Linear
Rumen pH	6.31	6.33	6.26	6.38	0.06	0.541
Rumen NH_3-N (mg/dL)	19.41[a]	17.46[ab]	16.31[b]	15.18[b]	0.78	0.003
Total VFA (mmol/100 mol)	103.30[a]	104.63[a]	103.01[ab]	100.33[b]	0.87	0.024
Individual VFA (mmol/100 mol)						
Acetate	70.93[a]	69.71[a]	69.44 [a]	66.99[b]	0.70	0.004
Propionate	21.14	23.79	22.35	22.25	0.91	0.653
Butyrate	11.24	11.13	11.23	11.11	0.29	0.82
Acetate:propionate ratio	3.36	2.96	3.11	3.02	0.14	0.186

Key Words: Baluchi sheep, pistachio by-product

W126 Substitution of ground corn with different levels of coarsely ground wheat in the diets of dairy cows on feed intake, nutrient digestion, microbial N supply, and plasma metabolite profiles. Y. Guo*, Y. Zou, S. Li, Z. Cao, X. Xu, and Z. Yang, *State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing, China.*

The effects of increasing concentrations of coarsely ground wheat (CGW, 3-mm screen, geometric mean particle sizes: 1,139μm) substituted for ground corn (GC, 3.5-mm screen, geometric mean particle sizes: 666μm) on feed intake, nutrient digestion, microbial N supply and plasma metabolites were evaluated using 8 multiparous Holstein cows (569 ± 47 kg of BW, 84 ± 17 DIM) in a duplicated 4 × 4 Latin square design with 21-d periods. The 4 diets contained 0, 9.6, 19.2, and 28.8% CGW and 27.9, 19.2, 9.6, and 0% GC (DM basis), respectively. The cows were fed a TMR, with a 47:53 forage to concentrate ratio, where forage was 27% corn silage, 14% alfalfa hay, and 6% Chinese wild rye. Increasing CGW in the diets resulted in a quadratic response ($P = 0.07$) in feed intake with numerically greater intake at 9.6 and19.2% of diet DM. Apparent digestibility of CP and starch were not affected by dietary treatments; however, apparent digestibility of NDF and ADF decreased significantly ($P < 0.01$) when cows were fed 28.8% CGW diets. Apparent digestibility of DM ($P = 0.02$) and OM ($P = 0.01$) decreased linearly with increasing CGW in the diets. The appropriate amount of CGW can promote microbial N supply, and the optimal value is in 9.6% CGW diets; however, the calculated absorption of purine derivatives ($P = 0.04$) and intestinal flow of microbial N ($P = 0.02$) decreased significantly when cows were fed 28.8% CGW diets. With increasing the level of dietary CGW, plasma BHBA ($P = 0.07$), cholesterol ($P < 0.01$), and triglycerides ($P = 0.06$) decreased linearly, whereas plasma glucose ($P = 0.08$) and insulin ($P = 0.02$) increased linearly at 6h after morning feeding. These data indicate that CGW is a suitable replacement for CG in dairy cow diets when fed up to 19.2% of diet DM; however, the substitution percentage should not be too high, a great amount of CGW in the diets may increase the risk of digestive disturbance, depress microbial N supply, perturbs the patterns of plasma metabolites in lactating dairy cows.

Key Words: dairy cow, nutrient digestibility, wheat

W127 Particle size distribution of corn can predict starch degradability in rumen. Y. Zou*, Z. Yang, S. Li, and Z. Cao, *State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing, China.*

A study using 5 Holstein cows with ruminal cannulas were conducted to evaluate the degradation mechanisms of different particles, and to establish the relationship between ruminal degradation dynamics and particle size distribution. The particle size of corn grain was prepared to pass 5 sieves: 6000, 2360, 600, 450, and 300 μm. All nylon bags containing the tested corn were placed in rumen simultaneously, and 2 bags of each cow were removed at each time point after 2, 4, 8, 12, 24, and 48 h of incubation. In general, in situ disappearance and degradation curves of DM and starch were linearly ($P < 0.05$) increased from grounded (300 μm) to coarsely rolled (6000 μm) corn because of destruction of crystallization of corn. R^2 varied from 0.6790 ($P = 0.086$) to 0.9344 ($P = 0.008$) of DM and from 0.7467 ($P = 0.059$) to 0.9908 ($P < 0.001$) of starch disappearance, and for degradable variables varied from 0.6188 ($P = 0.115$) to 0.9010 ($P = 0.014$) of DM and from 0.6243 ($P = 0.112$) to 0.9290 ($P = 0.008$) of starch, expect for starch degradability at 0 h ($R^2 = 0.3113$, $P = 0.328$). Overall, a simple way for evaluating degradation characteristics of mixed particle corn in feed was established, dynamic degradability and degradation variables can be predicted using the product of corresponding value of each particle calculated in the linear formula and the percentages of corn on each screen of a standard test sieve.

Table 1. Dry matter and starch degradation variables of corn kernel with 5 different particle sizes incubated in situ

Particle	DM disappearance				Starch disappearance			
size, μm	a	b	K_d	RDDM	a	b	K_d	RDS
300	45.62^{a}	54.03^{b}	6.62^{a}	73.96^{a}	43.04^{a}	56.63^{b}	7.38^{ab}	74.28^{a}
450	32.82^{b}	62.51^{ab}	6.15^{ab}	64.46^{b}	25.55^{c}	67.53^{ab}	9.14^{a}	66.31^{b}
600	34.47^{b}	64.49^{ab}	3.63^{b}	58.79^{c}	36.53^{b}	62.55^{ab}	4.66^{bc}	63.87^{b}
2360	27.48^{c}	70.58^{ab}	3.47^{ab}	53.34^{c}	27.12^{c}	72.02^{ab}	3.81^{bc}	55.09^{c}
6000	12.61^{d}	84.67^{a}	2.29^{b}	36.00^{d}	15.99^{d}	83.66^{a}	2.28^{c}	39.03^{d}
SEM	0.591	3.802	0.489	0.656	0.703	0.962	4.574	6.281
Regression								
Intercept	39.53	58.57	5.61	67.96	36.43	60.84	7.21	70.12
Slope	−4.60	4.48	−0.61	−5.48	−3.49	3.93	−0.91	−5.36
R^2	0.854	0.901	0.619	0.879	0.653	0.862	0.624	0.929

^{abc}Different superscript letters with the same column represent a significant difference between treatments ($P < 0.05$).

Key Words: degradability, lactating cow, starch

W128 Ruminal fermentation kinetics of finishing feedlot beef diets with increasing levels of whole cottonseed. V. N. Gouvea*[1], J. T. Neves Neto[2], D. B. Galvani[3], M. V. C. Ferraz Junior[1], J. A. Faleiro Neto[1], M. V. Bieh[4], J. J. R. Fernandes[2], and A. V. Pires[4], *[1]University of São Paulo, Pirassununga, SP, Brazil, [2]Federal University of Goiás, Goiânia, GO, SP, Brazil, [3]EMBRAPA Goats and Sheep, Sobral, CE, Brazil, [4]University of São Paulo, Piracicaba, SP, Brazil.*

Whole cottonseed (WC) is the primary by-product included in Brazilian finishing feedlot beef diets. Because a high level of WC in the diet can impair animal performance, the objective of this study was to evaluate the in vitro fermentation kinetics of diets containing 0, 8, 16, 24, or 32% of WC (DM basis). Diets were composed of 0.85 concentrate and 0.15 of forage (corn silage), being formulated to meet protein and energy requirements of Nellore bulls (2.2% of N and 80% TDN, respectively). Samples of each diet (0.8 g) were weighed into 160 mL serum bottles, with 8 mL of inoculum and 72 mL of a buffer solution. Rumen inoculum was collected before the morning feeding from 2 Holstein cows fitted with permanent ruminal cannula and fed ad libitum a total mixed ration consisting of 0.30 commercial concentrate and 0.70 corn silage. Four bottles for each diet, plus 4 additional bottles containing buffered medium and rumen fluid inoculum only (blanks) were used. As the bottles were filled they were immediately closed with rubber stoppers, shaken and placed in the incubator at 39°C. The volume of gas produced was recorded at 2, 4, 6, 8, 10, 12, 15, 18, 21, 24, 36, 48, 72, and 96 h of incubation using the pressure reading technique. To estimate kinetic parameters of gas production (GP) data were fitted to the model $G = A[1-\exp^{-c(t-L)}]$, where: G (ml) is the cumulative gas production at time t; A (ml) is asymptotic gas production; c (/h) is the fractional rate of gas production; and L (h) is the lag time. Increasing WC level in the diet linearly increased ($P < 0.001$) the fractional rate of gas production (0.048, 0.052, 0.053, 0.058, and 0.064/h). Discrete lag time also linearly increased (3.69, 3.79, 4.08, 4.42, 4.95 h; $P < 0.05$), while the asymptotic gas production decreased ($P < 0.05$) when the level of WC was greater than 8% in the diet (333.80, 353.65, 333.28,

320.03 and 323.55 mL/g DM), probably due to great contents of ether extract (17.5%) and lignin (13.0%) in the WC. Including WC in feedlot finishing diets for beef cattle at levels greater than 8% can impair ruminal fermentation.

Key Words: by-product, gas production, lag time

W129 Animal performance and fractional volatile fatty acid absorption rate through the rumen wall in lactating cows receiving a corn straw or mixed forage diet. X. X. Weng[2,3], J. Q. Wang*[1,2], D. P. Bu[2], Y. D. Zhang[2], and F. D. Li[3], *[1]Agronomy College of Heilongjiang August First Land Reclamation University, Da qing, Heilongjiang, China, [2]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [3]College of Animal Science and Technology, Gansu Agricultural University, Lanzhou, China.*

Objective of this experiment was to investigate effects of 2 types of forage diets on animal performance and fractional absorption rate of volatile fatty acids (VFA) through the rumen wall. Ten primiparous, rumen-cannulated Holstein dairy cows in late-lactation were randomly assigned to mixed forage diet (MF, forage: concentrate = 60: 40) with Chinese wildrye, alfalfa hay and corn silage as the forage source or corn straw diet (CS, forage: concentrate = 40: 60) with corn straw as the forage source. Cows were fed their respective diet for 58 d, following which n-valeric acid and Co-EDTA were used as markers for measuring ruminal VFA absorption and passage rates. Rumen fluid was collected from ventral sac of the rumen. Feed intake, body weight and milk production were monitored. Milk fat, protein, lactose and total solids were analyzed by near-infrared analysis. Results showed that dry matter intake was not affected ($P > 0.05$) by treatments, averaging 19.78 kg/d. Cows fed MF diet produced more 4% FCM ($P < 0.05$), milk fat ($P < 0.05$) and total solids ($P < 0.10$). Ruminal ammonia concentration was significantly higher in CS treatment ($P < 0.01$). Mixed forage treatment markedly increased rumen acetate concentration and acetate: propionate ratio ($P < 0.05$). Cows fed CS diet tended to have higher molar proportions of propionate and isobutyrate ($P < 0.10$). Fractional rates of total VFA absorption and passage from the rumen were not affected by dietary treatments, averaging 14.78 and 13.64%/h, respectively. However, cows fed MF diet had higher ($P < 0.05$) estimated clearance rate of acetate, as well as total VFA passage rate (mol/h). These results suggest that cows fed MF diet improve yields of 4% FCM, milk fat and total solids. Lower rumen ammonia concentration indicated a more efficient utilization of feed nitrogen in MF diet compared with CS diet. Dietary treatments did not affect fractional rate of VFA absorption in late lactating cows.

Key Words: animal performance, forage source, VFA absorption rate

W130 The use of Propolis in calf feeding: Effect on fecal score, health score and feed consumption behavior. P. Peravian*, K. Rezayazdi, G. Nehzati, and M. Dehghan-Bonadaki, *University of Tehran, Tehran, Iran.*

Forty female Holstein calves with 41 ± 1 kg birth weight were assigned to a completely randomized design with 4 treatments and 10 replicates (calves) in each treatment from 14 until 65 d of age. Treatments were (1) Control (without monensin in starter and without Propolis in milk), (2) starter without monensin and 500 ppm soluble Propolis powder in milk, (3) starter without monensin and 1000 ppm soluble Propolis powder in milk, and (4) monensin in starter and without Propolis in milk. During the experiment calves were inhabited in individual boxes and had free access to water and starter. The starter was formulated according to NRC 2001.To decrease the stress of weaning, calves stayed in their boxes after weaning for 9 d. Fecal score (fluidity score, 1 = normal, 2 = soft, 3 = runny 4 = watery) and health score (cough score: 1 = normal, 2 = induced single cough, 3 = induced repeated cough, 4 = repeated spontaneous cough, and nasal score: 1 = normal, 2 = unilateral cloudy discharge, 3 = bilateral cloudy discharge, 4 = copious bilateral discharge) were measured daily. dry matter intake behavior (time of feeding, ruminating, resting) was measured at the middle of the experiment. Means of fecal score (1.29, 1.21, 1.26, 1.22) ($P = 0.3$), nasal score (1.18, 1.19, 1.18, 1.17) and cough score (1.18, 1.19, 1.18, 1.17) ($P = 0.6$) for treatments 1–4 respectively, were not different among treatments. The times spent on feeding (147, 154, 154,180 min/d), ruminating (397, 370, 343, 376 min/d), resting (706, 660, 620, 637 min/d) were not influenced by treatments ($P = 0.7$). The results showed that Propolis in milk or monensin in starter did not affect fecal score, health score and feed consumption behavior of Holstein female calves.

Key Words: fecal score, Holstein female calf, Propolis

W131 Effects of three different diets on productive performance and archenteric pH values of dairy cows at late lactation. J. N. Li[1,2], D. P. Bu[1], J. Q. Wang*[1], P. Sun[1], F. D. Li[2], C. F. Qin[1], and P. Zhang[1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]College of Animal Science and Technology, Gansu Agricultural University, Lanzhou, Gansu, China.*

This study was to investigate the effects of 3 different types of diets on productive performance and archenteric pH values in late lactation dairy cows. Fifteen primiparous, permanently ruminally and duodenally fistulated Holstein cows at late lactation (DIM = 293 ± 5.34) were randomly assigned to 3 treatments (n = 5) mainly differing in forage: MF diet (alfalfa hay, Chinese wildrye, corn silage, soybean meal), CSA (corn straw, soybean meal), CSB (corn straw, cottonseed meal, corn gluten lipid, high protein corn meal). CP, NDF and NE_L in 3 diets were 18.02, 16.90 and 16.30%; 61.43, 56.73 and 57.06%; 1.48, 1.54 and 1.52 Mcal/kg, respectively. Dry matter intake and milk yield were recorded daily, body condition scoring (BCS) were conducted once weekly. Milk compositions were detected twice weekly, rumen and duodenum samples were collected with 2-h intervals and pH values were determined. Data were analyzed using the MIXED procedure (SAS 9.1). Compared with CSA treatment, cows fed MF diet had positive effect ($P < 0.05$) on composition of milk free fatty acid (FFA) (2.18 and 3.48%; $P < 0.05$), and tended to have negative effect on milk urea percentage (0.042 and 0.037%; $P = 0.09$). Cows in CSB group had higher FFA composition (2.18 and 2.76%; $P < 0.05$), somatic cell count (SCC) (155.43 and 179.16×10^3 mL^{-1}; $P < 0.05$) and lower density (1032.95 and 1031.93 g/L; $P < 0.05$) in milk compared with those in CSA group. There was no difference in other indexes of productive performance ($P > 0.05$). Compared with CSA treatment, the ruminal pH of MF group decreased at 1730 (6.80 and 6.25; $P < 0.01$), 1930 (6.44 and 6.10; $P < 0.01$), and CSB treatment decreased at 1730 (6.80 and 6.58; $P < 0.01$), and 2330 (5.92 and 6.06; $P < 0.05$). The population mean of duodenal pH in all treatments had no significant difference ($P > 0.05$). The results indicated that productive performance affected by forage patterns slightly, milk FFA composition, density and SCC of dairy cows at late lactation were influenced by different dietary protein sources. Ruminal and duodenal pH values were influenced by diet systems partly.

Key Words: archenteric pH, diet system, productive performance

W132 Influence of diets with different protein sources on productive performance and rumen microbial communities in dairy cattle. J. W. Zhao[1,2], D. P. Bu[1], J. Q. Wang*[1], S. G. Zhao[1], and C. F. Qin[1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]College of Animal Science and Technology, Inner Mongolia University for the Nationalities, Tongliao, Inner Mongolia, China.*

The objective of this experiment was to study the effects of diets with different protein sources on productive performance and composition of rumen microbial community in dairy cows. Ten Holstein cows (primiparous, DIM 314 ± 16 d, BW 540 ± 50 kg) were assigned to 2 groups randomly and fed with soybean meal diet (soybean meal, 23.6% DM) or miscellaneous meal diet (soybean meal, 3.3% DM; cottonseed meal, 2.6% DM; DDGS, 9.3% DM; Corn gluten lipid, 9.9% DM; and corn high meal, 11.9% DM). The content of crude protein of 2 diets was 18.02% DM and 16.90% DM, respectively. Completely randomized design was conducted and feeding lasted for 60 d. Ruminal fluid samples were collected from 6 dairy cows with rumen canullas on d 30. Total DNA were extracted and analyzed by denaturing gradient gel electrophoresis (DGGE) with subsequent analysis on sequences and clusters. Results showed that diets with different protein sources had no effects on dry matter intake, body weight, milk production, standard milk production, milk fat, milk protein, lactose, fat/protein ratio, milk urea nitrogen and free fatty acid contents ($P > 0.05$). According to the above synthesis evaluation of performance indexes, soybean meal could be replaced by miscellaneous meal effectively. DGGE profiles of rumen microbial community from 2 groups showed that the quantity and optimal density of the DGGE bands which were analyzed with Quantity one were changed significantly. Shannon-Weiner index showed no difference ($P > 0.05$) between 2 groups. Sequences analysis in 2 groups showed that the uncultured bacteria belonged to the phylum of *Bacteroidetes*, *Firmicutes*, *Spirochaetes*, *Proteobacteria* and *Planctomycetes*. These results revealed that bacteria community structure from diets with different protein sources were unique but no difference existed in diversity of rumen bacteria.

Key Words: dairy cow, productive performance, rumen microbial

W133 Screening and analysis of dipeptidyl peptidase IV from microbial metagenomic library in the rumen of dairy cow. J. W. Zhao[1,2], J. Q. Wang*[1], S. G. Zhao[1], P. Sun[1], D. P. Bu[1], X. L. Hu[1], Y. F. Lu[1], D. D. Wang[1], and D. Jin[1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]College of Animal Science and Technology, Inner Mongolia University for the Nationalities, Tongliao, Inner Mongolia, China.*

As the key enzyme of oligopeptides degradation, the study for sequence characteristics and enzymatic properties of dipeptidyl peptidases IV (DPP-IV) contribute to control the degrading of oligopeptides. Most of the DPP-IV sequences could not be obtained because limited culturable bacteria in the rumen. The purpose of this study was to reveal the characterization of DPP-IV sequences and enzymatic activity in the rumen of dairy cow by culturable-independent method. The dpp-IV degenerate primers were used to screen rumen microbial fosmid library including 17664 clones. The plasmids were extracted from the positive clones and digested by Hind III. The dpp-IV sequences were obtained by PCR, cloning and sequencing. The Fosmid end sequences and DPP-IV sequences of the positive clones were analyzed by blastx and blastp, respectively. The peptidase activity from the positive clones was measured using Gly-Pro-pNA as a substrate. Ten positive clones named DP1-DP10 containing dpp-IV fragment were obtained. 78% of the Fosmid end sequences could match with the known genes (similarity 44–94%). DPP-IV sequences contained N-conservative region (DWVYEEE) and C-catalytic domain (GWSYGG). DPP-IV sequences matched to *Cyclobacterium marinum* (43%), *Capnocytophaga* sp. (63%), *Prevotella ruminicola* 23 (66%) and *Solitalea canadensis* (50%). The activity of DP7 peptidase is highest (6.88 U/mg). Ten positive clones obtained from rumen microbial fosmid library had different sequence characteristics and peptidase activity. In the future, we will overexpress the DPP-IV in vitro, and characterize the enzyme kinetics.

Key Words: dipeptidyl peptidase IV, enzyme activity, fosmid library

W134 Adhesion molecules of the immune system of dairy cows fed with n-3 and n-6 fatty acid sources in the transition period and early lactation. L. C. Verdurico*, J. R. Gandra, R. D. Mingoti, R. V. Barletta, J. E. Freitas Junior, L. Oliveira, G. D. Calomeni, R. Gardinal, C. S. Takyia, T. H. Vendramini, and F. P. Renno, *Universidade de Sao Paulo, Pirassununga, Sao Paulo, Brazil.*

The aim of this study was to evaluate effect of omega 3 and omega 6 supplementation, on expression of adhesion molecules of Holstein cows during transition period and early lactation. Forty-eight Holstein cows were divided in 4 experimental groups in randomized design. Animals were assigned to receive one of 4 treatments: 1) control (C; n = 12), without fat sources in pre- and postpartum; 2) flaxseed (FS; n = 12), fed 60 and 80 g/kg of DM of flaxseed in pre and postpartum; 3) whole raw soybeans (WS; n = 12), fed 120 and 160 g/kg of DM of whole raw soybeans in pre and postpartum; 4) calcium salts of unsaturated fatty acids (CSFA; n = 12; Megalac-E), fed 24 and 32 g/kg of DM of calcium salts of unsaturated fatty acids in pre and postpartum. Experimental diets were fed from 35 d before the estimate calving until 84 d of lactation, formulated to meet nutritional requirements of each period. Blood samples were taken −21, −14, −7 d in relation to prediction of birth, at birth and +7, +14, +21, +42, +84 d postpartum. Data were analyzed using the PROC MIXED of SAS 9.1 with fixed dietary effect, time effect, interaction between diet and time. Data were analyzed by orthogonal contrasts C vs. WS+CSFA+FS (C1); FS vs. WS+CSFA (C2); and WS vs. CSFA (C3). Was measured expression of adhesion molecules (cluster of differentiation) CD4+, CD8+, CD25+ and CD62L. Cows fed the FS, WS and CSFA treatments had higher expression of adhesion molecules CD4+, CD8+, CD25+ and CD62L than those fed the C diet. However, cows fed WS and CSFA treatments had higher expression of adhesion molecules CD14+ than those cows fed the FS diet peripartum period (30.6 and 25.1 vs. 18.2% of positive cellules respectively). The inclusion of sources of fatty acids omega 3 and 6 in the diet of dairy cows improved the expression of adhesion molecules in the transition period.

Key Words: dairy cow, fat source, immune function

W135 Regulation of pancreatic amylase synthesis by leucine and phenylalanine is associated with the changes in mRNA abundance and/or phosphorylation of 4E-BP1. Z. Yu, K. Liu, Y. Liu, M. Xu, and J. Yao*, *College of Animal Science and Technology, Northwest A&F University, Yangling, Shaanxi, China.*

Insufficient pancreatic amylase secretion may be the critical limiting factor of low starch digestibility in the small intestine of ruminants. The present experiment, therefore, aimed to evaluate the regulating mechanism of duodenal leucine (Leu) and phenylalanine (Phe) to pancreatic enzyme activities. Twenty yearling ewe goats with duodenal catheters were used in a completely randomized design experiment. All goats

were fed the same diet twice daily at 0800 and 1800, and were randomly assigned to 4 treatments: duodenal infusion of water, 3 g/d Leu (3L), 9 g/d Leu (9L), and 2 g/d Phe (2P) for 21 d. On d 21, all goats were slaughtered for blood and pancreatic tissue sample collection. Pancreases were weighed, subsampled, frozen in liquid N_2, and stored at −80°C for the subsequent analysis. Pancreatic DNA concentration was reduced ($P < 0.05$) by 9L treatment. Pancreatic protein:DNA ratios increased markedly ($P < 0.05$) in 9L and 2P treatments. Both Leu and Phe infusions increased ($P < 0.05$) pancreatic amylase activity. Pancreatic trypsin activity (U/mg of protein) decreased ($P < 0.05$) when 2P was infused, while when expressed by per milligram DNA, pancreatic trypsin activity increased ($P < 0.05$) in 9L group. Pancreatic lipase activity (U/mg of DNA) was improved by 9L and 2P treatment. Amylase mRNA levels were higher ($P < 0.05$) in 9L and 2P groups. The Leu and Phe infusions had no effects ($P > 0.05$) on trypsin mRNA levels. Lipase mRNA levels were increased ($P < 0.05$) by 2P treatment. Leu infusions significantly stimulated ($P < 0.05$) phosphorylation of 4E-BP1, while no effects ($P > 0.05$) were observed when goats were infused Phe. Leu infusions also increased ($P < 0.05$) pancreatic free Leu concentration. Phe infusion trended to increase plasma CCK concentration ($0.05 < P < 0.10$). Leu and Phe infusions did not influence plasma insulin concentration ($P > 0.05$). These results indicate that cell size, not cell number, is critical for digestive enzyme production. Duodenal Leu and Phe infusions regulate pancreatic amylase expression mainly through transcriptional and/or translational events.

Key Words: amino acid, pancreatic amylase, regulation

W136 Microbial protein synthesis in sheep supplemented with extracts of *Salix babylonica* and exogenous enzymes. K. I. Valdes[1], A. Z. M. Salem*[1], M. Gonzalez-Ronquillo[1], R. Rojo[2], H. Gado[3], N. Rivero[1], and N. Odongo[4], *[1]Facultad de Medicina Veterinaria, Universidad Autonoma del Estado de Mexico, Mexico, [2]CU-UAEM Temascaltepec, Mexico, [3]Department of Animal Production, Faculty of Agriculture, Ain Shams University, Qalubia, Egypt, [4]Animal Production and Health Section, Joint FAO/IAEA Division of Nuclear Techniques in Food and Agriculture, International Atomic Energy Agency, Vienna, Austria.*

The aim of this study was to estimate microbial protein synthesis and urinary excretion of purine in lambs. In a completely randomized design, 16 male growing Suffolk lambs (27.5 ± 2.5 kg LW) were used, which were assigned to 4 treatments in individual pens. Treatments were: control (lambs were fed on 30% concentrate and 70% corn silage at 0700h and 1600h; SB: control diet supplemented with *Salix babylonica* extract (30 mL); EZ: control diet supplemented with 10 g exogenous enzymes of Zado and SBEZ: control diet supplemented with *Salix babylonica* extract and exogenous enzymes of Zado. Enzyme product of Zado is commercially available multi-enzyme feed additive in a powder form produced from *Ruminococcus flavefaciens* and manufactured by the Academy of Scientific Research and Technology in Cairo, Egypt. Average daily gain was increased ($P = 0.001$) with EZ, while dry matter intake was increased with SBEZ. Allantoin and xanthine concentrations were increased ($P < 0.001$) with SBEZ supplementation compared with the other treatments. Uric acid and total purine derivatives were increased ($P < 0.001$) with EZ addition in diets. The combination of the 2 additives increased ($P = 0.025$) allantoin-to-creatinine ratio compared with control diet. As a conclusion the addition of 10 g of exogenous enzymes of Zado or in combination with *Salix babylonica* extract in lamb's diet, increased the microbial protein synthesis.

Key Words: lamb, purine derivative, *Salix babylonica*

W137 Changes in the relative population size of target ruminal bacteria following a grain-induced challenge in beef cattle receiving viable and nonviable active dried yeast. R. Mohammed[1], D. Vyas*[1], A. Uwizeye[1], W. Z. Yang[1], K. A. Beauchemin[1], and N. Walker[2], *[1]Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada, [2]AB Vista, Marlborough, Wiltshire, UK.*

This study was conducted to characterize changes in the relative population size (RPS) of selected ruminal bacteria in cattle fed active dried yeast (*Saccharomyces cerevisiae*) following an induced ruminal acidosis. Six ruminally cannulated beef heifers fed a 50:50 forage:concentrate diet (DM basis) were used in a double 3 × 3 Latin square design. Treatments were control (Ctrl; no yeast), active dried yeast (ADY; 4 g providing 10^{10} cfu/g; AB Vista, UK), and killed dried yeast (KDY; 4 g autoclaved ADY). A day before acid challenge (d21), intakes were restricted to 50% of ad libitum intake. Acidosis was induced on d22 by adding barley grain (amount equivalent to 25% of DMI) directly into the rumen before feeding. Ruminal digesta was collected on d22 of each period at time 0 (before feeding), 3, 6, 9, 12, 24 h, and 168 h. Real-time PCR data from the liquid and solid ingesta were summed by cow at each time and reported as % (16S copies for time t relative to time 0). The RPS of *S. ruminantium* was greater ($P = 0.03$), and that of *R. flavefaciens* tended to be greater ($P = 0.06$), for heifers fed ADY and KDY compared with Ctrl. Treatment × time interactions were not significant. There was a time effect on the RPS of *S. ruminantium* reaching peak values 12 h post-challenge. The RPS of *F. succinogenes* decreased until 9 h post-challenge and recovered to the 0 h value by 168 h. The RPS of *S. ruminantium* ($r^2 = 0.62$; $P < 0.01$), *M. elsdenii* ($r^2 = 0.57$; $P < 0.01$) and S. bovis ($r^2 = 0.31$; $P = 0.03$) were positively related to lactate concentration, while RPS of *F. succinogenes* ($r^2 = 0.30$; $P = 0.03$) was negatively related to lactate. The RPS of *S. ruminantium* ($r^2 = 0.62$; $P < 0.01$) and *M. esldenii* ($r^2 = 0.38$; $P = 0.01$) were negatively related to ruminal pH while RPS of F. succinogenes ($r^2 = 0.43$; $P = 0.01$) and *R. flavefaciens* ($r^2 = 0.38$; $P = 0.01$) were positively related to pH. Feeding active dried yeast, regardless of its viability, during a period of acidosis can help increase the RPS of *S. ruminantium* that utilize lactic acid and *R. flavefaciens* that digest fiber.

Key Words: acid-challenge, active dry yeast, ruminal bacteria

W138 Effect of ensiling high moisture corn with aspen wood byproducts on in situ dry matter disappearance of the final ensiled product. E. Caldera*, J. J. Wagner, and T. E. Engle, *Colorado State University, Fort Collins.*

The objective of this study was to investigate the effect of ensiling high moisture corn (HMC) with aspen wood byproducts (bark, shavings, and saw dust) on in situ dry matter disappearance (DMD) of the final ensiled product. Treatments consisted of (1) 100% HMC; (2) 90% HMC, 10% bark; (3) 90% HMC, 10% shavings; (4) 90% HMC, 10% saw dust; (5) 100% bark; (6) 100% shavings; and (7) 100% saw dust; with 5 replications per treatment. All ratios were calculated for similar DM. Treatments were individually packed by placing each experimental silo (0.368 m × 0.302 m × 0.267 m) into a modified press. A torque wrench was used to apply the same packing pressure (2.76 kg·m) and densities across treatments. Prior to packing each silo, 50 kg of HMC was prepared by mixing water and dry rolled corn at a desired ratio (29.4% water to 70.40% dry rolled corn) then mixed with each aspen wood byproduct specific for each treatment. After 30 d of storage in a well-ventilated room at 25°C, silos were opened, weighed, and subsampled for DM determination. Following DM analysis, samples were ground through a 2 mm screen and composited. Two sets of in situ bags for each treatment (including blank bags) were prepared for 6 different time periods (0, 6, 12, 24, 48,

and 72 h; in triplicate) and placed in 2 fistulated steers maintained on a roughage based diet for 3 weeks before in situ incubation. Steers were then switched to a high concentrate diet for 3 weeks and the in situ incubation was repeated. Area under the curve (AUC) was calculated for each replicate within each treatment over the 72-h incubation time period. Using the DMD results from the 100% HMC, bark, shavings, and saw dust treatments, a predicted digestion curve was generated for treatments 2, 3, and 4. Predicted and actual AUC were compared for treatments 2, 3, and 4. In situ DMD AUC for predicted and actual digestion curves in roughage and concentrate fed steers were similar across treatments 2, 3, and 4. These data indicate that under conditions of this experiment, ensiling HMC with aspen wood byproducts had no effect on in situ DMD of the final mixture.

Key Words: ensiling, in situ, wood

W139 Neutrophil (PMN) expression of extracellular trap formation and immunometabolic genes in response to prepartal energy intake and postpartal intramammary lipopolysaccharide challenge in postpartal dairy cows. K. M. Moyes*[1], D. E. Graugnard[2], J. K. Drackley[2], M. J. Khan[2], M. Bionaz[2], and J. J. Loor[2], *[1]University of Maryland, College Park, [2]University of Illinois, Urbana.*

Our objectives were to determine the effect of intramammary (IM) LPS challenge during the postpartal period on the expression of key genes associated with extracellular trap formation and immunometabolic response in blood neutrophils (PMN) for cows fed control (CON; 1.34 Mcal/kg dry matter; n = 8) or excess energy (OVE; 1.62 kg/dry matter; n = 5) during the dry period (~45 d before expected calving date). All cows were fed a common lactation ration after parturition. At 7 d in milk, all cows received LPS (200 mg) into one rear mammary quarter. Blood PMN were isolated before (0 h) and after (12 h) after IM LPS challenge for gene expression analysis using real-time quantitative PCR (qPCR). The effect of time, diet and their interaction was analyzed using the MIXED procedure of SAS with repeated measures. Regardless of prepartal diet, intramammary (IM) LPS challenge increased the expression of genes associated with the immune response (i.e., SELL, STAT3 and SOD2). Diet altered gene expression where cows fed CON during the prepartal period had decreased expression of genes associated with inflammation (ALOX5; −8.8-fold change) and metabolism (PLA2GA4; −2.3-fold change) when compared with OVE cows. At 0 h, we observed a −2.5-fold change in expression of S100A9, a gene associated with extracellular trap formation, for CON when compared with OVE cows. At 12 h, NFKB1 expression, a key gene associated with the inflammatory response, decreased (−1.5-fold change) for CON when compared with OVE cows. Results suggest a downregulation of genes associated with extracellular trap formation and the immunometabolic response after postpartal IM LPS challenge in blood PMN from cows fed a controlled energy diet during the prepartum period.

Key Words: immune, metabolism, neutrophil

W140 The effect of feeding competition on pre- and postweaning performance of dairy calves. E. K. Miller-Cushon*[1], R. Bergeron[2], K. E. Leslie[3], G. J. Mason[4], and T. J. DeVries[1], *[1]Department of Animal and Poultry Science, University of Guelph, Kemptville Campus, Kemptville, ON, Canada, [2]Department of Animal and Poultry Science, University of Guelph, Campus d'Alfred, Alfred, ON, Canada, [3]Department of Population Medicine, University of Guelph, Guelph, ON, Canada, [4]Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada.*

This study examined how reduced access to teats and feed buckets during the milk-feeding stage affects preweaning performance and postweaning response to competition for feed. Twenty Holstein bull calves were housed in pairs and provided milk replacer (MR) and starter ad libitum via either (1) 2 teats and 2 feed buckets/pen (non-competitive feeding; NCF), or (2) 1 teat and 1 feed bucket (competitive feeding; CF). Weaning occurred in wk 7 through incremental dilution of MR from 150 g/L to 0 g/L. Postweaning, calves were provided a complete pelleted diet and followed for 6 wk. In wk 8, 9, 12, and 13, all pens were fed noncompetitively via 2 feed buckets/pen. In wk 10 and 11, pens were fed competitively with 1 bucket/pen. Intake was recorded daily and calves were weighed 2×/wk. Data were analyzed in a repeated measures general linear mixed model. MR intake was subject to a treatment by week interaction ($P < 0.001$); NCF pens had initially greater intake (wk 2, 9.6 vs. 8.3 L/calf/d; SE = 0.6) and CF pens increased intake in later weeks (wk 5, 13.4 vs. 11.7 L/calf/d; SE = 0.3). Correspondingly, ADG evolved differently over time ($P = 0.003$), but BW was similar at weaning (103.6 kg; SE = 3.9; $P = 0.9$). Solid feed intake was greater for NCF pens before weaning (0.15 vs. 0.12 kg/d; SE = 0.01; $P = 0.009$) and similar during weaning (1.1 kg/d; SE = 0.04; $P = 0.9$). Postweaning, previously CF pens had greater intake than NCF when fed non-competitively ($P = 0.02$; in wk 8 and 9, 2.9 vs. 2.6 kg/d/calf, SE = 0.09, and wk 12 and 13, 4.9 vs. 4.5 kg/d/calf, SE = 0.1). During the competitive feeding period (wk 10 and 11), intake was subject to a treatment by day interaction ($P = 0.04$); previously NCF pens had initially lower intake but rapidly increased intake. Calves in previously CF pens tended to have greater ADG in noncompetitive weeks (1.4 vs. 1.2 kg/d; SE = 0.1; $P = 0.08$) and similar ADG in the competitive weeks (1.2 kg/d; SE = 0.1; $P = 0.5$). Final BW was similar between treatments (147.2 kg; SE = 4.5; $P = 0.8$). These results suggest that calves are able to adapt to moderate competition for feed in the milk-feeding stage and that prior exposure to competition influences response to feeding competition.

Key Words: dairy calf, competition, feeding

W141 Measurement of feeding motivation in limit-fed dairy heifers. A. M. Greter[1], T. F. Duffield[2], B. W. McBride[3], T. M. Widowski[3], and T. J. DeVries*[1], *[1]Dept. of Animal and Poultry Science, University of Guelph, Kemptville Campus, Kemptville, ON, Canada, [2]Dept. of Population Medicine, University of Guelph, Guelph, ON, Canada, [3]Dept. of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada.*

The objective of this experiment was to determine whether, and how hard, limit-fed heifers were motivated to work, both immediately post-feeding and following a short-term period of feed deprivation, for parcels of a low-nutritive feedstuff (i.e., oat straw) to ameliorate health concerns and meet foraging needs. Ten Holstein heifers (291.6 ± 39.2 d of age, weighing 324.2 ± 61.2 kg) were exposed to each of 2 dietary treatments, in a random order, over 2 successive 26-d treatment periods (14-d adaptation and a 12-d data collection) using a crossover design. The treatments were (1) a high-forage control TMR (60% DM; C) and (2) a limit-fed, low-forage TMR (50% DM; LF) at 2.05% BW. During the data collection period, heifers were fed at 1100 h and then tested for feeding motivation using a push-door apparatus 3 h later (1400 h) and 21 h later (0800 h). Intakes and feeding behavior were recorded during the last 7 d of each period. Rumination was recorded during 3 d of each period. The amount of weight pushed as a % of BW and latency to access the push-door were recorded 3 times for each heifer at each time point on each treatment. Data were analyzed in a general linear mixed model. DMI was greater on the C treatment (12.9 vs. 7.2 kg/d; SE = 0.6; $P < 0.001$). Heifers on the C treatment spent more time feeding (209.3 vs. 82.4 min/d; SE = 6.2; $P < 0.001$) and ruminating (452.2 vs. 318.3 min/d; SE = 15.8; $P < 0.001$), as well as consumed their feed slower across the day (0.06 vs. 0.09 kg/min; SE = 0.004; $P = 0.001$) than heifers on the LF treatment. On the LF treatment heifers tended to pushed more weight at 3 h (4.5 vs. 1.9% of BW; SE = 1.0; $P = 0.09$) and did push more weight at 21 h (9.3 vs. 2.8% of BW; SE = 1.0; $P < 0.001$) after feed delivery. Latency to access the door was similar between treatments at 3 h (96.7 ± 45.0 s) and 21 h (113.8 ± 45.0 s) after feed delivery. In summary, heifers will work harder, spend less time feeding and ruminating, and consume feed faster when provided a low-forage, limit-fed ration compared with a high-forage, ad-libitum-fed ration, providing evidence that limit-fed animals are experiencing feelings of hunger and may not be physically or behaviorally satisfied.

Key Words: feeding behavior, limit feeding, motivation

W142 Do limit-fed heifers prefer supplementary long or short straw? A. M. Greter[1], T. F. Duffield[2], B. W. McBride[3], T. M. Widowski[3], and T. J. DeVries*[1], *[1]Dept. of Animal and Poultry Science, University of Guelph, Kemptville Campus, Kemptville, ON, Canada, [2]Dept. of Population Medicine, University of Guelph, Guelph, ON, Canada, [3]Dept. of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada.*

The objective of this study was to determine whether limit-fed heifers will choose to consume long, rather than short, particles of a low-nutritive feedstuff to ameliorate rumen function and meet foraging needs. Ten Holstein heifers (261.6 ± 39.2 d of age, weighing 303.3 ± 56.2 kg) were exposed to each of 2 dietary treatments, in a random order, over 2 successive 7-d treatment periods (4-d adaptation period and a 3-d data collection period) using a crossover design. The treatments were (1) provision of long particle oat straw (85% of particles >8 mm; LS) and (2) provision of short particle oat straw (45% of particles >8 mm; SS). Both treatments were offered following consumption of a limit-fed, nutrient-dense TMR fed at 2.05% of BW. Following these 7-d periods of exposure to each type of straw (long and short), heifers were given access to both types during an additional 2-d preference period. Individual intakes, feeding and lying behavior were recorded during the last 3 d of each treatment period. Intake and behavior data were analyzed in a general linear mixed model. Preference ratio (LS consumed/total straw intake) was tested for a difference from 0.5 using a *t*-test. Dry matter intake of both the TMR (6.3 ± 0.4 kg/d) and straw (0.36 ± 0.06 kg/d) was similar between treatments. Heifers fed LS spent more time feeding (197.7 vs. 175.2 min/d; SE = 5.7; $P = 0.01$) than heifers fed SS due to the increase in time required to consume long particles in the LS (59.8 vs. 34.2 min/d; SE = 5.0; $P = 0.007$). Daily lying time (974.7 ± 11.4 min/d) and time spent standing without eating (278.9 ± 10.4 min/d) was similar between treatments. The preference period showed a strong preference ratio for LS rather than SS (preference ratio = 0.83; SE = 0.06; $P < 0.001$), with heifers consuming 0.43 ± 0.2 kg/d of LS and 0.07 ± 0.1 kg/d of SS. In conclusion, heifers will consume similar amounts of supplementary long or short straw if provided to them alongside of a limit-fed

TMR. Limit-fed heifers do, however, show a clear preference for LS when offered the choice, suggesting that they find LS to be more satisfactory for achieving rumen fill and/or meeting their behavioral foraging needs.

Key Words: feeding behavior, limit feeding, preference

W143 The effect of calving environment on the behavior, metabolism, and milk yield of Holstein heifers. S. Y. Morrison*, P. Ji, H. M. Gauthier, S. E. Williams, and H. M. Dann, *William H. Miner Agricultural Research Institute, Chazy, NY.*

This study determined the effect of the calving environment on periparturient behavior and its potential effect on behavior, blood metabolites, and milk yield of Holstein heifers during the first 21 DIM. Heifers (n = 54) were housed in a bedded pack enhanced with a 4.6x4.0 m calving blind during a 21-d close-up period and then were either moved when calving was imminent to an individual pen (IND; n = 24) or left in the pack (GRP; n = 30). After calving heifers were housed in a freestall pen, fed a TMR, and milked 3×/d. Calving, standing, and rumination behaviors were monitored using visual observations, video review, and data loggers. Calving difficulty (1: easy to 5: difficult) was recorded. Serum was analyzed for nonesterified fatty acids (NEFA) and β-hydroxybutyrate (BHBA) on 0, 7, 14, and 21 DIM. Data were analyzed as a completely randomized design using the MIXED procedure of SAS with repeated measures as appropriate. Twelve GRP heifers calved in the blind and 6 IND heifers were in the blind at the time they were moved to the individual pen. IND heifers were in the individual pen for 89 ± 10 min before calving. Labor was 98 and 124 min for GRP and IND heifers (SEM = 12 min; $P = 0.11$), respectively. Calf birth weight (38.0 ± 1.1 kg) and calving difficulty score (1.7 ± 0.2) were not affected by treatment ($P > 0.10$). During the 2 h before calving, treatment did not affect standing (49 ± 5 min; 3.2 ± 1.2 bouts; 21 ± 5 min/bout) or rumination (10 ± 2 min). During the 12 h after calving, treatment did not affect standing (504 ± 14 min; 11.5 ± 0.8 bouts; $P > 0.10$), but GRP heifers tended to spend more time ruminating (78 and 60 min; SEM = 7; $P = 0.07$). During the first 21 DIM, treatment did not affect ($P > 0.10$) NEFA (0.35 ± 0.02 mEq/L), BHBA (5.9 ± 1.0 mg/dL), standing (849 ± 16 min/d; 57 ± 1 min/bout), or milk (30.7 ± 1.3 kg/d). Daily rumination was greater for GRP than IND (367 and 324 min; SEM = 15; $P = 0.03$). The calving blind was used by 40% of GRP heifers at calving and may indicate a desire for seclusion at calving. Management decisions around parturition should be considered to minimize disruptions that may delay normal calving progress and resumption of rumination after calving.

Key Words: calving, behavior, cow

W144 Rumination and feeding behavior before and after calving. K. Schirmann*, N. Chapinal, L. A. Vickers, D. M. Weary, and M. A. G. von Keyserlingk, *Animal Welfare Program, Faculty of Land and Food Systems, The University of British Columbia, Vancouver, BC, Canada.*

The objectives of the current study were to describe the changes in rumination and feeding behavior around calving. Rumination time, feeding time and dry matter intake were monitored in 11 Holstein cows from 96 h before to 48 h after calving. Data were initially summarized in 2-h periods; these data were first averaged across cows and plotted to describe the pattern relative to time of calving. Ruminating and feeding started to decline approximately 4 and 8 h (respectively) before calving and increased in the 4 and 6 h (respectively) after calving. Data were then averaged within cow to form daily values relative to calving time; the period from 96 to 24 h before calving was averaged to calculate one baseline value per cow. These data were analyzed using the mixed models in SAS with day as a repeated measure and Dunnett's 2-tailed test was used as a post-hoc test to evaluate differences between baseline and subsequent days. Compared with baseline (baseline rumination time: 426.1 ± 26.5 min/d; baseline feeding time: 205.1 ± 13.2 min/d), cows spent 63 ± 30 min less time ruminating and 66 ± 16 min less time feeding during the day before calving. These behaviors remained lower than baseline the day after calving when, compared with baseline, cows spent 133 ± 35 min less time ruminating and 82 ± 18 min less time feeding. Cows also tended to decrease dry matter intake by 3.8 ± 1.9 kg DM the day before calving as compared with baseline (baseline: 15.7 ± 1.5 kg DM/d); dry matter intake returned to baseline values by the day after calving. In conclusion, time spent ruminating and time spent feeding show promise as tools to identify cows as they approach calving.

Key Words: welfare, parturition, dry matter intake

W146 Social constraints and motivation of dairy cows to work for access to pasture. A. C. Andressa[1,2], J. A. Fregonesi *[2], D. M. Weary[1], and M. A. G. von Keyserlingk[1], [1]*Univerisity of British Columbia, Vancouver, British Columbia, Canada,* [2]*Universidade Estadual de Londrina, Londrina, Paraná, Brazil.*

In social species such as cattle, motivation to access resources may depend upon the location and behavior of social partners. This study tested how the motivation of lactating dairy cows to access to pasture, varied with the presence of familiar and unfamiliar social partners. We used a total of 24 lactating dairy cows. Twelve Holstein cows were trained to push a weighted gate to access fresh TMR, and the other 12 cows formed the unfamiliar group. The weight started at 14 kg and was increased by 7 kg/d until cows were no longer willing to perform the task. Cows were then individually allowed to push the gate to access pasture for 3 d under each of 3 conditions: (1) familiar social group on pasture, with weight set at the maximum pushed for TMR + 7 kg; (2) unfamiliar group on pasture with weight set as in treatment (1); and (3) familiar social group on pasture, with weight set at the maximum pushed for TMR + 14 kg. The number of cows pushing the gate to have access to pasture was compared using Fisher's Exact test. Cows pushed on average a maximum of 36.6 ± 9.1 kg during the TMR test and 50.4 ± 8.8 kg in treatment (3). The number of cows accessing pasture was higher in treatment 1 versus 2 (6.5 ± 0.7 versus 1.0 ± 0.0; $P = 0.01$), but similar for Treatment 3 (4.5 ± 2.1; $P = 0.12$). The results indicate that motivation to access pasture is stronger when paired with access to familiar social companions.

Key Words: social behavior, operant test, welfare

W148 Combined wavelet and linear regression techniques to model cattle behavioral responses to changes in forage allowance. M. S. Gadberry*[1], W. Whitworth[2], and G. Montgomery[2], [1]*University of Arkansas, Cooperative Extension Service, Little Rock,* [2]*University of Arkansas, Southeast Research and Extension Center, Monticello.*

As forage availability diminishes, cattle compensate, in part, by increased grazing time. As a result, the visual cue of activity throughout the day may help delineate conditions whereby available forage negatively affects productivity. This study attempted to model dawn to dusk changes in grazing, lying, and indeterminate activity for varying amounts of available forage during summer months. Activity was visually assessed for 16 h at 1 h intervals for 3 (2010 and 2011) or 2 herds (2012) of predominately Beefmaster cows (nonlactating). To create variability in available forage without negatively influencing herd productivity, 3 (yr 1 and 2) or 2 (yr 3) pastures of different sizes were assigned to the study. Herd size was fixed at 20 cows within herd in yr 1 and 2 and 30 in yr 3. Each herd was assigned to a pasture, grazed for a 2-wk adaptation and observed during wk 3. At the conclusion of the observation wk, herds were re-assigned

pastures so all herds were grazed and observed on all pastures. Forage allowance (FA) ranged from 12.8 to 56.5 kg DM/100 kg BW. Proportional behavior responses to change in FA were transformed to Haar wavelet coefficients. ANOVA at the 2, 4, and 8 h scales indicated similar coefficient variability ($P > 0.10$) among FA allocations. Correlation between FA and individual wavelet coefficients was determined. Linear models to predict coefficients were constructed for the significant correlations that occurred for lying at level 1, position 1 and standing at level 0. The lying coefficient was predicted as 0.011944 × FA – 0.641426 ($r^2 = 0.47$); and the grazing coefficient was predicted as 0.009547 × FA – 0.847766 ($r^2 = 0.52$). Based on the predicted coefficients, from 600 to 900 h, lying activity increased as FA increased; however, from 1000 to 1300 h, lying activity decreased as FA increased then converged for 1400 to 2100 h. Prior to 1300 h, more cattle were predicted grazing as FA increased. Following 1300 h, the proportion of cattle grazing increased as FA decreased. These results indicate FA changes affect morning lying and afternoon grazing activity.

Key Words: grazing behavior, model, wavelet analysis

W149 Determinants of body temperature and feed intake in beef cattle during summer heat. A. K. Curtis*, B. Scharf, P. A. Eichen, M. S. Kerley, J. R. Russell, and D. E. Spiers, *Division of Animal Sciences, University of Missouri, Columbia.*

Heat stress in cattle has long been known to affects well-being and decrease performance. The challenge comes in determining reliable predictors of heat stress in the form of measurable, independent variables that indicate current and near-future changes in performance. A 42-d study, including 25 crossbred Angus (*Bos taurus*) steers with a body weight of 347 ± 29 SD kg, was conducted during summer 2011 to identify animal and environmental determinants of core body temperature (Tcore) and feed intake (FI). Animals were stratified by weight and housed among 5 different pens. Ambient temperature (Ta) during this period ranged from 17.3 to 40.7°C with a mean of 27.2°C. Steers were provided a feedlot diet and water ad libitum and Tcore was measured hourly using intrarumenal telemetric boluses (SmartStock, Pawnee, OK). Electronic ID tags (Allflex US Inc., Dallas-Fort Worth, TX) connected to a GrowSafe FI system (GrowSafe Systems Ltd., Airdrie, AB, Canada) provided FI. Data loggers (Hobo H8 Pro; Onset Computer, Bourne MA; accuracy: ±0.2°C and ±3% relative humidity) recorded ambient conditions in sun and shade, along with black globe temperature (BG). Temperature-Humidity Index (THI) was calculated for all combinations. Analysis of FI used the daily sum of animal values to determine population FI, whereas Tcore used hourly daylight (0700–1900) values. Both stepwise and multivariant linear and polynomial regression analyses (JMP statistical software; SAS Institute; Cary, NC) were used for 0 to 4-d delay evaluations. Best FI predictor, based on highest R^2 was mean THI using BG in the sun, with a 3-d delay ($R^2 = 0.24$, $P < 0.005$). Analysis of Tcore used group averages for each hour. Both regression analyses identified Ta alone with no delay as the best indicator of Tcore ($R^2 = 0.62$, $P < 0.005$). These results indicate that although air temperature alone may be the best predictor of core temperature in the heat, radiant heat load may be a better determinant of feed intake over time.

Key Words: heat stress, beef cattle, telemetry

W150 Influence of pen-shade on feedlot performance of Bos indicus growing heifers under hot weather conditions. J. A. Vazquez[1], B. J. Cervantes[2], A. Camacho[3], M. A. Espino[3], T. J. Heras[3], L. R. Flores[3], J. J. Lomeli[3], and R. Barajas*[3], *[1]CUALTOS, Universidad de Guadalajara, Tepatitlan, Jalisco, Mexico, [2]Ganadera Los Migueles, S.A. de C.V., Culiacan, Sinaloa, Mexico, [3]Facultad de Medicina Veterinaria y Zootecnia, Universidad Autonoma de Sinaloa, Culiacan, Sinaloa, Mexico.*

Pen-shade has shown to be beneficial to feedlot performance of cattle under hot weather conditions. Most experiments have been conducted using *Bos taurus* cattle. However, differences in heat tolerance and greater use of *Bos indicus* in hotter areas of the world suggest that we should focus on evaluating the utility of pen-shade use in these cattle as well. In this study 60 *Bos indicus* heifers (initial BW = 195.8 ± SD 2.936 kg) were used to evaluate the influence of pen-shade on feedlot performance of *Bos indicus* growing heifers under hot weather conditions. Heifer were weighed individually and blocked by Initial BW. Groups of 5 heifers were placed in each pen, and the pen constituted the experimental unit. In a complete randomized block design experiment, within a block, pens were randomly assigned to receive one of 2 types of allotment: (1) dirt-floor pens (6 × 12 m) without shade (Control); and (2) Control plus shade (Pen-shade). Shade was provided by a ceiling of 6 × 4 m of metal sheeting positioned 3.7 m over soil level. Cattle were weighed on d 1 and 84 when they finished the experiment. Feed intake was recorded daily. Samples of food (1 kg) were taken weekly for DM determination (110°C/24 h). Results were analyzed by ANOVA for a randomized complete block design. The daily variation ($P < 0.01$) of temperature and relative humidity is described for its mean ± SE observed values of 28.35 ± 1.32°C (maximum 40.5°C, minimum 21.1°C) and 76.0 ± 5.98%, respectively. Cumulative rain was 504 mm; air velocity 7.65 ± SE 2.59 km/h, and sun radiation of 872 ± SE115 W/m^2. Compared with heifers housed in the control pens, heifers housed in the pen-shade group had higher final weight (284.4 vs. 275.0 ± SE 2.113 kg; $P = 0.02$), superior average daily gain (1.05 vs. 0.94 ± SE 0.026 kg/d; $P = 0.02$), and a better feed efficiency (0.17 vs. 0.15 ± SE 0.003 kg of gain/kg of DMI; $P < 0.01$). Dry matter intake was not affected by treatments (6.25 vs. 6.23 ± SE 0.070 kg/d; $P = 0.84$). It is concluded, that provision of pen-shade contributes to improve the feedlot performance of *Bos indicus* growing heifers under hot weather conditions.

Key Words: *Bos indicus*, feedlot performance, hot weather

W151 Behavior of horses kept in large groups in a feedlot environment. J. H. Higginson Cutler*[1], M. Robertshaw[1], E. A. Pajor[2], L. J. Keeling[3], L. Burwash[4], C. Dewey[1], and D. B. Haley[1], *[1]University of Guelph, Guelph, ON, Canada, [2]University of Calgary, Calgary, AB, Canada, [3]Swedish University of Agricultural Sciences, Uppsala, Sweden, [4]Alberta Agriculture, Food and Rural Development, Airdrie, AB, Canada.*

Horses kept for meat production, a legal practice in Canada, are commonly kept in large social groups; however no data about the behavior or welfare of horses in these conditions is available in the literature. The objective of this study was to describe the general activity of horses kept in large groups under dirt dry-lot conditions in western Canada. Observations were made on 18 d spread evenly over a period of time from June 1 to August 19, 2010. Scan samples were completed every 10 min to count the number of horses performing various behaviors during the following blocks of time: 0700–0900, 1000–1200, 1300–1500, and 1600–1800h. Environmental conditions at the time of observations were also recorded. Two pens of horses grouped by age were observed. The number of animals in the pens ranged from 124 to 182 in one pen and 100–200 in the second pen. The proportion of animals performing each behavior divided by the number of animals in the pen was determined for each behavior. A mean (±SE) of 25.2 (±0.3)% of horses were eating, 1.1 (±0.02)% drinking, 11.9 (±0.4)% lying, 6.1 (±0.1)% moving, 46.4 (±0.6)% standing, 1.3 (±0.06)% playing, and 4.5 (±0.1)% grooming throughout the scan samples. Preliminary statistics examining the relationship between pen, weather (rain vs. no rain), time period, and date were analyzed using mixed models. The number of horses performing behaviors was affected by date of observation ($P < 0.05$). Rain altered the number of horses performing all behaviors ($P < 0.05$) except playing ($P = 0.35$), with lying, eating, drinking and

grooming decreasing during rain while standing increased. The number of horses performing certain behaviors was also altered by time of day, with grooming increasing throughout the day, play increasing until the final daily observation period, and lying decreasing throughout the day ($P < 0.05$). Knowledge gained regarding the behavior of horses housed in large social groups will allow for improved management practices to ensure appropriate resources are provided for these animals.

Key Words: equine, group size, behavior

W152 Barrow approachability to a novel object when selected for feed efficiency. J. Colpoys*[1], N. Gabler[1], A. Keating[1], S. Millman[2], J. Siegford[3], and A. Johnson[1], *[1]Animal Science, Iowa State University, Ames, [2]Veterinary Diagnostics and Production Animal Medicine, Iowa State University, Ames, [3]Animal Science, Michigan State University, East Lansing.*

The objective of this study was to determine if divergent selection for residual feed intake (RFI) influenced barrows' approach to a novel object, an orange traffic cone. Twenty low-RFI (high FE) and 20 high-RFI (low FE) barrows (BW 49 ± 9.2 kg) from 8th generation Yorkshire RFI selection lines were randomly selected and evaluated once over a 4-wk period using a novel object test (NOT). The NOT arena measured 4.9 m long × 2.4 m wide, with black corrugated plastic walls 1.2 m high. The arena floor was divided into 4 zones; zone 1 being the traffic cone while zone 4 was furthest from the traffic cone and was the point where the pig entered the arena. Between 1300 and 1700 h pigs were moved individually from their home pen and into a weigh scale for 1 min. Pigs then entered the NOT arena and were video recorded for 10 min. Video was then continuously scored by one observer for latency, duration, and total number of freezing postures (defined as whole body still for ≥ 3 s). Latency, duration, and total number of zone visits were also collected. Data were analyzed with PROC Glimmix and the experimental unit was the barrow. Latency to show the first freeze posture and total length of time freezing did not differ between selection lines ($P > 0.28$). However, low-RFI froze fewer times compared with high-RFI barrows ($P = 0.003$). Latency to enter zones: low-RFI barrows took longer entering zone 2 ($P = 0.02$), but did not differ entering zone 1 or 3 when compared with high-RFI barrows ($P > 0.17$). Duration of time within a zone: low-RFI barrows tended to spend less time in zone 3 compared with high-RFI barrows ($P = 0.09$). For all other zones there was no difference in time spent in the zones ($P > 0.36$). Number of visits: low-RFI barrows visited zones 3 and 4 less often compared with high-RFI barrows ($P < 0.02$). For all other zones there was no difference in number of visits ($P > 0.24$). These data suggest that differences exist in the response to a novel stressful situation between barrows of different RFI lines. Therefore, the ability of livestock to recognize and cope with stress may be related to RFI and feed efficiency.

Key Words: novel approach, residual feed intake, pig

W153 Influence of dietary flavors on sheep feeding behavior and nutrient digestibility. J. J. Villalba*[1], A. Mereu[2], and I. R. Ipharraguerre[2], *[1]Utah State University, Logan, [2]Lucta, S.A., Montornés del Vallés, Spain.*

A variety of flavored feeds may enhance intake relative to a monotonous diet. The aim of this study was to assess whether the feeding pattern displayed by sheep exposed to a monotonous ration is modified when the same ration is presented in a diversity of flavors and if such diversity influences nutrient digestibility. Twelve wethers (3 lambs/group/period) were housed in metabolic crates during 2 successive periods. One group of lambs [Diversity (D)] was fed simultaneously an unflavored TMR of alfalfa, barley, beet pulp, and urea (55:35:9:1) and the same ration supplemented (0.2%) with one of 2 flavors: 1) sweet, and 2) umami. The other group [Monotony (M)] received just the unflavored TMR. All animals were fed their respective rations ad libitum from 0800 to 1600. The first 20 d of each period were used for adaptation, and the last 6 d were used for sample collection. On d 20, intake was assessed every 30 min for 8 h (feeding pattern). Intake was estimated by subtracting the amounts of feed offered and refused. Intake values were matched with composited samples of feces to determine digestibility. The design of the experiment was a split-plot design with lambs nested within groups and period, day and time interval (feeding pattern) as repeated measures. On average, lambs in D tended to consume more feed than lambs in M ($P = 0.08$). Lambs in D showed greater intakes than M during 30 ($P = 0.006$), 60 ($P = 0.02$), 90 ($P = 0.02$), 120 ($P = 0.04$), and 180 min ($P = 0.07$) after offering the rations. Digestibility of CP ($P = 0.08$) tended to be lower for lambs in D than for lambs in M. Lambs in M and D digested the same amount of DM, NDF, ADF, and N ($P > 0.10$). Flavor diversity did not affect N retained, N retained/N consumed, or ruminal pH 1 h after feeding ($P > 0.10$). In conclusion, exposure to diverse flavors in the same ration has the potential to increase feed intake relative to monotonous rations due to changes in feeding patterns occurring within the first 180 min of feeding. This enhanced consumption likely contributed to the slight decline observed for DM and CP digestibility. The amount of nutrients digested, however, was not influenced by such a decline.

Key Words: flavor, behavior, intake

W154 Metabolic profile of sheep and their lambs in an artificial nursing system. L. H. Díaz-García*, L. P. López-Huitrado, A. Muro-Reyes, H. Gutiérrez-Bañuelos, and J. A. López-Román, *Universidad Autónoma de Zacatecas, Zacatecas, México.*

The artificial nursing system is a methodology that must be used in most sheep farms as it can help reduce the high mortality rates of lambs in the first days of life. The aim of this study was to evaluate seric blood concentrations of glucose (GL), triglycerides (TG; mg/dL) and total protein (TP) (gr/dL) in ewes (SH) and their lambs (LB) during artificial (AN) and natural nursing (NN). Samples were obtained by jugular venipuncture at 1, 8, 15 and 22 d (experimental period) after birth, and chemical profile obtained by spectrophotometry. We used 20 third-parity SH (10 per treatment) and their respective LB, divided into 2 treatments (Tx): artificial nursing (AN, n = 13; lambs did not nurse their dams) and natural nursing (NN, n = 12; lambs nursed their dams). Data were analyzed with PROCGLM, running an ANOVA to detect differences between Tx and animal type. Also, Pearson correlation coefficients (PROC CORR) were run to assess relations between variables. All data was computed by SAS statistical package. Data are shown on Table 1. No differences were found ($P > 0.05$) between Tx for SH in any of the variables evaluated. For LB, both GL and TG differs ($P < 0.001$ and < 0.05, respectively). It was concluded that the type of nursing does not influence the chemical blood parameters of sheep, and nonetheless GL and TG differs on lambs, both chemical variables are within normal ranges.

Table 1. Means (±SD) for each metabolite by treatment (artificial nursing, AN, and natural nursing, NN) and animal type (ewe, lamb)

	Ewe		Lamb	
Variable	AN	NN	AN	NN
Glucose	40.44 ± 17.79	40.66 ± 23.6	52.27 ± 26.8[b]	84.77 ± 29.28[a]
Triglycerides	26.13 ± 15.67	27.07 ± 13.2	68.01 ± 35.72[b]	89.16 ± 30.93[a]
Total protein	7.3 ± 1.39	6.82 ± 1.6	4.45 ± 1.62	5.05 ± 1.47

[abc]Different superscripts represent significant difference ($P < 0.05$) between treatments.

Key Words: sheep, lamb, artificial nursing

W155 Individual behavior of lambs confined in enriched environment. J. P. A. Lorenço[1], P. A. Bustos Mac-Lean*[1], N. Mora[1], J. M. Malheiros[2], T. Zunino[1], C. G. Titto[3], B. S. Lala[1], and F. A. F. Macedo[1], *[1]State University of Maringa, Maringa, PR, Brazil, [2]Faculty of Agriculture and Veterinary Sciences, Jaboticabal, SP, Brazil, [3]University of São Paulo, FZEA/USP, Pirassununga, SP, Brazil.*

This research aimed to investigate the influence of environmental enrichment with brushes on individual behavior of confined lambs. The project was lead at Maringá-PR, October to December 2012. Were used 6 Pantaneira lambs allotted in individual pens. The behavior was measure by the focal method on 6 separate days, 5 h in afternoon each day (which heat stress increases due to combination of high temperature air and relative humidity in tropical climates). The behavioral assessment divided the 2 treatments, and the first 3 observations without the object and the other 3 observations, put up a brush located in the region above the feeder. The activity patterns of the animals were recorded in an ethogram field every 5 min, and were noted the times of posture (standing or lying) and activities (eating, drinking, ruminating, idleness, brushing and other activities). Behavior data were analyzed by Student's *t*-test to compare means before and after introduction of environmental enrichment using SAS-STAT at a significance level of 0.05. The air temperature and relative humidity within the stall had a variation 25.7 to 35.2°C and 47 to 81%, respectively, causing heat stress to the animals. Table 1 shows that the frequency of the lying position and ruminating activity was significantly higher in the evaluation of lambs when there was enrichment in the pens and this behavior shows that the animals are under a high level of welfare. When lambs remain standing for long, they may be trying to lose heat to the environment. Thus, environmental enrichment alters the behavior of lambs in the hottest hours of the day and can be a tool to reduce stress in confined animals.

Table 1. Frequency of behaviors (means ± SE; %/5 h) observed in lambs with and without environmental enrichment

Behavior	Without brush	With brush
Posture		
Standing	41.4 ± 0.1[a]	32.2 ± 0.1[b]
Lying	58.6 ± 0.1[b]	67.8 ± 0.1[a]
Activity		
Eating	20.0 ± 0.1[a]	10.4 ± 0.1[b]
Drinking	2.3 ± 0.04[b]	3.8 ± 0.06[a]
Ruminating	11.8 ± 0.1[b]	18.4 ± 0.1[a]
Idleness	43.3 ± 0.1[a]	39.4 ± 0.1[b]
Brushing	0.0 ± 0.0[b]	11.8 ± 0.1[a]
Other	22.6 ± 0.1[a]	16.1 ± 0.1[b]

[a,b]Means followed by different small letters in column differ by *t*-test ($P < 0.05$).

Key Words: environmental enrichment, welfare, lambs

W156 Creation and persistence of conditioned aversion to grape leaves and sprouts for grazing sheep in vineyards. C. L. Manuelian[1], E. Albanell[1], M. Rovai[1], A. A. K. Salama[1,2], and G. Caja*[1], *[1]Group of Ruminant Research (G2R), Universitat Autonoma de Barcelona, Bellaterra, Spain, [2]Animal Production Research Institute, Dokki, Giza, Egypt.*

Sheep grazing is a sustainable and environmentally friendly alternative to the traditional vineyard weed control without using machinery and herbicides. However, vineyard grazing has its drawbacks; sheep are attracted by grape leaves and sprouts. Sheep grazing in vineyards usually damages vines, compromising grape quantity and quality. With this in mind, 2 midterm and consecutive experiments were conducted with 12 Manchega and 12 Lacaune ewes, consisting of Exp. 1: Aversion induction to grape leaves (novel food) and persistence evaluation under simulated grazing conditions; and Exp. 2: Descriptive study in a commercial vineyard. In Exp. 1, ewes were allocated into 4 groups (6 ewes/group and breed) in which grape leaves intake was measured after dosing lithium chloride (AV, 225 mg LiCl/kg BW) or water (C, control). Induced aversion was created after offering individually 100 g of grape leaves (var. Tempranillo) in pens for 30 min, and orally administering a single LiCl dose post-consumption; validation was done individually for 3 d. Aversion persistence on a simulated vineyard (2 kg leaves and sprouts var. Tempranillo in wood frames on a ryegrass prairie) was tested during 30 min in 11 sessions (d 5 to 375). Intake data was analyzed by a nonparametric Mann-Whitney U-test using SPSS v.19.0.0 of IBM. On average, C ewes avidly ate grape leaves whereas AV ewes fully refused them, either during validation in the pens (95.1 ± 1.9 vs. 0 g/d and ewe; $P < 0.001$) or in the simulated vineyard (1.47 ± 0.06 vs. 0 kg/group; $P < 0.001$). In Exp. 2, AV ewes were moved to a commercial vineyard (var. Merlot; Penedes county, Barcelona, Spain) and allowed to rotationally graze for 3 h/d during 10 d (d 401 to 410). Averted ewes reduced grass cover between vine lines by 70% but they started to bite grape leaves and sprouts when grass was scarce (d 403 to 410); no significant damage in the vines was visually appreciated. In conclusion, aversion to grape leaves and sprouts persisted in the AV ewes for 1 yr but, in practice, the use of a reinforcing LiCl dose after this time is recommended for assuring an effective aversion behavior in grazing sheep.

Key Words: aversion, grazing, sheep

W157 Feed management of psittacines in captivity using energy requirement equations. V. M. Pereira, T. S. G. Carvalho, V. D. L. Assis, F. M. O. B. Saad, and C. E. P. Saad*, *Federal University of Lavras, Lavras, Minas Gerais, Brazil.*

Captive birds have decreased energy requirement as a result of reduction in living space. Furthermore, ad libitum feeding can induce overweight and may favor the selection for fruits and the rejection of extruded feedstuffs. The selection of feeds by parrots can cause an imbalance of the diet and induce nutritional disorders. Selection also increases feed wastage, mainly of extruded feeds. Two Red Macaws (*Ara chloroptera*), three Blue Macaws (*Anodorhynchus hyacinthinus*), and three Purple Breast Parrots (*Amazona vinacea*) from the "Fundação Zoobotânica" Zoo, Belo Horizonte, Brazil, were used. Before the experiment birds were fed ad libitum. During the trial, birds were fed according to their energy requirement, calculated as body weight to the 0.75 power multiplied by (156 kcal/kg $BW^{0.75}$) for 28 days. The diet contained 70% of extruded dry feed (corn, wheat germ, soybean meal, egg powder, wheat bran, beet pulp, minerals and vitamins) and 30% of fruits (papaya, banana, orange, and apple). The birds were weighed initially and weekly until the end of the experiment and the initial and final weight compared by Student's t-test. Even with restricted feeding, the bird's weight showed no statistical differences ($P > 0.05$) between the initial and final weight. It can be concluded that using formulas based on energy requirements for maintenance do not affect the bird's body weight and contribute to avoid waste of food. Acknowledgment: Fundação Zoobotânica of Belo Horizonte city, CAPES and FAPEMIG.

Key Words: parrot, energy, controlled feeding

Undergraduate Student Competition: ASAS Undergraduate Student Poster Competition

W158 Comparison of pre-race behaviors of Thoroughbred race horses on finish order and finish type. A. McDuff*, K. William, J. Gregory, and C. E. Ferguson, *McNeese State University, Lake Charles, LA.*

This study compared various pre-race behaviors of Thoroughbred (TB) race horses (n = 1018) at Delta Downs (Vinton, LA) with their performance. The horses were evaluated based on their behavior by 4 experienced horse persons and the pre-race period was divided into 3 sections: pre-saddling (BSAD), which was the time the horse entered the saddling paddock until the saddling, saddling (SAD), which was the time from saddling until the jockeys prepared to mount the horse, and post-parade (POSTP), which consisted of the time the jockey mounted and rode the horse in the parade. The behavior was classified as calm, nervous, or ready and they were also scored numerically from 1 to 5 with 1 being only minimal movement and 5 being a horse that reared, flipped over or pawed several times during the each evaluation period. The horses received a separate behavior type and numerical score for BSAD, SAD and POSTP. Following completion of the race the horses finish order and method of finishing the race (running, tired, or pulled-up) was recorded. Statistically evaluations were performed in SAS and chi-squared analysis was performed to determine statistical differences. Horse scored as nervous during BSAD were more likely ($P < 0.001$) to finish the race tired (68%) compared calm or ready horses (34% and 35%), respectively. Being nervous during BSAD significantly ($P < 0.006$) decreased the horses chances of finishing first to third (17%) compared with calm or ready horses (36% and 38%), respectively. More ($P < 0.0001$) horses that were nervous during SAD finished tired (63%) compared with calm or ready horses (31% and 36%), respectively. Also, horses that were nervous during POSTP were more likely ($P < 0.004$) to run tired (59%) compared with calm or ready horses (34% and 35%), respectively. The BSAD, SAD and POSTP behavior score did not affect finish type ($P < 0.4$, $P < 0.14$, $P < 0.76$) or the percent finishing fourth or better ($P < 0.18$, $P < 0.56$, $P < 0.26$), respectively. Horses with no chain or it used as a regular lead shank were more likely ($P < 0.01$) to run first to fourth (64%) compared with horses with a chain used over their nose or in their lip (47%).

Key Words: horse racing, Thoroughbred, behavior

W159 Alleviation of pain associated with disbudding. A. Mathias*, J. Gilliam, D. Stein, and M. Calvo-Lorenzo, *Oklahoma State University, Stillwater.*

Disbudding, the removal of the horn buds of a calf, is a necessary management procedure because it eliminates costs associated with horns and improves safety. However, disbudding is known to cause pain and distress in calves. Extra-label use of some pharmaceuticals allows for some of the alleviation of the pain and distress, but it is not the best way. A FDA-approved pharmaceutical would be the best option to alleviate the pain and distress, however one does not exist. Therefore, pharmaceuticals are often used extra-label to alleviate pain and distress. This study evaluates the effectiveness ethyl alcohol (EtOH) to produce a cornual nerve block, when the area surrounding the horn is numb. To test this, calves were given 1 of 4 treatments: 5 mL saline solution (SAL), solution mixture of 2.5 mL 2% Lidocaine and 2.5 mL 75% EtOH (MIX), or 5 mL 75% EtOH (ALC). The calves were needle pricked in the area surrounding the horn bud at 5, 10, 15, 20, 30, and 60 min after the treatment on d 1 to determine the onset of the cornual nerve block. To test the duration of the cornual nerve block they were pricked once daily from d 2 - 14. The behavioral response to the prick test was evaluated as either "blocked" or "not blocked." "Blocked" was defined as no movement in response to the prick test, and "not blocked" was defined as pulling on halter, throwing head back, backing away from handler, or falling down. The study found that SAL calves exhibited "not blocked" behaviors at all needle pricking time points; all other treatments exhibited initial "blocked" behaviors at 5 min post-treatment. The study also found that the MIX and ALC treatments were effective at maintaining a cornual nerve block for 2 weeks when needle pricked daily from d 2–14. These results indicate there is potential in utilizing EtOH as a form of non-restricted pain relief for disbudding calves, which would be beneficial for management practices on farms today. Future research incorporating the removal of the horn buds after EtOH administration will further evaluate the effectiveness of EtOH as a cornual nerve block.

Key Words: dehorning, calf, ethyl alcohol

W160 Factors affecting neonatal dairy calf mortality in a hot-arid environment. E. L. Lopez Rodriguez*, M. Mellado, F. G. Veliz, M. A. de Santiago MIRAMONTES, and J. E. Garcia, *Autonomous Agrarian University Antonio Narro, Torreon, Coahuila, Mexico.*

A field study involving 7734 Holstein calves from 8 large intensive dairy herds in northern Mexico (26° N; 24.2°C mean annual temperature; same location) was conducted to determine some factors affecting early postnatal (one to 21-d of age) dairy calf mortality, and to assess its association with climatic conditions. The effects of season of birth, size of dairy operation, birth type (single or twin), sex of calves, and temperature-humidity index (THI) shortly before, during or shortly after calving were analyzed by the GENMOD procedure of SAS. The total mortality incidence was 14%. Mortality of calves was altered by the THI during birth, with a decreased ($P < 0.05$) mortality rate from 16 to 12% when THI was 81 or higher. Mortality levels were 4 percentage point higher ($P < 0.05$) in winter than all other seasons. Single-born calves had fewer deaths (14%) than twin-born calves (19%). The mortality rate was higher ($P < 0.05$) in male than in female calves (17 vs. 12%). Calves that were born in dairy operations > 1800 cows had a greater risk of dying than calves born in smaller dairies (16 vs. 13%). Both respiration rate (74.4 ± 15.6 vs. 67.8 ± 16.3; means ± SD) and heart rate (119.2 ± 19.6 vs. 113.9 ± 17.0; means ± SD) were higher ($P < 0.05$) in calves born in winter than in summer. Rectal temperature was not altered by high ambient temperature and panting was not observed in calves during high ambient temperature. It was concluded that in this particular zone characterized by an intense heat load for the most part of the year, calf mortality was not linked to high ambient temperature around calving. Instead, survival of calves was negatively affected by winter weather. Thus, efforts to protect calves from cold weather would alleviate calf losses.

Key Words: calf, mortality, climate

W161 GALNT13, a positional candidate gene on bovine chromosome 2 for heifer pregnancy, is only expressed in nervous tissue. J. N. LaMastro*[1], W. A. Khan[1,2], S. O. Peters[2,3], O. O. Ajayi[1],

M. De Donato[1,4], W. Bai[1,5], and I.G. Imumorin[1], *[1]Cornell University, Ithaca, NY, [2]University of Veterinary and Animal Sciences, Lahore, Pakistan, [3]Berry College, Mt. Berry, GA, [4]Universidad de Oriente, Cumana, Sucre, Venezuela, [5]Shenyang Agricultural University, Shenyang, China.*

Genetic improvement programs for reproductive traits have been much slower to develop than improvement programs for growth and carcass traits for reasons including low heritability of fertility traits. In our previous study, a Bayesian based association mapping combined with alignment to differentially expressed hypothalamic transcriptome from RNA-seq data helped to identify candidate genes that may be responsible for the variation in heifer pregnancy on bovine chromosome 2. One of these candidates is uridine diphospho N-acetylgalactosaminyltransferase 13 (GALNT13), belonging to a family of enzymes involved in mucin-type O-glycosylation of serine and threonine residues of polypeptide acceptors. Bovine GALNT13 has 11 exons with mixed structures in its secondary structures predicted using the GORIV tool showing that it possesses the glycosyltransferase and ricin domains. We analyzed expression of bovine GALNT13 using reverse transcriptase-PCR amplification of 290 bp from exon 1. Like its murine and human counterpart, bovine GALNT13 is expressed in brain and spinal cord and not in liver, heart, kidney and lymph node. Our results appear to support previous studies in mouse that GALNT13 is a major enzyme responsible for the synthesis of O-glycan residues in neurons, which is consistent with being expressed only in nervous tissue.

Key Words: GALNT13, bovine, brain

W162 Combining ruminally protected choline and flaxseed in cattle diets to increase assimilation of n-3 fatty acids from the diet . C. P. Weiss*, C. L. Van Bibber-Krueger, K. A. Miller, C. A. Alvarado-Gilis, and J. S. Drouillard, *Kansas State University, Manhattan.*

Crossbred heifers (n = 108; initial BW = 285 ± 13.6 kg) were used in a randomized complete block experiment with a 2 × 2 factorial treatments arrangement to evaluate effects of ruminally-protected choline and ground flaxseed on changes in plasma concentrations of long-chain fatty acids, glucose, and L-lactate. Heifers were stratified by initial BW and allocated randomly, within strata, to 36 feedlot pens with 3 heifers/pen (9 pens/treatment). Factors consisted of level of ruminally-protected choline (C) fed at 0 or 113 g/d (Robert Morgan Inc.) and level of an extruded mixture of flaxseed, wheat middlings, vitamins, and minerals (F) fed at 0 or 10% of diet DM (Great O3 Premium Feed). Heifers were fed a basal diet (DM basis) of 25% corn silage, 15% alfalfa, 25% wet corn gluten feed, steam-flaked corn, and supplement. Cattle were fed their respective diets ad libitum at 1600 h daily. On d 0 and 14 of the study, cattle were weighed, blood was sampled via jugular venipuncture and centrifuged to recover plasma. Plasma glucose and L-lactate were measured using a YSI 2100D analyzer and fatty acid methyl esters (FAMEs) were measured by gas chromatography. Data were analyzed as a mixed model with choline, flaxseed, day, and all interactions as fixed effects, weight block as a random effect, and pen as the experimental unit. There were no significant interactions between C and F for performance or blood constituents ($P > 0.05$). Feeding C tended to improve gain efficiency (0.284 vs. 0. 313) for 0 and 113 g/d feeding levels, respectively; $P = 0.06$); but did not affect ADG, DMI, or blood constituents ($P > 0.10$). Gain, DM intake, gain efficiency, and plasma glucose and lactate were unaffected by feeding F ($P > 0.10$), but plasma concentrations of α-linolenic acid were greater for cattle fed F compared with those without ($P < 0.01$). Ruminally protected choline yielded efficiency responses comparable to those observed in previous studies. The Great O3 feed used in this study increased plasma concentrations of n-3 fatty acids, but including choline provided no further improvement in assimilation of dietary fats.

Key Words: FAME, glucose, lactate

W163 Kyphosis induced by maternal vitamin D intake is not explained by a reduction in vertebrae body mineral content of pigs at birth or weaning. L. M. Vanderwerff*, L. A. Rortvedt-Amundson, and T. D. Crenshaw, *University of Wisconsin, Madison.*

Kyphosis, an idiopathic disease characterized by abnormal outward spinal curvature, commonly affects the 14th to 16th thoracic vertebrae. In recent experiments kyphosis was induced in young pigs produced by sows fed diets with no supplemental vitamin D_3 (D) throughout gestation and lactation. The current objective was to assess variation in mineral content of regions along spinal columns of pigs produced by gilts fed diets varying in D. Regions were examined to determine if a reduction in percent ash (%ash) predisposed specific vertebrae to conformational deformities associated with kyphosis. Spinal columns were collected from pigs at birth (d 0, n = 12) and weaning (d 25, n = 15). Gilts that produced the pigs were fed diets containing 0, 325, or 1,750 IU D/kg from breeding through lactation. After euthanasia, the spinal column was removed and vertebrae bodies were dissected, then extracted with ether and ashed. Data from individual vertebral bodies were grouped into regions (n = 3/region) and numbered 1 to 7 consecutively from the 1st rib through the last lumbar vertebra. Regions of 3 adjacent vertebrae were selected based on the definition of kyphosis. Differences due to maternal diets were not detected in vertebrae % ash of pigs at birth (44.4, 43.6, and 44.8%) or weaning (37.4, 37.1, and 39.9%). Vertebrae % ash decreased ($P < 0.05$) from d 0 to d 25 (44.3 vs. 38.1%) but these differences varied by region within the vertebral column (age X region interaction, $P < 0.01$) as shown below. The 6% decrease in % ash with age was due to a 4-fold increase in bone organic matrix (0.11 vs. 0.49 g) that exceeded the 3-fold increase in bone mineral (0.09 vs. 0.31 g). At d 0, the % ash was essentially constant across regions but at d 25, % ash increased, especially in the more distal regions. At d 25, % ash values in regions associated with kyphosis were greater, implying that kyphosis may result from an overgrowth of organic matrix not from a lack of matrix mineralization.

Table 1. Ash (%) values of different vertebral regions

	Vertebral region (3 vertebrae/region)							Pooled
Age, d	1	2	3	4	5	6	7	SEM
0	43.8	43.8	44.1	44.3	44.2	45.0	44.9	0.07
25	36.5	37.3	37.6	38.4	39.0	39.5	38.5	0.08

Key Words: bone ash, bone matrix, vitamin D

W164 Effect of sex, pen density and season on feedlot performance. J. H. Moss*, C. L. Maxwell, and C. R. Krehbiel, *Department of Animal Science, Oklahoma State University, Stillwater.*

There are a variety of factors that can affect feedlot performance for both steers and heifers. The objective of this study was to quantify factors that affect DMI, ADG, and efficiency of cattle during the finishing phase. Factors that were evaluated were sex and season of cattle closeout. Trial data from 2003 to 2012, including initial BW, final BW, DMI, ADG, G:F, from the Willard Sparks Beef Research Center was compiled and analyzed. The data set consisted of 933 pens, 647 pens of steers (3,706 steers) and 286 of heifers (1,800 heifers). The effect of sex was analyzed using PROC MIXED (SAS 9.3, Cary, NC), initial

BW was used as a covariate when necessary ($P < 0.05$) to determine the difference in performance and efficiency between steers and heifers. Steers consumed 14.5% more feed (10.29 vs. 8.99, kg/d), gained 16.9% faster (1.66 vs. 1.42, kg/d), and were 3.2% more efficient than heifers (0.162 vs. 0.157; $P < 0.01$). Season was evaluated to determine the effect of seasonal variation on performance. Season was divided into 4, 3 mo periods 1(Jan-Mar), 2(Apr-Jun), 3(Jul-Sep), 4(Oct-Dec). Cattle finished in season 4 consumed 5% more feed (10.02 vs. 9.54 kg/d; $P < 0.01$) compared with the other 3 seasons. Cattle in seasons 2 and 4 had a 5.2% improvement in ADG compared with season 1 (1.61 vs. 1.53 kg/d) and an 11.0% improvement in ADG compared with season 3 (1.61 vs. 1.45; $P < 0.01$). Cattle in season 2 and 4 were 4.1% more efficient than cattle in season 1 and 3 (0.164 vs. 0.157, $P < 0.01$). A strong positive correlation existed between initial and DMI for heifers ($r^2 = 0.54$; $P < 0.01$), as well as steers ($r^2 = 0.40$; $P < 0.01$). Using PROC REG, dry matter intake for this data using only initial BW was estimated by the equation DMI, kg/d = 6.75 + (initial BW, kg*0.162) ($P < 0.01$). Actual DMI was positively correlated to predicted DMI (Eq.7–2, NRC, 2000; $r^2 = 0.40$, $P < 0.01$). The results of this study indicates that steers have increased DMI, ADG, and feed efficiency during the finishing period compared with heifers, and that cattle closed out in the spring and fall of the year experience improved feedlot performance compared with cattle closed out in the winter and summer.

Key Words: sex, season, feedlot performance

W165 Phosphorus status of grazing beef cattle in Virginia's Chesapeake Bay watershed. S. J. Neil*, D. D. Harmon, and M. A. McCann, *Virginia Polytechnic Institute and State University, Blacksburg.*

Phosphorus loads in the Chesapeake Bay are a focus of environmental concern. Animal agriculture's contribution to this problem has been documented and efforts are focused on mitigating the issue. Major research and extension efforts have focused on concentrated animal feeding operations (mainly dairy and poultry); however, 400,000 beef cows are located in Virginia's Chesapeake Bay watershed counties. The objective of this study was to document phosphorus (P) supplementation in free choice minerals, soil test P, forage P and manure P levels of grazing beef cows in Virginia's Chesapeake Bay watershed. Producers could submit more than one set of samples if a full complement of samples was collected and the samples represented another land area or herd. Thirty-four producers from 2 counties cooperated with sample collection (n = 80) and completed a questionnaire related to their management practices. Soil test P values were characterized as low (14%), medium (29%), high (27%) and very high (13%) based on Virginia Cooperative Extension Soil Test guidelines. Phosphorus content of pasture forage grab samples (mean = 0.36%, SD = 0.10) was correlated to soil phosphorus levels (r = 0.42), but manure total P was lowly related (r = 0.05) to soil P values. Forage P levels were compared with Beef Cattle NRC (2001) P requirements for a 545-kg cow (peak milk, 13.6 kg/d). All forage samples were sufficient in P content to meet a dry cow's requirements, 98% met the requirements for late gestation and 87% met the peak lactation P requirement. Farm mineral supplements were categorized into 4 levels of P content (0, 1.0–2.5, 3.0–5.0 and >6.0%). Forage P content did not affect mineral selection by producers. The mean forage P content for the 4 mineral categories were 0.27, 0.37, 0.37 and 0.46%, respectively. Manure TP increased as mineral P content increased, 0.54, 0.65, 0.80 and 0.88% respectively. All farms surveyed required little or no phosphorus supplementation in regard to cow nutrient requirements. Sixty-five percent of participating cattlemen were receptive to modifying their P supplementation based on forage test results while only 6% were opposed to any modification.

Key Words: phosphorus, beef cattle

W166 Effect of anabolic implants on adrenal cortisol synthesis in beef cattle. K. A. Branham*[1], J. O. Ellison[1], B. I. Gomez[1], A. D. Stapp[1], C. A. Gifford[1], C. R. Kreihbel[1], B. C. Bernhard[1], C. L. Maxwell[1], D. M. Hallford[2], and J. A. Hernandez Gifford[1], *[1]Oklahoma State University, Stillwater, [2]New Mexico State University, Las Cruces.*

Implantation of anabolic steroids to increase growth rate in beef cattle affects adrenal glucocorticoid production. The mechanism by which trenbolone acetate and estrogen reduce cortisol (C) biosynthesis in heifers is not clear. The objective of this study was to determine serum C concentrations and adrenal steroidogenic enzyme mRNA levels in heifers implanted with Revalor 200. On d 0 of a 90-d finishing phase, 187 predominantly Angus heifers were randomly assigned to 3 treatments: non-implanted controls (con); Revalor 200 implant for 90 d of finishing phase (early); or Revalor 200 for last 30 d of finishing phase (late). On d 0, BW was 363, 359, and 361 kg for con, early and late treatments, respectively. At d 60, BW for early implanted heifers (458 kg) was greater ($P < 0.01$) than con (439 kg) and late implanted (436 kg) heifers. Final BW (d 90) was greater in early (519 kg) and late (510 kg) implanted heifers compared with con (492 kg). In a subset of heifers (n = 49) peripheral blood was collected to quantify serum C concentrations at d 0, 30, 60 and 90. Serum C was similar among groups at d 0 ($P = 0.65$); however, at d 30 heifers receiving implants had a marked reduction ($P < 0.01$) in serum C concentrations (31 ng/mL) compared with con (47 ng/mL) and late (48 ng/mL). At d 90, con heifers had a serum C value of 43 ng/mL compared with 25 ng/mL in both early and late implanted heifers ($P < 0.01$). At harvest (d 90) adrenal tissue was collected (n = 6/group) for mRNA analysis of steroidogenic enzymes cytochrome P450, family 21, subfamily A, polypeptide 2, cytochrome P450, family 11, subfamily B, polypeptide 1 and melanocortin 2 receptor. Despite decreased serum C in implanted heifers, no difference among treatments was detected for expression of the steroidogenic enzymes or the ACTH receptor in adrenal glands indicating other components of the hypothalamic-pituitary-adrenal axis are responsible for the observed decrease in serum C.

Key Words: adrenal, cortisol, implant

W167 Expression of WNT signaling transcripts at specific stages of follicle development in bovine granulosa cells. A. J. Potts*[1], A. D. Stapp[1], B. I. Gómez[1], K. B. Parker[1], C. A. Gifford[1], D. M. Hallford[2], and J. A. Hernandez Gifford[1], *[1]Oklahoma State University, Stillwater, [2]New Mexico State University, Las Cruces.*

Follicular maturation is a dynamic process requiring input from pituitary gonadotropins and ovarian derived factors. Members of the wingless-type mammary tumor virus integration-site (WNT) signaling pathway have been recognized to be differentially expressed and hormonally regulated in rodent ovaries, and we recently reported that WNT2 is regulated by FSH in bovine granulosa cells. However, the role and expression of WNT signaling molecules in ovarian follicle development in cattle is unknown. Therefore, the objective of this study is to characterize components of the WNT signaling pathway at specific stages of follicular development by real-time PCR. To identify gene expression changes in bovine folliculogenesis, granulosa cells and follicular fluid were collected from ovary pairs containing a stage III CL (d 11 to 17 of an estrous cycle). Granulosa cells were isolated from small (1 to 5 mm; n = 4) and

large (8 to 22 mm; n = 4) follicles, and the corresponding CL (n = 3). Intra-follicular estradiol and progesterone concentrations were used to identify large dominant follicles (estradiol:progesterone >1). Real-time PCR quantification of select WNT family members was evaluated at distinct stages of development. Compared with small follicle granulosa cells, expression of the WNT transcriptional co-factor, CTNNB1 was similar in large dominant follicles ($P = 0.95$) but was decreased in the CL ($P = 0.06$). Expression of WNT ligands also demonstrated stage specific regulation as WNT2B was reduced in large dominant follicles ($P = 0.02$) but similar in CL ($P = 0.53$) compared with small follicles. A comparable pattern of expression was demonstrated for WNT5A as small follicles had greater expression compared with large follicles ($P < 0.01$) and was similar to CL ($P = 0.37$). However, WNT2 mRNA expression was unchanged throughout follicle maturation ($P = 0.47$). Previous work in our laboratory demonstrated WNT3A is antagonistic to FSH signaling in cultures of primary rat granulosa cells. Results from the current experiment indicate that WNT signaling molecules may be inhibitory to follicle development and luteinization in cattle.

Key Words: folliculogenesis, ovary, WNT

W168 Solubility of copper sulfate and three sources of dicopper chloride trihydroxide. C. S. Park* and B. G. Kim, *Konkuk University, Seoul, Republic of Korea.*

Copper sulfate ($CuSO_4$) and dicopper chloride trihydroxide (dCCTH) are widely used as Cu sources in swine diets. The objective of this study was to determine the solubility of Cu in $CuSO_4$, and 3 sources of dCCTH consisted of α-form (dCCTH-α), β-form (dCCTH-β), or a mixture of α and β-form (dCCTH-α·β) at different pH and an in vitro digestion procedure using a shaking incubator at 39°C. In Exp. 1, $CuSO_4$, dCCTH-α, dCCTH-β, and dCCTH-α·β were incubated in buffer at pH 2.0, 3.0, 4.8, and 6.8 for 4 h. Copper sulfate was completely dissolved within 15 min except at pH 6.8. At pH 2.0, solubility of Cu in dCCTH-α and dCCTH-α·β was greater (42.5 and 34.9 vs. 17.2%; $P < 0.05$) than dCCTH-β at 15 min and Cu in all dCCTH was completely dissolved at 4 h. In pH 3.0 and 4.8 buffers, all sources of dCCTH were dissolved at less than 22% and 3%, respectively, when incubated for 4 h. Copper in dCCTH sources was not dissolved at pH 6.8. Exp. 2 was conducted to determine the solubility of Cu in the same Cu sources as in Exp. 1 using an in vitro digestion assay simulating digestion procedures of pigs. All sources of Cu were completely dissolved at pH 2.0 when incubated for 2 h in a phosphate buffer. In Exp. 3, the 5 diets consisted of a control diet and diets supplemented with 250 ppm of Cu as $CuSO_4$, dCCTH-α, dCCTH-β, or dCCTH-α·β were prepared to determine the solubility of Cu during an 3-step in vitro digestion assay. Solubility of Cu in diets supplemented with $CuSO_4$ and dCCTH sources was greater ($P < 0.05$) than the control diet in step 1 and 2. These results indicate that solubility of $CuSO_4$ and dCCTH is affected considerably by pH of digesta. Among dCCTH sources, the solubility of Cu in dCCTH-α is greater than in other dCCTH sources at pH 2.0.

Key Words: in vitro digestion, swine, trace mineral

W169 Effects of poor maternal nutrition on GH, IGF-I, insulin, and leptin concentrations in pregnant ewes. M. E. Forella*, K. N. Peck, M. L. Hoffman, A. R. Fox, K. E. Govoni, and S. A. Zinn, *Department of Animal Science, University of Connecticut, Storrs.*

Maternal hormones affect fetal growth and development through their effect on nutrient partitioning and placental development. Maternal diet is one factor regulating maternal hormone concentrations. We hypothesized that during gestation, diet alters concentrations of maternal metabolic hormones. Pregnant ewes (n = 36; 12/treatment) were individually fed 1 of 3 diets [100% (CON), 140% (OVER), or 60% (RES) NRC requirements] from wk 5 of gestation until parturition. Weekly blood samples (20 mL) were obtained via jugular venipuncture and BW was measured. Concentrations of GH, IGF-I and leptin were determined by RIA. Insulin was determined by ELISA. Data were analyzed using ANOVA. By the end of gestation (wk 20), RES ewes (89.3 ± 3.6) were lighter ($P < 0.01$) and OVER ewes (119.7 ± 3.6 kg) were heavier ($P < 0.1$) than CON ewes (112.9 ± 3.6 kg). However, compared with CON ewes (0.27 ± 0.01 kg), ADG was increased ($P < 0.01$) in OVER ewes (0.35 ± 0.01 kg) and decreased ($P < 0.01$) in RES ewes (0.12 ± 0.01 kg). Concentrations of GH were greater ($P < 0.01$) in RES ewes (6.4 ± 0.6 ng/mL) than CON ewes (3.2 ± 0.6 ng/mL) and OVER ewes (2.3 ± 0.6 ng/mL). Average concentrations of IGF-I were greater ($P < 0.1$) in OVER ewes (197.7 ± 14.5 ng/mL) compared with CON (163 ± 14.5 ng/mL) and RES (146.35 ± 14.5 ng/mL) ewes, but there was no difference between CON and RES ewes ($P < 0.42$). Average concentrations of insulin were greater ($P < 0.01$) in OVER ewes (0.61 ± 0.7 ng/mL) than RES (0.31 ± 0.7 ng/mL) and CON (0.32 ± 0.7 ng/mL) ewes. Leptin averaged 2.3 ± 1.4, 1.5 ± 1.4, and 4.3 ± 1.4 ng/mL in CON, RES, and OVER ewes, respectively, but there were no differences in leptin due to diet ($P > 0.32$). In conclusion, poor maternal diet during gestation affects circulating concentrations of GH, IGF-I, and insulin, and this may contribute to developmental changes in the fetus.

Key Words: insulin, maternal diet, somatotropic axis

W170 In vitro fermentation of high forage substrate with addition of direct fed microbials and/or monensin. K. E. Roberts*, K. M. Anderson, N. M. Kenney, K. R. McLeod, and E. S. Vanzant, *University of Kentucky, Lexington.*

This study was conducted to determine in vitro ruminal fermentation characteristics with addition of direct fed microbials (DFM) and/or monensin (MON) to a high forage TMR. ANKOM RFS fermentation vessels received either 50 µg lactose (control) or 50 µg DFM containing 50,000 cfu lactic acid bacteria (LifeProducts 10G) whereas MON was applied in the feed of the inoculum donor steers. Four ruminally cannulated steers received a high forage diet either with (n = 2) or without (n = 2) 440 mg/hd/d MON. Rumen fluid for each pair of steers was combined before inoculating fermentation vessels. Gas production was measured in each vessel for 24 h. At termination, fluid samples were collected from each vessel for measurement of VFA, ammonia, and pH. The best-fit model of 10 gas production models evaluated was used to quantify gas production parameters for individual vessels. Data were analyzed with the GLM procedure of SAS with a model appropriate for a completely randomized design with treatments arranged in a 2 × 2 factorial structure. Treatments did not influence ($P > 0.10$) total VFA concentrations (m*M*) or gas production (mL). Gas production rates were decreased slightly ($P = 0.06$; 0.236 mL/min and 0.224 mL/min ± 0.004) by DFM and were unaffected by MON ($P = 0.89$). Interactions between DFM and MON were detected ($P \leq 0.08$) for NH3 concentration and molar proportions of all VFA except propionate. In the absence of MON, DFM had no influence ($P > 0.10$) on any of these variables. With MON, acetate proportion was decreased ($P < 0.06$; 56.8 vs. 53.7 ± 1.10%) by DFM, whereas molar proportions of the remaining VFA (except propionate) were increased ($P < 0.10$; 11.9 vs. 13.2 ± 0.43%; 4.4 vs. 5.2 ± 0.28%; 2.1 vs. 2.4 ± 0.09%; 4.7 vs. 5.5 ± 0.28%; for butyrate, valerate, isobutyrate, and isovalerate) by DFM, as was NH3 concentration (1.6 vs. 2.8 ± 0.43 m*M*). Although MON decreased pH slightly ($P < 0.01$; 6.86 vs. 6.73 ± 0.015), DFM had no effect ($P = 0.30$) on pH. Results indicate that the effects of DFM on VFA profiles and ammonia concentrations with in vitro fermentation of a high forage substrate were dependent on the presence of MON.

Key Words: direct-fed microbial, VFA, gas production

W171 Effects of poor maternal nutrition on gene expression in bone marrow stromal cells from lambs. D. M. Kaelin*, S. Neupane, M. L. Hoffman, K. N. Peck, S. A. Zinn, and K. E. Govoni, *University of Connecticut, Storrs.*

Poor maternal nutrition can reduce growth rate, reduce bone development, and increase fat deposition in offspring. Bone marrow stromal cells (BMSC) are multipotent stem cells that can differentiate into several cell types including osteoblasts and adipocytes. Poor maternal nutrition may commit these cells to the adipocyte lineage, contributing to increased adipose tissue and reduced bone; however the mechanisms are not well established. We hypothesized that poor maternal nutrition would alter gene expression in BMSC. Pregnant ewes (n = 24) were randomly assigned to a diet of 100% (CON), 60% (RES), or 120% (OVER) of NRC requirements beginning at d 114 ± 10 of gestation. Within 24 h of birth, lambs were euthanized (n = 3/treatment), BMSC were isolated from the femur, cultured until 80% confluent, and RNA was extracted using TriReagent and ethanol precipitation. Real-time reverse transcriptase (RT)-PCR was used to determine mRNA expression. Data were analyzed by ANOVA. We did not observe an effect of treatment on markers of adipogenesis [CCAAT-enhancer binding protein (CEPB)-α, proliferation-activation receptor (PPAR)-γ, Pref-1; $P \geq 0.29$]. Maternal diet did not affect runt-related transcription factor (Runx)2 ($P \geq 0.45$), a key transcription factor in osteoblast differentiation, as well as various transcription factors involved in osteoblast development [dickkopf-related protein (DKK)2, low density lipoprotein receptor-related protein (Lrp)4, Lrp5, glycogen synthase kinase (GSK)-β and β-Catenin; $P \geq 0.3$]. mRNA expression of T-box (Tbx)-3, a key transcription factor in development and osteoblast function, tended ($P = 0.1$) to be reduced 1.6 ± 0.2-fold in RES. Expression of P2Y14 receptor, a key factor in lineage commitment of BMSC, was reduced 3.8 ± 0.1-fold in OVER ($P = 0.03$). Expression of CEBP-β was reduced 2.0 ± 0.1 and 2.2 ± 0.1-fold in RES and OVER, respectively ($P \leq 0.02$). In conclusion, poor maternal nutrition during gestation alters the expression genes involved in the commitment of BMSC to osteoblast and adipocytes cell lineage, which may contribute to altered body mass and composition of offspring.

Key Words: maternal nutrition, bone marrow stromal cells, sheep

W172 Effects of maternal dietary yeast supplementation on foal growth and development. E. R. Share*, J. M. Reddish, and K. Cole, *Department of Animal Sciences, The Ohio State University, Columbus.*

Dietary yeast supplementation in horses has been reported to influence nutrient digestibility and milk production in mares. Altering the nutrient composition of the milk from mares may influence the growth of their foals. The objective of this study was to determine if dietary yeast supplementation of the maternal diets would influence foal growth and development. Eight Quarter Horse mares (14.5 ± 7.5yr) were randomly assigned to one of 2 groups: Yeast or Control. All mares received 0.5% BW of a 16% CP pelleted concentrate, with water and mixed grass hay ad libitum. Mares in the yeast treatment group were fed a targeted dose of 1 g/ 45.4 kg of BW per day of a live culture of *Saccharomyces cerevisiae* for a period of 180 d. Growth measurements (body weight, body length, heart girth, wither and hip height, upper and lower leg length, and front/rear cannon bone circumference) were taken on d 0, 7, 14, 21, 28, 35, 42, 49, 56, 70, 84, 98, 112, 126, 140, 154 and 168. Data were analyzed using the PROC Mixed procedure of SAS. Average daily gain (ADG) of the foals was not influenced by the addition of yeast to the maternal diets. Hip height and wither height were highly correlated (r = 0.99). Although upper leg length and wither height were highly correlated (r = 0.93), lower leg length and wither height were not (r = 0.72). No significant differences in foal growth and development due to dietary yeast supplementation of the

Key Words: foal, growth, yeast

W173 Effects of poor maternal nutrition during gestation on gene expression in renal adipose tissue of lambs. A. M. Bush*, M. L. Hoffman, K. N. Peck, S. A. Zinn, and K. E. Govoni, *Department of Animal Science, University of Connecticut, Storrs.*

Poor maternal nutrition impairs postnatal growth and development of the animal, particularly decreasing carcass quality with an increase in fat deposition. We hypothesized that poor maternal nutrition would alter expression of key genes involved in adipogenesis in lambs. Thirty-six multiparous Dorset (n = 25), Shropshire (n = 7), and Southdown (n = 4) ewes were individually housed and fed either 100% (CON), 60% (RES), or 140% (OVER) of requirements for ewes pregnant with twin lambs (NRC, 1985) starting at d 31 ± 1.3 of gestation. Lambs were euthanized within 24 h after birth (n = 18) and perirenal adipose tissue was collected immediately and snap frozen in liquid nitrogen. Gene expression was determined by RNA extraction using Tri-Reagent, an RNeasy Mini Kit, and real-time reverse transcriptase-PCR. Data were analyzed using ANOVA with significance considered as $P \leq 0.05$. To determine if maternal diet affected markers of adipogenesis, we quantified expression of peroxisome proliferator-activated receptor gamma (PPAR-γ) and CCAAT/enhancer binding protein β (CEBP-β). We did not observe a change in expression of either gene in lambs born to RES and OVER ewes relative to controls at birth ($P \geq 0.27$). In addition, we did not observe an effect of maternal diet on glucose transporter type 4 (GLUT-4), a marker of nutrient uptake, in RES and OVER lambs relative to controls at birth ($P = 0.17$). Maternal diet did not effect adiponectin (ADIPOQ), a marker of energy homeostasis, in RES and OVER groups relative to controls ($P = 0.07$). These findings suggest that during fetal development, poor maternal nutrition does not alter expression of key markers of adipogenesis. Further analysis is needed to determine if poor maternal nutrition alters gene expression in adipose tissue at later stages of development when fat accretion is more rapid.

Key Words: maternal nutrition, adipose tissue, sheep

W174 Uterine flux of estrone sulfate in an ovine maternal nutrient restriction model during melatonin supplementation. L. J. Grossner*[1], L. E. Camacho[2], D. M. Hallford[3], K. A. Vonnahme[2], and C. O. Lemley[1], *[1]Mississippi State University, Mississippi State, [2]North Dakota State University, Fargo, [3]New Mexico State University, Las Cruces.*

Previous data from our laboratories showed an increase in uteroplacental secretion of progesterone and estradiol 17β in nutrient restricted vs. adequate fed ewes. The current objectives were to examine the effects of dietary melatonin supplementation and nutritional plane on uteroplacental estrone sulfate flux and placental protein expression of steroidogenic acute regulatory protein (StAR) and aromatase. From d 50 to 130 of gestation, 31 primiparous ewes received 100% (ADQ) or 60% (RES) of nutrient requirements and were supplemented with 5 mg of melatonin per day (MEL) or no melatonin (CON). At d 130, uterine artery blood flow (BF) was determined under general anesthesia. Blood samples were collected from maternal saphenous artery, gravid uterine vein, umbilical artery, and umbilical vein. Estrone sulfate was not detected in the umbilical vein or umbilical artery samples (concentration ≤0.01 ng/mL). Uterine flux of estrone sulfate was calculated as maternal arterial-venous difference × uterine BF. Maternal artery estrone sulfate was increased ($P < 0.01$)

in RES (5.3 ± 1.4 ng/mL) vs. ADQ (0.7 ± 0.3 ng/mL) ewes. Similarly, uterine vein estrone sulfate was increased ($P < 0.05$) in RES (5.1 ± 1.5 ng/mL) vs. ADQ (1.5 ± 0.7 ng/mL) ewes. Maternal arterial-venous difference of estrone sulfate was increased ($P = 0.01$) in CON-RES (1.9 ± 1.0 ng/mL) vs. CON-ADQ (−1.1 ± 1.0 ng/mL), while MEL-RES (−2.1 ± 1.0 ng/mL) was not different ($P > 0.50$) from CON-ADQ. Uterine flux of estrone sulfate was decreased ($P < 0.01$) in MEL-RES (−3.4 ± 1.4 μg/min) vs. CON-RES (2.2 ± 1.4 μg/min), while neither was different ($P \geq 0.07$) from CON-ADQ (−1.5 ± 1.5 μg/min). Placental StAR protein expression was increased ($P < 0.05$) in RES vs. ADQ ewes at d 130, while placental aromatase protein was not different ($P > 0.60$) across all treatment groups. Maternal nutrient restriction interacted with dietary melatonin supplementation to alter uterine flux of estrone sulfate. Moreover, the previously observed increase in steroid secretion from nutrient restricted dams is associated with an increase in placental StAR protein.

Key Words: estrone sulfate, melatonin, uterine flux

W175 Reproductive indices of quail hatching eggs under semi-intensive management system. O. T. F. Abanikannda, A. M. Adeyeye*, A. O. Leigh, and A. A. Olubunmi, *Lagos State University, Ojo, Lagos, Nigeria.*

The supply of day old chicks is very important for successful hatchery operations and the future of quail production, breeding and management. This is predicated not only on the number produced but also the fertility and hatchability of the eggs. Fertility and hatchability are 2 major indices for assessing reproductive performance which are mostly sensitive to environmental and genetic influences. This study was aimed at assessing the fertility and hatchability of quail eggs under semi-intensive management. A total of 985 eggs were sourced from a quail farm in the Savannah region of Nigeria. The breeders were kept in cages and were freely pen-mated with a sex ratio of one male to 5 female birds. Eggs were cleaned, labeled, measured, fumigated, incubated and classified as fertile or not fertile after incubation. Measurements included egg weight, length, width, vertical and horizontal circumferences, while computed indices were egg density, surface area and volume (Table 1). All statistical analyses (exploratory, correlation and logistic fit) were done with JMP$^{(R)}$ software. Fertility was 74.92%, while hatchability was 67.82% in the entire study but 90.51% within the fertile eggs group. There was no statistical significance ($P > 0.05$) in mean of all variables in the 2 groups (fertile and not fertile) and a further logistic fit of the 2 groups based on the measures was not significant ($P > 0.05$). In a similar way, hatchability was not significantly influenced by the pre-hatch measures of the eggs. It can be concluded from the study that physical characteristics of the eggs as reflected by the measured variables and indices was not the significant factor in the determination of the fertility and hatchability of the eggs.

Table 1. Descriptive statistics of measured variables

Variable	Fertile	Not fertile
Sample size (no.)	738	247
Egg weight (g)	9.90 ± 0.03	9.93 ± 0.06
Egg length (mm)	30.46 ± 0.05	30.62 ± 0.09
Egg width (mm)	24.54 ± 0.04	24.49 ± 0.04
Horizontal circumference	8.37 ± 0.02	8.34 ± 0.02
Vertical circumference	9.25 ± 0.02	9.23 ± 0.03
Egg density	1.05 ± 0.01	1.05 ± 0.01
Egg surface area	22.61 ± 0.06	22.66 ± 0.10
Egg volume	10.33 ± 0.05	10.34 ± 0.07

Key Words: fertility, hatchability, logistic fit

W176 Effects of maternal 25-hydroxycholecalciferol (25OHD3) supplementation on fetal bone development in pigs. K. K. McFadden*[1], M. L. Hoffman[1], J. D. Starkey[2], J. D. Coffey[2], E. A. Hines[2], C. W. Starkey[2], and K. E. Govoni[1], *[1]University of Connecticut, Storrs, [2]Texas Tech University, Lubbock.*

Lameness in pigs is often due to poor bone development and creates a major health issue for the swine industry. The majority of bone development occurs during fetal and early postnatal development and vitamin D is required for proper bone development. It has been shown in swine that 25OHD3, a metabolite of vitamin D, is more bioavailable than vitamin D_3. We hypothesized that providing vitamin D as 25OHD3 to pregnant gilts would increase markers of bone formation in the bones of fetuses. Forty PIC Camborough-22 gilts were randomly assigned to one of 2 corn-soybean meal-based diets. The control diet contained 2,500 IU of vitamin D_3 per kg of diet. The experimental diet contained 500 IU D_3 per kg of diet plus 50 μg of Rovimix Hy-D (DSM Nutritional Products Ltd., Basel, Switzerland) the 25OHD3 form. Beginning 43 d before gestation, gilts were fed 2.7 kg of their assigned diet once a day until 90 d of gestation. At d 90 ± 1 femurs from the 2 median BW fetuses per gilt (1 male and 1 female) were collected (n = 22: control; n = 28: 25OHD3). mRNA was extracted from the mid-diaphysis for gene expression analysis using real time-reverse transcriptase (RT)-PCR. Data were analyzed using ANOVA with significance considered at $P \leq 0.05$. Specifically, we evaluated mRNA expression of markers of bone formation [osteocalcin, alkaline phosphatase (ALP), and type I collagen], as well as, vitamin D receptor, parathyroid hormone receptor (PTHR), and fibroblast growth factor-23 (FGF-23), molecules critical for bone development and known to interact with the vitamin D pathway. We did not observe an effect of maternal 25OHD3 supplementation on the expression of any of the genes evaluated ($P = 0.32$). In addition, we did not observe an effect of gender ($P = 0.25$) or a treatment × gender interaction ($P = 0.46$). These data suggest that maternal supplementation with 25OHD3 does not alter the expression of these genes at this time during fetal development (90 d of gestation). Further studies are needed to determine if maternal vitamin D supplementation will affect markers of bone formation later during fetal development and postnatal growth.

Key Words: vitamin D, swine, bone

W177 Pituitary genomic expression profiles of steers are altered by grazing of high (HE) versus low (LE) endophyte-infected pastures. R. M. Hegge*, J. A. Boling, and J. C. Matthews, *University of Kentucky, Lexington.*

Consumption of ergot alkaloids in endophyte-infected tall fescue induces a distinct set of physiological and whole-animal performance parameters collectively known as "fescue toxicosis." It is estimated that fescue toxicosis-associated animal performance losses cost cattle farmers about $1 billion annually. Many of these parameters, such as decreased fertility and milk production are consistent with impairment of pituitary functions. The goal of this study was to test the overall hypothesis that consumption of endophyte-infected tall fescue would alter pituitary genomic expression profiles, including genes involved with prolactin (PRL) metabolism, a known marker of fescue toxicosis. Total RNA was extracted from pituitaries of 16 Angus-cross steers (BW = 266 ± 10.9 kg) that had been randomly assigned (n = 8) to graze either HE or LE pastures for 89 d, and for which serum PRL levels of HE steers was only 10% of LE steers (JAS, 2009, 87:748–760). RNA was subjected to microarray analysis using a custom platform (WT Btau 4.0 Array, Affymetrix). Raw expression intensity values were adjusted using Robust Multichip Averaging and then normalized using the GeneChips and Media Polish Summarization algorithms (Partek). Pearson (linear)

Correlation Analysis revealed a high (>0.98) correlation among all chips. ANOVA testing found differential ($P \leq 0.001$) expression of 592 RNA transcripts in HE vs. LE pituitaries. Hierarchical clustering analysis (Partek) of differentially-expressed genes revealed that each animal segregated within its respective treatment group. Bioinformatic analysis identified decreased (17 to 63%) expression in HE steers of genes for prolactin signaling and regulation of lactotroph, gonadotroph, and thyrotroph proliferation (GPR101, DRD2, PCSK1, PRL, PRLR), and altered expression of another 13 genes for gonadotropin releasing hormone-mediated signaling. In conclusion, steers grazing HE pastures had altered pituitary genomic profiles, in a manner consistent with reduced blood PRL and altered whole-body metabolism, hallmarks of fescue toxicosis.

Key Words: pituitary, gene expression, ergot alkaloid

W178 Excess estrus in meat goats: 1-year summary. B. A. Schulte*, L. S. Wilbers, J. D. Caldwell, C. Clifford-Rathert, and A. K. Wurst, *Lincoln University, Jefferson City, MO.*

Excess estrus (EE) occurs when animals exhibit behavioral estrus, or standing heat, after conception. Excess estrus can occur frequently in some domestic farm animals; however, information regarding its frequency in goats is limited. The causes and effects of EE on the reproductive cycle and pregnancy in goats have not previously been studied. The objective of this project was to determine the frequency of EE in meat goats. Hormone profiles of estradiol-17β (E_2) and progesterone (P_4) during pregnancy and quantity of embryonic and fetal losses (near d 25, 40, 60, and 110) were recorded to determine if does displaying EE were more prone to reproductive dysfunction. In winter 2011, ultrasonographic examination was used to determine pregnancy in 132 bred Boer and Boer-cross does. One vasectomized buck fitted with a marking harness was placed with does following breeding to detect does displaying EE (EE does). Does were checked for breeding marks daily. Results of this study indicate that of 105 does confirmed pregnant, 21 (20%) showed EE at least once during pregnancy. Concentrations of E_2 and P_4 were lower in EE does compared with does not displaying EE near d 25 of pregnancy (5.9 vs. 7.3 pg/mL; 7.5 vs. 10.8 ng/mL, respectively). Concentrations of P_4 remained lower in EE does through d 40 (8.7 vs. 10.2 ng/mL) and tended ($P = 0.07$) to remain lower through d 60 (10.2 vs. 11.9 ng/mL) of pregnancy. On a percentage basis, fetal and embryonic losses were greater in EE does (29% vs. 15%); however, there was not enough animals to determine significance. Of does kidding, kidding rate of EE does compared with does that did not show EE was not different (1.6 vs. 1.5 kids/doe, respectively; $P = 0.72$).These results suggest that EE may occur in a significant portion of pregnant meat goats and may be associated with differences in embryonic and/or fetal losses of these animals. This project was supported by USDA-NIFA Cooperative agreement.

Key Words: goat, estrus, behavior

W179 Physicochemical analyzes of Longissimus dorsi muscle for checking the quality of meat from cattle Nellore (*Bos indicus*) selected for production. J. M. Malheiros*[1], W. A. Baldassini[2], L. A. L. Chardulo[3], J. A. V. Silva[2], and L. G. Albuquerque[1], *[1]UNESP-FCAV, Jaboticabal, SP, Brazil, [2]UNESP-FMVZ, Botucatu, SP, Brazil, [3]UNESP-IB, Botucatu, SP, Brazil.*

Tenderness is a major quality attribute of beef that affects consumer satisfaction, consumption habits and retail preferences. Hence, breeding programs that focus on meat tenderness are important for Brazil given the prevalence of *Bos indicus* breeds in the cattle industry [1]. The present work aims to determine traits in meat quality in Longissimus dorsi muscle of Nellore cattle from 10 farms in 5 Brazilian states that currently are selecting for meat tenderness traits in their breeding programs including analysis shear force (SF), rib eye area (REA), fat thickness (FT), myofibrillar fragmentation index (MFI) and total lipids (TL). The results of the analysis in this study show verified average and standard deviation for each analysis and the correlation of this with the value of shear force. It is the average value and standard deviation of 4.3 ± 1.25 for SF analysis, which confirms the tenderness of the meat in question since it did not exceed the limit accepted for the meat to be considered tender, ie, 4.5 kg [2]. The MFI value found was heavily influenced by postmortem, where the meat showed satisfactory average 63.19 ± 16.26 denoting high tenderness of the analyzed meat, as Culler et al. (1978) [3] values above 60 to qualify as tender flesh. It has been shown a significant correlation ($P < 0.01$) between SF and MFI, as these characteristics are inversely proportional. It has also been found significant correlations ($P < 0.05$) for the analysis of REA (65.49 ± 7.98) and TL (0.76 ± 0.36). For FT (5.26 ± 3.2) there was not a significant correlation ($P < 0.05$) with SF. Therefore, the use of physical and chemical analysis and correlations with shear force, can be used as a tool in verifying the quality of beef, mainly for Nellore (*Bos indicus*), showing a herd with a deficit for such.

Key Words: meat tenderness, myofibrillar fragmentation index, shear force

W180 Bioanalytical methods for calcium proteomic study on tenderness Longissimus muscle of Nellore cattle (*Bos indicus*). W. A. Baldassini[1], J. M. Malheiros*[2], L. A. L. Chardulo[2], J. A. V. Silva[2], L. G. Albuquerque[2], and P. M. Padilha[3], *[1]UNESP/FMVZ, Sao Paulo State University, Botucatu, Brazil, [2]UNESP/FCAV, Sao Paulo State University, Jaboticabal, Brazil, [3]SUNESP/IB, Sao Paulo State University, Botucatu, Brazil.*

The calpain system is a complex of proteases activated by calcium as the μ-calpain and m-calpain and its endogenous inhibitor, the calpastatin and are related to proteolysis and meat tenderness [1]. This study examines the separation of skeletal muscle proteins by 2D-PAGE and performing the identification of calcium ions in the protein spots by x-ray fluorescence (SR-XRF) for the 20 Nellore cattle (*Bos indicus*) contrasting meat tenderness: tough (TO) and tender (TE) meat animals. A third group (PI) with Piedmontese cattle (*Bos taurus*) was used as a comparative model of meat tenderness degree. The 3 groups were selected according by the rib eye area and backfat as well the shear force values [2]. The resolution of the gels (matching > 50%) and the image analysis between groups TO, TE and PI showed a correlation between gels of (n = 3) 82%, 54% and 53%, respectively. The average numbers of protein spots in repetitions gels were 176 ± 22, 172 ± 31 and 204 ± 33 for the groups TO, TE and PI, respectively. This standard deviation below 20% can be regarded as a good indication of the proteins fractionation by 2D-PAGE [3]. In the study images of the gels were estimated correlations between protein spots for the groups. The correlation between the spots of the protein was varied in the different groups TE and PI (R > 0.85) as well the gels of the TO and PI groups (R > 0.73). In the qualitative assessment of calcium ions by SR-XRF were randomly chosen 60 protein spots from the experimental groups, with molar weight (MW) between 20 and 97 kDa [4]. There was higher detection (56%) of calcium by SR-XRF in protein spots TE group, a factor that may be indicative of proteolytic activity in meat after slaughter. The 2D-PAGE in the evaluation study of the calpain system was effective in the fractionation of proteins present in Longissimus muscle. The correlations obtained in the 2D gels indicated that the procedures for extraction of total protein were

efficient and preserved the metal-protein structure. However, it was possible to make a detection of calcium in protein spots by SR-XRF with MW between 20 and 97 kDa.

Key Words: calpain system, 2D-PAGE, shear force

W181 The effects of selecting for the myostatin F94L polymorphism on reproductive traits in pubertal heifers. E. D. Forbes*[1], O. L. Swanson[2], A. K. McNeel[3], R. G. Tait Jr.[3], T. P. L. Smith[3], G. L. Bennett[3], T. A. Hoagland[1], S. A. Zinn[1], C. A. Lents[3], G. A. Perry[2], and R. A. Cushman[3], *[1]University of Connecticut, Storrs, [2]South Dakota State University, Brookings, [3]US Meat Animal Research Center, Clay Center, NE.*

The myostatin F94L polymorphism influences carcass traits in steers; however, the influence of this polymorphism on female reproductive performance should be characterized as part of using it for marker assisted selection. Results from USMARC indicate that heifers that are homozygous for the L allele (L) reach puberty later than heifers that are homozygous for the F allele (F, wild-type), but no one has investigated the influence of this polymorphism on reproductive function in pubertal heifers. We hypothesized that reproductive function would be decreased in heifers that were L. Homozygous heifers that were pubertal (n = 5/genotype) were synchronized with 2 shots of PFG2a given 11 d apart and observed every 4 h for behavioral estrus with the aid of estrus detection patches. Heifers were slaughtered on d 4 after estrus, and the uterus, ovaries, and anterior pituitary were collected, measured, and weighed. A representative piece of one ovary was fixed for histological evaluation, and a sample of subcutaneous adipose was collected and frozen to measure relative levels of chemerin mRNA, a marker of adiposity. Follicular fluid was aspirated from all small follicles (1–5 mm), pooled within heifer, and frozen. Data were analyzed using a MIXED model with genotype as a fixed effect. Heifers that were F had lighter birth weights than heifers that were L ($P = 0.04$), but there was no difference in weaning weight, slaughter weight, or chemerin mRNA levels in the adipose. Heifers that were L exhibited behavioral estrus 14 h sooner after PGF2a than heifers that were F ($P = 0.06$). There was no difference in reproductive organ measurements or numbers of follicles in the ovaries between genotypes. Follicular fluid estradiol concentrations tended to be greater in L heifers than F heifers ($P = 0.10$). Reproductive tract development is not altered in heifers homozygous for the L allele, although they reach puberty later. A shorter time from PGF2a to estrus indicates that timing of insemination in timed-AI protocols may need to be altered for L heifers. USDA is an equal opportunity provider and employer.

Key Words: heifer, myostatin, puberty

W182 Epidemiology of synchronization programs for breeding management in US dairy herds. A. H. Souza*[1,2], P. A. Carvalho[1], R. D. Shaver[1], M. C. Wiltbank[1], and V. Cabrera[1], *[1]Department of Dairy Science, University of Wisconsin, Madison, [2]Ceva Sante Animale, Libourne, France.*

The aim of this study was to evaluate the use of synchronization programs in US dairy herds. Reproductive records from DHIA (AGSource, Agritech, and DRMS) were analyzed. The final data set included artificial insemination records from 2008 to 2012 and restricted to AI-breedings with confirmed pregnancy outcome. Only herds reporting at least 30 breedings in the last 12 mo were included. A total of 1,142,821 breeding records from 40 states were available for the 1st analysis. Breeding codes were classified within herd into either AI-to-estrus (EAI) or synchronized-AI (SAI) based on weekly insemination profile for each herd. Within-herd, synchronized breedings were assumed when more than 30% of the breedings happened on the same day of the week, remaining breedings for the same herd were considered non-synchronized. Overall, 29.9% of the breedings happened after the use of synchronization programs, with great variation throughout states. The leading states in terms of proportion of SAI that reported more than 5,000 breedings were SD = 56%, WI = 46%, IA = 43%, OH = 40%, MI = 32%, NY = 29%, PA = 27%, MN = 24%, VA = 23%, and SC = 23%. Out of all SAI breedings, 78% happened on Thursdays and Fridays. There were no significant differences in conception results between SAI (32.6%) and EAI (33.4%), with no interactions with breeding month. Herd size information was available for a further data set from WI herds with 207,506 breedings. Findings in regards to herd size and use of SAI at 1st AI in herds in WI are shown in Table 1, which indicates that SAI is used in most 1st postpartum AIs and larger herds seem to use more SAI at 1st AI and have lower days to 1st AI without compromising conception outcomes. In summary, these results indicate that most dairy herds in US use synchronization strategically as part of their breeding program. Supported by Accelerated Genetics.

Table 1.

Herd size	ME305 (kg)	SAI – 1st AI (%)	DIM at 1st AI (d)	P/AI at 1st AI (%)
<300 (n = 54,199 AI)	13,104[a]	47.4[a]	80.2[a]	36.5[a]
300-1000 (n = 89,336 AI)	14,082[b]	66.4[b]	76.0[ab]	35.5[a]
>1000 (n = 63,971 AI)	14,527[c]	75.3[c]	72.0[b]	35.1[a]

Key Words: dairy farm, timed AI, synchronization

W183 Effects of different stall type and bedding materials on lactation length, milk yield and some health problems in dairy herds. N. K. Kara*[1], A. Galiç[2], and M. Koyuncu[1], *[1]Uludag University, Bursa, Turkey, [2]Akdeniz University, Antalya, Turkey.*

This study was carried out to determine effects of 2 different stall types and 3 different bedding materials on lactation length, milk yield and some health problems in dairy herds. 477 lactation cows in 37 herds in Bursa were examined. Mean of lactation length (day) and milk yield of cows in the same herd was calculated to determine the effects. A *t*-test was used to compare the means of free-stall or tie-stall herds, and one-way ANOVA was used to compare the means of herds with concrete, sand or rubber bedding. To test the association between stall type or bedding material and some health problems, Chi-squared test was used. According to the results, a significant difference was determined between 2 stall types, in terms of milk yield ($P < 0.01$), while mean of milk yield and lactation length of herds with rubber bedding were found higher than the others ($P < 0.01$). The associations between stall type and repeat breeding, dystocia and retained placenta were found to be significant ($P < 0.01$, $P < 0.01$ and $P < 0.05$, respectively). Also, it was found that repeat breeding and clinical mastitis were associated with bedding material ($P < 0.05$ and $P < 0.01$, respectively). The results of the present study indicate that by providing suitable stall type with better bedding materials, animals can be kept healthy, expenditures on medical treatments can be minimized and consequently profitability can be increased.

Key Words: bedding material, stall type, lactation length

W184 Genetic and phenotypic trends for milk yield in Holstein populations in Mexico. H. O. Toledo[1], F. J. Ruiz[2], C. G. Vazquez[1], J. M. Berruecos[1], and M. A. Elzo*[3], *[1]Universidad Nacional Autonoma de Mexico, Ciudad de Mexico, DF, Mexico, [2]INIFAP, Queretaro, Queretaro, Mexico, [3]University of Florida, Gainesville.*

The objectives were to evaluate genetic and phenotypic trends from 2007 to 2011 for milk yield in 3 Holstein populations representing 14% of the milk production in Mexico. Data consisted of first-lactation milk yields adjusted to 305 d, adult equivalent and 2 milkings/d. Records were from the Holstein Association of Mexico (HAM; n = 43,668), the National Bank of Dairy Information (NBDI; n = 120,217), and the National Breeding Program of Mexico (NBPM; n = 163,885) which included records from HAM and NBDI. Best Linear Unbiased Predictions of breeding values (BV) were computed with ASREML using a mixed animal model. Fixed effects were herd-year-season. Random effects were animal and residual. Weighted and unweighted yearly means of sire BV were computed for HAM, NBDI, and NBPM. Weights were numbers of daughters per sire per year. Weighted yearly means of sire BV in NBPM were also computed by country of origin (USA, Canada, México, Other). Lastly, yearly means of cow BV and phenotypic values (PV) were obtained for HAM, NBDI, and NBPM. The mean BV and PV of cows for milk yield in the HAM, NBDI, and NBPM populations increased between 2007 (BV = 108.4 ± 5.7 kg; PV = 217.3 ± 25.4 kg) and 2011 (BV = 242.9 ± 3.3 kg; PV = 486.3 ± 14.0 kg). Differences between yearly means indicated that cow BV from HAM tended to be higher than cow BV from NBDI (from 32.2 kg in 2009 to 47.2 kg in 2010). Holstein sires from the US tended to have substantially higher yearly mean BV for milk yield (from 722.4 kg in 2008 to 991.3 kg in 2010) than Holstein sires from Mexico. Breeders from HAM tended to choose sires with higher BV for milk yield (401.9 ± 15.1 kg) than those from NBDI (396.5 ± 11.0 kg). However, differences in weighted yearly means (from 221.9 kg in 2008 to 101.8 kg in 2010) suggested that NBDI breeders used sires with higher BV for milk yield more frequently than HAM breeders. Greater utilization of sires with increasingly higher BV for milk yield allowed dairy breeders in Mexico to consistently increase cow genetic and phenotypic means from 2007 to 2011.

Key Words: genetic trend, phenotypic trend, milk yield

W185 Genetic parameter estimates for rump traits and teat length in a multibreed dairy cattle population in Thailand. B. Wongprom[1], S. Koonawootrittriron[1], M. A. Elzo*[2], and T. Suwanasopee[1],

[1]*Kasetsart University, Bangkok, Thailand,* [2]*University of Florida, Gainesville.*

Hip width (HW, cm), pin width (PW, cm), hip to pin length (HP, cm), hip height (HH, cm) and teat length (TL, cm) of cows are important for reproduction and production efficiency of a dairy business. Most dairy cattle in Thailand and other Asian tropical countries are multibreed where Holstein is a major component breed (mean = 87%; SD = 9%) and both purebred and crossbred animals are regularly selected as parents of the next generation. The objective of this study was to estimate genetic parameters for rump traits (HW, PW, HP and HH) and TL of dairy cattle in a multibreed dairy population in Thailand. The data set consisted of pedigree and phenotypic information for HW, PW, HP, HH, and TL from 868 cows located in 122 farms across Thailand. The data were analyzed using a multiple-trait animal model that accounted for the fixed effects of herd, Holstein fraction, and age of cow, and the random effects of animal and residual. An average information-restricted maximum likelihood procedure was used to estimate variance components. Estimates of variance components were subsequently used to compute heritabilities and genetic correlations. Means and SD were 55.13 cm and 4.91 cm for HW, 18.49 cm and 2.40 cm for PW, 51.74 cm and 3.27 cm for HP, 134.07 cm and 5.52 cm for HH, and 5.07 cm and 1.43 cm for TL. Heritability estimates were high for HW (0.42 ± 0.10), medium for PW (0.23 ± 0.09) and HP (0.25 ± 0.10), and low for HH (0.11 ± 0.08) and TL (0.12 ± 0.09). Most genetic correlations ranged from medium (0.35 ± 0.28 between HP and PW) to high (0.91 ± 0.45 between PW and HH). The only low correlations were between TL and PW (0.14 ± 0.39) and between TL and HH (0.19 ± 0.54). These estimates of heritability and genetic correlations indicated that it would be feasible to develop a genetic improvement program for rump traits and teat length in this multibreed population.

Key Words: dairy, genetic parameter, type trait

W186 Genotype by environment interaction effect on lactation pattern and milk production traits in an Ethiopian dairy cattle population. G. Gebreyohannes[1], S. Koonawootrittriron[1], M. A. Elzo*[2], and T. Suwanasopee[1], [1]*Kasetsart University, Bangkok, Thailand,* [2]*University of Florida, Gainesville.*

The objective of this study was to evaluate the effect of genotype by environment interaction (GEI) on lactation pattern and milk production traits in an Ethiopian multibreed dairy cattle population. The analyses used 4,488 lactation milk records of 1,320 cows born from 254 sires and 896 dams collected in 2 research centers (Bako and Holetta) from 1979 to 2010. Breeds present in the population were Horro, Boran, Friesian, Simmental and Jersey. Traits were lactation milk yield (LY), initial milk yield (IY), peak milk yield (PY), average milk yield per day (YD), lactation length (LL) and days to peak (DP). The effect of GEI was tested using a fixed linear model that considered herd-year-season, parity, environment (Bako and Holetta), breed and the interaction between breed and environment as fixed effects, and residual as a random effect. Lactation length was considered as a covariate for the analysis of LY. Least squares means (LSM) were compared among subclasses of each factor. All factors in the model affected LY, IY, PY, YD and LL ($P < 0001$). The effects of breed and breed by environment interaction on DP were not significant. All traits had significantly ($P < 0001$) higher LSM values in Holetta than Bako. Friesian crossbred cows in Holetta had significantly higher LSM for LY (2111.9 ± 16.87 kg), IY (9.2 ± 0.08 kg), PY (11.6 ± 0.08 kg) and YD (6.6 ± 0.05 kg) than Simmental and Jersey crosses. The LSM for LY, PY and YD were significantly ($P < 0.0001$) higher for Friesian and Simmental than for Jersey crossbreds in Bako. However, the LSM IY and LL were not significantly ($P > 0.05$) different among Friesian, Simmental and Jersey crossbred cows. The LSM of LY, IY, PY, YD and LL for Boran and Horro were not different in both environments. In Holetta, the Jersey and Simmental were not significantly different for the LY, IY, PY and YD. Thus, Friesian sires can be recommended for crossbreeding with Boran or Horro in Holetta, and Friesian, Simmental and Jersey sires in Bako.

Key Words: dairy cattle, genotype by environment interaction, multibreed

W187 Impact of sire by region interaction on first-lactation traits of dairy cows raised under tropical conditions in Thailand. P. Yodklaew[1], S. Koonawootrittriron[1], M. A. Elzo*[2], and T. Suwanasopee[1], [1]*Kasetsart University, Bangkok, Thailand,* [2]*University of Florida, Gainesville.*

Initial yield (IY), peak yield (PY), days to peak yield (DP) and persistency (PS) are traits associated with milk yield (MY) in dairy cattle. Daughters of the same sire could have different lactation curve traits (IY, PY, DP, and PS) and MY in different regions. Thus, the objective of this study was to investigate the effect of sire-by-region interaction on first-lactation traits in 3 regions of Thailand. The data set contained 27,276 monthly test-day records from 2,431 first-lactation cows raised in 294 farms located in Central, Northeastern and Southern Thailand. Wood's gamma function was used to estimate IY, PY, DP, PS, and MY for individual cows using their monthly test-day records. A fixed linear model was used to avoid sire-by-region interactions due to unequal numbers of daughters per region. The fixed linear model included herd-year-season, calving age, Holstein fraction, and interaction between sire and region as fixed effects, and residual as a random effect. Sires were ranked in each region using their least squares means and correlations between sire rankings across regions were computed. Herd-year-season affected ($P < 0.001$) all lactation traits and calving age only influenced PY ($P = 0.02$). Holstein fraction had no effect on any trait and sire-by-region interaction had an effect only on PY and MY ($P < 0.001$). Correlations between sire rankings in the Central and Northeastern regions, Central and Southern regions, and Northeastern and Southern regions were low or close to zero for PY (−0.01 to 0.05) and MY (0.03 to 0.29). These results suggested that sires would affect their daughter's first-lactation PY and MY differently if they were located in different regions of Thailand. Thus, sires would need to be selected based on their genetic superiority in each region to optimize genetic improvement for milk production in this Thai population.

Key Words: dairy cattle, interaction, tropical

W188 Optimal age at first calving for US dairy cattle. J. B. Cole, J. L. Hutchison*, D. M. Bickhart, and D. J. Null, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

Heifer rearing is a major expense for the US dairy industry that accounts for 15 to 20% of the total cost of producing milk. Selecting for an optimal age at first calving (AFC) in US dairy cattle could reduce these costs while still providing animals with high lifetime yields. Records from 9,502,802 Holstein (HO), 611,939 Jersey (JE), and 46,580 Brown Swiss (BS) cows with first calvings from January 1, 1997 to present were selected for analysis. A linear model included the fixed effects of herd-year of calving, year-state-month of calving, and AFC, grouped into 50-d intervals. The traits analyzed included, milk yield, composition, and persistency; fertility; and longevity. Contrary to current age adjustment factors, the highest first-lactation milk yield occurred at an AFC between 651 to 700 d (21 to 23 mo) for HO, resulting in an increase in milk production of 58 kg compared with animals with an AFC between 701 to 750 d (23 to 25 mo). Similarly, fat, protein, and persistency of milk in HO showed an increase of 1.86 kg, 2.08 kg, and 0.05, respectively, for the same AFC

interval. For JE, the highest yields occurred at 601 to 650 d (20 to 21 mo), with increases of 129 kg, 5.18 kg, 4.45 kg, and 0.12 for milk, fat, protein, and persistency of milk, respectively. The greatest yields for BS occurred between 701 to 750 d, although they did not differ from the yields of the 651 to 700 d or 751 to 800 d groups. Heifers from all breeds calving between 601 to 750 d showed an increase in heifer and cow conception rates compared with those calving later. Lifetime traits (up to 5 parities) showed the same optimal HO AFC, with differences between 651 to 700 d and 701 to 750 d of +589 kg, +21.14 kg, +18.23 kg, +11 d, and +0.90 d for milk, fat, protein, days in milk, and days open. For JE, differences between 601 to 650 d and 701 to 750 d were +1397 kg, +64.21 kg, +50.03 kg, +33 d, and +0.72 d, respectively. These results show that the optimal AFC is actually 75 to 130 d less than the breed averages published in 2010, suggesting that a reduction in AFC may improve profitability and fertility in HO and JE cattle.

Key Words: age at first calving, milk production, fertility

W189 Evaluation of genetic advance of production traits in Shenxing dairy farm from 2002 to 2012. G. Yao[1], H. Liming[2], L. Guanglei*[1,2], Z. Changbin[1], and F. Fengshou[1], *[1]Shanghai Dairy Breeding Center Co., Ltd., Shanghai, China, [2]State Key Laboratory of Dairy Biotechnology, Shanghai Bright Holstan Co., Ltd., Shanghai, China.*

Genetic trends of milk, fat and protein yield (305 d, 1st lactation) from the Shenxing dairy farm in Shanghai were evaluated for genetic trend by best linear unbiased prediction. Original data consisted of 13,548 production records between 2002 and 2012 were obtained from Dairy Herd Improvement (DHI) project of Shanghai Dairy Breeding Center. Generation interval from sire to daughter was 6.48 years and from dam to daughter was 5.84 years, with an average of 6.16 years. Heritability of milk, fat and protein yield was calculated by half-sister correlation analysis. Heritability estimates were 0.27, 0.16 and 0.14 for milk, fat, and protein yield. Average genetic trend for milk yield was about 71 kg per year over 11 years, an increase about 0.84% per year (60 to 67 kg per year in the first 6 years, about 0.71 to 0.79% of average genetic progress; about 70 to 86 kg in the later 5 years, approximately 0.82% to 1.01% of average genetic change). Average genetic advance of fat and protein yield were about 2.1 kg and 1.1 kg per year, the average genetic progress were about 0.45% to 0.82% in fat yield and 0.37% to 0.56% in protein yield. Our results showed that the genetic level of yield traits in Shanghai Holstein herd have increased in the past 11 years, and that meant the improvement project of Shanghai Holstein herd is effective.

Key Words: genetic advance, generation interval, heritability

W190 Genetic parameters for test-day milk, fat, protein and mozzarella yield using random regression models in buffaloes. N. Hurtado-Lugo*[1,2], R. Aspilcuelta[1], G. M.F. de Camargo[1], M. Cerón[2], and H. Tonhati[1], *[1]State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, São Paulo, Brazil, [2]University of Antioquia, Medellín, Antioquia, Colombia.*

Buffalo milk is used mainly for the production of milk derivatives due to the compositional and physicochemical quality of its components. Random regression models (RRM) can be applied to test-day milk yield as an alternative to standard procedures used for the genetic evaluation of longitudinal traits in dairy cattle. We aim was to estimate covariance functions for additive genetic and permanent environmental effects and, subsequently, genetic parameters for milk (MY), fat (FY) protein (PY) yields and mozzarella cheese production(MP) in buffaloes from Colombia using RRM with orthogonal Legendre polynomials (LP). Data of test-day MY, FY, PY and MP of 1884 first lactation buffaloes were analyzed. They were daughters of 228 sires from 14 herds in Colombia with calving between 1995 and 2011. For test-day, 10 mo classes of lactation days were considered. Herd-year test day was used as a contemporary group. The random effects in the model included: additive genetic effect, permanent environment and residual and the fixed effects of contemporary group, buffalo age at calving (linear and quadratic effect) and mean lactation curve of the population modeled by LP of 3rd order. The residual variances were modeled with homogeneous structures and many heterogeneous classes. The variance components were estimated using the statistical package WOMBAT. According to the REML test, the best model for MY was with 4 classes of residual variances, considering LP of 3rd and 5th order for additive genetic and permanent environment effects respectively. For FY, PY and MP, the best model was with 4 classes of residual variances, considering LP of 3rd and 4th order for additive genetic and permanent environment effect respectively. The heritability estimates for MY, FY, PY and MP varied from 0.38 to 0.05, from 0.67 to 0.11, from 0.50 to 0.07 and from 0.50 to 0.11, respectively. In general, the RRM were adequate do describe the genetic variation in test-day of MY, FY, PY and MP in Colombian buffaloes.

Key Words: animal model, heritability, mozzarella

W191 Rate of genetic progress and breeding values in commercial dairy herds using young versus daughter proven sires. C. D. Dechow*[1] and G. W. Rogers[2], *[1]Penn State University, University Park, [2]Geno Global Ltd., Hamar, Norway.*

The objective of this study was to evaluate the rate of genetic progress and breeding values (BV) of cows in commercial dairy herds using young sires (YS) with genomic BV versus daughter proven sires (PS). Genotypes were simulated at 1000 loci for a nucleus herd of 1000 animals (500 bulls and 500 cows) born each year and a commercial herd with 500 cows born annually. Allele effects were −1 or 1 for all loci and accuracy was 100% for initial scenarios as BV was obtained by summing allele effects across loci. Young bulls and cows were selected beginning at 2 years of age and ending at 3, versus a range of 6 to 7 years for PS. Young sires and dams from the top 10% of BV were selected for the nucleus herd. Sires for commercial cows were selected from the top 10%, 25%, or 100% of the nucleus population. Thirty years of selection were simulated and results among scenarios were compared for years 11 to 30. The average generation interval for the nucleus herd was 2.22 years and the actual genetic progress of 0.75 additive genetic standard deviations per year was close to expectations from the genetic progress formula (0.79). The rate of genetic progress in commercial herds (0.73 to 0.77) was nearly identical to progress in the nucleus herd regardless of whether YS or PS were selected. The BV of cows in PS scenarios lagged behind cows in YS scenarios by 4 years when selection intensity was identical between YS and PS, which was equivalent to the difference in generation interval. The lag was reduced to 1.5 years when the top 10% of PS were selected versus the top 100% of YS. Scenarios were considered where accuracy was reduced by adding a random noise term to the BV before making selection decisions. Higher accuracy for PS further reduced the lag between YS and PS scenarios. It was concluded that the rate of genetic progress in commercial herds may not differ for YS versus PS selection strategies, but that average BV at a specific point in time will vary depending on differences in generation interval, selection intensity, and accuracy. Genetic progress predictions may need to consider interdependencies among selection pathways.

Key Words: genomic, genetic progress

W192 Evaluation of sources of variation and estimation of productive parameters using multi-trait animal models in dairy buffaloes in Pakistan. S. M. Suhail*[1,2], M. S. Qureshi[2], I. Ahmed[2], H. Akbar[1], M. J. Khan[1], and J. J. Loor[1], *[1]University of Illinois, Urbana, [2]KPK Agricultural University, Peshawar, Pakistan.*

Buffalo is the major source of milk production in Asia. Production performance of buffaloes raised at 3 state farms of Pakistan was studied using complete milk records from 5,026 lactations. Economic traits including lactation yield (LY), standard 305-d yield (SY), peak daily milk yield (PY), average daily milk yield (DY) and lactation length (LL) were studied. A general linear model (GLM) procedure was used to study the effect of herd, year, season of calving and sire nested into herd, parity and age at puberty × season of calving on production traits. Birth weight, square of birth weight, lactation length, calving interval, age at puberty and age at first calving were used as covariates. Average LY was 2,076 ± 4.94 (1,524 to 3,723 kg) while SY was 2,200 ± 5.93 kg (1,540 to 3,852 kg). PY and DY averaged 9.9 ± 0.05 and 7.1 ± 0.02, respectively. Mean LL was 294 ± 0.49 (181 to 435 d). Herd, sire nested into herd and parity had a significant effect on lactation yield, while the effects of year, season of calving, year × season and age at puberty × season were nonsignificant. Among covariates, birth weight and lactation length had a significant effect on lactation yield. Similarly, standard 305-d milk yield was significantly affected by sire within herd and parity. Among covariates birth weight, square of birth weight, lactation length and calving interval affected the SY. Year and season of calving and their interaction affected PY. Among covariates the length of lactation affected the PY. Herd, sire within herd and parity significantly affected DY. Among covariates, birth weight, square of birth weight and lactation length affected the DY. Lactation length was affected by herd, sire nested into herd and parity. Standard 305 d milk yield was affected positively by birth weight while increasing parity increased milk yield up to third parity. It is concluded that the milk production ability of dairy buffaloes improves by increasing the birth weight and maturity, while keeping the calving interval shorter and the parity up to third lactation.

Key Words: lactation, animal model, dairy buffalo

W193 Development of a Monte Carlo simulation model to quantify genetic progress from an emerging in vitro fertilized embryo transfer dairy reproduction system. K. Kaniyamattam*, J. Schneider, and A. De Vries, *University of Florida, Gainesville.*

Objective of this study was to develop a Markov chain Monte Carlo simulation model to quantify genetic progress from an emerging in vitro fertilized (IVF) embryo transfer dairy reproduction system. The hypothesis is that IVF coupled with genomic testing of calves will rapidly accelerate the genetic gain from the female side. The model simulated individual dairy young stock and cows day by day for 20 years into the future. Individual animal performance was modeled using functions for feed intake, milk production, reproduction, body weight, risk of culling and genetic merit. The model was parameterized to represent an average US Holstein dairy herd. Phenotypic milk production was dependent on genetic merit. All heifer calves born were assumed to be genomically tested and ranked based on a Net Merit index, drawn from a normal distribution. A fixed cow herd size was assumed. The extra heifer calves were sold and the bull calves were sold within 2 weeks after birth. The top 5% of heifers from 10 mo of age to 5 mo of pregnancy were used as oocyte donors. The donor list was updated each month. Oocytes were collected from each donor 4 times per month. The collected oocytes were in vitro fertilized. On average there were 5 transferable embryos per collection. All open eligible heifers and cows were observed for estrus 3 d after giving prostaglandin. It was assumed that only 66% of eligible animals came into estrus. The recipients were randomly chosen. The recipients on d 6, 7, 8 of the estrus cycle were transferred with a d 7 embryo. Surplus embryos were frozen if there were not enough recipients available and AI was used if there were not enough embryos (fresh or frozen) available. The model was developed in JAVA. Preliminary results showed an increase in Net Merit of $30 per year based on selection on the female side. The model will be further used for evaluations and sensitivity analyses of management factors that affect genetic progress and profitability of this reproduction system such as genomic testing strategy and selection of recipients.

Key Words: in vitro fertilization, embryo transfer, genetic gain

W194 Heritability estimates of performance and health traits of Holstein calves. M. Mousa*[1,2], A. Seykora[2], H. Chester-Jones[3], D. Ziegler[3], and J. Cole[4], *[1]Department of Animal Production, Faculty of Agriculture, Assiut University, Assiut, Egypt, [2]Department of Animal Science, University of Minnesota, Saint Paul, [3]University of Minnesota, SORC, Waseca, [4]Animal Improvement Programs Laboratory, ARS-USDA, Beltsville, MD.*

The objective of this study was to estimate heritabilities of performance and health traits of Holstein calves. These traits were available on 6,390 AI sire-identified Holstein heifer calves reared at University of Minnesota, SROC facility. Calves were picked-up at 2 - 4 d old from 3 Minnesota commercial dairy farms during the period April 2003 to May 2012. Calves were removed from the data set if they were in sire progeny groups of less than 2, leaving 6,189 observations for analyses. Performance traits were BW (W56) and hip height (HH56) at 56d of age, BW (LBW) and hip height (LHH) at approximately 200d of age, daily gains in the nursery from arrival to weaning at 56d of age (WADG) and from arrival to 200d of age (LADG). Health traits were coded relative to number of incidences that required treatment during the first 56d of age (0, 1, 2 treatment incidences). The Proc MIXED procedure of SAS 9.1 was used to estimate variance components with sire fitted as a random variable. Significant fixed effects ($P < 0.01$) in the model were year of birth, month of birth, year of birth × month of birth, arrival BW and serum protein level fit as a covariate. Performance traits were moderately heritable, with estimates ranging from 0.25 to 0.37. Health traits had low heritabilities, ranging from 0.01 to 0.06. Results suggest that calf performance and health can be improved genetically.

Table 1. Performance and health traits

Performance trait	Average	SD	Sire variance	Residual	Heritability
W56 (kg)	74	9.38	2.5447	35.9814	0.26
HH56 (cm)	90	3.29	0.3357	5.128	0.25
LBW (kg)	206	21.90	29.9901	285.46	0.37
LHH (cm)	114	3.66	0.8692	8.9867	0.35
WADG (kg/d)	0.62	0.13	0.0008	0.0115	0.26
LADG (kg/d)	0.86	0.09	0.0004	0.0056	0.29

	Incidence occurrence (%)					
Health trait	0	1	2	Sire variance	Residual	Heritability
Scours	49.78	50.05	0.17	0.0034	0.2417	0.06
Respiratory	99.48	0.51	0.01	0.0005	0.0485	0.04
Navel	99.57	0.38	0.05	0.0002	0.0592	0.01

Key Words: heritability estimate, performance and health traits, Holstein calf

Breeding and Genetics: Applications and Methods in Animal Breeding—Pigs, Poultry, Sheep, and Horses

W195 Genetic analysis of the stayability for running of Thoroughbred horses. J. A. V. Silva*, L. H. Kato, A. M. Maiorano, R. A. Curi, and M. D. S. Mota, *Faculdade de Medicina Veterinaria e Zootecnia, UNESP, Botucatu, Sao Paulo, Brasil.*

Stayability is an economically relevant trait; it is directly associated with profitability of the production system by its relationship to specific costs or with efficiency. In this work, stayability is analyzed in racehorses and defined as stayability for running up to 4 years old (STAY4) and up to 6 years old (STAY6). Inclusion of this trait in genetic evaluation programs may permit selection of stallions that will have offspring with a greater probability of remaining productive (running) for a longer period of time. The objectives of the current study were to assess the feasibility of using stayability for running traits to improve the genetic potential of Thoroughbred horses and to examine the genetic relationship between STAY4 and STAY6. Stayability was considered to be a categorical trait and defined as whether a horse (male or female) that remained running up to the age of 4 (STAY4) and 6 (STAY6) yr of age, given that the opportunity to participate in races was provided. Data was gathered for 23,009 and 20,005 animals for STAY4 and STAY6, respectively, born from 1989 onward with performances between 1992 and 2010 analyzed using 2 trait animal threshold model based on Gibbs sampling algorithm. The matrix relationship included 35,422 animals until 6th generation. 60% and 17% were scored 1 for STAY4 and STAY6, respectively. Animals with stayability for running until evaluated ages were scored as 1, and those that failed were scored as 0. Analysis included fixed effects of breeder, breeding season, age at first competition and the linear covariate, the number of races to ages studied, in addition to the random animal effect. The sex and race distance effects were not include in the model because these were not significant. Heritability estimates for STAY4 and STAY6 were 0.12 ± 0.03 and 0.13 ± 0.03, respectively. The genetic and residual correlation estimates between the 2 traits were 0.48 ± 0.18 and 0.92 ± 0.03, respectively. Based on the results of this study, STAY can be used for selection of stallions for horse racing. Competition data provide a good tool for measuring the stayability for running in horses.

Key Words: heritability, genetic correlation, residual correlation

W196 Population parameters in Quarter Horses in Brazil. M. D. S. Mota, R. A. Curi, G. L. Pereira, A. C. Verdugo, and J. A. V. Silva*, *Faculdade de Medicina Veterinaria e Zootecnia, UNESP, Botucatu, Sao Paulo, Brasil.*

The Quarter Horse was first bred in Brazil from horses imported from the King Ranch in Texas, United States. Since the founding of the Brazilian Association of Quarter Horse Breeders (ABQM) in 1969, there have been approximately 360,000 animals and just over 61,000 breeders, owners and associated in ABQM. In 2012, breeders conducted auctions involving 5,372 horses at an average price of US$15,000. The objective of this study was to estimate population parameters of Quarter Horses registered by ABQM. We considered 122,355 animals born from 1950 to 2009. Of this total, 5,397 (4.41%) were inbred, with an average inbreeding coefficient of 8.56% and a maximum of 37.5%. To study the probability of origin of genes, we established a reference population of 56,329 animals born between 1980 and 2009. The number of founders (animals with unknown ancestors in the pedigree) was 5,479, while the effective number of founders reached 669.5. The difference between these 2 values indicates that not all horses' founders contributed equivalently to the population. The evaluation of the effective number of ancestors indicates that the 100 main breed males account for 30.13% of the genetic diversity of the population reference, while the top 10 account for approximately 7.5%.

Key Words: genetic diversity, inbreeding, pedigree

W197 Understanding the impact of frozen semen on swine production systems. D. Gonzalez-Pena*, N. V.L. Serão, R. Knox, and S. L. Rodriguez-Zas, *University of Illinois at Urbana-Champaign, Urbana.*

Frozen-thawed (FRO) boar semen preparation can intensify the dissemination of top genetics, reduce animal maintenance costs, enable genetics banking, and facilitate biosecurity compared with fresh-refrigerated (FRE) preparation. However, the freezing process can result in lower farrowing rate and litter size. The goal of this study was to compare the effect of FRO and FRE preparations on genetic improvement and profit. For a 3-tier system, average daily gain (ADG) was the trait studied. The cross of 2 nucleus breeds A and B (500 sows/breed) generated 200,000 AB sows at the multiplier level. The AB sows were mated to breed C boars (originated from 500 breed C nucleus sows) at the commercial level resulting in 4,500,000 weaned pigs/year. To understand the effect of preparation on genetics and profit, the simulation assumed 2.1 semen doses/estrus, 2.25 farrowings/year, 50 collections/boar/year, 6 FRO time spans (one to 6 semesters), 4 farrowing rates levels (60–90%), 9 litter sizes classes (7–15 pigs alive/litter), and 7 boar:sow ratios for FRE (1:172–1:258) and FRO (1:77–1:115) based on 27 and 12 doses/ejaculate for FRE and FRO, respectively. Sow stayability ranged from 1 year (nucleus) to 3 years (commercial) and the involuntary culling was approximately 32%. The 378 simulated scenarios were evaluated in ZPLAN. The average genetic gain for ADG was 19.33g/semester. Line C had the highest ADG of all lines (34% above the mean) and contributed 61% of the total ADG return. Per semester, the profit increased $0.14 and $0.33 per 5% increase in farrowing rate for FRE and FRO semen, respectively. The net profit increased $0.37 and $0.38 per additional piglet in the litter for FRE and FRO, respectively. The use of FRO for 6 semesters resulted in 6% higher genetic gain than the use of FRE from a boar for 2 semesters. Optimal profit was attained when FRO was used for 4 relative to one semester (16.6% difference). The use of FRO in swine production units for 4 semesters at a boar:sow ratio of 1:115 is profitable and accelerates the genetic improvement relative to FRE.

Key Words: frozen semen, fresh semen, simulation

W198 Estimation of the additive and dominance Variances in South African Duroc pigs. D. Norris* and J. W. Ngambi, *University of Limpopo, Sovenga, South Africa.*

The objective of this study was to estimate dominance variance for number born alive (NBA), 21-d litter weight (LWT21) and interval between parities (FI) in South African Duroc pigs. A total of 10,703 NBA, 6883 LWT 21, and 6881 FI records were analyzed. Preliminary analysis showed low level of inbreeding and the elements of the dominance relationship matrix (D) were calculated using values of the additive relationship matrix, A. Bayesian analysis via Gibbs sampling was used to estimate variance components and genetic parameters. Estimates

of additive genetic variance were 0.554, 16.84, and 4.535 for NBA, FI, and LWT21, respectively. Corresponding estimates of dominance variance were 0.246, 9.572, and 0.661 respectively. Dominance effects were statistically not significant for all traits studied. Further research utilizing a larger data set is necessary to make concrete conclusions on the importance of dominance genetic effects for the traits studied.

Key Words: pig, additive, dominance

W199 Accounting for population structure when predicting litter size in commercial pig lines. L. Tusell*[1], S. Forni[2], P. Pérez[1], and D. Gianola[1], [1]*Dept. of Animal Sciences, University of Wisconsin, Madison,* [2]*Genus Plc, Hendersonville, TN.*

Two pig lines (A and B) showed clusters of individuals in plots of the 2 largest principal components extracted from genomic and pedigree-based relationship matrices. This hidden population structure may be due to family aggregation. We assessed whether predictive ability of yet to be observed litter size phenotypes using genome-enabled models would be larger within clusters than within random samples of the whole population. Data from the A and B lines represented 2,598 and 1,604 sows that were assigned into 3 and 2 clusters (i.e., subpopulations), respectively, by visual separation of points observed in the principal component plots of the genomic relationship matrix. The target variable was the average number of piglets born per sow, pre-corrected for systematic environmental effects. Genotypes were obtained using the Illumina PorcineSNP60 BeadChip. Within subpopulations, a 10-fold cross-validation assessed predictive ability of genomic BLUP (GBLUP), reproducing Kernel Hilbert spaces with kernel averaging (RKHS), and a radial basis function neural network (RBFNN). Random samples with the same subpopulation size were used as benchmark, i.e., without accounting for population structure. Predictive ability, measured as the correlation between predicted and observed phenotypes in the testing set (r), was very low in 2 subpopulations of the A line: with RBFNN (the model with the highest r in these subpopulations) r decreased −0.10 and −0.05 relative to their corresponding random samples using the same model. However, r (model with the highest r in each subpopulation shown in parentheses) was slightly better in all other subpopulations with an increase of +0.04 in the remaining A subpopulation, and +0.06 (GBLUP) and +0.04 (RKHS) in the 2 B subpopulations with relative to those observed in the corresponding random samples. This approach could be exploited to potentially increase overall accuracy in predictions within purebred lines.

Key Words: genomic prediction, population structure, pig

W200 Partitioning of within-litter birth weight variation and its distribution in piglets. T. J. Zindove*[1], E. F. Dzomba[1], A. T. Kanengoni[2], and M. Chimonyo[1], [1]*University of KwaZulu-Natal, Pietermaritzburg, KwaZulu-Natal, South Africa,* [2]*Agricultural Research Council, Pretoria, Gauteng, South Africa.*

Increasing within-litter birth weight variation in pigs affects litter performance. The objective of the study was to characterize within-litter birth weight variation in piglets. The study was conducted using 1 788 litters from 740 sow records collected between January 1998 and September 2010 from a Large White × Landrace pig herd in South Africa. The factors affecting within-litter birth weight coefficient of variation (CVBWT) were analyzed using the General Linear Model procedure (SAS, 2008). The number of piglets born alive (NBA) ranged from 3 to 18. The mean CVBWT was 17.64% and CVBWT ranged from 0.47 to 50.65%. The distribution of CVBWT in the herd was positively skewed. Year and month of farrowing did not affect CVBWT ($P > 0.05$). Multiparous sows farrowed litters with higher ($P < 0.05$) CVBWT than gilts. The litter weight (LWT) and NBA, fitted as covariates, also affected ($P < 0.05$) CVBWT. The correlation between CVBWT and NBA was 0.299. Estimated phenotypic correlation between mean birth weight (MBWT) and CVBWT was relatively strong (−0.309). The phenotypic correlation between LWT and CVBWT was low (0.058), but significantly different from zero ($P < 0.05$). To enhance profitability of pig enterprises, the selection for NBA should, therefore, be accompanied by selection for CVBWT.

Key Words: parity, litter weight, coefficient of variation

W201 Genetic analysis of longitudinal measurements of feed intake in Piétrain sire lines. M. Dufrasne*[1,2], V. Jaspart[3], J. Wavreille[4], and N. Gengler[1], [1]*Gembloux Agro-Bio Tech, University of Liege, Gembloux, Belgium,* [2]*FRIA, Brussels, Belgium,* [3]*Walloon Pig Breeding Association, Ciney, Belgium,* [4]*Walloon Agricultural Research Centre, Gembloux, Belgium.*

Feed efficiency (FE) is a very important trait in pig production because of the large part of feeding cost in production costs. Because FE involves feed intake (FI), it is useful to develop selection strategies that allow for a reduction of FI while keeping growth rate at least constant. The aim of this study was to estimate the genetic parameters for longitudinal measurements of feed intake (FI) in a crossbred population of pigs. An additional objective will be to develop a genetic evaluation model for the estimation of breeding values for FI of Piétrain boars. Data were collected on crossbred pigs in test station in the context of the genetic evaluation system of Piétrain boars in the Walloon Region of Belgium. Trait analyzed was the individual cumulated FI throughout the progeny-test. Because there were no facilities to record individual FI in the Walloon test station, individual FI were assumed to be averaged on the total pen FI. The edited data set consisted of 4,095 measurements of FI recorded on 2,127 crossbred pigs from 84 purebred Piétrain sires and 163 Landrace dams from the hyperprolific Landrace K+ line. A random regression animal model was used in this study to estimate variance components. Fixed effects were sex and batch. Random effects were additive genetic, permanent environment and residual. Random additive genetic and permanent environmental effects were modeled with quadratic Legendre polynomials. Estimated heritability for cumulated FI increased with age from 0.06 to 0.45 between 50 and 150 d of progeny-test. The average heritability over this period was 0.66. Estimated genetic correlations between adjacent ages were high and decreased when age interval increased. Negative genetic correlations were found between the very beginning and the very end of the testing period. Because heritability tended to increase with time, it seems that FI data at the end of the growing period is more informative. Moreover, a high FI at the beginning does not necessarily match a high FI at the end. Eventually, FI may be influenced by different genes during the growing period.

Key Words: feed intake, pig, random regression

W202 General and specific combining abilities for reproductive and growth performance of three color variants of Nigerian indigenous turkeys. M. A. Adeleke*[1], R. O. Ojo[1], S. O. Peters[2], and M. O. Ozoje[1], [1]*Department of Animal Breeding and Genetics, Federal University of Agriculture, PMB 2240, Abeokuta, Ogun State, Nigeria,* [2]*Department of Animal Science, Berry College, Mount Berry, GA.*

This study was designed to estimate combining abilities for some reproductive and growth traits of 3 color variants of Nigerian indigenous

turkeys. Two hundred and fifty poults consisting of 41 White × White (W×W), 40 Black × Black (B×B), 32 Lavender × Lavender (L×L) purebreds; 26 White × Black (W×B), 24 Black × White (B×W), 22 White × Lavender (W×L), 20 Lavender × White (L×W), 23 Black × Lavender (B×L) and 22 Lavender × Black (L×B) crossbreds were generated using artificial insemination. The poults were raised from day-old to 20 wk of age. A 3 × 3 diallel design was set up to estimate general combining ability (GCA) and specific combining ability (SCA) for reproductive traits (fertility, hatchability, weak-in-shell, dead-in-shell, dead-in-germ) and growth parameters (body weight, breast girth, body length and thigh length) according to Hayman (1954) using Genstat (1996) and Dial 98 package. The highest GCA for fertility (4.44) and weak-in-shell (WIS) (0.32) were observed in B×B. The highest GCA for hatchability (5.39) and dead-in-germ (0.64) were recorded in L×L while W×W had the highest GCA for dead-in-shell (2.60). SCA for fertility was the highest in W×B (0.07). W×L had highest SCA (3.28) for hatchability. The highest GCA for body weight at week 20 was recorded for W×W (90.83). The highest SCA for body weight at wk 20 was 0.62 for W×L. B×B had highest GCA values for breast girth, body length and thigh length at wk 20 (1.46, 0.46 and 0.41 respectively). B×W had the highest SCA (0.94) for breast girth; W×L gave the highest SCA (2.34) for body length while the highest SCA (0.89) for thigh length was observed in B×L turkey genotype. The study showed that additive variance was more important for growth parameters, fertility and dead-in-germ while dominance variance was higher and more important in controlling hatchability, weak-in-shell and dead-in-shell. Dams from B×W crossbred indigenous turkeys could be used to improve growth performance while W×L could be used to achieve best combiners for improvement of reproductive traits in Nigerian indigenous turkeys.

Key Words: turkey, combining ability

W203 Quail chick weight prediction using pre-hatch egg measurements and indices. O. T. F. Abanikannda*, A. O. Leigh, and A. M. Adeyeye, *Lagos State University, Ojo, Lagos, Nigeria.*

The weight of chicks at hatch is a good indicator of the future productivity of the bird and it is positively correlated to faster weight gain, increased final weight, reduced age at puberty, higher number of eggs laid and heavier eggs. This study was aimed at predicting the hatch weight of Quail chicks using pre-hatch egg parameters. An initial total of 987 hatching Quail eggs were sourced from a commercial farm in Jos in the Savannah region of Nigeria. Eggs were labeled and set in demarcated chambers covered with a net to prevent crossing at pip-out. Pre-hatch egg measurements include weight (Eggwt), length (Egglt), width (Eggwd), vertical circumference (VerCir), horizontal circumference (HorCir), egg weight at 14th day of incubation (14Dwt), while indices include shape index (ShpInd), egg volume (EggVol), egg surface area (EggSSA), egg density (EggDens), surface area to volume ratio (SSAVol) and percent weight difference (WtdiffP); chick weight (Chkwt) and shell thickness (Shltkn) were taken at hatch (n = 612). All statistical analyses (exploratory, normality test, descriptive, correlation and modeling) were done using Minitab statistical software. Out of the 14 variables studied, only ShpInd and Shltkn did not significantly ($P > 0.05$) correlate with chick weight, while egg weight was significantly ($P < 0.05$) correlated to all variables except ShpInd, and were thus eliminated from the final model, given as $Y = \beta_0 + \beta_1X_1 + \beta_2X_2 + \beta_3X_3 + \ldots\ldots\ldots\ldots + \beta_kX_k$. All the regressors in the model significantly ($P < 0.01$) affected chick weight, with egg density and d 14 incubation egg weight accounting for 30 and 26%, respectively. The model provides a veritable method for predicting chick weight based on pre-hatch egg parameters.

Table 1. Summary statistics and coefficients of variables

Variable	Mean ± SE	Correlation with chick weight
EggWt (g)	9.91 ± 0.04	0.54
EggLt (mm)	30.46 ± 0.05	0.40
EggWd (mm)	24.52 ± 0.04	0.38
VerCir (cm)	9.25 ± 0.02	0.30
HorCir (cm)	8.37 ± 0.01	0.30
ShpInd (%)	80.60 ± 0.16	−0.01
14Dwt (g)	8.89 ± 0.04	0.51
WtDiffP (%)	10.33 ± 0.20	−0.13
EggVol	10.32 ± 0.05	0.44
EggSSA	22.59 ± 0.07	0.46
EggDens	1.05 ± 0.001	0.54
SSAVol	2.20 ± 0.003	−0.44
ShlTkn (mm)	0.173 ± 0.001	0.05
ChkWt (g)	6.11 ± 0.03	1.00

Key Words: quail, Nigeria, chick weight

W204 Genetic parameters of body weight at multiple ages in meat-type quails. L. Silva*[1,2], D. González-Pena[2], J. Ribeiro[1], A. Crispim[1], S. Rodriguez-Zas[2], and R. Torres[1], *[1]Departament of Animal Sciences, Federal University of Viçosa Universidade Federal de Viçosa, Viçosa, MG, Brazil, [2]Departament of Animal Sciences, University of Illinois at Urbana-Champaign, Urbana.*

The domestic quail (*Coturnix coturnix*) is an accepted model to study the genetic parameters of meat production in domestic poultry due to the similar traits, low maintenance cost, and low generation interval. The estimation of the genetic variability and correlation associated with body weight (BW) at multiple ages can offer insights into effective selection strategies that maximize the genetic gain for BW at later ages while minimizing undesirable effects of higher BW at earlier ages. The aim of this study was to estimate the genetic variances and covariances of BW at multiple ages in meat-type quail. A total of 16,617 BWs from 4,777 quails across 13 generations of selection for higher body weight were measured at 0 (hatch), 14, 28, and 42 d of age. A multi-trait model including the fixed effects of generation and hatch (16 levels) and sex (2 levels), and the random additive genetic effect was used. The pedigree matrix included 8,755 quails, with an average inbreeding coefficient of 0.78 and REML parameter estimates were obtained using the software Wombat (Version 30/05/12). The mean (and standard deviation) phenotypic values were 9.62 g (1.09 g), 86.19 g (16.26 g), 210.24 g (29.76 g) and 274.30 g (36.71 g) for BW at 0, 14, 28, and 42 d, respectively. The heritability estimates (and standard errors) of BW at 0, 14, 28, and 42 d were 0.61 (0.02), 0.30 (0.03), 0.29 (0.03), and 0.27 (0.03), respectively. The higher heritability at 0 d may be due to the lower coefficient of phenotypic variation and similar genetic variation relative to the average of the reminder days. The genetic correlations (and standard errors) were 0.36 (0.06), 0.42 (0.05), 0.47 (0.06); 0.79 (0.06), 0.52 (0.07); and 0.65 (0.07) for 0 with 14, 28, and 42 d; 14 with 28 and 42 d; and 28 with 42 d, respectively. The higher correlations among BWs at later days suggest higher similarity on the genetic components of these BWs. The genetic correlation estimates indicate that it is possible to identify quails with high genetic potential for BW at older ages and low BW at earlier ages thus minimizing higher maintenance costs at earlier ages.

Key Words: coturnix, genetic correlation, heritability

W205 Genetic relationships between cloacal gland area and fertility traits in meat quail. L. Silva*[1,2], D. González-Pena[2], G. Caetano[1], R. Pacheco[1], S. Rodriguez-Zas[2], and R. Torres[1], *[1]Department of Animal Sciences, Federal University of Viçosa Universidade Federal de Viçosa, Viçosa, MG, Brazil, [2]Department of Animal Sciences, University of Illinois at Urbana Champaign, Urbana.*

Quail production has experiencing substantial growth in world markets, constituting a considerable niche business. However, selection based on growth in quail may have a negative effect on reproduction. The cloacal gland area (CAREA) has been proposed as an indicator of fertility because can be measured earlier, and less expensively than hatchability and fertility. This work aimed to investigate the genetic correlation between CAREA and other indicators of reproductive fitness in meat quail. Data from 189 males, generated from 51 females and 48males selected for higher BW. Males were allocated to individual cages and the width and height of the cloacal gland were measured using precision calipers (0.01mm) at 49 d of age. CAREA was estimated as the product between width and height. These males were mated to one fertile female each; the eggs were collected within 10 d, and placed on hatching trays. Eggs were candled after 9 d and after 17 d the number of chicks hatching alive was recorded. Fertility was computed as the proportion of fertile eggs among the incubated eggs, and hatchability was computed as the percentage of chicks that hatched among the incubated eggs. Multi-trait mixed models including the fixed effect of generation (2 levels) and a random additive genetic effect were used to estimate the genetic correlation between CAREA and fertility or hatchability. Pedigree matrix included 337 quails with an average inbreeding coefficient of 0.78 and REML parameter estimates were obtained using the software Wombat (Version 30/05/12). The mean (standard deviation) phenotypic values were 340.17mm^2 (106.52 mm^2), 0.81 (0.23), and 0.80 (0.22) for CAREA, fertility, and hatchability, respectively. Heritability estimates (standard errors) were 0.36 (0.16), 0.02 (0.18), and 0.41 (0.27) for CAREA, fertility, and hatchability, respectively being consistent with the literature. Genetic correlations (and standard errors) were 0.51 (0.35) and 0.68 (0.17) between CAREA and hatchability or fertility respectively. Results suggest that correlated responses in reproductive performance can be achieved by selection based on CAREA.

Key Words: coturnix, fertility, hatchability

W206 Genetic variation in Afec-Assaf ewes differing in their lamb survival rate at birth. A. Lam, A. Rosov, E. Seroussi, and E. Gootwine*, *Institute of Animal Science, The Volcani Center, Bet Dagan, Israel.*

High prolificacy is a desirable trait in sheep kept under intensive management. The prolificacy of Afec-Assaf ewes is high, being 2.5 ± 0.7 lambs born/ewe lambing (LB/EL), with 0.8 ± 0.2 lamb survival rate at birth (LSRAB). Investigating 419 lambing records (980 lambs) revealed lamb mortality rates of 0.0, 0.07, 0.24, 0.28, 0.21 and 0.72 for lambs born in litter sizes of 1, 2, 3, 4, 5 and 6, respectively. ANOVA that included crop, parity, sex, litter size and lamb viability in the model showed that average birth weight of liveborns (4.0 ± 0.1 kg) was significantly heavier ($P < 0.0001$) than that of stillborns (3.5 ± 0.1 kg). However, the average crown rump length (0.51 ± 0.01 m) was similar among these groups, suggesting that fetal mortality occurred at the late stage of pregnancy following an intrauterine fetal growth restriction. To investigate the effect of the maternal genome on LSRAB, DNA was extracted from blood samples of 71 high prolific ewes with an average prolificacy of 3.04 LB/EL based on 4–8 lambing records and LSRAB varying from 0.00 to 0.95. Whole genome association analysis was performed utilizing a 50K single nucleotide polymorphism (SNP) beadchip (Illumina). Association between 10-SNP haplotypes and LSRAB was carried out using PLINK package. Haplotypes located in altogether 14 regions of chromosomes: 1, 8, 10, 26 and X were found to be associated ($P < 10^{-7}$) with LSRAB. Analysis by the EMMAX software that controls for genetic relatedness within the sample supported the existence of QTL for LSRAB on 10 of the chromosomal regions. Within the 10 regions, candidate genes associated with stillbirth and with fetal growth restriction were chosen from public genomic databases. We further characterized the SMOC2 gene on chromosome 8, for which increased expression has been previously associated with stillbirth in cattle. Deep and direct sequencing revealed copy number variation within the ovine SMOC2 gene in the Afec-Assaf sheep. Further study is needed to establish the link between this locus and LSRAB; and to investigate the effect of the fetal genome on perinatal lamb mortality.

Key Words: Afec-Assaf, lamb survival, GWAS

W207 Factor analysis of biometric traits among the Djallonke sheep of Northern Ghana. P. T. Birteeb[1], S. O. Peters[2], and M. O. Ozoje*[3], *[1]Department of Animal Sciences, University for Development Studies, Tamale, Ghana, [2]Department of Animal Science, Berry College, Mount Berry, GA, [3]Department of Animal Breeding and Genetics, Federal University of Agriculture, Abeokuta, Nigeria.*

This study aimed at using multivariate approach to describe the body structure of Djallonke sheep in Northern Ghana. Live weight (LW) and linear body measurements traits (heart girth (HG), neck girth (NG), chest depth (CD), height at withers (HW), rump height (RH), body length (BL) and pin-bone width (PBW)) were obtained from 172 sheep, between 2 and 3 years old. The fixed effects of sex and age were tested using the a generalized linear model, while the nearest neighbor method of hierarchical cluster analysis was used to group body traits into clusters. Principal component factor analysis was used to describe variation in body traits where extracted factors were Varimax rotated to enhance interpretability. The ANOVA revealed significant ($P < 0.01$) differences in the morphological traits of the 2 sexes with higher values recorded for the male in all traits except PBW. Age had no effect ($P > 0.05$) on all body traits. On the average these sheep weighed 26.92 ± 0.89kg and measured 71.74 ± 1.23, 40.52 ± 0.79, 27.73 ± 0.52, 60.72 ± 0.86, 59.61 ± 0.87, 58.87 ± 1.06 and 12.81 ± 0.23 cm respectively for HG, NG, CD, HW, RH, BL and PBW. The product moments of correlation were positive and significant ($P < 0.05, 0.01$; r = 0.18–0.99) for all pairs of traits. These traits were categorized mainly into 2 clusters. HG, HW, RH and BL formed the first cluster, while NG, CD and PBW formed the second cluster. The grouping of the traits was however different in Factor analysis, where 2 underlying principal components (PC) were extracted to discern the variance structure of the Djallonke. The first consisting of CD, HW, RH, BL and PBW explained 61.26%, while the second consisting of HG and NG explained 12.92%, giving a maximum of 74.17% generalized variance in body measurements. The traits loaded on the first PC are closely associated with bone growth; while the traits on the second PC described only the thoracic region. In conclusion, both hierarchical cluster analysis and factor analysis grouped body traits similarly. However, the later is recommended because of its additional ability to indicate the amount of variation explained by the developed factors.

Key Words: Djallonke, factor analysis, body structure

W208 Evaluation of economic traits in Romanov × Iranian fat-tail sheep breed in the first generation (F_1). M. J. Najafpanah*[1,2], H. Mousapour[2], N. Feiz[1], M. H. Moradi[2], and B. Ghorbani[1], *[1]Center*

of Advance Research and Development of Elite Affairs, Tehran, Iran, [2]University of Tehran, Tehran, Iran.

Governments all over the world have tried to provide healthy, sustainable, and cheap food for their people. Sheep are an important part of the agricultural economy and may be a medium of trade in barter economies. Besides, sheep are one of the most important livestock to meat supply and employment in Iran. Prominent features of Iranian breeds have a fat-tail and low lambing and/or litter size. The aim of this study was to compare some phenotypic traits of economic in purebred lambs (Afshari) and crossbred lambs (Romanov × Afshari in F_1). The experimental broodstock was included of 40 Afshari pluriparous ewes. They were artificially inseminated with Canadian Romanov semen using laparoscopy. After the lambing, we observed all crossbred lambs were thin-tailed. The model that used for analysis contained the fixed effects of group (purebred and crossbred) and sex, the random effect of animal and a regression for dam's weight. The results proposed the dominance of the thin tail phenotype and suggesting that a few number of genes are associated with fat storage in the tail. We observed significant differences ($P < 0.05$) between the 2 groups in terms of weaning weight, weight in 6 mo, Adg_{0-3} and Adg_{3-6} while the differences between male and female lambs were not significant. The characteristics of other phenotypic traits presented in the Table 1. Our results revealed that crossbred lambs in F_1 have better performance for other phenotypic traits comparing to purebred lambs. In conclusion, this study showed that the efficiency of meat production in Afshari breed can improve using crossbreeding with Romanov breed.

Table 1. The characteristics of economical important traits in Iranian fat-tail sheep breed and their crossbred lambs (raw means ± SD)

	Purebred		Crossbred	
Item	Male	Female	Male	Female
Birth weight (kg)	4.42 ± 1.29	4.17 ± 0.68	4.47 ± 0.41	4.38 ± 0.33
Weaning weight (kg)	29.5 ± 4.23	26.5 ± 2.88	30.7 ± 6.14	27.63 ± 3.40
Weight in 6 mo (kg)	41.24 ± 5.31	38.7 ± 2.03	44.33 ± 7.36	40.68 ± 2.57
Preweaning daily gain (kg)				
Adg_{0-3}	0.327 ± 0.054	0.294 ± 0.03	0.307 ± 0.034	0.341 ± 0.061
Adg_{3-6}	0.130 ± 0.011	0.135 ± 0.016	0.151 ± 0.020	0.149 ± 0.019
Adg_{0-6}	0.229 ± 0.027	0.215 ± 0.028	0.246 ± 0.032	0.226 ± 0.021

Key Words: crossbred lamb, Romanov, fat-tail sheep

W209 Phenotypic and genetic changes of ewe economic traits in the Makooei sheep. H. M. Shahrbabak*[1], H. Mohammadi[2], and A. H. F. Khaltabadi[3], *[1]Department of Animal Science, Academic of Agronomy and Animal Science, University College of Agriculture & Natural Resources University of Tehran, Karaj, Alborz, Iran, [2]Department of Animal Sciences, Faculty of Agriculture, University of Tabriz, Tabriz, Iran, [3]Department of Animal Science, Faculty of Agriculture, University of Arak, Arak, Iran.*

In this study 3418 records from the Makooei sheep stud were used to predict phenotypic, genetic and environmental change in ewe traits from 1996 to 2009. Best linear unbiased predictions (BLUP) of breeding values were estimated by restricted maximum likelihood (REML) procedure using single and multi-trait animal model with ASReml program. Phenotypic, genetic and environmental trends were calculated by regressing of the average phenotypic values, predicted breeding values and environmental values in the year of ewe birth respectively. The estimated phenotypic trends were –0.1005 kg for ewe body weight, 0.447% for conception rate, 0.0002 for number of lambs born per ewe lambing, 0.0064 for number of lambs weaned per ewe lambing, 0.0270 kg for total birth weight per ewe exposed and 0.4522 kg for total weaning weight per ewe exposed. The estimated genetic trends were 0.0472 kg, −0.0004 kg, 0.0253%, 0.0015, 0.0005, 0.0040 kg and 0.0122 kg from single-trait analysis and 0.0365 kg, −0.0005 kg, 0.0074%, 0.0017, −0.0006, 0.0050 kg and 0.0157 kg respectively from multi-trait analysis. The estimated phenotypic and environmental trends were significant ($P < 0.05$) but genetic trends were not significant ($P > 0.05$) for all traits. Results from this study agree with those of the previous studies of the other sheep breeds that multi-trait analysis should be used rather than single-trait analysis when estimating genetic changes because of the effect thatincluding correlated traits has on estimates of breeding values of other traits.

Key Words: phenotypic trend, genetic trend, ewe trait

W210 Estimation of genetic trends for live weight traits in Raeini goats. H. M. Shahrbabak*[1], H. Mohammadi[2], and A. H. F. Khaltabadi[3], *[1]Department of Animal Science, Academic of Agronomy and Animal Science, University College of Agriculture & Natural Resources, University of Tehran, Karaj, Alborz, Iran, [2]Department of Animal Science, Faculty of Agriculture, University of Tabriz, Tabriz, Iran, [3]Department of Animal Science, Faculty of Agriculture, University of Arak, Arak, Iran.*

The aim of this study was to estimate genetic trends for live weight traits at different ages in Raeini goat. The data were collected from Baft city Breeding Research Station in southeastern Kerman province, Iran. Data were collected over the years 1982 to 2009, with records on total of 4,219 kids descended from 263 sires and 1653 dams. Major reasons for culling were old age, mastitis, and bad udder. Throughout the study replacement bucks and breeding does were selected on the basis of phenotypic characteristics such as visual conformation and WW. The investigated traits were birth weight (BW), weaning weight (WW), 6 mo weight (6W), 9 mo weight (9 W) and yearling weight (YW). Number of observations for BW, WW, 6W, 9W and YW were 4219, 3473, 2692, 1641 and 1021, respectively. The (co)variance components and corresponding genetic parameters were estimated by restricted maximum likelihood method based on a single trait animal model, using ASReml program (Gilmour et al., 2006). The fixed effects of sex, birth year, dam age and birth type and the random effects of direct and maternal genetics were included in the model for all traits. Age of kid at weighing (in days) was fitted as a covariate. Genetic trends were estimated by regressing estimated breeding values on year of birth. The mean predicted breeding values of Goat kids generally show an increase over time for all studied traits. The additive direct genetic trends for BW, WW, 6W, 9W and YW were 2 ± 0.28, 95 ± 11.31, 65 ± 8.7, 18 ± 6.2 and 17 ± 4.9 g per year, respectively. Higher genetic trends for WW and 6W than other traits might be attributed to the relatively higher additive genetic variation in those traits. Results of this work showed, in general, low genetic improvement in the studied traits during the period of study. The main reason for this could be the absence of clear and focused selection criteria during the period of the study. The genetic trends estimates show that there has been a positive genetic improvement in all studied traits and indicate that selection would be effective.

Key Words: genetic trend, weight trait, goat

W211 Linear models versus threshold models for predicting direct and maternal genetic effects on number of lambs weaned in Iranian Makooei sheep. H. M. Shahrbabak*[1], H. Mohammadi[2], and A. H. F Khaltabadi[3], *[1]Department of Animal Science, Academic of Agronomy and Animal Science, University College of Agriculture & Natural Resources, University of Tehran, Karaj, Alborz, Iran, [2]Department of Animal Science, Faculty of Agriculture, University of Tabriz, Tabriz, Iran, [3]Department of Animal Science, Faculty of Agriculture, University of Arak, Arak, Iran.*

Meat quantity has traditionally contributed most of the net return in the sheep farmers of Iran. Recent high prices for sheep meat are likely to increase the interest in, and importance of the reproductive rate in sheep herds. The number of lambs weaned (NLW) can be a good criteria for reproductive performance in a sheep herd. This reproductive trait is recorded in discrete category but analyses as a continuous trait. The objective of this study was to compare the accuracy of a threshold animal model to a linear model for direct and maternal genetic evaluation of NLW in Iranian Makooei sheep. The information of NLW was extracted from data notebooks of Makooei sheep breeding station from 1996 to 2009. The number of lambs weaned was recorded in 2 categories (0 and 1) and a total of 3418 records were available. Most of the records categorized in class1 (77.6%) and the average number of weaned lambs was 1.09. Analyses were performed using an animal model (linear and threshold) with a maternal effect. Year of birth and sex were considered as fixed effects and age of dam as a covariate in all models. A cross-validation method was used to assess the predictive ability of the models. The estimates of direct and maternal variances and also covariance between direct-maternal were obtained larger in threshold model comparing to the linear model. Larger estimates of heritabilities also were obtained when the threshold model was employed. For the direct additive genetic effect, the correlation from the threshold model was 10% higher than the linear model (0.53 vs. 0.48) and the maternal effects followed the same pattern with 6% increasing (0.57 vs. 0.52). The results confirmed the better performance of a threshold animal model compared with a linear animal model for genetic evaluation of NLW. However, the advantage of using a univariate threshold model instead of a linear model was small. Further investigation is needed for fully judge the predictive ability of the 2 models.

Key Words: threshold model, lambs weaned, prediction

W212 Effect of egg weight on hatching weight and incubation period in Giant African land snail (*Archachatina marginata*). J. A. Abiona*, Y. F. Sokoya, A. O. Osinowo, A. O. Ladokun, and M. O. Abioja, *Federal University of Agriculture, Abeokuta, Abeokuta, Ogun State, Nigeria.*

An experiment was conducted to determine the effect of egg weight on hatching weight and incubation period in the Giant African land snail. A total of 30 *Archachatina marginata* eggs comprising of 4 weight range categories (1.24–1.55, 1.56–2.14, 2.15–2.83 and 2.84–3.20 g) were obtained from Dams of different body weight ranges (100g-150g, 151–200g, 201–250g) from the Snail Physiology Research Unit of the College of Animal Science and Livestock Production, Federal University of Agriculture, Abeokuta, Nigeria. Eggs were incubated, after which both incubation period and hatching weight after hatching were monitored. Results obtained showed that egg weight group had significant effect ($P < 0.001$) on hatching weight. Egg weight with weight range of 2.84–3.20 had the highest hatching weight, followed by 2.15–2.14 while other 2 (1.24–1.55 and 1.56–2.14 g) were not significantly different from each other. Furthermore, egg weight had no significant effect ($P > 0.05$) on incubation period. A positive significant correlation (Pearson) was obtained between egg weight and hatching weight, and also dam weight and hatching weight. It was concluded that egg weight had effect on hatching weight of eggs. It was also discovered that egg weight had no meaningful effect on incubation period.

Table 1.

Egg weight group	No. of observations	Hatching weight (g)	Incubation period (d)
1.24–1.55	6	0.947 ± 0.087^{c}	32.5 ± 2.325
1.56–2.14	6	1.100 ± 0.087^{c}	33.5 ± 2.325
2.15–2.83	6	1.555 ± 0.087^{b}	24.7 ± 2.325
2.84–3.20	5	2.118 ± 0.095^{a}	29.6 ± 2.546

Key Words: egg weight, incubation period, hatching weight

W213 Effect of Chy-Max M on proteolysis during ripening of natural cheese, and functionality of process cheese. A. C. Biswas*, C. Marella, and L. E. Metzger, *Dairy Science Department, South Dakota State University, Brookings.*

Recombinant bovine chymosin is an enzyme routinely used in cheese manufacture. Recently, recombinant camel chymosin (Chy-Max M) has also been developed and is commercially available as a milk coagulant for natural cheese manufacture. Previous research has determined that recombinant camel chymosin has a higher clotting activity, and is less proteolytic as compared with recombinant bovine chymosin. However, the effect of reduced proteolysis from recombinant camel chymosin on process cheese functionality has not been studied. The objective of this study was to determine the effect of Chy-Max M on proteolysis during ripening of natural cheese, and functionality of process cheese, as compared with cheese manufactured from recombinant bovine chymosin (Chy-Max Extra). Three replicates of natural cheese with a range in composition (37.73 - 43.49% moisture, 28.87 – 34.11% fat, 21.16 – 26.06% protein, and 1.60 – 2.24% salt) were manufactured with different protocols (cook temperature, curd washing, and salting rate) for each replicate. In each replicate a cheese was produced with Chy-Max M and Chy-Max Extra using the same protocol. The level of proteolysis in each cheese was determined at 2 weeks, 1, 2, and 3 mo of ripening. Additionally at 1 mo of ripening each natural cheese was utilized to produce process cheese that was standardized to 30% fat, 18% protein, 2.2% salt and 42.5% moisture using a formulation that contained water, sodium citrate, butter, salt, and deproteinized whey. In the natural cheese there was not a significant ($P > 0.05$) difference in fat, protein, moisture or pH between the Chy-Max M and Chy-Max Extra treatments. However, the level of primary proteolysis was significantly ($P < 0.05$) lower in the Chy-Max M treatment at all ripening times. In the process cheese the viscosity after manufacture and the TPA hardness of the Chy-Max M formulation was significantly ($P < 0.05$) higher than the Chy-Max Extra. These results demonstrate that Chy-Max M results in a reduced level of primary proteolysis in natural cheese and when utilized in process cheese results in an increase in viscosity and firmness.

Key Words: chymosin, proteolysis, process cheese

W214 High pressure processing of Queso Fresco: Effects on textural and rheological properties over 12 wk of storage. D. L. Van Hekken*[1], M. H. Tunick[1], N. Farkye[2], and P. M. Tomasula[1], *[1]USDA, Agricultural Research Service, Wyndmoor, PA, [2]California Polytechnic State University, San Luis Obispo.*

High pressure processing (HPP) is a non-thermal post-packaging process with the potential to improve cheese safety and shelf life because of its lethality to bacteria (spoilage and pathogens) and ability to inactivate many enzymes. Queso Fresco (QF), a high moisture Hispanic-style cheese popular in the US, could benefit from improved safety and shelf life but more information is needed to understand the effect that HPP has on the textural and rheological qualities of the cheese once it is placed in storage. A starter-free QF, made from pasteurized and homogenized milk, was vacuum packaged and then processed at 600 MPa for 3 or 10 min and stored at 4 or 10°C; controls were not HPP. After 1, 4, 8, and 12 wk of storage, QF were assayed for compositional, textural (texture profile analysis), and rheological (torsion and small amplitude oscillatory shear analyses) properties. After 1 wk of storage at 4°C, the control QF consisted of 56.4 ± 0.3% moisture, 15.4 ± 1.5% protein, 22.3 ± 0.3% fat, 2.9 ± 0.1% lactose, and 2.0 ± 0.3% salt; pH 6.31 ± 0.03. Free whey accumulated in packaging following HPP and over time resulting in decreased moisture contents ($P < 0.05$). Controls decreased 2.0% in moisture over 12 wk while samples lost about 2.5% moisture after HPP treatment and another 2% by the end of the study; HPP QF stored at 10°C tended to have the lowest moisture contents. HPP QF were harder, more rigid, and fractured at higher stress than controls ($P < 0.05$); QF processed for 10 min tended to be firmer than samples processed at 3 min and QF stored at 10°C were firmer than QF stored at 4°C. Within a treatment, the textural and rheological properties were stable over 12 wk of storage. Loss of free whey, considered a defect by American consumers, was enhanced after HPP treatment and affected the moisture content, texture, and rheology of the cheese. As new post-processing steps are explored, it is essential to monitor texture and rheology to maintain the quality traits of the cheese that are expected by the consumer.

Key Words: cheese, high pressure processing, rheology

W215 Reducing fat levels in Cheddar-like goat cheese: Effect on proteolysis and rheological properties over 6 months of refrigerated storage. D. L. Van Hekken*[1], Y. W. Park[2], and M. H. Tunick[1], *[1]USDA, Agricultural Research Service, Wyndmoor, PA, [2]Fort Valley State University, Fort Valley, GA.*

Development of low-fat goat cheeses that appeal to health conscious consumers requires information on how the reduction of fat affects the quality traits of the cheese, such as its proteolysis and rheology. Goat milk samples containing 3.6, 2.0, 1.0, and < 0.5% fat were processed into full-fat (FF), reduced-fat (RF), low-fat (LF), and non-fat (NF) high-moisture Cheddar-like cheeses, respectively, vacuum sealed in pouches, and stored at 4°C. Compositions of the cheeses were determined after 1 mo of storage, protein profiles were compared between 1 and 6 mo of storage, and rheological properties were measured after 1, 3, and 6 mo of storage. The FF, RF, LF, and NF cheeses contained 26.3, 19.0, 9.65, and 1.50% fat; 48.7, 50.0, 51.5, and 55.2% moisture; and 21.0, 24.9, 35.9, 38.5% protein, respectively. The FF, RF, and LF cheeses had similar proteolysis with a 40% decrease of intact caseins (α_s- and β-CN) while the intact caseins in the NF cheese decreased by 14%. The NF cheese, with its dense protein matrix had the highest values for hardness, chewiness, cohesiveness, fracture stress, elastic modulus, and viscous modulus. Although the LF cheese was harder, chewier, more cohesive, and fractured at higher stress than the FF and RF cheeses, it softened somewhat with age while the NF cheese remained a hard mass. The FF and RF cheeses had similar rheological properties and had the softest and most flexible textures. It was concluded that fat can be reduced to 19% in a Cheddar-like goat cheese with minimal effect on rheology which will help in developing reduced-fat goat cheese products.

Key Words: goat milk cheese, low fat cheese, rheology

W216 Influence of temperature and milk on $W_1/O/W_2$ double emulsions made with anhydrous milk fat. D. B. Clayton and D. J. McMahon*, *Western Dairy Center, Utah State University, Logan.*

Water (W_1) in oil (O) in water (W_2) double emulsions ($W_1/O/W_2$) have been added to milk to improve texture and to add fiber to low-fat cheese. Our objective was to determine stability, and suitability for cheesemaking, of a $W_1/O/W_2$ emulsion made using anhydrous milkfat (AMF) as the oil phase. Because the melting range of AMF covers typical cheese

manufacturing temperatures, we were concerned that an AMF $W_1/O/W_2$ emulsion would be unstable in cheese milk. The primary (W_1/O) emulsion was prepared by adding water (50°C) dropwise, under low shear into AMF (50°C) containing 8% polyglycerol polyricinoleate in a 40:60 (W_1:O) ratio. The W_1/O emulsion was then added to water containing 2% whey protein concentrate (50°C) in a 20:80 (W_1/O: W_2) ratio using low shear. The mixture was then subjected to high shear using an Omni GLH mixer at 5,000 rpm for 1 min to create a $W_1/O/W_2$ emulsion. Presence of double emulsions was verified through optical microscopy. Temperature stability of $W_1/O/W_2$ emulsions was measured by placing 5 to 7 mL of emulsion in test tubes that were held at 30, 35, 40, or 50°C for 3 h. In comparison, a canola oil $W_1/O/W_2$ emulsion was used as control. Light backscattering from the test tubes was measured every 15 min in a Turbiscan for 3h to determine instability of the emulsions due to creaming. The $W_1/O/W_2$ emulsion was also added to skim milk at 1:20 ratio and held at 32°C for 3 h then viewed using optical microscopy to see if the $W_1/O/W_2$ remained or reverted to an O/W_2 emulsion. The AMF $W_1/O/W_2$ emulsion was most stable at 30°C, with only a 4.11 mm change in backscattering after 3 h as shown by Turbiscan measurements, compared with 4.49, 4.57, and 5.71 mm for emulsions stored at 35, 40, and 50°C, respectively. After 3 h in milk, the initial $W_1/O/W_2$ emulsions were not stable, with the inner primary phase being lost resulting in an O/W_2 emulsion. This problem was solved by adding 0.4% NaCl to the W_1 before making the emulsion to balance osmotic pressure with milk, and $W_1/O/W_2$ emulsion droplets in milk were still visible after 3 h. We concluded that a double emulsion made using this process is sufficiently stable to be used in the manufacture of cheese.

Key Words: emulsion, cheese

W217 Cheese milk fortification with denatured whey/buttermilk blend—Effect on rennet gel characteristics. M.-P. Gauvin*[1], M. Britten[2], and Y. Pouliot[1], *[1]STELA Dairy Research Center, Institute on Nutrition and Functional Foods (INAF), Université Laval, Quebec, Quebec, Canada, [2]Food Research and Development Center (FRDC), Agriculture and Agri-Food Canada, St-Hyacinthe (Québec), Canada.*

Thermal aggregation of whey protein concentrate with buttermilk has been studied as a way to produce a new enrichment ingredient for cheese making. The purpose of this work is to describe the effect of adding whey protein/buttermilk denatured blend to cheese milk in terms of gelation and rennet gel properties in comparison with the use of 100% whey protein or buttermilk aggregates. Whey protein, buttermilk and a 1:1 combination of whey protein and buttermilk were reconstituted from powders to 3.15% protein (wt/wt) and heat denatured (80°C, 30 min, pH 4.6) under stirring. After cooling, the mixtures were adjusted to pH 6.5 and homogenized. The ingredients were added to reconstituted skim milk and milk protein concentrate to constitute 17.7% (wt/wt) of the total protein of a 5.1% protein dispersion (wt/wt). To discriminate the contributions from the colloidal and soluble phases of the ingredients, cheese milks were also formulated after removing colloidal material by centrifugation (30,000 × *g*, 1 h). Cheese milks were renneted and coagulation kinetics, gel rupture properties and syneresis were measured. All experiments were performed in triplicate. Milk gelation was accelerated with increasing amount of buttermilk in the ingredient. For the milks containing buttermilk (B) or whey protein only (WP), lag phase (Tlag) and maximum gelation rate (Vmax) ranged from 23 to 28 min and from 0.027 to 0.034 min^{-1} respectively. Tlag and Vmax values obtained with the milk enriched with whey protein/buttermilk blend (WP/B) were 26 min and 0.032 min^{-1}. The WP/B and B gels showed very similar rupture stress (284 and 291 Pa respectively), greater than the value obtained for gels containing whey protein only (WP) (236 Pa). Along with WP gels, WP/B gels showed lower syneresis (64.8 and 63.9%) compared with B gels (66.3%). WP/B gels were therefore more humid. Milk fortification with WP/B blend tends to give rennet gels with intermediate characteristics when compared with WP and B. However, discriminating the contributions from the colloidal and soluble phases provides a better understanding of the ingredient behavior in cheese milk.

Key Words: whey protein, buttermilk, cheese

W218 Physicochemical and sensory properties of Prato cheese made with different coagulants. L. S. Alves[1], C. Merheb-Dini*[1], E. Gomes[2], R. da Silva[2], and M. L. Gigante[1], *[1]Faculty of Food Engineering, University of Campinas - UNICAMP, Campinas, SP, Brazil, [2]Instituto de Biociências, Letras e Ciências Exatas, UNESP - Univ Estadual Paulista, São José do Rio Preto, SP, Brazil.*

Prato cheese is a typical Brazilian variety, obtained by enzymatic curdling. It is made from a semi-cooked, washed and pressed mass, which is ripened for at least 25 d. The aim of this work was to compare the effect of coagulant type on Prato cheese yield and sensory acceptance. Cheeses were manufactured from 50 L of milk in vats with a heating-cooling jacket, stirrers and speed control, according to traditional methodology using the following coagulants: laboratory obtained protease, from the fungus Thermomucor indicae-seudaticae N31, recently isolated in Brazil (Thermomucor cheese) and commercial coagulant from *Rhizomucor* sp. (Alternative, Bela Vista) (Control cheese). For both chesses the amount of enzyme added was calculated to achieve milk clotting in ≈35 min. The experiment was repeated 3 times and the results were evaluated by ANOVA and mean values were compared by Tukey's test ($P < 0.05$). Milk, whey and cheese composition were evaluated and cheese yield was calculated. After 25 d of ripening, sensory acceptance was evaluated by 100 consumers who were asked to score each sample with respect to their degree of liking or disliking the appearance, aroma, taste, texture and overall liking using a 9-point hedonic scale. The different coagulants did not affect cheese composition, which exhibited average content of 42.68% ± 1.87 for moisture, 41.52% ± 0.69 for protein (dry base) and 49.83% ± 0.22 for fat (dry base). Protein and fat recovery and, consequently cheese yield, were not affected by the coagulants as well. No significant differences were observed in respect to sensory properties among the cheeses, which had good acceptability with overall liking scores of 7.06 ± 1.33 and 7.13 ± 1.30 for Thermomucor cheese and Control cheese, respectively, both representing the 'like moderately' category. The gathered data suggest that the new protease from Thermomucor indicae-seudaticae N31 has technological potential to be used in cheese making and, therefore, has potential to be produced in large scale. Acknowledgments: FAPESP, CNPq

Key Words: cheese yield, composition

W219 The effect of cation substitution on the flavor of reduced-fat, reduced-sodium Cheddar cheese. H. H. Chang*[1], E. J. Kang[1], R. E. Miracle[1], D. J. McMahon[2], and M. A. Drake[1], *[1]North Carolina State University, Raleigh, [2]Utah State University, Logan.*

Sodium and fat reduction in dairy products are critical as diets high in sodium and fat are associated with many chronic diseases. However, sodium and fat play important roles in Cheddar cheese flavor development, and consumers are willing to purchase foods with reduced sodium and fat only when flavor profiles are similar to full fat and sodium counterparts. A previous study demonstrated that cation salts other than sodium could be used in place of sodium with minimal sensory effects up to 50% sodium replacement. The objectives of this

study were to determine the effect of cation substitution on the flavor of reduced sodium and fat (50% reduction) Cheddar cheese. Eight 50% reduced-fat Cheddar cheeses with different ratios of sodium, potassium, calcium and magnesium cations were manufactured. Traditional sodium chloride (NaCl) (1.7% wt/wt) and low sodium chloride (0.7% wt/wt; LC) cheeses served as controls. Cheeses were manufactured in triplicate, and analyzed for organic acids (HPLC), volatile compounds (SPME GCMS), and descriptive analysis (8 trained panelists with an established lexicon) across 9 mo ripening. Consumer acceptance testing was conducted with regular and sodium-restricted diet consumers (n = 100 each group) after 3 and 6 mo. No differences ($P > 0.05$) due to cation substitution were observed in organic acids, but higher concentrations of citric, pyruvic and lactic acids were present in LC compared with other reduced fat cheeses. Volatile compound differences were observed when more than 50% sodium was replaced. Trained panelists documented differences ($P < 0.05$) in flavor and basic tastes with more than 25% sodium substitution. The largest sensory impact was increasing intensities of bitter taste with sodium substitution. Sulfur and brothy flavors increased with decreased NaCl. Consumer acceptance scores, on regular or salt-restricted diets, were not different in overall liking up to 50% replacement of KCl with NaCl. Differences due to cation substitution are not likely to affect consumer liking and flavor chemistry up to 50% sodium replacement in reduced fat Cheddar cheeses.

Key Words: cheese, reduced sodium, reduced fat

W220 Comparison of physicochemical properties of Asiago cheese added with nanopowdered red ginseng and powdered red ginseng during ripening (II). K. H. Choi*, P. Ganesan, and H. S. Kwak, *Sejong University, Seoul, South Korea.*

Red ginseng which contains various ginsenosides is known to have various health benefits, such as antiinflammatory, anticancer, antitumor, antidiabetic. However, the low oral bioavailability of red ginseng is a major obstacle to its applicability as a functional food material. To overcome the obstacle, red ginseng was milled to nano scale (200 nm) and it was added into Asiago cheese. Therefore, this study was carried out to investigate physicochemical properties of different concentrations (0.1, 0.3, and 0.5%) of nanopowdered red ginseng (NRG) and powdered red ginseng (PRG)–added Asiago cheeses (AC). The proximate composition, lactic acid bacteria (LAB) counts, color, texture, and sensory analysis were measured to compare NRGAC and PRGAC during ripening at 14°C for 4 mo. The proximate composition such as moisture, protein, and fat contents were similar in NRGAC and PRGAC during ripening. LAB counts were not found significantly different between NRGAC and PRGAC during ripening ($P > 0.05$). However, L* value of 0.1% NRGAC showed significantly lower than that of PRGAC during the ripening. In texture, hardness was significantly increased during ripening in both NRGAC and PRGAC. In sensory analysis, the overall acceptability of 0.1% NRGAC was similar to control during ripening. In conclusion, the addition of NRG into cheese was slightly influenced to the properties of Asiago cheese, and 0.1% NRGAC was quite similar to control that may be worth developing functional cheese.

Key Words: Asiago cheese, nanopowdered red ginseng, physicochemical property

W221 Monitoring water-soluble compounds of Swiss cheese before cold room by attenuated total reflectance-Fourier transform infrared spectroscopy (ATR-FTIR) . N. Cheng*, W. J. Harper, and C. Wick, *Ohio State University, Columbus.*

Eye formation plays an important role in Swiss cheese quality and consumer acceptance. Critical amount production of gas and rheological properties were reported to cause eye formation in Swiss cheese. This study focused on monitoring the water-soluble chemical compounds profile of Swiss cheese before cold room by Fourier transform infrared spectroscopy (Varian 3100, Varian Inc., Hercules, CA). Ten vat makes of Swiss cheese were sampled out of press, out of pre-cool and out of warm room stages. Water extract of each sample was made by using chloroform and ethanol and then vacuum dried on a triple-reflection ZnSe crystal mounted on an attenuated total reflectance (Pike Technologies, WI) accessory. Four spectra were collected for each sample from 4000 to 700 cm^{-1} with a resolution of $8cm^{-1}$ and 64 scans were co-added per spectrum to enhance signal-to-noise ratio. All spectra were analyzed using soft independent modeling by class analogy (SIMCA, Pirouette 4.0, Infometrix Inc., WA). The discriminating wave number included fatty acids, amino acids and amide I and amide II compounds. The amino acid and amide bands indicate protein degradation that favors formation of eyes. The fatty acids probably arise from the formation of acids related to lactose degradation (probably acetic, propionic and butyric) and their formation can be associated with gas formation. Amino acid is also known to stimulate the growth of propionic acid bacteria in secondary fermentation of Swiss cheese and lead to the production of carbon dioxide. Our study showed that there were differences of water soluble compounds among out of press, pre-cool and out of warm room stage, which were associated with amino acid and aliphatic chains of fatty acids.

Key Words: Swiss cheese, eye formation, FTIR

W222 Survival of free and microencapsulated *Lactobacillus acidophilus* La5 in probiotic Prato cheese during simulated gastrointestinal conditions. C. Gebara, M. C. E. Ribeiro*, K. S. Chaves, F. N. Souza, C. R. F. Grosso, and M. L. Gigante, *Faculty of Food Engineering, University of Campinas, Campinas, SP/Brazil.*

The aim of this study was to evaluate the survival of free and microencapsulated *L. acidophilus* La5 added to Prato cheese during exposure to simulated gastrointestinal conditions. The probiotic was microencapsulated using citrus pectin by ionotropic gelation and coated with whey protein by complex coacervation. Three treatments were studied: Prato cheese with free La5, Prato cheese with La5 microencapsulated in pectin and Prato cheese with La5 microencapsulated in pectin coated with whey protein. After 30 d of storage at 12°C, the cheeses were exposed to conditions simulating the passage through the gastrointestinal tract: artificial gastric juice at pH 3.0 with addition of mucin and pepsin at 37°C for 120 min and followed by artificial intestinal juice at pH 7.0 with addition of pancreatin for 300 min. The cheeses were also exposed to bile solution (0.5%, pH 7.0) for 300 min. The effect of the treatments (free or microcapsulated probiotic) on the survival of the microorganism exposed to the gastrointestinal conditions was evaluated by ANOVA and Tukey's test for comparison between means ($P < 0.05$). The treatments did not significantly affect the probiotics survival during the exposure to simulated gastrointestinal conditions. For both free and encapsulated microorganism, a significant decrease of *L. acidophilus* La5 was not observed. The results suggest that regardless of microencapsulation, the fat-protein matrix of Prato cheese provides, by itself, protection to the microorganism during passage through gastrointestinal tract, allowing the probiotics to be delivered to its site of action, maintaining the initial population present in the product. Acknowledgments: FAPESP, CNPq.

Key Words: microencapsulation, probiotic, enteric resistance

W223 Evaluation of flavor variation in Swiss cheese from five factories using SIFT-MS, descriptive sensory analysis, and consumer sensory testing. K. Taylor[1], M. Leidheiser[1], M. A. Drake[2], S. Barringer[1], and W. J. Harper*[1], *[1]The Ohio State University, Columbus, [2]North Caroline State University, Raleigh.*

Variation in Swiss cheese flavor has become a problem in the Swiss cheese industry. The objective of this study is to identify the compounds and flavor attributes causing variation in Swiss cheese flavor by using selected ion flow tube-mass spectrometry (SIFT-MS), descriptive sensory analysis, and consumer sensory testing. Three Swiss cheese samples were obtained from each of 5 different factories for a total of 15 samples. These cheeses varied in manufacturing dates, as well as the vat and block location. The trained panelists in the descriptive analysis found significant differences between the cheeses from different factories. Although there are some similarities between factories, there are also attributes that distinguish samples and are unique to each factory. To determine consumer preferred flavors this study utilized an untrained consumer panel of 100 people who consume Swiss cheese, to determine which cheeses were liked the most, met expectations, and had the highest liking rating. Overall, one factory was liked the most and was the best balanced in all attributes. SIFT-MS showed that the cheeses contained varying concentrations and odor activity values (OAV) of high impact volatile organic compounds (VOCs). OAVs (concentration/threshold) were utilized to discriminate all factories using soft independent modeling of class analogy (SIMCA) indicating unique flavor profiles. A variety of variables inherent to Swiss cheese manufacture may contribute to the variation in flavors associated with each factory. This study provided end-point flavor characteristics and compounds to be traced back through fermentation pathways to help determine the source of flavor variation.

Key Words: flavor, cheese, SIFT-MS

W224 Gas formation and growth characteristics of an oligotrophic *Lactobacillus* species isolated from Cheddar cheese. F. Ortakci*[1], C. Oberg[2,1], J. Broadbent[1], T. Oberg[1], and D. McMahon[1], *[1]Western Dairy Center, Utah State University, Logan, [2]Weber State University, Ogden, UT.*

A heterofermentative *Lactobacillus* (WDC04), isolated from gassy Cheddar cheese, was studied for growth and gas formation. Previously, WDC04 was shown to only use ribose (Rib) as a sugar source. Our aim was to determine rate and extent of growth, and gas production when grown anaerobically in various combinations of Rib and galactose (Gal) at 12, 25, and 37°C. Using MRS broth without glucose at pH 5.2, we added Rib and Gal individually or combined at 0.05%, 0.1%, 0.5%, 1.0% and 2.0%. The WDC04 isolate was grown to 7×10^8 cfu/mL in MRS (without glucose) + 0.5% Rib+1% Gal then inoculated into the various broths to an initial turbidity at 640 nm of 0.05 to 0.15 (~10^7 cfu/mL). Cell growth was monitored through turbidity change every 12 h. At all 3 temperatures, the most growth of WDC04 occurred in 1% Rib, 0.5% Rib + 0.5% Gal, or 1% Rib + 1% Gal. Stationary phase was reached in 180, 48 and 48 h at 12, 25 and 37°C, respectively. Cell numbers at stationary phase were similar (~10^9 cfu/mL) when WDC04 was grown at 12 and 25°C, but lower (~10^8 cfu/mL) when grown at 37°C. Growth rates were similar when lower levels of Rib or Rib/Gal were used but extent of growth was less. When Gal was the only sugar source, growth of WDC04 was slower, with stationary phase at 25°C reached after 156 h in 0.5% Gal compared with 24 h in 0.5% Rib. When WDC04 was grown in Gal only at 37°C there was no further growth after the initial 12 h ($P > 0.05$). Gas formation was observed only when Gal were present and at 25°C either in the presence or absence of citrate. The similar growth patterns in 1% Rib and 0.5% Rib + 0.5% Gal indicates that WDC04 can utilize Gal for energy but transport of Gal into the cell is dependent on Rib metabolism. Furthermore, the metabolic pathways associated with Gal utilization appear to be required for gas production. To confirm the ability of WDC04 to cause late blowing in cheese, we made Cheddar cheese from milk inoculated (10^2 cfu/g) with WDC04 and stored the cheese at 6 and 12°C. After 3 mo at 12°C, gas formation was observed in the cheeses containing WDC04 while slower gas production occurred at 6°C.

Key Words: *Lactobacillus*, gas former, cheese late blowing

W225 Effect of oil-based and microencapsulated n-3 fatty acids on physical and chemical properties of processed cheese. M. Rouse, C. A. Boeneke, K. V. O'Brien*, and K. Aryana, *Louisiana State University, Baton Rouge.*

In recent years the benefits of n-3 fatty acids has been elucidated in numerous studies related to cardiovascular health, immune functioning, renal disorders, diabetes and cancer. Fish and fish oils are a good source of n-3 fatty acids; however, the recommended dietary amounts are not often achieved in the Western diet. The addition of fish oils to commonly consumed dairy products, such as yogurt or processed cheese, could serve as effective method to incorporate more n-3 fatty acids into the diet. The objective of this study was to evaluate several sensory qualities of a processed cheese containing varying levels of docosahexaenoic acid (DHA) and eicosapentaenoic acid (EPA). Fortification of this dairy product with DHA and EPA was achieved by the addition of microencapsulated fish oil during the melting stage of the processed cheese manufacture. The addition of 25 mg 2:1 DHA:EPA received the highest scores for both flavor and overall liking by testers; however, few significant differences were found between the samples. The flavor and aroma are the most deterrent factors in consumer acceptance of products fortified with fish oils due to relatively high rates of lipid oxidation and the resulting off flavors that can occur in the finished product. Microencapsulation of fish oils before addition may reduce the rate of oxidation and therefore improve marketability of dairy products fortified with fish oil.

Key Words: processed cheese, fish oil, microencapsulation

W226 Variability of volatile organic compounds profile during the manufacture of Swiss-type cheeses using selected ion flow tube mass spectrometry. H. Z. Castada* and W. J. Harper, *Department of Food Science and Technology, The Ohio State University, Columbus.*

The determination of the volatile organic compounds (VOCs) profile variability during the manufacture of Swiss cheese was achieved using static headspace sampling and quantitative analysis of the volatiles with selected ion flow tube-mass spectrometry (SIFT-MS). Cheese samples from 5 different vats at each of the 4 different stages of manufacture from a single factory were obtained. These stages include: out-of-press, end of pre-cool, end of warm room and at time of cutting. Two batches of samples and their subsequent stages from 2 different starting make dates were investigated in this study. Statistical analyses and comparison of VOC profile between vats and between stages of manufacture were applied using soft independent modeling of class analogy (SIMCA) and statistical analysis system (SAS). Significant VOC profile differences have been identified between the 4 stages of cheese manufacture. Multivariate stage-level (VOC concentrations were pooled from the 5 vats at each stage) classification using SIMCA showed significant discrimination between the 4 manufacturing stages. The key VOCs

that predominantly discriminated each stage after SIMCA analysis and subsequent least squared means analysis using SAS revealed that 2-methylpropanal, 3-methylbutanal, butanal and propionic acid were significantly highest at the time of cutting; acetic acid and methional at the end of warm room; butanoic acid, ethyl methyl sulfide and 3-methylbutanoic acid at the end of pre-cool; and ethanol and 2,3-butanedione in out-of-press samples. Another significant finding of this study was the apparent variability of the VOC profile in cheeses at each stage made in different vats and manufactured on the same day. Variability is most probably related to the changes in microflora and environmental conditions at each stage. Such findings could be used to explain and control the flavor and aroma heterogeneity of the cheese samples, especially for the cheeses at the time of cutting and packaging.

Key Words: Swiss cheese, volatile organic compounds (VOC), selected ion flow tube mass spectrometry (SIFT-MS)

W227 Tracking the progression of thermoduric bacteria during the manufacture of Cheddar cheese—A case study. K. Bhanduriya*, S. Anand, and L. Metzger, *Midwest Dairy Foods Research Center, Dairy Science Department, South Dakota State University, Brookings.*

Many groups of thermoduric bacteria are known to cause slits, weak body or blowing defects in Cheddar cheese. These organisms are likely to increase during a typical Cheddar cheese making long run of 18 to 20 h, because of in-process multiplication and concentration. The present study was conducted to scan the thermoduric progression during Cheddar cheese manufacture in a commercial cheese plant. Three independent cheese manufacture runs were analyzed at monthly intervals. The entire process was divided into 3 sampling stages; raw milk, pasteurized milk, and cheese blocks. Samples were drawn in duplicates at 4 different time intervals; start of the cycle, pre mid-day wash, post mid-day wash, and end of the cycle. The microbiological analysis was conducted for thermoduric mesophiles and thermoduric thermophiles using standard techniques. Analysis of variance was used to compare mean counts. The average mesophilic counts in raw milk samples were log cfu 4.6/mL, of which, log 1.9 were thermodurics. Pasteurization process was able to bring down the total mesophilic count by 3–4 logs. The thermoduric mesophiles did not increase during the pasteurization duration. The average counts of thermoduric thermophiles in raw milk were log cfu 1.5/mL. These counts were shown to increase by about 1.0 log during pasteurization run of 9–10 h, which indicates a build-up of thermoduric thermophiles during the process of pasteurization. Mid-day wash was able to reduce this thermophilic increase by about 1.5 logs, as established by pre and post mid-day wash counts. However, the thermophilic build up during pasteurization was noticed again near the end of the 20-h run. Similarly, the cheese made early in the day or soon after the mid-day wash showed lower thermoduric thermophiles (average 2.15 log cfu/g) as compare with the cheese made before mid-day wash or at the end of the production run (average 2.7 log cfu/g). Further studies related to the effect of long production run hours on the population of thermodurics during ripening and its effect on cheese quality parameters are under progress.

Key Words: thermoduric, thermophile, Cheddar cheese

W228 Causative organisms for slit defects in Cheddar cheese samples—A case study. K. Bhanduriya*, S. Anand, and L. Metzger, *Midwest Dairy Food Research Center, Dairy Science Department, South Dakota State University, Brookings.*

Appearance of slits due to gas production, during ripening of Cheddar cheese, is a sporadic yet reoccurring problem faced by cheese manufacturers. A wide variety of facultative and obligate heterofermentative bacteria have been associated with these defects. The present study was conducted to identify the causative bacteria in Cheddar cheese samples with slits to help design a control strategy later on. The cheese samples drawn from 10 (18-kg) cheese blocks of 2 different lots, aged about 3 mo, were obtained from a commercial cheese manufacturing plant. The slits were spherical or oval in shape, and majority of them were concentrated toward the center of the sampled blocks. In the case of plug samples, the slits were observed to be unevenly distributed. Some of the plug samples were very fragile due to the gas holes. Two samples of 100 g each were drawn from the cheese blocks and 11g samples were plated in duplicates for the species of *Lactobacillus* on de Man, Rogosa, and Sharpe (MRS) agar, *Lactococcus* on M17 agar with 10% added lactose, coliforms on violet red bile agar (VRBA), anaerobic spore-formers on reinforced clostridial medium agar (RCM), and yeast and molds on potato dextrose agar (PDA). Statistical comparison of counts within spoiled samples indicate RCM counts were significantly different between the lot ($P < 0.0001$) whereas M17 and MRS were not. Representative colonies of the isolates were Gram stained for purity, and were tested for gas production in skim milk with 1% glucose, and the organism specific media broths with the inverted Durham tubes. Biochemical identification of the isolates was performed using API CH50 strips. The gas producing isolates from MRS agar were identified to be *Lactobacillus fermentum*, and from the RCM belonged to genus *Clostridium*. *Lactobacillus* isolates were observed to be of both thermophilic and mesophilic types, while the *Clostridium* isolates were thermoduric mesophiles. The present study thus indicates the involvement of lactobacilli and clostridia in causing the slit defects in Cheddar cheese samples.

Key Words: Cheddar cheese slits, *Lactobacillus*, *Clostridium*

W229 Impact of cation substitution on composition and microbiology of reduced-fat Cheddar cheese. D. J. McMahon*[1], C. J. Oberg[2,1], L. V. Moyes[2,1], M. A. Drake[3], and N. Farkye[4], *[1]Western Dairy Center, Utah State University, Logan, [2]Department of Microbiology, Weber State University, Ogden, UT, [3]Department of Food, Bioprocessing, and Nutrition Sciences, North Carolina State University, Raleigh, [4]Dairy Products Technology Center, California State Polytechnic University, San Luis Obispo.*

Substituting potassium (K) for sodium (Na) in cheese can assist in reducing overall dietary Na intake. Our objective was to evaluate the effect of partial Na substitution on composition and microbiology of 50% reduced-fat (RF) Cheddar cheese. Seven RF Cheddar cheeses were made with molar salt contents equivalent to 2.1% (wt/wt) NaCl but with different ratios of Na, K, Ca and Mg cations, along with a cheese containing 0.7% NaCl. Cheese was made using pre-acidification to pH 6.35 and adding lactococcal starter and a lactococcal/lactobacilli adjunct culture. Control cheese was made using 100% NaCl and then 10%, 25%, 50% and 75% substitution with KCl. Additional cheeses were made with 50% NaCl, 40% KCl and 10% $CaCl_2$ or $MgCl_2$. During 6 mo storage at 6°C we measured pH, water activity, water-soluble N (WSN), organic acids, total lactic acid bacteria (LAB), lactococci, and nonstarter LAB (NSLAB). Control cheese had a mean composition of 48.4% moisture, 35% FDB, 27.0% protein, and 2.12% salt. Cheeses with K substitution had similar composition. When 10% Ca was added during salting, cheese moisture was lower at 43.7% ($P < 0.05$). There was no difference in water activity among full salt cheeses with mean value of 0.963 while the low salt cheese was 0.015 higher ($P < 0.05$). Changes in most of the organic acids followed similar trends for all 2.1% cheeses. Lactic acid

was initially lowest (and pH highest) in cheeses with higher Na levels, and increased during storage till by 3 mo all cheeses were similar. All cheeses had mean lactococci levels of 10^7 to 10^8 cfu/g and NSLAB of $\leq 10^2$ cfu/g. Lactococci stayed dominant throughout storage at ~10^6 cfu/g and for most cheeses the NSLAB were $\leq 10^4$ cfu/g. There was no apparent difference in bacterial numbers between cheeses containing 2.1% or 0.7% salt. In conclusion, differences in whey syneresis of RF compared with full-fat cheese was that calcium had been reduced from 0.8% to 0.6% and that dominance of lactococci throughout storage was a combined effect of a slightly lower salt-in-moisture content (4.3% versus 4.8%) and addition of the adjunct culture. Otherwise, substituting K for Na had little effect on cheese microbiology.

Key Words: cheese, sodium, potassium

W230 Production of reduced-fat Majorero cheese using supercritical CO_2. D. Sanchez-Macias*[1,2], A. Laubscher[1], N. Castro[3], A. Arguello[3], and R. Jimenez-Flores[1], *[1]California Polytechnic State University, San Luis Obispo, [2]Agroindustrial Engineering Department, Universidad Nacional del Chimborazo, Riobamba, Ecuador, [3]Department of Animal Sciences, Universidad de Las Palmas de Gran Canaria, Arucas, Spain.*

Consumer trends for healthier food choices and preferences for low-fat products have increased the interest in low-fat cheese and nutraceutical dairy products. However, consumers still value flavor over attributes in food. There are several strategies to produce low fat cheese. The method reported in this manuscript is another option to the conventional cheese-making strategy to produce reduced/low fat cheese. Using CO_2 as supercritical fluid ($scCO_2$) offers an alternative to reduce fat in cheese after ripening, maintaining the initial characteristics and flavor. The aim of this experiment was to evaluate the effect of pressure (100, 200, 300 and 400 bar) of the $scCO_2$ on the amount of fat extracted, microbial population, polar lipids profile, and microstructure of 2 varieties of goat cheese: Majorero (a PDO cheese from Spain), and goat Gouda-type cheese. The amount of fat was reduced 50–57% and 48–55%, for Majorero and goat Gouda-type cheeses, respectively. Higher content of sphingomyelin and phosphatidylcholine on fat basis were found in Majorero cheese compared with the control, and also compared with goat Gouda-type cheese. The microbial population was reduced after the supercritical fluid extraction in both cheeses, and the lethality was higher as pressure increased in Majorero cheese, most noticeably reductions on lactococcus and lactobacillus bacteria. Gouda-type cheese did not contain any lactobacillus. Micrographs obtained from confocal laser scanning microscopy showed a more open matrix and whey pockets in the Majorero control cheese. This could explain the effective fat extraction and significant reduction on the microbial counts in this cheese after the treatment with $scCO_2$. The results of this study demonstrated that the supercritical fluid extraction with $scCO_2$ process has potential in the dairy industry and commercial applications. Majorero cheese obtained after the SFE treatment is an excellent candidate to be considered as reduced fat goat cheese, with significant lower cholesterol, but still with all the flavor and health benefits inherent to the goat milk.

Key Words: reduced-fat cheese, supercritical CO_2, goat cheese

W231 Effect of post manufacture thermal dip treatment on proteolysis of commercial string cheese during refrigerated storage. M. K. Hsu* and P. S. Tong, *California Polytechnic State University, San Luis Obispo.*

Due to its convenience, nutritive value, and fun appeal, string cheese is a popular snack for kids today. It can string in fibers when pulled apart and this quality has transformed how consumers eat cheese. Graders judge string cheese by its stringiness; samples with copious string are highly awarded. But just as the texture of natural cheeses softens with time, the stringy texture of string cheese can diminish with age too. Age related softening in cheese is due mainly to proteolysis. Previous research has examined the effects of changing curd-cooking and curd-stretching temperatures on the extent of proteolysis in Mozzarella. Increasing the temperatures for both cooking and stretching processes were successful in decreasing the amount of α_{S1}-CN breakdown, the action that causes softening. We reason that a post manufacture heat treatment of cheese could inactivate proteolytic enzymes. The main objective of this study was to determine the effects of a post manufacture thermal dip treatment on proteolysis in packaged, commercial string cheese. Proteolysis was observed by using urea-PAGE electrophoresis and by measuring % water-soluble nitrogen (%WSN). String cheese was sourced on 2 occasions and treated 6 d after manufacture. Treatment consisted of dipping cheese in water at 55°C, 75°C, and 95°C for 30 and 60 s at each temperature. String cheese that did not undergo treatment served as a control. Cheeses were stored at 4°C until sampling for urea-PAGE and WSN extraction on d 1, 11, 22, 29, 49, 91, and 172 after treatment. The degree of β-CN breakdown did not change between all treatments throughout storage. This was expected since Mozzarella should have higher plasmin activity due to inactivation of plasmin inhibitors and activation of plasminogen from any thermal process. There was a trend of slightly more intact α_{S1}-CN in the most severely treated cheese (95°C for 60s) compared with the control at the final time point. However, only ripening time had a significant effect on %WSN ($P < 0.0001$). Extending the storage time may show a clearer effect of the treatment on secondary proteolysis.

Key Words: string cheese, proteolysis, thermal treatment

W232 Effect of partial substitution of sodium chloride with potassium chloride on physicochemical composition and sensory acceptance of Minas frescal cheese. J. M. V. Pires, A. T. B. Vieira, J. B. Miazaki, A. M. T. Roque, P. C. B. Vianna, and C. M. V. B. De Rensis*, *Universidade Norte do Paraná, Londrina, Paraná, Brazil.*

A high intake of sodium chloride causes negative effects on human health, because it is increasing the risk of heart attack and high blood pressure. Reducing the sodium content in cheese is expected to contribute to reducing the overall intake of sodium by world's consumers. Potassium chloride (KCl) has been studied as a salt (sodium chloride, NaCl) replacer in chesses. The effect of partial substitution of NaCl with KCl on physicochemical composition and sensorial acceptance of Minas frescal cheese was investigated. Two batches of Minas frescal cheese were made and kept in 3 different brine solutions (20%, wt/wt), including A) NaCl only, B) and C) 1NaCl:1KCl and then stored at 4°C for 1 h. After 5 d of manufacture cheeses were analyzed for pH, titratable acidity, fat, moisture, protein, ash and salt contents. Sensory acceptance and purchase intention were performed on d 7 of manufacture cheese with 36 untrained panelists. Results were analyzed by ANOVA and Tukey's test ($P < 0.05$). No significant difference was found in physicochemical composition. The cheeses showed no significant differences ($P > 0.05$) regarding to attributes appearance, overall impression and texture. 1NaCl:1KCl cheese received lower scores for flavor and purchase intention showing that this cheese was not well accepted.

Key Words: acceptance, Minas frescal cheese, salt

W234 Effects of chelating agents on texture of low-fat Cheddar cheese. M. Poveda*, M. Arnold, and N. Farkye, *California Polytechnic University-San Luis Obispo, San Luis Obispo.*

Effects of 2 types of chelating agents on proteolysis and texture properties of low-fat Cheddar cheese (LFC) were analyzed and compared with full fat Cheddar (FFC) control during ripening for 120 d. We hypothesized that chelating agents would bind calcium ions from cheese matrix to give a softer curd due to decrease of protein-protein interactions and simultaneously increase in cheese moisture. Whole milk was skimmed to 0.57% fat for LFC manufacture. The LFC milk was divided into 3 lots (A, B, and C). Sodium citrate (SCLFC) and disodium EDTA (SELFC) were added to A and B at the rate of 0.02% and 0.2%, respectively. C served as control (CLFC). LFC milk (88°F) was preacidified to pH 6.2 before setting using 34 mL chymosin/454 kg and starter culture addition. After cutting, curd was cooked to 96°F in 30 min and held for 10 min. After cooking, the curd was washed, salted, hooped and pressed. FFC was made using the same batch of whole milk by the stirred curd method. Cheesemaking was replicated 5 times. Table 1 shows composition, water-soluble nitrogen (WSN) and TPA hardness of the cheeses. Results suggest that chelation of calcium in low-fat cheese reduces cheese hardness and improve texture of low-fat Cheddar cheese.

Table 1. Composition, WSN and TPA hardness of low-fat and full-fat Cheddar cheeses

	FDM	Protein	Ca	WSN (%)			TPA Hardness (g)		
Cheese	(%)	(%)	(g/kg)	7 d	60 d	120 d	7 d	60 d	120 d
FFC	50.1	27.2	730	5.65	14.26	20.31	8657.7	6562.7	5527.7
CLFC	12.3	37.5	622.5	6.91	16.5	21.04	12747.6	9965.2	8111.5
SCLFC	13.0	37.3	477.5	6.86	14.87	20.57	10552.1	8664.7	7317.7
SELFC	13.3	35.6	502.5	6.76	16.62	22.17	10046.8	9121.4	7445.7

Key Words: proteolysis, texture, low-fat Cheddar cheese

W235 Heating curd grains during cheese-making could affect the appearance of fat and the phospholipids content in cheese. D. Sánchez-Macías[1,2], A. Laubscher[1], N. Castro[3], A. Argüello[3], and R. Jimenez-Flores*[1], *[1]Dairy Products Technology Center California Polytechnic State University, San Luis Obispo, [2]Agroindustrial Engineering department, Universidad Nacional del Chimborazo, Riobamba, Ecuador, [3]Department of Animal Science, Universidad de Las Palmas de Gran Canaria, Arucas, Las Palmas, Spain.*

Analyzing the phospholipids content in different dairy products, it is affirmed that the ruptured membrane parts will preferentially migrate to the serum phases, resulting in an alteration of the phospholipid/lipid ratio in cheese. The literature reports that heating the curd grains induced the formation of fat globules aggregates, and pressing of the curd grains resulted in the greatest disruption of milk fat globules, their coalescence and the formation of nonglobular fat (free fat). Using CO_2 as supercritical fluid ($scCO_2$) offers an alternative to reduce fat in cheese after ripening, maintaining the initial characteristics and flavor. The aim of this experiment was to evaluate the effect of pressure (100, 300 and 400 bar) of the $scCO_2$ on polar lipids profile and microstructure of 2 varieties of goat cheese: Majorero, (an artisan cheese from Spain), and commercial goat Gouda-type cheese. Sphingomyelin and phosphatidilcholine were detected in Majorero cheese. In Gouda cheese, a little sphingomyelin was detected in the treated cheeses. In majorero control cheese, the fat seems to have a coalesced or nonglobular appearance into the whey pockets. In Gouda-type control cheese, fat appears as nonglobular fat. Because heating the curd grains is part of the Gouda making-cheese, but not in Majorero, it could explain the large fat globules found in the images of control goat Gouda-type cheese, compared with control Majorero cheese. The shape of fat in control Gouda-type cheese images obtained with CLSM in this study and the lower phospholipids content found in the TLC analysis are results that concord with the heating curd grains during cheese-making.

W449 Evaluation of off-flavor development in Alpine cheese using selected ion flow tube mass spectrometry (SIFT-MS). E. Berusch, K. Taylor, and W. J. Harper*, *The Ohio State University, Columbus.*

A manufacturer of Alpine cheese has found that within three weeks of removing their product from vacuum packaging, off-flavors start to develop in the cheese. It was speculated that the development of these off-flavors was caused by lipid oxidation. The objective of this study was twofold: determine if the flavor change is, in fact, caused by lipid oxidation, and if it is not, find the agent causing the flavor profile to change. Both goals were met by using selected ion flow tube-mass spectrometry (SIFT-MS) to evaluate two different lots of Alpine cheese, #153 and #160. SIFT-MS is a direct mass spectrometric technique used to quantify volatile compounds in the headspace of a sample in real time. To prepare the samples, both cheeses were divided in half and grated – one part vacuum sealed and the other part exposed to oxygen. Over the course of 56 days, both the cheese exposed to oxygen and the vacuum-packed cheese were examined for development of off-flavors using SIFT-MS for cheese #153 and #160. Concentrations of 32 compounds in the cheeses, including alcohols, aldehydes, ketones, esters, sulfur compounds, and pyrazines, were analyzed. The results showed that 6 to 7 compounds, which changed in concentration over the testing period in samples exposed to oxygen, were derived from degradation of amino acids and lipids. This suggests that the off-flavor production in the Alpine cheeses are due to amino acid degradation as well as lipid oxidation. The compounds that underwent significant concentration changes, however, varied between cheese #153 and #160. In addition, the impact of time and oxygen on cheese #160 appears to be far greater than that on cheese #153. Further studies will be done to narrow down the causes of the changes in the Alpine cheese flavor profile and to determine ways to prevent the development of these off-flavors.

Key Words: oxidation, cheese, SIFT-MS

Companion Animals:
Companion Animal and Comparative Animal Nutrition

W236 Compositional analysis of various whole grains and whole grain dog treats. A. N. Beloshapka*[1], P. R. Buff[3], and K. S. Swanson[1,2], [1]*Department of Animal Sciences, University of Illinois, Urbana,* [2]*Division of Nutritional Sciences, University of Illinois, Urbana,* [3]*The Nutro Company, Franklin, TN.*

Whole grains, including the resistant starch (RS) components, may be beneficial to canine health through the use of a baked treat matrix; however, the use of whole grains in pet food has not been thoroughly evaluated. Our first objective was to measure the chemical and starch composition of various whole grains, processed grains and grain components which may be incorporated into baked treats for dogs. Thirty-one grain samples, including whole yellow corn, conventional quinoa, organic spelt hull pellets, conventional whole millet, conventional hulled millet, sorghum, brown rice, rice, rice flour, rice bran, whole wheat, potato flake, whole pearled barley, barley flake, cut barley, pearled barley flakes, steamed rolled barley, ground pearled barley, malted barley, groats, steel cut groats, ground steamed groats, steamed rolled oat groats, instant oats, quick oats, regular rolled oats, oat fiber, oat bran #1, oat bran #2, oat flour, and oatmeal (ground) were analyzed. The grains contained the following: crude protein (1.71–17.04% DMB), fat (1.28–8.49% DMB), total dietary fiber (2.16–85.16% DMB), and RS (0.0–9.38% DMB). Because cooking alters RS content of whole grains, our second objective was to evaluate the chemical composition, starch composition and gelatinization score of commercial baked whole grain dog treats and baked whole grain dog treats processed to alter the RS content. Ten treat samples were analyzed, including 4 commercially available canine treats (Nutro Natural Choice Lite All Natural Biscuits, Nutro Natural Choice Skin and Coat All Natural Biscuits, Nutro Ultra Healthy Skin and Coat Blend All Natural Biscuits, Nutro Ultra Healthy Digestion Blend All Natural Biscuits) and 6 test dog treats processed to alter the resistant starch content. The treats contained the following: crude protein (9.80–19.72% DMB), fat (6.27–15.55% DMB), and RS (1.29–5.60% DMB). Based on our compositional analysis, whole grains vary greatly in nutritive value, but some may provide a generous amount of functional nutrients (i.e., total dietary fiber and RS) to dogs, but more research is needed to test the effects of whole grain containing dog treats in vivo.

Key Words: canine, treats, grain

W237 Increasing dietary water content increases voluntary physical activity in healthy adult cats. P. Deng*[1], M. Pallotto[1], and K. Swanson[1,2], [1]*Department of Animal Sciences, University of Illinois, Urbana,* [2]*Division of Nutritional Sciences, University of Illinois, Urbana.*

Low physical activity has been identified as a major risk factor for the development of feline obesity and diabetes. Increased dietary water content has been suggested as a method to reduce dietary energy density to maintain body weight (BW) in cats. The objective was to evaluate the effect of increasing dietary water content on voluntary physical activity in healthy adult cats fed to maintain BW. Ten healthy adult neutered male cats (4.39 ± 0.43 kg BW; 4.5–5 BCS on 9-point scale) were used in a crossover design consisting of 52 d (two 26-d periods). Both periods included a 14-d adaptation phase, a 7-d phase for voluntary physical activity measurement via Actical activity collars, and a 5-d phase for fecal and urine collection. Cats were randomly assigned to 2 rooms (5 cats per room) under a 16 h light:8 h dark cycle and remained in the same room throughout the study. Cats were group-housed in the rooms for 22 h/d and were individually housed 2 h/d in cages at feeding times (0900–1000 h and 1500–1600 h). Cats were fed the Royal Canin Adult Fit 32 diet without or with added water (added to kibbles to reach 70% water content 1 h before feeding) at amounts to maintain BW and BCS. Drinking water was available ad libitum. Activity levels were expressed as 'activity counts' per epoch (15 s). Daily average activity level of cats fed the 70% hydrated diet tended to be higher ($P = 0.06$) than cats fed the dry diet, especially during the dark period ($P = 0.007$). Two-h food anticipatory activity before the afternoon meal for cats fed the 70% hydrated diet was lower ($P = 0.05$) than cats fed the dry diet, but not at the morning meal. Despite no differences in fecal score or total fecal weight, cats fed the 70% hydrated diet had greater ($P = 0.002$) total urinary volume and lower ($P = 0.003$) urinary specific gravity, and tended to have greater ($P = 0.06$) fecal moisture compared with cats fed the dry diet. In conclusion, increasing water content without changing energy intake or dietary macronutrient composition appears to promote physical activity and influence urinary specific gravity, which may aid in weight loss or maintenance in cats.

Key Words: physical activity, dietary water content, cat

W238 Chemical composition of dietary items consumed by two lemur species (*Varecia variegata* and *Propithecus diadema*) in the Analamazaotra Special Reserve, Madagascar. B. C. Donadeo*[1], V. R. A. Randrianindrina[2], K. R. Kerr[1], S. L. Burke[3], E. E. Louis Jr.[3], C. L. Morris[3,4], and K. S. Swanson[1], [1]*University of Illinois at Urbana-Champaign, Urbana,* [2]*Université d'Antananarivo, Antananarivo, Madagascar,* [3]*Omaha's Henry Doorly Zoo & Aquarium, Omaha, NE,* [4]*Iowa State University, Ames.*

The objective of this study was to determine the nutrient concentrations of selected fruits and leaves consumed by free-ranging black-and-white ruffed lemurs (*Varecia variegata*) and diademed sifakas (*Propithecus diadema*) that had been re-located to the Analamazaotra Special Reserve in eastern Madagascar. Twelve known groups of *P. diadema* (1 to 4 lemurs) and 2 known groups of *V. variegata* (3 to 4 lemurs) were observed from October 2008 to March 2009 to determine the predominant food items consumed in the wild. Plant samples were collected the day after lemurs were observed feeding from them. After collection, samples were dried at 57°C and secured in heat sealed bags for transport to Omaha's Henry Doorly Zoo (OHDZ). The Nutrition Department at OHDZ then ground the samples and dried them at 105°C to obtain absolute dry matter (DM) values, after which a subsample of each was analyzed for organic matter (OM), gross energy (GE), and crude protein (CP) concentrations. Samples were then stored at 4°C until shipment to the University of Illinois (UI). At UI, 13 species (n = 36) were selected to allow analysis of both fruits (n = 15) and leaves (n = 21) from each species. Fat concentrations were determined via acid hydrolysis. Dietary fiber fractions of the samples were determined using the total dietary fiber (TDF), neutral detergent fiber (NDF), and acid detergent fiber (ADF) assays. Samples were also examined for free sugars and hydrolyzed monosaccharides via HPLC. Fat values for the fruit samples (range = 3.1% to 23.1%; median = 7.9%) were higher ($P < 0.05$) than those from the leaf samples (range = 1.5% to 11.1%; median = 3.7%). The protein:ADF ratio of fruits ranged from 0.10 to

0.97, while leaves ranged from 0.11 to 0.66. Median ADF concentration was 42.9% (range = 9.8% to 65.9%), which far exceeds the minimum 10% recommendation from the NRC's Nutrient Requirements of Non-Human Primates (2003). The data from this study will aid in improving understanding of the nutrient composition of dietary items available to wild lemurs and allow comparison to captive diets.

W239 Inclusion of fresh pork pancreas in raw pork-meat based diets for African wildcats (*Felis silvestris tristrami*) does not affect macronutrient digestibility. C. L. Morris*[1,2], S. L. Burke[2], and C. L. Bexten[2], *[1]Iowa State University, Ames, [2]Omaha's Henry Doorly Zoo and Aquarium, Omaha, NE.*

Small exotic felids are frequently fed raw meat-based diets in managed environments, including zoological institutions. In addition, feeding raw meat-based diets to domestic companion animals (dogs, cats) is becoming more common. Many companion animal owners feeding raw meat diets indicate improvements in macronutrient digestibility when raw pancreas is included in the diet, particularly for senior animals or for clinical conditions including pancreatic insufficiency; however, data to substantiate these claims are lacking. The objective of this study was to determine the influence of fresh pork pancreas inclusion, in a raw pork-based diet for African wildcats, on apparent total tract macronutrient digestibility. Four animals were used (2 males, 2 females) in a randomized crossover design that consisted of 4 raw meat diets including the standard beef-based zoological formula [Beef; 33.4% dry matter (DM), 56.9% crude protein (CP), 29.4% crude fat (CF) and 6.3 kcal/g gross energy (GE)]; pork with 0% added pancreas (P0; 31.1% DM, 54.1% CP, 32.6% CF, 6.3 kcal/g GE); pork with 3% (wt/wt as fed) (P3; 31.9% DM, 53.8% CP, 31.1% CF, 6.4 kcal/g GE); pork diet with 5% (wt/wt as fed) (P5; 31.7% DM, 54.2% CP, 31.3% CF, 6.3 kcal/g GE). Apparent DM (87.0 to 89.5%), OM (90.8 −92.7%), CF (97.5–98.6%) and GE (92.5–94.2%) digestibility values were high for all diets and were not affected by treatment. Crude protein apparent digestibility was higher ($P < 0.05$) in cats fed P3 (96.4%) compared with cats fed Beef (93.8%). Apparent CP digestibility for P5 and P0 were 94.8 and 95.0%, respectively and did not differ. Beef CP digestibility (93.8%) was lower ($P = 0.02$) than all 3 pork diets (95.4%) when contrasts were analyzed statistically; therefore, the difference between Beef and P3 was likely a result of the different protein source, not the inclusion of pancreas. Inclusion up to 5% fresh pancreas did not increase macronutrient digestibility in healthy animals. Additional research may be warranted to determine if inclusion of pancreas can improve digestibility in senior or GI-compromised animals.

Key Words: cat, raw diet

W240 Neither enzymes nor synbiotic supplementation influenced nutrient digestibility or fecal characteristics of dogs. B. S. Obeidat*, K. K. Guatam, and M. A. Ballou, *Texas Tech University, Lubbock.*

The objectives of this study were to determine the influence of enzymes or synbiotic supplementation on nutrient digestibility and fecal characteristics of adult mixed breed dogs (BW = 23.6 ± 2.45; n = 4) using a 3 × 3 Latin square design. Treatments were a control (CON), enzyme mixture (ENZ), or synbiotic (SYN). Each dog in the CON treatment was supplemented with 4 g/d of maltodextrin; whereas in the ENZ treatment, each dog was supplemented with 2 g/d of maltodextrin and 2 g/d enzyme mixture (fungal amylase, hemicellulase, xylanase, lipase, fungal protease, and acid stable protease). Dogs in the SYN were supplemented with 1.47 g/d of maltodextrin, 2 g/d of FOS, 0.5 g/d of MOS, and 109 cfu/d each of *Bacillus subtilis* and *Enterococcus faecium*. Each treatment was top dressed to ensure complete consumption of the 4 g. In each period, one of the treatment groups had 2 dogs while the other 2 groups had 1 dog (a total of 4 dogs per treatment). Dogs were housed in individual pens. Each period composed of 10-d as adaptation and 4-d period for data collection. During the collection period, total fecal was collected from each dog and frozen at −80°C for later analysis. Fresh fecal sample was taken during the last day of the collection period and analyzed for dry matter (DM), unbound water, pH, ammonia, and volatile fatty acids (VFA). A commercial dog food (Adult Large Breed; Hill's Pet Nutrition; Topeka, KS) was offered at 1.25% of metabolic BW. Body weight was measured at the beginning and end of each period. Enzyme or synbiotic supplementation did not ($P > 0.05$) change the BW. Nutrient digestibilities were not influenced ($P > 0.05$) by the enzymes or synbiotic supplementation. There were no differences ($P > 0.05$) observed for the fecal DM, unbound water, ammonia, or VFA concentrations between treatment groups. In summary, results demonstrate that enzymes or synbiotic supplementation did not affect performance of adult mixed breed dogs.

Key Words: canine, enzyme, synbiotic

W241 Prediction of metabolizable energy value of extruded dog food: Comparing values generated by equations proposed in the literature and values obtained in vivo. F. S. Ebina, R. C. S. Ogoshi, M. G. Zangeronimo, P. B. Rodrigues, F. M. O. B. Saad, and C. E. P. Saad*, *Federal University of Lavras, Lavras, Minas Gerais, Brazil.*

The most exact metabolizable energy (ME) estimation method of extruded dog foods is through in vivo digestibility trials. However, due to the difficulty in performing this methodology in commercial routine, faster, low cost, and accurate alternative is warranted. Various equations are already proposed in literature and are widely used. However, due to the differences in ingredients, formulations and analytical methods, it is important to evaluate if this equations are apt in predicting ME in Brazilian rations. The objective of this study was to evaluate the adjustment of equations existent in literature for the prediction of ME in extruded dog foods produced in Brazil and, to do this, digestibility trials were performed of 40 dry extruded food on adults Beagle dogs. Each food was offered in controlled amounts (130 kcal/kg $BW^{0,75}$) to 6 Beagle dogs, individually housed in metabolic cages during 10 d, with 5 d being of adaptation period and 5 d of total feces and urine collection. The ME in vivo values were compared with the values predicted by the equations that used the data of the chemical composition of the ingredients to calculate the energies. Segmentations were done on diets with ether extract (EE) above or below 12% and crude fiber (CF) above or below 2.5% to test the adjustments. The adjustments were evaluated by means of the standard error of estimate, of the coefficients of determination and by the acceptance of the hypotheses tests (a = 0; b = 1) of the linear adjustment (y = a + bx) when observed values of energy were compared with the predicted. The model ME = Digestible Energy – 1,07*Crude Protein (%) (NRC, 2006) was the best in the diet segments of EE above 12% ($r^2 = 0.70$), in the diets of CF above 2.5% ($r^2 = 0.90$) and CF equal or below 2.5% ($r^2 = 0.79$). For the diets of EE equal or below 12%, the best model was: ME = 0.84DE – 0.6 ($r^2 = 0.32$) (Kendall et al., 1985). None of the tested equations adapted satisfactorily to the prediction of the energy values of the 40 dog foods. Acknowledgment: CAPES and FAPEMIG.

Key Words: pet food, energy estimation, canine

W242 Prediction of digestible and metabolizable energy value in Brazilian extruded dog foods. F. S. Ebina[1], J. S. Dos Reis[1], J. Franca[2], C. E. P. Saad[1], and F. M. O. B. Saad*[1], *[1]Federal University of Lavras, Lavras, Minas Gerais, Brazil, [2]Federal University of Uberlandia, Uberlandia, Minas Gerais, Brazil.*

In Brazil, the cereal cultivars which generate the byproducts used in dog rations are different than those used in the USA and Europe and this possibly generates differences in the food's nutritional composition. It is also known that pluviometric index (i.e., amount of rain) and the duration of the rainy season may affect the nutritional value. There are also processing differences for animal meal, such as drying time, bone and blood inclusion, among others. Thus, the adequacy of the models currently used for energy prediction in diets fabricated with ingredients cultivated and processed in Brazilian soil is questioned. This study aimed at obtaining digestible energy (DE) and metabolizable energy (ME) prediction equations that attend the Brazilian market of extruded dog foods. Forty dry extruded dog diets were evaluated through in vivo digestibility trials. Each food was offered in controlled amounts (130 kcal/kg $BW^{0.75}$) to 6 Beagle dogs, individually housed in metabolic cages during 10 d, with 5 d being of adaptation period and 5 d of total feces and urine collection. Analysis of crude protein (CP), crude fiber (CF), ether extract (EE) and gross energy (GE) of the ingredients and DE obtained in vivo as independent variables, were used for the formation of the equations. The best DE and ME estimation models were selected. The evaluation of the energy prediction equation adjustments was done through simple linear regression between the in vivo energy values and the predicted values, the nullity hypothesis test and the evaluation of the coefficient of determination. The best models were: DE = −1628.58 + 1.20 GE (r^2 = 0.84) and ME = −1127.26 + 1.02 GE (r^2 = 0.71). Segmentations were done according to the levels of EE and CF; the selected equations were the following: EE above 12%, ME = −352.81 – 19.32 CP + 43.11 EE – 39.51 CF + 0.88 GE (r^2 = 0.90); CF above 2.5%, ME = 100.06 – 92.5 CF + 0.97 DE (r^2 = 0.94). Finally, to present reliability, it is necessary to validate the equations obtained in this trial using in vivo digestibility data obtained from extruded foods different than those used in this experiment. Acknowledgment: CAPES and FAPEMIG.

Key Words: equation, energy estimation, canine

W243 Joint R&D prospects for dairy development in India. J. Parekh*, *Dairy Consultant, Mumbai, India.*

The Indian dairy industry is a top ranker in the global dairy bandwagon, with an incredible milk production 120 million tonnes last year. However, the success and statistics certainly do not satisfy India's need for self-sufficiency in production and supply of this essential commodity. There is room, a joint one indeed, to tap the big opportunities which lie in the dairy sector, and the apparent high potential of industry in the wake of growing global demand. In this rapidly changing world and a highly competitive globalized economy, there is a need to exploit the available resources to the maximum. The best technologies developed in India and abroad should be brought to use to cope with the rising domestic demand for dairy products. Second, more emphasis on improving productivity of cattle is needed. While a lot of attention is being given to the dairy industry, little effort has been made in improving the productivity of cow or buffalo. When it comes to productivity we are among the last. Whatever we see in terms of increased productivity is on account of increase primarily in numbers and to some extent increasing crossbred population. It is time for the policy makers to focus on right inputs in terms of genetic constitution, better feeding practices, improved fodder and ensure equitable opportunities to the private sector in the Indian dairying. The whole eco system around dairying lacks capacity of building the farmers toward better productivity, animal health, breeding practices, clean milk production and better use of animal wastes. The whole world is becoming more and more environment conscious, therefore, dairy emissions is an important area to be controlled through intensive knowledge sharing and dissemination. There is a need to strengthen the milk processing industry also in terms of technology, carbon foot print and water miles. The production levels could really make India the dairy basket of the world. Indian dairy industry incurs high costs of production due to lack of scale, poor product mix, high wastage, costly cold chain and lack of R&D in the sector for both products and packaging.

Key Words: India, dairy sector, R&D prospects

W244 Improving the textural properties of non-fat yogurt by addition of milk-based protein additives. B. Delikanli and T. Ozcan*, *Uludag University, Bursa, Turkey.*

In recent years low fat and non-fat yogurts is becoming popular due to the increased demand for low calorie products. However, these products exhibit weak body, poor texture, and whey separation since fat and total solids contents are reduced. Thus, innovative practices and fortification of milk with some additives is essential to improve the textural properties of reduced-fat yogurts. The addition of dairy-based ingredients is a preferential technique to reduce syneresis in yogurt by increasing the density of protein matrix in the gel microstructure. The aim of this study is to investigate the effect of fortification with dairy-based ingredients on the textural properties of non-fat yogurts. These ingredients are sodium caseinate (Na-CN), calcium caseinate (Ca-CN), milk protein concentrate (MPC) and whey proteins; namely whey protein concentrates (WPC), whey protein isolates (WPI) and whey protein hydrolysates (WPH). Yogurt samples were manufactured with reconstituted skim milk using milk proteins at a level of 1%. Textural parameters (hardness, adhesiveness, cohesiveness, and springiness) were evaluated by TA-XT plus Texture Analyzer in yogurt samples at the 14th day of storage. Using milk proteins in yogurt manufacturing caused a more compact structure consisting of stiff casein particles and large aggregates along with increased hardness which also increase cohesiveness and springiness values resulting in improved textural properties ($P < 0.01$). Yogurts fortified with Na-CN, Ca-CN and MPC had higher values of textural properties than whey protein-based ingredients (WPC, WPI, WPH). The results revealed that the textural characteristics might be influenced by the differentiations within the milk protein ingredients that resulted from variations of composition, casein to protein ratios and production methods. It could be concluded that fortification of the milk base ingredients that increased gel matrix compactness might play a beneficial role in improving textural properties of set type non-fat yogurt and might be used to develop functional dairy products.

Key Words: yogurt, milk protein, texture

W245 Viability of probiotic bacteria in lactose-hydrolyzed milk. F. R. Zamariano, D. V. Tenan, P. C. B. Vianna, and C. M. V. B. De Rensis*, *Universidade Norte do Paraná, Londrina, Paraná, Brazil.*

Hydrolysis of lactose by β-galactosidase is one of the main technologies applied in the production of dairy products with low lactose. There is a general agreement that probiotics dairy products relieve the symptoms of lactose intolerance, such as intestinal discomfort. The aim of this research was to evaluate the viability of probiotic bacteria in lactose-hydrolyzed milk pasteurized. Three types of lactose-hydrolyzed milk were produced: control (without probiotic), with *Lactobacillus casei* (LC) and with *Lactobacillus acidophilus* (LA). The hydrolysis of lactose from raw milk was carried out, with β-galactosidase enzyme at 40°C/4 h. The milk was pasteurized at 68°C/2 min and cooled to 4°C. Each block of design was repeated twice in a total of 6 experiments. The results for physicochemical composition were analyzed by ANOVA and Tukey's test ($P < 0.05$). Glucose was quantified in diluted aliquots by employing the glucose oxidase colorimetric method. After 120 min about 98% of the lactose had been hydrolyzed. Pasteurized milk was evaluated on d 1, 7, 14 and 21 after manufacturing, by enumeration of probiotic bacteria, titratable acidity and pH. The physicochemical composition of milk was performed on the day of the manufacture and Difference from Control test was carried out after 3 d. Regarding the physicochemical composition, LC milk showed higher titratable acidity compared with the control milk. During refrigerated storage, there was an increase in titratable acidity for all treatments. Probiotics bacteria showed good viability in the milk with populations about 10^7 cfu/g and 10^6 cfu/g for LA and LC milks, respectively. For sensory analysis only LC milk was different from control milk. The probiotics bacteria remained viable throughout the storage period of the product with populations $>10^6$ cfu/g. Therefore, this food would be a good vehicle for adding such bacteria. LA milk would be the most appropriate, since showed higher counts of viable bacteria and furthermore, no difference was detected when compared with milk without addition of probiotics bacteria by the sensory panelists.

Key Words: β-galactosidase, milk, probiotic bacteria.

W246 Encapsulation yield, gastrointestinal resistance and storage stability of *Lactobacillus acidophilus* microencapsulated by spray-drying using sweet whey and skim milk. G. M. Maciel, K. S. Chaves*, C. R. F. Grosso, and M. L. Gigante, *Faculty of Food Engineering, University of Campinas, Campinas, SP/Brazil.*

The aim of this study was to evaluate the effect of the encapsulating matrix on the encapsulation yield, resistance to the passage through simulated gastrointestinal conditions and on the viability of L. acidophilus La-5 during storage. The samples were produced from solutions of reconstituted sweet whey or skim milk (30% total solids), inoculated with a suspension of *L. acidophilus* (1% vol/vol) and subjected to spray-drying at inlet and outlet temperature of 180°C and 85–95°C, respectively. The samples were packed, vacuum sealed, and stored at 4°C and 25°C. The encapsulation yield, moisture content and the resistance of the microencapsulated La5 compared with the free cells (control) during exposure to in vitro gastrointestinal conditions (pH 2.0 and pH 7.0) were evaluated. The probiotic viability was assessed at 0, 7, 15, 30, 45, 60 and 90 d of storage. All experiments were repeated 3 times and the data were analyzed by ANOVA and Tukey's test for the comparison between means ($P < 0.05$). Using skim milk as encapsulating matrix and storing the particles at 4°C resulted in the best protection of the L. acidophilus. However, regardless of the encapsulating matrixes and the storage temperatures, the encapsulated probiotic presented counting values $>10^6$ cfu/g after 90 d of storage, decreasing 0.43 cycles log, on average, after this period. The results indicate that both skim milk and sweet whey have technological potential for delivering spray-dried probiotic cultures without affecting its resistance to simulated gastrointestinal conditions, and also have the advantage of being able to be stored in room temperature. Acknowledgments: CNPq.

Key Words: probiotic, microencapsulation, gastrointestinal simulation

W247 Selective methodology for enumeration of *Lactobacillus acidophilus* in yoghurt and Prato cheese. K. S. Chaves*[1], C. Gebara[1], M. C. E. Ribeiro[1], A. L. N. Gandara[2], and M. L. Gigante[1], *[1]Faculty of Food Engineering, University of Campinas, Campinas, SP/Brazil, [2]Technical High School of Campinas, University of Campinas, Campinas, SP/Brazil.*

The choice of a suitable selective methodology for counting probiotic strains in combination with starter cultures depends on the microorganisms present in the product and its matrix. The aim of this study was to evaluate different methodologies for selective enumeration of *L. acidophilus* in probiotic yogurt produced with *Lactobacillus delbruecki* ssp. *bulgaricus* and *Streptococcus thermophilus* and probiotic Prato cheese produced with lactococci starter cultures. The conditions used for the selective count of L. acidophilus were: MRS-bile agar and MRS-clindamycin agar, incubated at 37°C for 72 h under anaerobic conditions; MRS-sorbitol agar incubated at 37°C and 45°C for 72 h under anaerobic conditions. For counting of *L. bulgaricus*, MRS agar at pH 5.2 and RCA at pH 5.3 were evaluated, both incubated at 45°C for 72 h under anaerobic conditions. *S. thermophilus* was evaluated in ST agar incubated at 30°C for 72 h and M17-lactose agar at 45°C for 72 h, both aerobic conditions. The lactococci starter culture was evaluated using M17-lactose agar incubated at 30 and 37°C for 72 h under aerobic conditions. The methodologies were used for the enumeration of pure cultures, and probiotic yogurt and Prato cheese. The experiment was carried out in a randomized block design with 3 replications. The results showed that the selective medium for counting *L. acidophilus* in yogurt was the MRS-bile agar incubated at 37°C for 72 h, while in Prato cheese was the MRS-sorbitol agar incubated at 45°C for 72 h both under anaerobic conditions. For counting of *L. bulgaricus*, *S. thermophilus* and lactococci starter culture, the selective media were RCA agar at pH 5.3 at 45°C, ST agar at 30°C and M17-lactose agar at 30°C, respectively. Evaluation of selective media for the enumeration of probiotics in dairy products proves to be necessary, because the presence of different strains may affect the results and, therefore, lead to erroneous conclusions about the presence of probiotics in products. Acknowledgments: FAPESP, CAPES.

Key Words: yoghurt, cheese, selective methodology

W248 Effects of various chain lengths inulin on the properties of yogurt with *Lactobacillus rhamnosus*. Z. Canbulat and T. Ozcan*, *Uludag University, Bursa, Turkey.*

Probiotics can be defined as living microorganisms that have proved beneficial effects on health of the host and that improve the intestinal microbial balance. *Lactobacillus rhamnosus*, which is one of the widely known probiotics is frequently used in infants formulas and children's food due to preventive and curing effects on diarrhea, dental caries, allergy etc. Inulin is a prebiotic food ingredient that increases the activity of *L. rhamnosus*, increases calcium absorption and is a good source of dietary fiber. Polymerization degree of the inulin and probiotic bacteria strain affects the growth and viability of probiotic cultures in the probiotic fermented dairy products with inulin. The objectives of this study were to determine the effects of inulins with various chain lengths (short and long) on yogurt fermentation and survival of *L. rhamnosus* in yogurt during 28 d of storage. Inulins of short and long chain lengths were incorporated at 2% (wt/wt) of the yogurt mix and inoculated with *L. rhamnosus* and mixed cultures of *Lactobacillus delbrueckii* ssp. *bulgaricus* and *Streptococcus thermophilus*. In this study, viability of *L. rhamnosus*, physico-chemical and sensory properties (appearance, body and texture, flavor, taste and color) in the yogurt samples were evaluated. Organic acid (e.g., lactic, acetic, citric and propionic) profile was determined using a HPLC method. The result indicates that viability of *L. rhamnosus* in probiotic yogurt was enhanced by using short-chain inulin. Increased degree of polymerization led to decreased rate of consumption of inulin by *L. rhamnosus*. Syneresis was increased with addition of short chain inulin with high titratable acidity but higher flavor and taste scores than the yogurt containing long-chain inulin. However chain lengths of inulins did not affect consistency, color, and appearance and organic acid profile. Long-chain inulin did not influence *L. rhamnosus* bacteria viability during the storage of yogurt than short-chain inulin. Therefore, it is not recommended to use inulin with long-chain to improve the viability of the probiotic strain and sensory properties of yogurts.

Key Words: yogurt, *L. rhamnosus*, inulin

W249 Effect of chymosin on the functional and rheological properties of fresh Kou Wan Lao. Guo Ling*[1] and Jiang Yan[1], *[1]Key Lab of Dairy Science, Ministry Education, College of Food Science, Northeast Agricultural University, Harbin, Heilongjiang, China, [2]Key Lab of Dairy Science, Ministry Education, College of Food Science, Northeast Agricultural University, Harbin, Heilongjiang, China.*

Kou Wan Lao (KWL, also called as Gua-nai by researchers in the United States) is a traditional dairy product in China, which was manufactured by the milk-clotting enzymes from Chinese wine cake culture raised on steamed glutinous rice (sweet rice). Its smooth taste and attractive flavor are preferred by many Chinese, but its soft texture and complex manufacture method limits its industrial production. This study investigated the contribution of adding chymosin as the same time to the functional and rheological properties of KWL to decreasing manufacturing time and improving the texture. KWL was manufactured from pasteurized, homogenized milk using a commercial Chinese wine cake culture. Chymosin was added at different levels. The functional and rheological properties were determined after 1 to 8 d of storage at

4°C. At all chymosin levels, KWL were bright white and pale yellow. The micrograph of environment scan electronic microscopy (ESEM) showed that structure of KWL was sandwich-like. The thickness of layers became denser with increasing chymosin concentration. The results will be useful in commercialization of this traditional dairy-based product with optimum quality.

Key Words: Kou Wan Lao, chymosin, rheology

W250 Preliminary studies on the use of a novel electromagnetic fluid conditioner to modify the functional properties of nonfat yogurt. S. Menard, S. Bala, J. K. Amamcharla*, and K. Schmidt, *Department of Animal Sciences and Industry, Kansas State University, Manhattan.*

The present study evaluated the potentiality of a novel electromagnetic fluid conditioning (EFC) treatment to skim milk to modify the functional properties of nonfat yogurt. The EFC generates concentrated magnetic field that provides a temporary change in the physical properties in aqueous phase. It has been reported that the EFC alters the surface tension and interfacial tension of oil and water. Consequently, the EFC provides unique changes in functionality in dairy products that can be exploited to improve quality. Hence, the objective of the study was to evaluate the EFC on the functional properties of nonfat yogurt. For this purpose, commercial skim milk was obtained from the Kansas State Dairy Plant and divided into 3 sub-samples. Two of the sub-samples (E30+ and E30−) were treated using the EFC at 30VDC in positive and negative directions, respectively. The third sub-sample served as a control. The maximum magnetic flux density was found to be 3380 gauss at the center of the EFC. The control and magnetically treated samples were then heated to 90°C for 10 min, cooled to 43°C, and inoculated with a commercial yogurt culture. The milks were then incubated at 43°C. When the pH reached 4.5, the yogurt samples were stored at 4°C and performed water holding capacity (WHC), firmness, and syneresis using well established respective methods. Three independent replications were carried out on 3 different days. Titratable acidity and pH of the yogurt samples were not significantly different ($P > 0.05$). Also, WHC of magnetically treated yogurt samples was not significantly different from control ($P > 0.05$). However, syneresis of magnetic treated samples was significantly lower ($P < 0.05$) than the control. Consequently, firmness of control was found to be significantly higher ($P < 0.05$) than the treated samples. Based on the data obtained, EFC treatment of skim milk has potential to modify some functional properties of nonfat yogurt. However, further experiments are needed to study the intrinsic changes that are taking place in milk during the EFC treatment.

Key Words: electromagnetic fluid conditioner, nonfat yogurt, functional properties

W251 Microbiological and physical-chemical characteristics of fermented milk beverages. E. H. P. Andrade, M. O. Leite*, M. M. O. P. Cerqueira, L. M. Fonseca, C. F. A. M. Penna, M. R. Souza, T. Roza, B. S. Assis, M. F. S. Resende, A. F. Drummond, and N. M. A. Silva, *Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil.*

This work aimed to evaluate microbiological and physical-chemical characteristics of fermented milk beverages available in big supermarket chains in Belo Horizonte, Minas Gerais State, Brazil. A total of 40 samples of fermented milk beverages were collected at the market, being 8 samples from 5 brands. The samples were analyzed in the last week of their shelf-life. The parameters evaluated were: total and thermotolerant coliforms, *Salmonella* spp. presence, coagulase positive staphylococci count, mold and yeasts count, total count of lactic acid bacteria, water and volatiles content, total solids, protein content, fat content, pH and titratable acidity. These samples showed satisfactory microbiological quality. The lactic acid bacterial counts were higher than the minimum required by the Brazilian legislation. The morphological and biochemical characteristics of the isolates suggested the presence of *Streptococcus* spp. and *Lactobacillus* spp., which was confirmed by PCR-ARDRA 16S-23S, in products from all brands. It was also possible to identify *Lactobacillus delbrueckii* in 3 brands. Means of fat content, protein content, titratable acidity, pH, water and volatiles content and total solids ranged from 1.24 to 1.98%, 1.88 to 2.22%, 0.54 to 0.66%, 3.91 to 4.16%, 81.18 to 83.25% and 16.75 to 18.82%, respectively. Means of protein content were higher than the minimum required by the Brazilian legislation.

Key Words: fermented milk beverages, microbiology, physical-chemical

W252 Assessment of the viability of *Lactobacillus casei* in carbonated milk beverage. C. S. Jadão, S. A. M. Floriano, C. M. V. B. de Rensis, G. A. N. Costa, and P. C. B. Vianna*, *Universidade Norte do Paraná (UNOPAR), Londrina, PR, Brazil.*

The aim of this study was to produce a carbonated milk drink with probiotic and evaluate the viability of *Lactobacillus casei* during refrigerated storage. Milk beverage was produced with UHT milk and whey in the ratio of 70:30. Whey powder was reconstituted in water to 14% solids and then added to the UHT milk. The mixture was heated to 90°C/5 min, cooled to 10°C and added with 5% sugar and 5% passion fruit pulp, previously mixed and heated to 90°C/1 min. Milk beverage was then cooled to 4°C and divided into 2 treatments: (1) milk beverage added of *Lactobacillus casei* (2%) and without CO_2 addition; (2) milk beverage added of *Lactobacillus casei* (2%) and CO_2. The CO_2 was bubbled directly into the sample and the concentration was monitored by the reduction of titratable acidity. *L. casei* was added after carbonation. After treatment the samples were packed in sealed PET bottles and stored at 4°C. The pH, acidity and *L. casei* count were evaluated after 1, 7, 15 and 30 d of refrigerated storage. Results were evaluated by ANOVA and Tukey's test at the 5% significance level. The pH and acidity were affected only by storage time. Regardless of the treatment was observed a decrease in pH and an increased acidity in milk beverages with and without CO_2 addition. It may indicate post-acidification caused by probiotic action. The *Lactobacillus casei* count was not influenced by treatments, storage time and the interaction between these factors. *L. casei* inoculum has a concentration of 7.1×10^8 cfu/mL. The milk drink without CO_2 addition had initial and final *L. casei* counts of 1.6×10^7 and 1.1×10^8 cfu/mL, respectively. Carbonated drink milk showed values, for initial and final *L. casei* counts, of about 5.2×10^7 and 1.7×10^8 cfu/mL respectively, showing that CO_2 did not influence the probiotic count. Thus, the milk beverages can be considered probiotics, since presented *L. casei* count above 10^6 cfu/mL and this probiotic has remained viable during the storage time of the product.

Key Words: probiotic, carbon dioxide, milk beverage

W253 Production and sensory evaluation of high γ-aminobutyric acid-enriched fermented milk by *Lactobacillus plantarum*. T. Yan[2], C. Man[1], Y. Shan[1], J. Wang[2], X. Yang[2], Y. Deng[2], Y. Guo[2], M. Guo*[3], and Y. Jiang[1,2], *[1]National Dairy Engineering and Technology Research Center, Northeast Agricultural University, Harbin, Heilongjiang, China, [2]Department of Food Science, Northeast Agricultural*

University, Harbin, Heilongjiang, China, [3]Department of Nutrition and Food Sciences, The University of Vermont, Burlington, VT, USA.

γ-Aminobutyric acid (GABA) is a nonprotein amino acid that has been reported to reduce blood pressure in experimental animals and man. Dairy products such as functional probiotic-enriched fermented milk are good vehicle to transfer these beneficial microorganisms and valuable nutrients to consumers. The objective of this study is to produce fermented milk containing GABA by using *Lactobacillus plantarum* NDC75017 which isolated from traditional yogurt in Inner Mongolia of China. The fermentation parameters of *Lb. plantarum* NDC 75017 were optimized and the GABA content of yogurt was measured by high performance liquid chromatography (HPLC). Results showed that the maximum GABA concentration in fermented milk was 61 mg/100 g by the following conditions: 100 mmol/L L-sodium glutamate (L-MSG), 20 μmol/L pyridoxal 5′-phosphate (PLP), 2% inoculation concentration, the ratios of *Lb. plantarum*, *Lb. delbrueckii* ssp. *bulgaricus* and *thermophilus* at 0.5:0.5:1.5 and 43°C incubation until desirable pH values of 4.5 were reached. Fermented milk was stored at 4°C until sensory evaluation by consumers on d 7, 14, 21. Viscosity, Viscosity index, gel firmness were measured as sensory properties parameters is 1466.54 g·s, 146.79 g·s, 44.55 g, respectively. Our result showed that the appearance, flavor, texture, viscosity, and overall quality of the functional yogurt were comparable and was similar to general yogurts in market. The results of the study suggested that the NDC 75017 possessed a prospect to be applied in dairy and other health products with high nutritive values and functional properties. This work was supported by National Science and Technology Project (2011AA100902), National Natural Science Foundation of China (31171718), and Key Project of Education Department of Heilongjiang Province (12511z005).

Key Words: γ-aminobutyric acid, *Lactobacillus plantarum*, yogurt

W450 Sensory analysis of commercial packed vanilla ice creams using traditional sensory method and E-tongue in Taiwan. C. H. Chang[1], C.-S. Chen[2], G. C. C. Chuang[3], and B. K. Liou*[1], *[1]Central Taiwan University of Science and Technology, Taichung City, Taiwan, [2]Tungnan University, New Taipei City, Taiwan, [3]China University of Science and Technology, Taipei City, Taiwan.*

The purpose of this study was to evaluate the sensory characteristics of 10 commercial packed vanilla ice creams, including 7 local and 3 foreign brand products in Taiwan market, using descriptive analysis, consumer test and e-tongue. The 10 products were evaluated 34 attributes by 12 well-trained panelists using a 15cm unstructured line in descriptive analysis, were performed with a 9-point hedonic test by 60 college students for consumer test and were tested using a-ASTREE E-tongue. The descriptive analysis using principal component analysis showed 5 products, containing 2 foreign products, had the stronger intensity in sweetness, milky candy flavor, margarine flavor, fineness, creaminess and viscosity, 4 products were a significant characteristic in milky flavor, coconut flavor, walnut flavor and mouth coating as well as a foreign product, claimed vanilla bean used, had the higher intensity in vanilla flavor, medical flavor and icy feeling. The first partial least square (PLS) regression, used to relate the consumer ratings and the descriptive analysis ratings, showed that consumers like the product had a strong characteristic in milky flavor, walnut flavor, coconut flavor, creaminess and fineness but dislike the higher intensity in sweetness, milky candy flavor and icy feeling. The second PLS regression, used to relate e-tongue ratings and the descriptive analysis ratings, revealed GA sensor was positively correlated with vanilla flavor, medical flavor, sweetness, cooked sugar flavor and milky candy flavor; BB was positively correlated with sweetness, cooked sugar and milky candy flavor; JE and CA were both positively with margarine flavor but negatively correlated with sweetness and cooked sugar flavor; JB could have a positive relationship with milky flavor. This study concluded that there is a significant discrimination between the foreign and the local products in flavor characteristics such as sweetness and coconut flavor, Taiwan's consumers prefer the stronger intensity in milky flavor instead of sweetness and milky candy flavor, and the e-tongue is capable to effectively discriminate ice cream products.

Key Words: ice cream, sensory analysis, E-tongue

W254 Effects of aerobic exposure of corn silage on fermentation end-products and intake. A. A. Rodríguez*, D. Luciano, E. Pacheco, and L. C. Solórzano, *University of Puerto Rico, Mayaguez Campus, Mayaguez, Puerto Rico.*

Aerobically exposed silage has been associated with a decrease in its nutritional value and animal intake. The objective of this experiment was to determine the effect of length of aerobic exposure (LAE) on pH, fermentation end products, and intake by meat-type goats. Corn was ensiled in 5 kg sealed plastic silos. After a 60-d fermentation period, corn silage was aerobically exposed for 72, 48, 24, or 0 h in a 4-compartment wooden feeder before measurements. At the 0 h time point, DMI was determined during one day using 4 goats that previously had not consumed silage. Silage consumption was monitored at 2, 5, 8, and 24 h (ITP) after the goats had access to the silages. The experiment was replicated 4 times. Fermentation end products and pH were analyzed as a completely randomized design with 4 replicates. Intake was analyzed as a completely randomized design with 4 (LAE silages) × 4 (intake time points) factorial arrangement of treatments. Tukey test was used for mean separation. Total acidity (4.54 vs. 4.24), lactic acid content (2.92 vs. 4.08%), and the ratio of lactic acid:acetic acid (5.19 vs. 7.06) tended to be lower ($P < 0.15$) in corn silages exposed to air for 72 h than in fresh silage, but were similar to those in silages exposed for 48 and 24 h. Acetic acid content (0.79 vs. 0.41%) was higher ($P < 0.05$) in fresh corn silage vs. that exposed for 72 h, but was similar to silages exposed for 24 or 48 h. Regardless of LAE, propionic and butyric acid contents were similar ($P > 0.05$). Corn silage exposed during 48 h had higher ($P < 0.05$) NH3-N/Total-N % than those exposed for 24 or 72 h (8.72 vs. 6.24% or 6.77%, respectively), but similar to that exposed for 0 h (5.41%). Silage intake as a proportion of total silage offered was similar ($P > 0.05$) among treatments for LAE, ITP, and their interaction, and averaged 68.3%. In summary, LAE affected the fermentation end products of corn silage, but did not influence silage intake by goats.

Key Words: aerobic exposure, corn silage fermentation, intake

W256 Biological and chemical additives on the fermentation and aerobic stability of corn silage. N. Da Silva, I. De Oliveira, M. Bastos, A. Do Rego, C. Avila, and T. Bernardes*, *University of Lavras, Lavras, Minas Gerais, Brazil.*

In warm climates, the aerobic stability of silage is a very important factor in determining its quality. Thus, the objective of this study was to evaluate 2 Lactobacillus buchneri strains (a commercial product and an indigenous specie) and sodium benzoate in improving aerobic stability of corn silage. A corn hybrid was grown at University of Lavras (21°14′S; 45°00′W) and harvested at 50% milk line stage (36.8% DM). Chopped forage was treated with (1) deionized water (CON); (2) a commercial *L. buchneri* (CLB; strain CNCM-4323); (3) an indigenous *L. buchneri* (ILB), which was isolated from tropical forages; or (4) sodium benzoate at 0.2% (SB). Both inocula were applied at a rate of 1×10^6 cfu of bacteria/g of forage. Five replicates of each treatment were ensiled in 15-L plastic jars for 103 d. At silo opening, silage was removed and subsamples were taken. Aerobic stability was defined as the number of hours the silage remained stable before rising more than 2°C above room temperature. Aerobic deterioration was defined as the sum of the daily temperature increases above the reference temperature in the first 5 d of aerobiosis. Data were analyzed by using the GLM procedure of SAS according to a completely randomized design. Silages inoculated with ILB had greater pH value (4.05) than other treatments ($P < 0.05$). Acetate was higher in ILB silages (0.85% DM, $P < 0.05$) compared with CON silages (0.36% DM), and CLB and SB silages showed intermediate concentrations (0.67 and 0.48%, respectively). SB silages showed higher lactic acid concentration (5.86% DM, $P < 0.05$) than ILB silages (2.17% DM), and CON and CLB silages had intermediate values. The number of yeasts and molds was similar among treatments. However, SB tended to affect yeasts number ($P = 0.069$). SB silages differed in aerobic stability and aerobic deterioration than other silages. SB was the most effective additive, producing well-fermented silage and a long aerobic stability (161 h).

Key Words: aerobic deterioration

W257 Effect of applying potassium sorbate or sodium benzoate at two rates on the fermentation and aerobic stability of corn silage. I. De Oliveira[1], N. Da Silva[1], J. Dos Santos[1], O. Pereira[2], A. Evangelista[1], and T. Bernardes*[1], *[1]University of Lavras, Lavras, Minas Gerais, Brazil, [2]University of Viçosa, Viçosa, Minas Gerais, Brazil.*

Tropical climate provides conditions for the growth of aerobic spoilage microorganisms, which reduce silage quality. For silage producers in warm environments, adherence to management practices is critical to prevent or minimize aerobic deterioration, particularly in corn silages. Thus, the objective of this study was to evaluate the efficacy of 2 chemical additives (sodium benzoate or potassium sorbate), applied at 2 rates (0.1 or 0.2%), in improving aerobic stability of corn silage. A corn hybrid was grown at University of Lavras (21° 14′ S and 45° 00′ W) and harvested at 50% milk line stage (36.8% DM). Chopped forage was treated with potassium sorbate (PS) or sodium benzoate (SB). Both additives were applied at a rate of 0, 0.1 (D1) or 0.2% (D2) of fresh forage. Four replicates of each treatment were ensiled in 15-L plastic jars for 88 d. At silo opening, silage was removed and subsamples were taken. Aerobic stability was defined as the number of hours the silage remained stable before rising more than 2°C above room temperature. Aerobic deterioration was defined as the sum of the daily temperature increases (°C) above the reference temperature in the first 5 d of aerobiosis. Treatments were arranged in a 2 (type of additive) × 3 (dose of additive) factorial design. The GLM procedure of SAS was used to analyze the data. No interactions were observed between types of additive and their doses. Regarding additives, both produced silages with high standard of fermentation, combined with an intermediate aerobic stability (on average 146 h). With relation to doses, when the additives were applied at 0.2% silages were more stable (256 h, $P < 0.05$) than D1 and untreated silages (119 and 61 h, respectively). Aerobic deterioration was more pronounced in untreated silages (16.6°C, $P < 0.05$) compared with D1 and D2 silages (2.7 and 1°C, respectively). PS or SB applied at 0.2% was more effective in improving aerobic stability.

Key Words: silage additive

W258 Feeding corn silage improves nursing performance of Awassi ewes when used as a source of forage. B. S. Obeidat*[1,2], M. S. Awawdeh[1], R. T. Kridli[1], H. J. Al-Tamimi[1], M. A. Ballou[2], M. A. Abu Ishmais[1], F. A. Al-Lataifeh[1], and H. S. Subih[2], *[1]Jordan University of Science and Technology, Irbid, Jordan, [2]Texas Tech University, Lubbock.*

Objective was to evaluate the effect of using corn silage (SILAGE) or wheat hay (HAY) as a source of forage on nursing performance of Awassi ewes. Forty ewes (BW = 43.5 ± 1.58 kg) and their single lambs (BW = 6.3 ± 0.28 kg) were randomly assigned to 2 diets; SILAGE vs. HAY (4 pens/diet; 5 ewes/pen). Concentrate feeding was restricted to 1.1 kg DM/ewe/d, whereas forage was offered ad libitum. The study lasted for 8 weeks. Ewes and lambs were weighed at the beginning and at the end of the study. Milk yield and blood samples were collected on wk 2, 3, 4, 5, 6, 7, and 8. Intakes of forage and total DM were greater ($P < 0.05$) in ewes fed SILAGE compared with those fed HAY. Intakes of crude protein, ether extract and energy were greater ($P < 0.05$) in SILAGE compared with HAY group. However, neutral and acid detergent fiber intake was greater ($P < 0.05$) in the HAY than in the SILAGE group. At the end of the study, SILAGE-fed ewes gained more BW and their lambs had greater ($P < 0.05$) average daily gain compared with HAY-fed ewes. Glucose concentration was greater ($P < 0.05$) in the SILAGE compared with the HAY group, while serum urea N did not differ between diets. Daily milk and milk protein yield was greater ($P < 0.05$) in the SILAGE group than in the HAY group during wks 6, 7, and 8. Total solid yield was greater ($P < 0.05$) for the SILAGE than for the hay during wks 6 and 8; whereas fat yield was greater for the SILAGE than for the HAY diet on wk 8. Total energy output was greater ($P < 0.05$) for the SILAGE compared with the HAY diet. In conclusion, replacing wheat hay by corn silage in the diet of early lactating Awassi ewes improved intake, yields of milk and milk components, ewe body weight, and lamb average daily gain.

Key Words: Awassi ewe, corn silage, wheat hay

W259 The effects of an exogenous protease on the fermentation and nutritive value of poorly processed or well-processed corn silage. M. Windle*[1], C. Merrill[1], M. Agarussi[1], L. Rosa[1], K. Freedman[1], C. Asay[1], N. Walker[2], and L. Kung Jr.[1], *[1]University of Delaware, Newark, [2]AB Vista, Marlborough, United Kingdom.*

The objective of this experiment was to evaluate the effects of an experimental protease on silage fermentation and 7 h in vitro starch digestibility (ST-D) of whole plant corn with different degrees of kernel processing. Chopped whole plant corn (37% DM) was either poorly processed (PP, processing score of 53.9%) or well-processed (WP, processing score of 91.3%) and untreated (CTR) or treated with 2000 ppm of an experimental protease (ENZ, AB Vista, Wiltshire, UK). Forages were ensiled in vacuumed and heat-sealed bag silos at 21–23°C for 45 d. Data were analyzed as a 2 × 2 × 2 factorial arrangement of treatments with main effects of processing (PP and WP), enzyme treatment (CTR and ENZ), time of ensiling (0 and 45 d), and their interactions. Treatment with ENZ and degree of processing did not affect the concentrations of lactic and acetic acids ($P > 0.05$) in silage. However, treatment with ENZ resulted in higher concentrations ($P < 0.01$) of ammonia-N, soluble protein (% of CP), and ethanol in both WP and PP. The concentration of starch was less in WP-ENZ after ensiling compared with d 0 (45 vs. 36%, $P < 0.01$) but only numerically lower for other treatments (ave. 44 vs. 41%). Higher ethanol and lower starch may have been an indication that treatment with enzyme increased available substrate for fermentation. Prior to ensiling, the ST-D of freshly treated forage was between 60 and 65% for PP-CTR, WP-CTR, and PP-ENZ ($P > 0.05$) but was 74% for WP-ENZ ($P < 0.05$) suggesting some immediate effect of the enzyme. After 45 d of ensiling, ST-D was 75, 77, 84, and 89% for PP-CTR, WP-CTR, PP-ENZ and WP-ENZ, respectively. Treatment with ENZ increased ST-D in silages regardless of degree of processing ($P < 0.01$). Although the concentrations of ammonia-N, soluble protein, and ST-D were numerically greater in WP-ENZ vs. PP-ENZ, these differences were not statistically different.

Key Words: protease, starch digestibility, corn silage

W260 The effect of an exogenous protease on the fermentation and nutritive value of corn silage. M. Windle*[1], C. Merrill[1], L. Rosa[1], M. Agarussi[1], R. Savage[1], C. Asay[1], N. Walker[2], and L. Kung Jr.[1], *[1]University of Delaware, Newark, [2]AB Vista, Marlborough, United Kingdom.*

Previous work from our lab showed that adding high levels (2000 ppm) of exogenous proteases improved 7-h in vitro ruminal starch digestibility (ST-D) in ensiled corn silage. The objective of the current experiment was to test a range of levels of an experimental protease to more precisely determine an optimal level of treatment. Whole plant corn (37.5% DM) was chopped and processed without protease (CTR), or treated with 20 ppm (E1 ×), 200 ppm (E10 ×), 1000 ppm (E50 ×), or 2000 ppm (E100 ×) of protease (AB Vista, Wiltshire, UK). Forages were ensiled in vacuumed and heat-sealed bag silos, and stored at 21–23°C for 45 d. Data were analyzed as a 5 × 2 factorial arrangement of treatments with main effects of protease (levels) and time (0 and 45 d), and their interaction. After 45 d of ensiling, treatment with protease did not affect the concentrations of lactic or acetic acids ($P > 0.05$). Concentrations of ethanol were higher in E50 × and highest in E100 × silages as compared with CTR ($P < 0.05$). Silages that were treated with E1 × , E50 × and E100 × had more yeasts ($P < 0.02$) as compared with CTR. Silages that were treated with E50 × and E100 × had higher concentrations of ($P < 0.01$) ammonia-N as compared with CTR and E1 × . Concentrations of soluble protein (% of CP) on d 0 ranged from 28 to 37%, but after ensiling, were highest for E100 × (72%), followed by E50 × (68%), and E10 × (59%), and were lowest in E1 × (46%) and CTR (44%) ($P < 0.01$). The ST-D on d 0 ranged from 60 to 67% but after ensiling it was higher ($P < 0.01$) in E100 × (84%), E50 × (83%), and E10 × (81%) compared with E1 × (75%) and CTR (74%). These data indicate that a 200 ppm dose of protease was able to statistically improve ST-D after 45 d of ensiling. Protease treatment may be beneficial in accelerating the increase in ST-D that is normally observed in corn silage during time in storage.

Key Words: protease, starch digestibility, corn silage

W261 Impact of grain deposition on maize plant composition and feeding value. P. Walker*[1], M. J. Faulkner[1], T. D. Kaufman[1], L. Brown[2], and F. N. Owens[2], *[1]Illinois State University, Normal, [2]DuPont Pioneer, Bloomington, IL.*

Grain content of maize silage can be limited by management, environmental, and genetic factors. Impacts of lower grain content on nutrient yield and plant composition were studied in 2 trials. In trial 1, 2 tropical maize hybrids that failed to produce grain were compared with 6 temperate grain-bearing silage hybrids. Sets of whole plants were harvested at 7 d intervals starting 102 d after planting. Dry matter content of tropical hybrids plateaued at 25% DM. Across harvest dates, tropicals averaged 37% less dry matter per plant, in vitro digestibility of NDF was lower (34 vs. 45%; $P < 0.01$), but soluble sugar content was greater (17 vs. 9%; $P < 0.01$). Calculated production (milk or beef) per ton and per acre were 50 and 74% lower for tropical hybrids. In trial 2, pollination was prevented in subsets of 3 different temperate commercial grain-bearing silage hybrids by covering emerging ear silks with paper bags. Replicate sets of 5 plants per hybrid harvested on 16 different harvest dates were assayed for nutrient content. On the first harvest date (28%

DM for pollinated plants), dry plant weights and compositions were similar for pollinated and non-pollinated plants, but dry weight was 45% lower for plants without grain when the DM of pollinated plants reached 40%. Non-pollinated plants remained below 30% DM though their sugar content exceeded 20% of DM. Averaged across harvest dates, DM, starch, NDF, ADF and ash as a fraction of DM and in vitro NDF digestibility all were lower ($P < 0.01$) for non-pollinated plants. NDF and ADF yields declined with harvest date. Preventing pollination reduced beef and milk per ton and per acre by 50 and 65%. Factors that inhibit grain production, through reducing the sink for sugar, will increase the sugar content of plants but retard increases in plant DM content. Reducing the grain content of maize plants or premature harvest will reduce potential beef and milk production through reducing yields of digestible nutrients.

Key Words: grain, maize silage, tropical

W262 Impact of orientation of planted maize seeds on composition and feeding value of maize plants. T. D. Kaufman*[1], P. Walker[1], L. Brown[2], L. Nuzback[2], and F. N. Owens[2], *[1]Illinois State University, Normal, [2]DuPont Pioneer, Bloomington, IL.*

When planted with the tip downward, maize seeds emerge earlier and the first leaf emerges on the germ side of planted seeds. Through altering shading among plants, spatial seed orientation may alter yield and composition of maize plants. In 2011 using a 2 × 2 × 3 factorial design, 16 rows of 2 Pioneer silage hybrids at 2 populations (69,000 and 84,000 plants per hectare) were planted at 3 seed orientations [randomly (R) with a mechanical maize planter or manually with kernel points downward with the germ of each kernel either facing other seeds within the same row (W) or facing adjacent rows of maize (A) in an alternating fashion]. Harvested at 33% plant DM, plant DM and starch yields did not differ between W and A, but yields from oriented kernels (average of W and A) were 16 and 27% greater ($P < 0.05$) than for R. When harvested at 42% DM, plant and starch weights were 29 and 20% greater ($P < 0.05$) for W than R leading to 15% greater ($P < 0.05$) predicted milk and beef per acre. In 2012 using a 3 × 2 x 3 factorial design with 3 Pioneer hybrids, 2 plant populations, and 3 seed orientations, plants were harvested on a single date (41% plant DM). Angles of leaves relative to the germ were measured for 160 plants at each seed orientation. The first leaf emerged parallel to the germ azimuth (0.7 ± 32.8 degrees). Plant dry weights were greater for A than W. Compared with R, yields from A were 25% greater ($P < 0.05$) while ADF and NDF contents were 5 and 3% lower ($P < 0.05$). Silage and starch yields were 25 and 29% greater for A than R leading to estimates of 2% more beef and milk per tonne and 29% more ($P < 0.05$) beef and milk per hectare. At harvest, the number of dead leaves and husks was greatest ($P < 0.05$) for R plants. Through altering plant competition and capture of sunlight by leaves, spatial orientation of planted maize seeds altered projected beef and milk yield through increasing plant mass without markedly altering nutrient composition.

Key Words: maize silage, seed, orientation

W263 Effect of different silage additives on the fermentation and aerobic stability of corn silage. K. G. Arriola[1], O. C. M. Queiroz[1], J. J. Romero[1], M. A. Zarate[1], L. G. Paranhos[1], E. Muñiz[2], Z. X. Ma*[1], and A. T. Adesogan[1], *[1]Department of Animal Sciences, University of Florida, Gainesville, [2]Embrapa Tabuleiros Costeiros, Aracaju, SE, Brazil.*

The aim of this study was to compare the efficacy of different experimental silage additives on the fermentation and aerobic stability of corn silage. Corn forage was harvested at 35% DM, chopped and ensiled in mini silos after application of (1) water (T1), or with inoculants containing (2) 1.5×10^5 cfu/g of *Lactobacillus buchneri* (T2), (3) 1.5×10^5 cfu/g of *Lactobacillus plantarum* (20%), *Enterococcus faecium* (30%), and *Lactobacillus buchneri* (50%) (T3), (4) 1.5×10^5 cfu/g of *L. plantarum* (30%), *E. faecium* (40%), *Lactococcus lactis* (30%), and sodium benzoate at 0.4 g/kg forage (T4), (5) 1.5×10^5 cfu/g of *L. plantarum* (30%), *E. faecium* (40%), and *L. lactis* (30%) (T5), (6) 1.5×10^5 cfu/g of *L. plantarum* (40%), *E. faecium* (30%), and *L. lactis* (30%) (T6), and 7) 1×10^5 cfu/g of *L. plantarum* (T7). Five replicates of each treatment were weighed (11 kg) into 20-L mini silos, sealed and stored for 100 d at ambient temperature. Five additional replicates of each treatment were weighed (3 kg) into polyethylene bags and stored for 2 d. After silos were opened, aerobic stability, chemical composition, and yeast and mold counts were determined. By d 2 of ensiling, the pH of T5, T6 and T7 silages were lower than those of the Control silage (4.05 vs. 4.11, $P < 0.05$). After 100 d of ensiling, chemical component concentrations were unaffected by treatment except that ash concentrations were greater in T2, T3, and T5 silages than in Control silages. The T2, T3, and T5 silages had greater pH than other silages (3.89 vs. 3.83, $P < 0.001$). Treatments T4, T5, and T6 had greater aerobic stability than T1 and T3 (36.8 vs. 13.5 h). Silages T2, T3 and T4 had lower total VFA than T1, T6 and T7 (8.8 vs. 11.6% of DM, $P < 0.05$) and had the lowest isobutyric acid (1.73 vs. 2.43% of DM) concentrations. Treatments T3 and T7 had greater DM loss compared with other treatments (9.1 vs. 6.1%, $P = 0.04$). Treatment T5 was the most promising because it reduced silage pH within 2 d of ensiling, did not increase DM losses or decrease total VFA concentration and it increased aerobic stability.

Key Words: corn silage, bacterial inoculant, aerobic stability

W264 Comparison of nutritional and digestive differences of corn cultivars grown in cooler climates and harvested as fresh forage in western Canada. S. Abeysekara, K. Theodoridou*, D. A. Christensen, and P. Yu, *Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada.*

This study investigated the nutritional value of corn varieties grown in cooler climates. Corn grown in Canadian prairies is known as cool season corn, and is different by agronomical factors from warm season corn varieties. Samples from 6 corn cultivars (Pioneer and Hyland) with 4 fields which reached target crop heat units (>2000) were compared for major nutrients and digestive characteristics by means of wet chemistry, rumen in situ degradability, CNCPS, NRC and PDI feed evaluation methods. Based on the chemical composition, fresh forage from corn cultivars were nutritionally dissimilar and Hyland cultivars had some nutrients (NDF, 50.0% DM; CP, 7.4% DM) higher than Pioneer but not starch (21.1% DM). Diverse CNCPS fractions were found among both groups. Hyland had higher levels of CA4 (16.2% CHO), CB2 (47.0% CHO) and CC. Pioneer 7443R and Hyland SR06 had similar protein fractions which were higher than other cultivars. NRC energy calculations favor Pioneer (TDN, 67.8% DM; DE, 2.9%) over Hyland. In situ rumen degradability of DM was not affected by cultivar, however, Hyland had higher soluble (S, 22.8%) fractions than others. High effectively degraded organic matter (385.3 g/kg DM) was found in Pioneer 7535R. NDF degradability was not affected; however, Hyland SR22 and Pioneers had high effective degradability of crude protein (>200 g/kg DM). Hyland SR06 had higher absorbable microbial synthesis in the rumen and higher truly absorbable rumen undegraded protein in the intestines. Based on detailed results of nutrient content, degradability, and digestive

characteristics, these fresh corn forages are equally nutritious to use as ruminant feed.

Key Words: corn forage, chemical profile and degradability, metabolic characteristic

W265 Effects of varying silage inoculant technology on fermentation characteristics of corn silage during short and long term storage in mini-silos. . Z. Sawall*[1], L. Roth[2], and N. B. Litherland[1], [1]*University of Minnesota, St. Paul,* [2]*Provimi, Elk River, MN.*

Eighty PVC mini silos were used to evaluate corn silage fermentation characteristics after short and long-term fermentation with 4 homo- or heterofermentative inoculants. Corn silage (DM 40.4%, Starch 36.8%, NDF 38.7%) was harvested using a John Deere pull type chopper equipped with a kernel processor and inoculants, Control (CON), Promote HN-3 (PHN), Promote LC-1000 (PLC) and Vigorsile EBL II (VEBL) were administered before packing and stored at room temperature. Silos were opened at d 30, 60, 90 and 120. Temperature was taken immediately and samples were frozen until further analysis using NIR and wet chemistry. Data were analyzed using PROC MIXED with 5 reps per treatment and lsmeans with pdiff for mean separation. We hypothesized that inoculant would lower % dry matter loss, decrease pH and increase lactic acid %. Final temperature and dry matter % recovery were similar among treatments and decreased with time. PLC tended to increase ($P = 0.09$) aerobic stability (AS) at 72 h. Addition of PLC and VEBL decreased pH over time. Lactic acid % was greater for PLC and there was no difference in acetic acid % among treatments. Neutral detergent fiber digestibility (NDFd) was similar among treatments. PLC had greater 7-h starch digestibility (IVSD) and increased with time. Mold count was similar among treatments and the addition of inoculants reduced yeast counts. In summary, PLC and VEBL reduced the pH and PLC had greater lactic acid % and starch digestibility.

Table 1. Effects of inoculants on corn silage fermentation

	Treatment					*P*-value		
Variable	CON	PHN	PLC	VEBL	SEM	Trt	Day	Trt × Day
Temp, °C	20.76	20.82	20.77	20.76	0.07	0.90	<0.01	<0.01
Aerobic stability, °C	20.74	20.51	20.32	20.50	0.22	0.63	<0.01	0.04
pH	3.73[a]	3.70[ab]	3.64[c]	3.69[bc]	0.01	<0.01	<0.01	0.20
Lactic, %	5.04[a]	5.24[a]	5.92[b]	5.20[a]	0.13	<0.01	<0.01	0.37
Acetic, %	0.84	0.80	0.78	0.85	0.04	0.54	0.16	0.02
NDFd, %	48.71	48.70	48.95	48.48	0.40	0.87	0.71	0.21
IVSD, %	86.98[a]	87.37[a]	88.04[b]	87.10[a]	0.17	<0.01	<0.01	0.03

Key Words: corn silage, silage inoculant, fermentation

W266 Effect of bacterial inoculants on the fermentation, aerobic stability and spoilage losses of corn silage produced in farm-scale silos. O. C. M. Queiroz[1], F. C. Basso[2], R. Daetz[1], A. Schlaefli[1], and A. T. Adesogan*[1], [1]*Department of Animal Sciences, University of Florida, Gainesville,* [2]*Department of Animal Sciences - UNESP, Jaboticabal, Sao Paulo, Brazil.*

This project aimed to determine the effects of applying 2 bacterial inoculants on the quality, aerobic stability and spoilage losses of corn silage produced in farm-scale silos. Corn forage was harvested at approximately 35% DM, chopped and treated with nothing (Control), M inoculant (M) containing *Lactococcus lactis* SR 3.54, *L. plantarum* CHCC6072, and *Enterococcus faecium* M74, or with A inoculant (AC) containing *Lactobacillus buchneri* Lb1819, *L. plantarum* CHCC6072 and *E. faecium* M74 (Chr. Hansen, Denmark). Both inoculants were applied at 150,000 cfu/g fresh forage. Forty-five tons of corn forage were packed into each of four 3.7 m-wide replicate bags per treatment and ensiled for 186 d. Silage was removed from the bags at the rate of 1000 kg/d for 42 d and separated into good or spoiled (visibly moldy, darkened or hot silage) silage, weighed and analyzed for DM. Weekly composites were analyzed for chemical composition, aerobic stability and fungal counts. The experiment had a completely randomized design and the statistical model included effects of treatment, time (repeated), and the interaction. Inoculation did not affect DM recovery (97.9%; SEM = 0.42), in vitro true digestibility (82.6%; SEM = 0.38), NDF digestibility (60.6; SEM = 0.77), or chemical composition of good silage. However, M treatment increased the percentage of good (98.6 vs. 97.2%; SEM = 0.35) and decreased that of spoiled silage by 50% (1.39 vs. 2.81%; SEM = 0.35). Inoculation did not affect pH (3.8; SEM = 0.02), ammonia-N (0.09%; SEM = 0.01) or organic acid concentrations of good silage, except that M silages tended to have greater butyrate concentration (0.03 vs. 0.01%; SEM = 0.01) than others. Inoculated silages had similar yeast population (2.83 cfu/g, SEM = 0.47). However, A silages had greater aerobic stability than the Control silage (106 vs. 77; SEM = 7.09). In conclusion, applying the inoculants did not affect the chemical composition of good silage but M reduced the percentage of spoiled silage and A increased the aerobic stability.

Key Words: inoculant, silage, aerobic stability

W267 A mixture of homo- and hetero-fermentative lactic acid producing-bacterial strains enhanced the fermentation characteristics of sugar cane silage. A. A. Rodríguez*, P. Ramos, and L. C. Solórzano, *University of Puerto Rico, Mayaguez, Puerto Rico.*

Fermentation characteristics and aerobic stability were determined on sugar cane (SC) ensiled with the microbial inoculant SiloSolve AS (Chr. Hansen Inc., Milwaukee, WI). Chopped SC (31.3% DM) was ensiled in 1.8 kg micro-silos and assigned to 1 of 3 treatments (TRT); no additive (C), or SiloSolve AS applied at the recommended rate of 10^5 or at 10^6cfu/g fresh forage (AS1 and AS2). After 3 and 60 d of ensiling (DE) 5 silos from each TRT were emptied and silage analyzed to determine pH and fermentation products. Statistical analysis was performed according to a completely randomized design with a 2 (DE) by 3 (TRT) factorial arrangement. Aerobic stability was determined after 60 d of ensiling. Temperature was monitored every 6 h from 0 to 96h after opening in 5 samples (800 g) from each treatment. Statistical analysis was performed as a split plot design with a 3 (TRT) by 16 time points (hours of aerobic exposure) factorial arrangement, using the silo as repetitive measurement. For both rates of inoculation SC silage treated with SiloSolve AS had lower ($P < 0.05$) pH (C= 3.96, AS1 = 3.65, and AS 2 = 3.64), acetic and butyric acids % (1.50, 0.70, and 0.75 and 0.13, 0.07, and 0.05% for C, AS1 and AS2, respectively), and NH_3-N/Total-N (C = 2.51, AS1 = 1.48, and AS2 = 1.51) and higher ($P < 0.05$) lactic acid and lactic acid:acetic acid ratio (2.28, 1.68; 3.84, 8.24; and 4.24, 12.52 for C, AS1, and AS2, respectively) than untreated silage. No differences ($P > 0.05$) were detected in the temperature of SC among treatments during aerobic exposure. In summary, SC inoculated with SiloSolve AS applied at 10^5 or 10^6 cfu/g of fresh forage enhanced the fermentation characteristics, but not aerobic stability.

Key Words: sugar cane, inoculant, fermentation

W268 Effect of alfalfa as hay or silage and roughage:concentrate ratio on in vitro fermentation. Y. J. Tian[1,2], Z. J. Cao[1,2], and S. L. Li*[1,2], *[1]College of Animal Science and Technology, China Agricultural University, Beijing, China, [2]State Key Laboratory of Animal Nutrition, Beijing, China.*

Alfalfa in early bloom stage was harvested from the same area and managed either as dry hay or as silage. The objective was to study the effects of that alfalfa as either hay (AH) or silage (AS) at various roughage:concentrate (R:C) ratios on in vitro fermentation characteristics. Comparisons of fermentation patterns of total gas, ammonia-N (NH3-N) and microbial protein (MCP) production were conducted using an in vitro batch culture. Three healthy Chinese Holstein heifers similar in age and weight, each with a permanent rumen fistula were used as rumen fluid donors. AH or AS was mixed with concentrate at 6 R:C ratios: i.e., 0:100, 25:75, 45:55, 55:45, 75:25, and 100:0, respectively. Ten ml rumen fluid, 20 mL buffer fluid, and 200 mg feedstuff were mixed for 24-h incubation at 39°C for each tube, with 6 replicates per treatment. Data were analyzed by ANOVA and GLM analysis procedures (SAS 9.1). Content of MCP, concentrations of NH_3-N, and total gas at 24 h were significantly affected by form (AH vs. AS) of alfalfa forage ($P < 0.05$) and by the R:C ratio ($P < 0.05$), respectively. Alfalfa as silage (AS) resulted in greater MCP, NH_3-N, and total gas than AH treatments. Interactions of forage type and R:C ratio were significant ($P < 0.05$) for MCP and NH_3-N.

Table 1. The effect of forage type, R:C ratio, and interactions on fermentation

Item	Ratio (R:C)	MCP (total purine, mmol)	Ammonia-N (mg/100 mL)	24-h gas (ML/g DM)
Alfalfa hay	0:100	5.38	23.94	134.38
	25:75	5.30	25.54	110.62
	45:55	5.43	26.04	107.49
	55:45	3.56	25.28	94.15
	75:25	4.00	25.99	87.12
	100:0	3.80	26.51	88.27
Alfalfa silage	0:100	5.38	23.94	134.38
	25:75	6.86	27.09	121.38
	45:55	5.01	25.15	112.63
	55:45	4.70	29.06	112.47
	75:25	3.34	27.72	104.01
	100:0	4.97	27.23	84.13
SEM		0.63	1.50	11.15
Forage	AH	4.53^{b}	25.49 ^{b}	103.67^{b}
	AS	5.02^{a}	26.52^{a}	113.45^{a}
Ratio	0:100	5.38^{ab}	23.94^{b}	134.38^{a}
	25:75	6.08^{a}	26.16^{a}	116.00^{b}
	45:55	5.22^{b}	25.59^{a}	110.06^{bc}
	55:45	4.13^{c}	26.79^{a}	103.3^{cd}
	75:25	3.67^{c}	26.85^{a}	95.57^{de}
	100:0	4.39^{c}	26.94^{a}	86.72^{e}
P-value	Forage	0.0437	0.0036	0.011
	Ratio	<0.0001	<0.0001	<0.0001
	Forage × Ratio	0.0220	0.0163	0.2058

$^{a–e}$Values with different small letter superscripts mean significant difference (PP.

Key Words: alfalfa hay:silage, roughage:concentrate ratio, rumen fermentation

W269 Interaction effects of a *Salix babylonica* extract with exogenous enzymes on in vitro gas production of a total mixed ration. A. Z. M. Salem*[1], H. Gado[2], H. Ammar[3], M. A. Rodriguez[1], L. M. Camacho[4], M. M. Y. Elghandour[1], and N. Odongo[5], *[1]Facultad de Medicina Veterinaria, Universidad Autonoma del Estado de Mexico, Mexico, [2]Animal Production Department, Faculty of Agriculture, Ain Shams University, Qalubia, Egypt, [3]Ecole superieure dagriculture de Mograne, Mograne-Zaghouan- Tunisia, [4]Facultad de Medicina Veterinaria y Zootecnia, Universidad Autonoma de Guerrero, Cd. Altamirano, Guerrero, Mexico, [5]Animal Production and Health Section, Joint FAO/IAEA Division of Nuclear Techniques in Food and Agriculture, International Atomic Energy Agency, Vienna, Austria.*

An in vitro gas production (GP) technique was used to investigate the combination effects of *Salix babylonica* extract (SB) with the exogenous fibrolytic enzymes cellulase (C) and xylanase (X), or their mixture (1:1, vol/vol) on in vitro fermentation characteristics of a corn and sorghum grains- based total mixed ration (208 CP and 364 NDF g/kg DM). Four levels of extracts (i.e., 0, 0.6, 1.2, and 1.8 mL/g DM) and 4 fibrolytic enzymes (1 µL/g DM; Control, X, C and XC (1:1, vol/vol)) were used in 4 × 4 factorial arrangement. The GP was recorded at 2, 4, 6, 8, 10, 12, 24, 36, 48, and 72 h of incubation. After 72 h, the incubation was stopped and supernatant pH was determined and then filtered to determine digestible dry matter (DDM). Fermentation parameters, such as the 24-h gas yield (GY_{24}), metabolizable energy (ME), and short chain fatty acid concentrations (SCFA) were estimated. There were significant ($P < 0.001$) interactions (extract × enzymes) associated with addition of SB extract at 1.2 mL/g DM with either enzyme compared with other SB levels in combination with individual enzymes. Those interaction effects included: decreased pH (6.63 vs. 6.67, SEM = 0.008); increased GP during all incubation times, with asymptotic GP (187 vs. 157 mL/g DM, SEM = 4.64); and increased GY_{24} (182 vs. 152 mL gas/g DDM, SEM = 5.28). The SB extract, C, and X effectively improved the in vitro fermentation, and the combination of enzyme with SB extract at the level of 1.2 mL/g DM was more effective than the other treatments.

Key Words: exogenous enzyme, in vitro rumen fermentation, *Salix babylonica* extract

W270 Aerobic stability, pH and yeast population of sugarcane ensiled with different particle sizes. A. F. Campos*[1], G. R. Siqueira[1,2], N. M. Jeronimo[2,3], F. D. Resende[1,2], and R. A. Reis[1], *[1]Sao Paulo State University, Jaboticabal, Sao Paulo, Brazil, [2]Agencia Paulista de Tecnologia dos Agronegocios, Colina, Sao Paulo, Brazil, [3]Centro Universitario de Barretos, Barretos, Sao Paulo, Brazil.*

The trial aimed to evaluate the aerobic stability, pH values, and yeast population of sugarcane silage with different particle sizes (0.61; 1.07; 1.37 and 1.63 cm). Different particle sizes were estimated by the method of Penn State Particle Size Separator. Variables were evaluated in 0, 4, 8 and 12 d after silos opening, with 56 d of fermentation. Temperature of each silage was measured with digital dataloggers, during total period of 12 d. Aerobic stability was calculated as the time spent in hours for the silage mass increased 2°C compare with ambient temperature. Results were analyzed in a completely randomized design with 3 replications, with time repeated measures. Statistical analyzes were performed using PROC MIXED procedure of SAS 9.0. There were no differences ($P > 0.05$) among treatment in pH or yeast populations after 56 d of fermentation. However, after opening, pH increased ($P < 0.001$) from 3.59 to 6.21 after 12 d of exposure. This is due to the use of silage soluble components such as sugars and organic acids as substrate for aerobic microorganisms. Yeasts

growth over exposure time was also significant ($P < 0.001$) from 6.10 to 7.74 cfu/g of silage. Breakage of aerobic stability occurred 38, 12, 13 and 35 h after the start of air exposure for treatments 1, 2, 3 and 4, respectively, but did not observe statistical differences ($P = 0.4256$). When observing the maximum temperature of each silage and time spent to achieve it, significant response was observed ($P < 0.05$) for the maximum time, resulting quadratic effect, but was not significant for temperature, averaging 41°C. Thus, it is concluded that the average particle size of silage sugarcane does not interfere with aerobic stability, pH and yeast growth.

Key Words: aerobic exposure, microorganism, temperature

W271 Chemical composition, fermentative losses, and the dynamics of yeasts and lactic acid bacteria populations of sugarcane ensiled at different particle sizes—Year 2. A. F. Campos*[1], G. R. Siqueira[1,2], N. M. Jeronimo[2,3], F. D. Resende[1,2], and R. A. Reis[1], *[1]Sao Paulo State University, Jaboticabal, Sao Paulo, Brazil, [2]Agencia Paulista de Tecnologia dos Agronegocios, Colina, Sao Paulo, Brazil, [3]Centro Universitario de Barretos, Barretos, Sao Paulo, Brazil.*

Study aimed to evaluate the chemical composition, gas production, recovery of dry matter, and population dynamics of yeasts and lactic acid bacteria (LAB) in silage sugarcane with different mean particle sizes (0.61, 1.07, 1.37, and 1.63 cm), estimated using a Penn State Particle Size Separator. Plastic buckets were used as experimental silos. Losses and microbial population dynamics were evaluated during the storage period of 0, 3, 7, 14, 28, and 56 d with chemical composition measured at 56 d. Results were analyzed in a completely randomized design with 3 replications, with time as a repeated measure. Statistical analyses were performed to using PROC MIXED of SAS 9.0 ($P \leq 0.05$). Differences were observed in concentrations of dry matter (DM), acid detergent fiber (ADF) and lignin, being 27.01; 46.17; 8.48 for 0.61 cm; 31.01; 43.25; 7.56 for 1.07 cm; 32.68; 43.50; 7.45 for 1.37 cm and 26.58, 45.78, 8.79 for 1.63 cm, respectively, in % of DM, giving a quadratic effect ($P < 0.05$), probably due to losses of soluble compounds affecting DM and fiber concentrations. There were no differences in ether extract (EE), with mean of 0.98% of DM, and in vitro dry matter digestibility (IVDMD, 55.42% of DM). The smallest particle size (0.61 cm) resulted in highest values of gas losses (% of DM) with means of 9.49 vs. 6.60; 7.47; 7.41 for 0.61 vs. 1.07, 1.37 and 1.63 cm of particle size, respectively, and lower final DM recovery ($P < 0.05$). There was no treatment effect for lactic acid bacterial population ($P > 0.05$) indicating independence of particle size. Compaction intensity was effective in maintaining the anaerobic environment favorable to microbial growth. There was an effect of days of storage with greater amounts of CFU observed at 3 days. Ensilage of sugarcane with small particles (0.61 cm) had greater losses, so larger sizes are recommended.

Key Words: fibrous fraction, gas production, microorganism

W272 Ensiling characteristics and aerobic stability of guinea grass fermented with microbial inoculants. A. A. Rodríguez*, E. Martínez, C. Rosario, A. Almeida, C. Ocasio, E. Delgado, and L. C. Solórzano, *University of Puerto Rico, Mayagüez, PR.*

We evaluated the ensiling characteristics and aerobic stability of guinea-grass (GG, *Panicum maximum* 'Tanzania') fermented with commercial additives containing combinations of the lactic acid-producing bacterial strains: *Lactobacillus plantarum* DSM 16568; *Enterococcus faecium* DSM 22502, *Lactococcus lactis* DSM 11037 and NCIMB 30177, and *Lactobacillus buchneri* DSM 22502. Guinea-grass (25.9% DM) was chopped at 2.5 cm and ensiled with one of 4 additives: control (no additive), SiloSolve-AS (Chr. Hansen Inc., Milwaukee, WI), SiloSolve EF, and SiloSolve MC. Additives were added to weighed portions of GG and packed into PVC micro-silos (1.8 kg) to ferment for 3 or 45d at 25–27°C. Three silos from each treatment and fermentation day were analyzed for pH, organic acids, and NH_3. Statistical analysis was performed as a completely randomized design with a 4 (additives) by 2 (3 and 45 d of fermentation) factorial arrangement. For aerobic stability, temperature was monitored every 6 h in 3 samples (800 g) from each treatment during 120 h. Statistical analysis was performed as a split plot design with a 4 (additives) by 21 (time points of aerobic exposure) factorial arrangement using the silo as repetitive measurement. Tukey's test was used for mean separation. Microbial additives did not influence pH and lactic acid content in GG silage. After 45 d of ensiling forage treated with SiloSolve MC and SiloSolve EF had lower ($P < 0.05$) acetic acid (2.91 and 3.32 vs. 3.96 and 3.72%), butyric acid (1.27 and 1.35 vs. 1.68 and 1.77%), and NH_3-N/total-N (8.60 and 7.80 vs. 15.20 and 10.80%) than control silage or GG fermented with SiloSolve AS. All silages were stable to aerobic conditions after 120 h of aerobic exposure. In summary, addition of SiloSolve MC and SiloSolve EF improved the ensiling characteristics of GG silage ensiled at 25.9% DM. Guinea Grass fermented with or without the microbial additives resulted in silages stable to aerobic conditions.

Key Words: guinea-grass silage, microbial additive, fermentation

W273 Characterization of nutritive value and aerobic stability of passion fruit (*Passiflora edulis*) rind silage. I. Espinoza-Guerra*[1], J. Avellaneda-Cevallos[1,2], A. Sánchez-Laiño[1,2], L. Montenegro-Vivas[1], G. Quintana-Zamora[1,2], D. Zambrano-Gracia[1], M. Medina-Villacís[3], M. Peña-Galeas[1,2], and L. López-Intriago[1,2], *[1]Facultad de Ciencias Pecuarias, Quevedo, Los Ríos, Ecuador, [2]Dirección de Investigación Científica y Tecnólgica, Quevedo, Los Ríos, Ecuador, [3]Unidad de Estudios a Distancia, Quevedo, Los Ríos, Ecuador.*

The objective of this study was to evaluate the effect of the addition of commercial inoculants on chemical composition and fermentation characteristics in passion fruit (*Passiflora edulis*) rind silage stored in PVC experimental microsilos with 3 kg of capacity. Treatments were: T1) passion fruit rind silage without inoculant; T2) passion fruit rind silage + inoculant (Lacto Silo) and T3) passion fruit rind silage + inoculant (Sil-All 4x4), evaluated during 3 periods of fermentation (7, 14, and 21 d). Samples of each treatment were collected to determine dry matter, organic matter, ash, protein, fat, nitrogen-free extract, pH and temperature. Aerobic stability was analyzed throughout the temperature variation of the microsilos and pH using a potentiometer in the aqueous extract of 10 g of silage in 100 mL of distilled water after a 30-min rest period. The results obtained showed that the pH in the silos of T2 and T3 (3.8 and 3.9), when opened at 7 d, was significantly higher ($P < 0.05$) than the pH of the silage without additive (T1: 3.7). The pH and temperature of the silos opened at 14 and 21 days had no statistical differences between treatments ($P > 0.05$). Also, silages treated with inoculants or without inoculants had similar nutritional composition ($P > 0.05$). In conclusion, while there were minor effects on pH, there was no effect of adding inoculants on the aerobic stability or nutritional composition of the passion fruit rind silages in this study.

Key Words: passion fruit rind, microsilo, microbial inoculant

W274 Effects of different shoot height on fermentation quality and digestibility of barley silage. D. H. Kim*[1], S. C. Kim[2], H. J. Lee[1], S. M. Amanullah[2], Y. J. Jae[1], Y. M. Song[3], H. Y. Kim[3], and I. H. Choi[4], *[1]Division of Applied Life science, Gyeongsang National University, Jinju, South Korea, [2]Department of Animal Science (Inst. Agric. Life Sci.), Gyeonsang National University, Jinju, South Korea, [3]Department of Animal Resource Technology, Gyeongsang National University of Science and Technology, Jinju, South Korea, [4]Department of Companion Animal & Animal Resource Science, Joongbu University, Geumsan, South Korea.*

This study was conducted to investigate the effects of shoot height on fermentation quality of barley silage and nutrient digestibility of total mixed ration formulated with barley silage. Barley forage (Yuyeon) was grown at Research farm, Sabong, Jinju, South Korea. Forage was harvested at 37% DM with 3 different shoot height (5, 10 and 15 cm), ensiled to bale silage (500 kg) for 200 d. The nutrient digestibility was estimated using 12 Hanwoo steers (average 455kg) assigned randomly into 3 treatments. The treatments contained total mixed ration prepared with one of either barley silage (5, 10 and 15 cm shoot height), and concentrate mixture. The animals were housed individually into the metabolic cage and fed 8 kg of diet for 3 weeks consisted 2 wk of adaptation and 1 wk of collection period. Feces were weighed daily and sub-sampled during the collection period. The mean concentrations of DM, CP and NDF of barley forage at 5, 10 and 15 cm of shoot height were 37.4, 5.5 and 67.3%, respectively. The concentrations of DM, CP, EE and crude ash of barley silage ensiled for 200 d were greater in 5 cm than 10 cm and 15 cm ($P < 0.05$). Acetate concentration was greater 15 cm than 5 cm and 10 cm silage (1.13 vs. 0.40 and 0.50%, $P < 0.05$). Mold was greater in 10 cm than 15 cm silage (4.05 vs. 3.28 $\log_{10}$ cfu/g, $P < 0.05$). Ether extract and NDF digestibility of Hanwoo steer fed the diet formulated with 15 cm silage were greater ($P < 0.05$) than those fed the diets formulated with 10 cm silage ($P < 0.05$). In contrary, ADF digestibility was greater in the diet formulated with 5 cm silage than 10 cm silage ($P < 0.05$). Therefore, shoot height can improve the fermentation quality and digestibility of barley silage.

Key Words: barley silage, shoot height, digestibility

W275 Effects of the additives on fermentation quality of barley silage. H. J. Lee[1], D. H. Kim[1], H. Yoon[1], S. M. Amanullah[2], S. C. Kim*[2], and I. H. Choi[3], *[1]Division of Applied Life Science (BK21 program), Jinju, South Korea, [2]Department of Animal Science (Inst. Agric. Life Sci.), Gyeongsang National University, Jinju, South Korea, [3]Department of Companion Animal & Animal Resource Sciences, Joongbu University, Geumsan, South Korea.*

This study was carried out to determine the effect of the additives on fermentation quality of barley silage. Youngyang barley forage was grown at Animal Research Unit, Gyeongsang National University, Jinju, South Korea, and harvest at 29% DM. Approximately 300kg of barley forage were chopped and assigned into 1 of 4 treatments with 4 replications, which were CON (no additive), T1 (1.2×10^3 cfu/g of *L. plantarum*), T2 (0.1% of propionate) and T3 (combo). Barley forage was ensiled into 10-L bucket silo for 2-, 7-, 48-, and 100-d periods. After 100 d of fermentation, DM, NDF and hemicellulose content of silage remained unchanged ($P > 0.005$) among the treatments. Crude protein content was lower in T1 ($P = 0.004$), which further expressed by higher ($P < 0.001$) ammonia-N (% of total N) in this group than in the control and other treatments. Crude ash and ADF contents were higher in the control than in other treatments. The in vitro DMD and NDFD were lowest ($P < 0.05$) in the control than other treatments. The control silage has the higher ($P < 0.05$) pH value; however, pH did not differ with the difference in additives. Lactate was higher in T2 and T3 than that in the control and T1, but acetate was highest ($P < 0.001$) in control silage (6.05%), followed by T3 (5.19%), T2 (5.06%) and T1 (4.18%). These results gave the highest lactate/acetate ration in T2 (2.59), followed by T3 (2.39), T1 (1.97) and the control (1.10). LAB (7.15 vs. 6.82 vs. 6.39 vs. 6.51 log10 cfu/g, $P = 0.055$) tended to decrease with additives. No difference was observed in yeast or mold count among the treatments. Therefore, applying additives can improve the fermentation quality of barley silage.

Key Words: barley silage, inoculant, propionate

W276 Effects of microbial inoculants on alfalfa, ryegrass, and grass clover mixture silages on silage pH, dry matter loss, and aerobic stability. A. Lanckriet*[1], J. Jatkauskas[2], V. Vrotniakiene[2], E. French[3], and T. Hemling[4], *[1]DeLaval N.V., Drongen, Belgium, [2]Lithuanian University of Health Sciences, Baisogala, Lithuania, [3]DeLaval Inc., Waunakee, WI, [4]DeLaval Inc., Kansas City, MO.*

An in vitro study using 3L glass mini silos was conducted to observe the effects of silage inoculants on nutrient composition, pH, VFA concentration, DM loss, and aerobic stability. Three silages were studied: alfalfa (AS), perennial ryegrass (RS), and a mixture of red clover:ryegrass:timothy (MIX). Nine treatments (control, DeLaval Feedtech (F10, F18, F22, F3000), Sil-All 4 × 4 (SA), Lalsil Dry, Bonsilage (BO), Bio-sil Stabil, were organized as a randomized complete bock design, with 5 replicates per treatment. Silos were filled to a target density of 0.2 kg DM/L and ensiled for 90 d at 20°C. After 90 d, silages were analyzed for DM loss and chemical composition (DM, CP, NDF, and pH). Silage VFA (g/100 g of DM) were analyzed by GLC. Aerobic stability was measured on d 90 by exposing the silages to air and measuring temperature until silages were 3°C above ambient temperature. Mean nutrient composition (%) was 33.8, 32.2, and 32.8 for DM, 20.6, 14.7, and 19.0 for CP, and 38.0, 44.1, and 42.2 for NDF for AS, RS, and MIX. Lactate increased in RS for F18 and F22 compared with other inoculants (9.1 v. 6.6; overall mean ± SEM, 6.8 ± 0.57; $P < 0.01$) and MIX for F10, F22, F3000, and ISA versus other inoculants (5.8 v. 4.3; 4.9 ± 0.2; $P < 0.01$). After 90 d, pH was lower in AS treated with F18, F22, F3000, and SA versus other inoculants (4.88 v. 5.02; 5.1 ± 0.01; $P < 0.01$), in RS for F10, F22, F3000, and SA versus other inoculants (4.02 v. 4.21; 4.13 ± 0.02; $P < 0.01$), and in MIX treated with F10, F22, and F3000 compared with other inoculants (4.02 v. 4.18; 4.15 ± 0.03; $P < 0.01$). Loss of DM was reduced in RS for F10, F18, F22, F3000, and BO compared with other inoculants (2.9 v. 3.8%; 3.5 ± 0.7; $P < 0.01$), and reduced in MIX for F10, F22, and F3000 compared with other inoculants (4.02 v. 4.18; 4.6 ± 0.4; $P < 0.01$). Adding inoculants improved ($P < 0.05$) aerobic stability compared with the control (AS, 229.8 v. 98.4; RS, 197.7 v. 96.0; MIX, 167.1 v. 80.4). Results demonstrate improved silage quality by adding inoculants. In particular, DeLaval Feedtech and Sil-All 4 × 4 inoculants consistently improved silage quality compared with other treatments.

Key Words: inoculant

W277 Effect of age at weaning and creep feeding on carcass composition and IGF-I concentrations in 5-month-old females calves. C. Viñoles*[1], A. L. Astessiano[2], D. Guggeri[1], A. Meikle[3], and M. Carriquiry[2], *[1]Instituto Nacional de Investigación Agropecuaria, Tacuarembó, Uruguay, [2]Facultad de Agronomía, Montevideo, Uruguay, [3]Facultad de Veterinaria, Montevideo, Uruguay.*

We tested the hypothesis that carcass composition and IGF-I concentrations are affected by age at weaning and plane of nutrition before weaning by assigning Hereford female calves (n = 21) to 3 different treatments between 2 and 5 mo of age: (1) early weaning at 2 mo of age (EW, n = 6); (2) late weaning at 5 mo of age (LW, n = 7) and (3) LW plus creep feeding (LW+CF, n = 8). Calves were weighed every 2 weeks from 2 to 5 mo of age, when a blood sample was collected and the urea dilution technique (Rule et al., 1986; J. Anim. Sci. 63:1935–1948) applied to evaluate the in vivo carcass composition (CL = carcass lipids; CP = carcass protein; CW = carcass water; EBW = empty body water; EBF = empty body fat). Data were analyzed using a linear mixed model and means were considered to differ when $P < 0.05$. LW+CF calves gained faster and were heavier at 5 months of age compared to LW calves, which were heavier that EW calves (Table 1). The carcass composition was not affected by age at weaning or creep feeding (Table 1). LW+CF calves had higher IGF-I concentrations that LW calves, and the latter higher concentrations than EW calves (Table 1). We conclude that age at weaning and creep feeding affect IGF-I concentrations, but not carcass composition.

Table 1. Average daily gain between 2 and 5 mo of age and live weight, IGF-I concentrations and carcass composition at 5 months of age in EW, LW, and LW + CF calves (LSM ± SEM)

	EW	LW	LW + CF
Average daily gain (kg/d)	0.333 ± 0.03[a]	0.764 ± 0.03[b]	0.926 ± 0.03[c]
Live weight (kg)	122 ± 7.5[a]	177 ± 7.2[b]	194 ± 4.2[c]
IGF-I (ng/ml)	47.8 ± 10.4[a]	80.6 ± 9.9[b]	158 ± 10.8[c]
CL (%)	20.5 ± 0.8	19.1 ± 0.9	19.4 ± 0.8
CP (%)	17.2 ± 0.2	17.0 ± 0.2	17.2 ± 0.2
CW (%)	58.6 ± 0.5	57.3 ± 0.5	57.6 ± 0.5
EBW (%)	59.7 ± 0.6	58.5 ± 0.6	59.1 ± 0.5
EBF (%)	17.9 ± 0.9	19.3 ± 0.8	18.2 ± 0.7

[a] versus [b] P.

Key Words: weaning, creep feeding, growth

W278 Effect of palmitoleic acid on body composition and adipocyte cell size in obese sheep. S. K. Duckett*, M. C. Miller, G. Volpi Lagreca, M. Alende, T. A. Burns, A. Wright, J. G. Andrae, and N. M. Long, *Clemson University, Clemson, SC.*

Southdown wethers (n = 15; 95 kg BW) were used to assess the effects of palmitoleic (C16:1) acid infusion on body composition and adipocyte cell size in obese sheep. An n-7 (omega-7) enriched oil (45% palmitoleic acid) was infused, twice daily for 28 d via indwelling jugular catheter at 3 levels of palmitoleic acid: 0 (CON), 5 (MED) or 10 (HI) mg·kg $BW^{-1}\cdot d^{-1}$. The oil was solubilized in 40% ethanol and immediately injected into the catheter at 0800 and 1600 h for each lamb. All lambs received the same amount of 40% ethanol per dose regardless of oil level. Blood samples were collected at 5 min post dosing on a weekly basis to assess uptake of palmitoleic acid into circulation. After 28 d, lambs were slaughtered. At slaughter, weights of omental and mesenteric adipose tissue were collected as well as hot carcass weight. At 24 h postmortem, carcass data was collected and samples obtained from subcutaneous and intramuscular adipose tissues for cell size determination. Serum palmitoleic acid contents (mg/mL) at 5 min post injection were 60% higher ($P < 0.05$) in HI compared with CON. Serum palmitoleic acid content also tended ($P = 0.09$) to be higher (+ 31%) in MED compared with CON. Serum *cis*-11 vaccenic acid was also elevated ($P < 0.05$) in HI compared with CON, which increased ($P < 0.05$) over time for HI but not in CON. The ratio of C16:1 to C16:0 was elevated ($P < 0.05$) in both the MED and HI treatments. Average daily gain during the 28 d treatment period was lower ($P < 0.05$) by 76% for HI compared with CON. Carcass parameters and visceral adipose depots were not different ($P > 0.05$) between treatments. Mean subcutaneous adipocyte size did not differ ($P > 0.05$) between treatments and averaged 92.2 μm. Mean intramuscular adipocyte size was reduced ($P < 0.05$; 66.1 vs. 74.2 μm) in HI compared with CON. Administration of an n-7 enriched oil to obese sheep increased circulating C16:1, reduced average daily gains and intramuscular adipocyte size.

Key Words: sheep, palmitoleic acid, adipocyte

W279 Palmitoleic (C16:1) acid alters glucose and insulin metabolism in obese lambs. T. A. Burns*, N. M. Long, M. Alende, G. Volpi Lagreca, A. K. G. Kadegowda, M. C. Miller, and S. K. Duckett, *Clemson University, Clemson, SC.*

Palmitoleic (C16:1) acid has been proposed to function as a lipokine and alter insulin sensitivity. The objective of this study was to assess C16:1 effects on glucose and insulin tolerance in obese sheep. Southdown wethers (86.7 ± 1.5 kg BW; n = 4) with indwelling jugular catheters were used in a crossover design. Treatments were intravenous infusion of 2 doses of C16:1, 0 (CON) or 5 (LIPO) mg/kg BW in 40% (vol/vol) ethanol, immediately followed by a glucose (0.25 g/kg) tolerance test. The design was repeated with CON and LIPO treatments immediately followed by an insulin (0.02 μU/kg) challenge. Catheters were inserted 1 d before first infusion. Lambs were fasted 18 h before treatment with 44 h rest between tests. Blood samples were collected at −15 min, immediately before infusion, and serially for 4 h. Plasma was analyzed for fatty acids using GLC, glucose using a colorimetric assay, and insulin using a commercial RIA. Repeated measures data were analyzed using Proc Mixed procedure. Plasma C16:1 was increased ($P < 0.01$) in LIPO compared with CON lambs. At 2 min post-infusion, percent C16:1, mg of C16:1/mL of serum, and ratio of C16:1/C16:0 was maximal with 9.5-, 10.9-, and 10.6-fold increase over baseline, respectively. By 30 min post-infusion, plasma C16:1 levels had returned to baseline. In addition, C17:0 and C18:0 (mg/mL) increased ($P < 0.05$) in LIPO compared with CON lambs. During the glucose tolerance test, C16:1-administration increased ($P < 0.05$) peak and overall glucose concentrations in LIPO lambs compared with CON. Glucose peaked at 2 min post-infusion and returned to baseline in both treatment groups by 180 min. During the insulin test, LIPO lambs had increased ($P < 0.05$) peak and overall plasma insulin compared with CON; in addition, glucose was greater ($P < 0.05$) in LIPO compared with CON lambs. Insulin peaked at 2 min post-infusion and returned to baseline in both treatment groups by 20 min. In conclusion, fatty acid profiles indicated rapid removal of C16:1 from plasma after pulse dose infusion. In addition, C16:1 infusion appears to affect insulin signaling to alter plasma glucose in obese lambs.

Key Words: palmitoleic acid, glucose, insulin

W280 Influence of maternal linseed supplementation on brain and muscles fatty acid composition in newborn lambs. A. Nudda, B. Gianni, R. Boe, M. Lovicu, NPP Macciotta*, and G. Pulina, *Dipartimento di Agraria, Sezione di Scienze Zootecniche, Universita di Sassari, Sassari, Italy.*

The increase of polyunsaturated fatty acids (PUFA) n3 content in meat has been a key objective of applied animal science. The metabolism of 18:3 n-3, by desaturation and elongation pathway, leads to the production of long-chain PUFA, including 20:5 n-3 (eicosapentaenoic acid; EPA), 22:5 n-3 (docosapentaenoic acid; DPA) and 22:6 n-3 (docosahexaenoic acid; DHA). Research on laboratory animals evidenced that the capacity to convert 18:3 n-3 into long-chain metabolites increases during pregnancy. Among vegetable sources, linseed has a high content of α-linolenic acid (C18:3 n-3; ALA) and can be used in animal diet to provide dietary n-3 PUFA. This study investigated the effect of linseed ALA dietary supplementation to dairy ewes during late-pregnancy on fatty acid (FA) profile of brain and muscles in newborn lambs. From the last 8 weeks of gestation, 8 pregnant Sarda ewes were divided into 2 groups fed 2 different diets: a control (CTL) diet and an ALA-enriched diet by adding linseed (LIN). Four lambs from each group were slaughtered at birth. Brain samples, and the Semitendinosus and Longissimus dorsi muscles of lamb carcasses were collected to determine their FA composition by GC. The LIN supplementation to the ewes increased ($P < 0.05$) the concentration of ALA (0.85 vs. 0.20 g/100 g of total FA; SE 0.164), C18:4 n-3 (0.035 vs. 0.010; SE 0.006), EPA (0.65 vs. 0.31; SE 0.036) and DPA (2.14 vs. 1.70; SE 0.164), but did not influence that of DHA (1.00 vs. 0.89; SE 0.099) concentration in the muscles of newborns. The maternal LIN supplementation increased ($P < 0.05$) the concentration of EPA (0.51 vs. 0.45; SE 0.020), DPA (1.38 vs. 1.00; SE 0.103), but did not influence that of DHA (10.97 vs. 10.48; SE 0.397; $P = 0.35$) in brain tissue. The ALA was not detected in lambs from CTL ewes and its concentration was low in LIN lambs (0.04 g/100 g FA; SE 0.006). In this study the maternal ALA supplementation during gestation increased the LC-PUFAn-3 but did not enhanced the concentration of DHA in muscles and brain tissues of newborn lambs. Acknowledgments: research supported by Cargill-Animal Nutrition Division, Milan, Italy.

Key Words: linseed, long-chain PUFA, lamb tissue

W281 Uptake of palmitoleic (^{13}C16:1) acid in blood and adipose tissue of obese lambs. T. A. Burns*, A. K. G. Kadegowda, M. C. Miller, A. M. Wright, and S. K. Duckett, *Clemson University, Clemson, SC.*

Palmitoleic (C16:1) acid is proposed to function as a lipokine and regulate metabolism. The primary objective of this study was to assess the uptake of U-^{13}C16:1 in circulation and adipose tissue of obese lambs. In addition, a secondary objective of this study was to evaluate blood glucose and serum insulin in response to C16:1 infusion. Southdown wethers (67.4 ± 1.4 kg; n = 3) were used in a 3 × 3 Latin square with a pulse dose infusion of U-^{13}C16:1 infused at 0 (CON), 2 (LOW), and 5 (HI) mg/kg BW in 40% ethanol (vol/vol). For each period, lambs were fitted with an indwelling jugular catheter 1 d prior and grain-fasted 18 h before treatment with 10 d rest between periods. Blood samples were collected before (−30, −15, and 0 min) and after U-^{13}C16:1 infusion at 15 min intervals for 3 h. Immediately following the last blood sample, an adipose tissue biopsy was performed at alternating sites within the tailhead region of each lamb. Blood glucose levels were monitored with a hand-held glucometer. Serum insulin was measured with a commercial ELISA. Fatty acids were quantified using GLC and enrichments were analyzed with GLC/mass spectrometry. Repeated measures data were analyzed using Proc Mixed procedure. At 15 min post-infusion, serum C16:1 (mg/mL) was elevated in LOW and HI lambs compared with CON by 1.8- and 3.1-fold increase, respectively. By 30 min, serum C16:1 did not differ ($P > 0.10$) between treatment groups. Enrichment of U-^{13}C16:1, however, peaked at 15 min and remained elevated ($P < 0.01$) in HI lambs compared with CON through 3 h. Also, LOW lambs had peak U-^{13}C16:1 at 15 min, but had returned to baseline by 60 min post-infusion. Blood glucose was also elevated ($P < 0.05$) in HI lambs compared with LOW and CON lambs from 15 to 60 min post-infusion. Serum insulin and adipose tissue fatty acid composition did not differ ($P > 0.10$) between treatment groups. In conclusion, U-^{13}C16:1 infusion induced a short-term increase in overall serum C16:1 concentrations, although enrichment of ^{13}C16:1 was maintained in serum for a slightly longer period. In addition, U-^{13}C16:1 increased blood glucose in a dose-dependent manner without affecting serum insulin.

Key Words: palmitoleic acid, isotope, lamb

W282 Nutritionally mediated prenatal growth restriction is associated with reduced somatotroph cell density in the late gestation ovine fetus. N. Craig[1], N. P. Evans*[1], M. Bellingham[1], C. L. Adam[2], J. M. Wallace[2], and J. E. Robinson[1], *[1]Institute of Biodiversity, Animal Health and Comparative Medicine, University of Glasgow, Glasgow, UK, [2]Rowett Institute of Nutrition and Health, University of Aberdeen, Aberdeen, UK.*

Maternal malnutrition during pregnancy adversely affects fetal nutrient supply and prenatal growth velocity leading to low body weight and altered organ development at birth. Such prenatal growth restriction (PGR) affects postnatal growth trajectories, body composition and reproductive performance. As the pituitary gland is central to both somatotropic and reproductive function we herein investigated whether PGR altered the population of GH and LHb cells in the fetal sheep pituitary. Singleton pregnancies to a single sire were established by embryo transfer and adolescent dams offered control (C, n = 24) or high dietary intakes (n = 24) during the first 2 thirds of pregnancy to induce normal or compromised placental size, respectively. The latter group was further categorized as PGR or non-PGR after determination of fetal weight at necropsy on d 130 of gestation on the basis of a minus 2 SD cut-off relative to the control group mean. Pituitaries were frozen at necropsy and the density of GH or LHb immunoreactive cells subsequently determined in 6 microscope fields/fetal pituitary. Both total placentome weight (511 ± 24, 389 ± 28 and 241 ± 12g) and fetal weight (4450 ± 84, 4273 ± 166 and 3037 ± 146g) were greater ($P < 0.001$) in C and non-PGR compared to the PGR group. While late gestation fetal growth status did not impact LHb cell density it did influence GH cell density. GH cell density was 5.64 ± 0.40, 5.53 ± 0.57 and 4.12 ± 0.40 cells/1000 μm^2 in C, non-PGR and PGR groups, respectively, with a significant post hoc comparison ($P = 0.012$) between C vs. PGR. This difference appears to be sex specific, being evident in female but not male fetuses [C vs. PGR GH cells/100 μm^2: Females 6.26 ± 0.39 (n = 17) vs. 4.64 ± 0.49 (n = 7), $P = 0.023$; Males 4.13 ± 0.74 (n = 7) vs. 3.52 ± 0.61 (n = 6), $P = 0.541$]. The attenuated GH cell density in severely nutritionally growth restricted lambs may affect somatotrophic axis function in postnatal life.

Key Words: somatotropic axis, pituitary, placentome

W285 Development of gravid uterus components in function of days of gestation and feeding level in pregnant Nellore cows. M. P. Gionbelli[1], M. S. Duarte[1], S. C. Valadares Filho[1,2], H. C. Freetly[3], P. V. R. Paulino[1], F. C. Rodrigues[1], B. C. Silva[1], T. R. Santos[1], D. F. T. Sathler[1], M. G. Machado[1], and M. I. Marcondes*[1,2], *[1]Universidade*

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Thirty-two multiparous Nellore cows with average initial body weight of 451 ± 10 kg, age of 5.6 ± 0.5 years were used in an experiment aiming evaluate the influence of maternal nutrition and days of gestation on development of gravid uterus components. Sixteen cows were fed 1.2 times maintenance and 16 cows were fed ad libitum a diet with 85% of corn silage and 15% of concentrate. Four cows of each group were harvested at 136, 189, 239 and 269 d of pregnancy and had their gravid uterus dissected into fetus, uterus, placenta and fetal fluids. The effect of feeding level and time of gestation was evaluated by a 2 × 4 factorial scheme. After, non-linear functions were fitted to the data to describe the development of gravid uterus components in function of time of gestation. For each function, an F-ratio was calculated to test whether estimation of parameters specific to each feeding level improved fit of the data relative to estimation of parameters from a pooled data set, ignoring the feeding level. Weight of fetus was greater ($P < 0.05$) in ad libitum cows compared to the 1.2 times maintenance cows at 269 days of gestation (29.7 vs. 24.4 kg) but not different in early gestation. No differences *(*$P > 0.05$) were observed on weight of uterus and fetal fluids in function of feeding level. The placenta weights from ad libitum fed cows were greater ($P < 0.05$) than placentas of 1.2 times maintenance cows (average of 1.12 vs. 0.90 kg). Logistic functions [Aexp(B – Ct) t] were those that better described the growth of uterus components in function of time of pregnancy (t, days). For fetus and placenta the F test showed better fit of non-linear functions when functions were estimated separated for the two levels of feeding, but for uterus and fetal fluids pooled equations showed better fit. The functions to describe the growth of fetus and placenta in function of time of pregnancy were: for 1.2 times maintenance cows, Fetus weight (kg) = $0.0000225\exp^{(0.10225 - 0.000188t)t}$ and Placenta weight (kg) = $0.01729\exp^{(0.02947 - 0.0000499t)t}$; for ad libitum cows, Fetus weight (kg) = $0.0003202\exp^{(0.07573 - 0.000123t)t}$ and Placenta weight (kg) = $0.05511\exp^{(0.02123 - 0.0000323t)t}$.

Key Words: fetal programming, gestation, maternal nutrition

W286 Residual feed intake and hormonal parameters in Nellore cattle. R. H. Branco*[1], C. F. Nascimento[1], E. Magnani[1], L. F. Oliveira[2], S. F. M. Bonilha[1], and J. N. S. G. Cyrillo[1], *[1]Centro APTA Bovinos de Corte, Instituto de Zootecnia, Sertaozinho, Sao Paulo, Brazil, [2]Departamento de Zootecnia, Universidade Estadual Paulista, Jaboticabal, Sao Paulo, Brazil.*

Residual feed intake (RFI) is used to identify more efficient animals in feed utilization. Its physiological bases are still unknown, but the insulin hormone, linked to the mechanisms of hunger and satiety, can elucidate such efficiency. The increase of insulin hormone triggers the release indirect of IGF-I. This hormone acts on cellular proliferation saving glucose and using fatty acids from adipose cells as energy. This study aimed to assess the relationships between RFI groups and concentrations of insulin and IGF-I in Nellore cattle. The experiment was conducted at Instituto de Zootecnia, São Paulo, Brazil. We utilized 118 Nellore steers, tested for feed efficiency (112 d in individual pens) and classified as low RFI (<mean − 0.5SD, n = 40), medium RFI (SD ± 0.5, n = 42) and high RFI (>mean + 0.5SD, n = 36). Blood samples were collected and analyzed for insulin and IGF-I determination. Differences were found for concentration of insulin and IGF-1 among RFI groups, which were greater in low RFI animals. This demonstrates that the increase in insulin concentration can cause effects on the growth axis stimulating the production of IGF-I, which acts on the proliferation of somatic cells with glucose economy and determines the animals´ satiety feeling. Therefore there are differences in growth mechanisms between RFI groups, in which low RFI animals have higher concentrations of insulin and IGF-I influencing the growth and feed efficiency.

Table 1. Insulin and IGF-I concentrations in blood of Nellore cattle classified for RFI

	Low RFI	Medium RFI	High RFI	P-value
Number	40	42	36	—
RFI, kg/d	$-0.33^{a} \pm 0.02$	$0.00^{b} \pm 0.02$	$0.34^{c} \pm 0.02$	<0.01
DMI, kg/d	$5.74^{a} \pm 0.11$	$6.07^{b} \pm 0.12$	$6.41^{c} \pm 0.11$	<0.01
IGF-I, ng/mL	$41.49^{a} \pm 1.69$	$43.82^{a} \pm 1.62$	$39.05^{b} \pm 1.76$	0.057
Log[1] Insulin	$1.63^{a} \pm 0.04$	$1.55^{a} \pm 0.04$	$1.46^{b} \pm 0.04$	0.017

[a–c]Means followed by the same letter, in the same row, do not differ significantly by testing t, 10% of probability.
[1]Log = transformation basis for variables that did not show normal distribution.

Key Words: growth, IGF-I, satiety

W287 Residual feed intake studies in cattle reveal a potential role for gonadotropin releasing hormone (GnRH) in regulating feed efficiency. S. D. Perkins*, C. D. Foradori, C. L. Bratcher, L. A. Kriese-Anderson, and T. D. Brandebourg, *Auburn University, Auburn, AL.*

Residual feed intake (RFI) is a heritable feed efficiency measure. Mechanisms underlying variation in feed efficiency are currently poorly understood. To address this issue, 48 Angus-sired steers were trained to the Calan Gate (Northwood, NH) system at the Beef Evaluation Unit at Auburn University to facilitate measurement of individual feed intake. Daily feed intake and RFI were assessed during a 70 d feeding trial. The test diet was 50% sorghum-sudan silage, 50% grain (2.9 Mcal ME/kg DM). Body weights and hip heights were recorded at 14 d intervals. Ultrasound measurements of rib eye muscle area (REA) and subcutaneous backfat (BF) were recorded initially and before slaughter. RFI was calculated for each animal as the difference between actual feed intake and the expected intake to create 2 divergent cohorts consisting of High (H) and Low (L) RFI individuals. Upon harvest, carcass characteristics were measured and hypothalamic tissue (HT) samples were collected to facilitate gene expression studies into the mechanisms underlying variation in RFI. As expected feed intake was higher for the H individuals versus the L steers ($P < 0.001$) while on test gain was not different between the 2 groups ($P < 0.87$). There were no differences in intramuscular fat ($P < 0.17$), BF ($P < 0.44$), or REA ($P < 0.33$) between L and H cohorts indicating there is no relationship between RFI and body composition. Targeted gene expression studies indicate that neuropeptide-Y (NPY), relaxin-3 (RLN3), melanocortin 4 receptor (MC4R), and GnRH mRNA expression was 64%, 59%, 58%, 86% lower respectively in the arcuate nucleus of low RFI steers while pro-opiomelanocortin (POMC) expression was 350% higher in these more efficient animals ($P < 0.01$). Pituitary expression of gonadotropin β subunits (FSHβ, LHβ) was correlated to hypothalamic GnRH levels (FSHβ: r = 0.580, $P < 0.01$; LHβ: r = 0.783, $P < 0.01$) suggesting changes in gene expression in the arcuate nucleus indeed had functional consequences. Furthermore, these expression profiles suggest GnRH may play a role in regulating feed efficiency.

Key Words: steer, RFI, GnRH

W288 Fatty acids profile of muscle and fat from Nelore bulls classified for residual feed intake. S. F. M. Bonilha*[1], K. Zorzi[2], R. H. Branco[1], M. M. C. Silva[3], J. N. S. G. Cyrillo[1], and M. E. Z.

Mercadante[1], *[1]Centro APTA Bovinos de Corte, Instituto de Zootecnia, Sertãozinho, São Paulo, Brazil, [2]Departamento de Zootecnia, Universidade Estadual do Norte Fluminense, Campos do Goytacazes, Rio de Janeiro, Brazil, [3]Departamento de Zootecnia, Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil.*

Residual feed intake (RFI) is defined as the difference between actual feed intake and expected requirements for maintenance and gain. Studies have shown association between RFI and BW gain composition, which could affect fatty acids (FA) profile of body lean and fat tissues. This study aimed to identify associations between RFI and FA profile of muscle and fat in Nelore bulls. Fifty-nine and 25 bulls were used, respectively, for longissimus muscle (LM) and kidney, pelvic and heart fat (KPH) FA profile determination. Bulls were divided into high (>mean+0.5 SD) and low (<mean-0.5 SD) RFI groups and slaughtered with 4 mm of ultrasound fat thickness between 12th and 13th ribs, with average BW and age of 421 kg and 552 d. Samples of LM and KPH were vacuum packed for FA profile determination. Data were analyzed using mixed model and LS means tested by *t*-test. The FA found in highest concentration in LM were the saturated palmitic (20.1%) and stearic (16.0%); the monounsaturated oleic (29.4%); and the polyunsaturated linoleic (14.1%), constituting 79.6% of the total FA identified. There were no significant differences between RFI groups for LM SFA, MUFA and PUFA concentrations. For KPH, the FA found in highest concentration were the saturated stearic (27.3%); and the monounsaturated oleic (38.9%) and myristoleic (23.0%), totaling 89.2% of FA identified. Significant differences between RFI groups were detected for oleic, SFA, and MUFA, having low RFI animals higher concentrations of oleic and MUFA, and lower concentration of SFA. Nelore bulls more efficient in converting feed into meat have similar lean tissue FA profile and different FA profile on fat tissue.

Table 1. Fatty acids profile of LM and KPH from Nelore bulls classified for RFI

	LM Low RFI	LM High RFI	*P*-value	KPH Low RFI	KPH High RFI	*P*-value
Number	32	27	—	13	12	—
Oleic, %	27.1 ± 1.17	25.6 ± 1.23	0.31	41.2 ± 1.16	36.4 ± 1.21	0.01
Linoleic, %	16.1 ± 1.04	17.7 ± 1.10	0.21	1.99 ± 0.13	1.98 ± 0.13	0.95
Linolenic, %	0.27 ± 0.13	0.48 ± 0.13	0.18	0.19 ± 0.02	0.21 ± 0.02	0.41
CLA, %	0.51 ± 0.04	0.55 ± 0.04	0.31	0.33 ± 0.04	0.26 ± 0.03	0.18
SFA, %	38.8 ± 1.08	38.0 ± 1.14	0.55	51.4 ± 1.34	56.8 ± 1.39	0.01
MUFA, %	36.1 ± 0.94	34.2 ± 0.99	0.10	44.4 ± 1.30	38.9 ± 1.35	0.01
PUFA, %	23.8 ± 1.50	26.5 ± 1.58	0.15	2.40 ± 0.15	2.41 ± 0.15	0.97

Key Words: beef, efficiency, lipid

Lactation Biology I

W289 Changes in parathyroid hormone-related protein concentrations in bovine milk from the early stage of lactation. K. Onda*, R. Sato, K. Kazama, H. Ochiai, and Y. Wada, *Azabu University School of Veterinary Medicine, Sagamihara, Japan.*

The concentration of parathyroid hormone-related protein (PTHrP) in the blood of healthy animals is extremely low. However, milk contains a relatively large amount of PTHrP, and the changes in its levels in the early stages of lactation and the biological implication of these changes in cows remain unclear. To understand the characteristics of parturient changes in milk PTHrP content, we first measured the changes in milk PTHrP concentrations as a function of time after parturition in 8 primiparous and 8 multiparous Holstein cows at 7 intervals until 21 d postpartum. Second, based on these results, we collected milk samples from 47 primiparous and 66 multiparous Holstein cows at 3 d postpartum and investigated the relationship between the milk PTHrP concentration and the age of the cow or milk yield. Consequently, the concentration of PTHrP in milk of both age groups of cows was lowest on the day of parturition (3.1 ± 1.5 n*M* in primiparous and 1.6 ± 0.8 n*M* in multiparous cows) and significantly increased on d 7 of lactation and stayed on the same level until d 21 of lactation (5.9 ± 2 n*M* in primiparous and 6 ± 1.3 n*M* in multiparous cows on d 21). Comparing the 2 groups, milk PTHrP concentrations in primiparous cows were higher than those of multiparous cows in the first 3 d of lactation ($P < 0.05$). The milk PTHrP concentration at 3 d postpartum exhibited a negative correlation with increasing age of cows ($r = -0.57$, $P < 0.0001$), and a positive correlation with milk yield was observed only in the multiparous cows ($r = 0.29$, $P < 0.02$). This experiment identified the unique characteristics of milk PTHrP in the early stage of lactation; milk PTHrP concentrations are higher in primiparous cows than in multiparous cows and lower in colostrum than in later milk. The difference in milk PTHrP concentration observed between primiparous and multiparous cows at 3 d postpartum was more strongly influenced by age than by milk yield.

Key Words: age, parity, PTHrP

W290 SND1 regulates milk protein synthesis of dairy cow mammary epithelial cells in vitro. W. W. Bi, C. C. Luo, Y. Lin, X. J. Gao*, and Q. Z. Li, *Key Laboratory of Dairy Science of Education Ministry, Northeast Agricultural University, Harbin, China.*

Tudor-SN (SND1, p100) has been shown to function as a transcriptional coactivator, which is highly conserved through evolution from yeast to mammals. The conservation of SND1 along evolution suggests it may have important functions. However, the physiological function of SND1 in mammary epithelial cells of dairy cow has not been characterized. In this study we constructed transfected dairy cow mammary epithelial cells (DCMECs) with SND1 to analyze the expression and localization of SND1 and the function in transfected DCMECs by CASY, fluorescent immunostaining, Western blot and RT-qPCR. Analysis indicated that SND1 was widely expressed in nucleus of DCMECs. Overexpression and siRNA inhibition of SND1 experiments showed that SND1 promoted the cells proliferation and lactation relative genes expression, regulated milk protein synthesis through Stat5 and mTOR pathway. These findings indicated that SND1 involves in regulation of milk synthesis, and sheds new insights for understanding the mechanisms of milk protein synthesis.

Key Words: SND1, dairy cow mammary epithelial cell, milk protein synthesis

W291 Heat-induced stress and response of bovine mammary epithelial cells. H. Hu, D. P. Bu, J. Q. Wang*, L. Y. zhou, and X. M. Nan, *Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Study objectives were to determine the cell-stress response to heat stress (HS) in Chinese bovine mammary epithelial cells (CMECs). CMECs were exposed to either 38 or 42°C for 0.5, 1, 3, 5, 8, and 12 h, and cell apoptosis rate and expression of apoptosis regulation genes were quantified by flow cytometry and qRT-PCR, separately. Calculation data of mean, SD, and *P*-values were performed on triplicate experiments using SARS (9.0). The Student's *t*-test was used to calculate *P*-values for comparison, and the significance was set at a *P*-value <0.05. Thermal temperature significantly induced cell apoptosis and the peak of apoptosis appeared at 3 h with the apoptosis rate up to 14% ($P < 0.05$). The expression level of heat shock proteins (Hsps), Bcl-2, caspases and tumor necrosis factor receptor (TNFR) family genes were detected to discuss the cell response to heat stress. The genes, which were in development of apoptosis, death receptor gene (TNF-R1), cysteine proteases genes (caspases-3, -7 and -8) and Apaf-1 were markedly upregulated by HS ($P < 0.05$). However, Fas, caspase-6 and -9 were downregulated ($P < 0.05$) with different exhibition. For Bcl-2 protein family, which plays a critical role in pro- or anti-apoptotic processes, the transcription levels of anti-apoptotic protein genes (Bcl-2, Bcl2Al and Mcl-l) were significantly increased ($P < 0.05$) and pro-apoptotic protein genes (Bax, Bak and Bid) were significantly decreased ($P < 0.05$) during thermal temperature treat. The gene ratio of Bcl/Bax shown positive suggested its blocking activity to apoptosis and determined the survival of cells following an apoptotic stimulus. Simultaneously, Hsps genes (hsp27, 70 and 90) were generally upregulated at 42°C and this was especially apparent for hsp70 transcription as it was increased 14-fold at 1 h ($P < 0.05$). The sudden increasing of Hsps promoted cells effective recovery and survival under HS conditions. The changes of cell apoptosis rate and gene transcription induce by HS began to recover to normal after 8 h. These results suggested that HS induced the apoptosis of CMECs, and aroused its intracellular thermotolerance machinery.

Key Words: bovine mammary epithelial cell, heat stress, apoptosis

W292 Study on differential intake free amino acids of mammary gland in dairy cows. X. Y. Wang, N. Zhang, Q. Z. Li*, and X. J. Gao, *Key Laboratory of Dairy Science of Education Ministry, Northeast Agricultural University, Harbin, China.*

Free amino acids in the blood constitute the major precursors of milk proteins, and the availability of these amino acids to the mammary system is critical to optimizing milk production. The study was to investigate the difference of amino acid intake between dairy cows producing high-quality milk and cows producing low-quality milk. Chinese Holstein dairy cows (n = 18) were allotted in 2 groups according to results of milk composition analyzer: one is high milk quality group (n = 9, high protein and fat ratio) and the other is low milk quality group (n = 9, Low protein and fat). We collected the blood from the external pudic artery and abdominal mammary vein of the 2 groups of cows, and used the amino acids autoanalyzer to determine 17 free amino acids concentration. The results showed that the concentration of 5 essential amino acids (Met, Leu, Ile, Thr, Val) of the high milk quality group were significantly higher than the low milk quality group ($P < 0.05$), and the concentration of 2 nonessential amino acids (Glu, Tyr) were

significantly higher than the low milk quality group ($P < 0.05$). The uptake rate of 6 essential amino acids (Thr, Val, Met, Ile, His, Arg) in the high milk quality group were significant higher than the low milk quality group ($P < 0.05$), and nonessential amino acids detected were also significantly higher than the low milk quality group ($P < 0.05$). In conclusion, differential utilization of Met, Leu, Ile in the High and Low milk quality groups maybe the main reason to cause the considerable difference of milk protein rate.

Key Words: dairy cow, milk quality, free amino acids

W293 Prolactin-inhibitor cabergoline hastened the mammary involution during drying-off in dairy cows. M. Boutinaud*[1,2], N. Isaka[4], A. Deflandre[4], E. Gandemer[1,2], P.-G. Marnet[1,2], F. Dessauge[1,2], and V. Lollivier[1,2], *[1]INRA UMR 1348 PEGASE, Saint Gilles, France, [2]Agrocampus UMR 1348 PEGASE, Rennes, France, [3]Université Européenne de Bretagne, Rennes, France, [4]CEVA Santé Animale, Libourne, France.*

In ruminants, the early phase of drying-off is a period of mammary gland involution that is marked by the cessation of prolactin (PRL) release. The analysis of the changes of mammary secretion composition can provide valuable information about the speed of the mammary involution. To assess the effect of PRL inhibition by cabergoline on mammary gland involution, 14 Holstein dairy cows were injected with a single i.m. administration of 5.6 mg cabergoline (n = 7) or placebo (n = 7) at the first day of drying-off (D0). Mammary biopsy samples were collected one week before drying-off (D-6), at D1 and at D8 and used for RNA extraction and RT-PCR analyses. Mammary secretion samples were collected using a teat-cannula once during lactation (D-6) and at D1, D2, D3, D4, D8 and D14 after the drying-off. The mammary secretion samples were used for milk fat, lactose, true protein, a-lactalbumin, lactoferrin and citrate analysis. The decrease in lactose content of mammary secretions seemed to be faster in cabergoline treated cows compared to controls, demonstrated by lower levels of lactose in cabergoline treated cows already by D1 than in control cows ($P < 0.05$). Cabergoline treatment tended to increase fat content at D3 after drying-off ($P < 0.10$), whereas an increase in fat content was only observed at D4 in the control group. The rise of lactoferrin was significant starting at D4 in the cabergoline treated cows whereas it only happened at D8 in controls, and overall there was a tendency towards greater lactoferrin content in cabergoline treated cows ($P = 0.10$). Cabergoline did not seem to alter citrate content. However, the decrease in lactoferrin/citrate ratio happened faster in cabergoline treated cows compared to controls on D1 ($P = 0.01$). No significant effects of cabergoline treatment were observed both in true protein and in a-lactalbumin contents in mammary secretions or in a-lactalbumin and k-casein mRNA levels in mammary tissues. These changes in lactose, lactoferrin, lactoferrin/citrate ratio and fat, indicate that cabergoline treatment was efficient to hasten the mammary gland involution without affecting milk synthesis in the mammary tissue

Key Words: cow, drying-off, prolactin

W294 Effects of omitting the dry period on plasma progesterone and prolactin during lactogenesis and on colostrum IgG content in dairy cows. R. S. Zbinden[1], H. A. van Dorland[1], G. Remmelink[3], B. Kemp[2], A. T. M. van Knegsel[2], and R. M. Bruckmaier*[1], *[1]Veterinary Physiology, Vetsuisse Faculty University of Bern, Bern, Switzerland, [2]Adaptation Physiology Group, Wageningen University, Wageningen, the Netherlands, [3]Livestock Research, Wageningen University and Research Centre, Lelystad, the Netherlands.*

Omitting the dry period represents a strategy that may reduce metabolic stress in early lactating cows. A drawback of continuously milking is discussed to be a compromised colostrum quality, although insufficient studies have been done to confirm this. The objective of this study was to evaluate the effects of omitting the dry period on key hormone patterns during lactogenesis and the IgG content of colostrum in periparturient dairy cows. Twenty Holstein-Friesian dairy cows were randomly assigned to 2 experimental groups (0 or 60 d dry period; DRY0 or DRY60, respectively). Milk yields were recorded daily and plasma concentrations of progesterone and prolactin were determined from d 5 pre- until d 3 postpartum. Milk samples were collected for analysis of IgG concentration from d 7 pre- until d 3 postpartum for DRY0, and from d 0 until d 3 postpartum for DRY60 cows. Data were analyzed with a mixed model procedure including dry period length, day and their interaction as fixed effects. Plasma prolactin did not differ between DRY0 and DRY60 and started to increase significantly from one day before calving in both groups ($P < 0.05$). Progesterone dropped prepartum and followed a similar pattern in both groups, but was significantly lower on one day before calving in DRY60 compared with DRY0. This may point to a stronger decrease in progesterone concentration for DRY0 and could imply a faster calving process after the progesterone drop. IgG concentration started to increase from d 6 prepartum in DRY0 cows. From calving up to d 3 postpartum, IgG level decreased, but no difference was observed between the groups. However, calculated IgG mass was significantly higher for DRY60 compared with DRY0 ($P < 0.05$) across the study time, due to the higher milk yield in DRY60 (21.8 versus 13.5 kg/d on d 0; $P < 0.05$). In conclusion, the endocrine profiles supporting lactogenesis remained unaffected, and the colostrum quality was not compromised by omitting the dry period in dairy cows. It can be speculated that milking related oxytocin releases during the peripartal period induced an increased labor activity and faster birth.

Key Words: colostrum, immunoglobulin, dry period

W295 Characterization of mammary circadian rhythms of wild-type C57BL/6J mice and the role of thyroid hormone responsive spot 14 (S14) in circadian regulation of milk fat synthesis. L. Ma*, Y. Ying, A. Clarke, P. Bartell, and K. J. Harvatine, *Penn State University, University Park.*

Peripheral circadian rhythms are well described in liver and adipose tissue and S14 expression follows a circadian rhythm. The objectives of the current study were to characterize the mammary circadian rhythm of wild-type (WT) mice and investigate the role of S14 in the rhythm of milk fat synthesis. Wild-type and S14 null mice were euthanized on d 14 of lactation (0600, 1200, 1800, or 2400 h; n = 6 per time point per genotype) and dam mammary tissue and pup stomach milk clots were collected. Dam intake and body weight and litter gain were recorded twice per day. Data were analyzed by ANOVA with genotype, time, and the interaction of genotype and time as fixed effects and second fit to a cosine function with a 24 h period for rhythm analysis. Wild-type mice consumed more feed during the dark than the light phase (66% vs. 34%; $P < 0.01$). Total intake and eating patterns were maintained in S14 null. Litters gained 22% more during daytime compared with nighttime in both WT and S14 null ($P < 0.05$). Pup milk clot fat concentration followed a circadian rhythm and the amplitude and phase were decreased and delayed by 18.7% and 15.6 h in S14 null mice ($P < 0.05$). In S14 null mice, the amplitude and phase of 16-carbon FA were decreased by 66% and advanced by 2.9 h, compared with WT ($P < 0.05$). In the mammary gland, expression of the core clock genes (CLOCK, BMAL1, CRY1&2, and PER1&2), lipogenic regulators (SREBP1c and S14), and lipogenic enzymes (FASN and SCD1) followed a circadian rhythm in

WT. A 15 to 23% decrease in the amplitude of BMAL1 and PER1&2 and a 58% increase in the amplitude of CRY1 rhythm were observed in S14 null mice, although the phases were similar ($P < 0.05$). Moreover, the amplitudes of SREBP1c and SCD1 were diminished by 52 and 19%, respectively ($P < 0.05$). In conclusion, there is a circadian rhythm in the mammary gland of wild-type C57BL/6J mice. Spot14 is important for maintaining the circadian rhythm of milk fat synthesis by affecting mammary core clock genes and expression of lipogenic enzymes.

Key Words: spot 14, circadian rhythm, milk fat synthesis

W296 Suitability of refractometer and densimeter for on-farm determination of colostrum quality in dairy cows and heifers. J. J. Gross*, E. C. Kessler, and R. M. Bruckmaier, *Veterinary Physiology, Vetsuisse Faculty University of Bern, Bern, Switzerland.*

Instruments for on-farm colostrum quality determination are increasingly used in dairy practice. The objective of this study was to elucidate the relationships between colostrum quality as assessed by 2 common on-farm instruments and composition in colostrum in cows and heifers. Twelve multiparous cows and 14 heifers were milked for the first time exactly 4 h post-calving. Colostrum was analyzed for total IgG by ELISA and for fat, protein and lactose by Foss Milkoscan (previously validated for use with colostrum). A Brix sugar refractometer (BRIX) and a Kruuse colostrum densimeter (DENS) were used to assess colostrum quality at 20°C. In cows, BRIX was closely correlated with DENS (r = 0.72, $P < 0.05$), protein (r = 0.88, $P < 0.01$) and lactose concentration (r = −0.85, $P < 0.01$). Also DENS showed a clear relationship with milk protein (r = 0.74, $P < 0.01$) and lactose (r = −0.73, $P < 0.05$) in cows. Both BRIX and DENS did not correlate with IgG concentration in cows. In colostrum of heifers, BRIX was less correlated with DENS (r = 0.43) and lactose (r = −0.50) than in cows, but still high with protein concentration (r = 0.75, $P < 0.01$). Also DENS was less correlated with protein (r = 0.44) in heifers than in cows. For heifers, BRIX and DENS did not correlate with IgG concentration. In conclusion, the refractometer and the densimeter closest correlated with protein content in colostrum but not necessarily with total IgG concentration. The easier handling of the refractometer and the higher correlations of its results with colostrum constituents make it a more reliable instrument than DENS for on-farm assessment of colostrum quality.

Key Words: colostrum, densimeter, refractometer

W297 PPARgamma agonists and antagonists fail to overcome *trans*-10, *cis*-12 conjugated linoleic acid (CLA) inhibition of lipogenesis and lipogenic gene expression in bovine mammary epithelial cell culture. D. E. Oliveira*[3,1], K. J. Harvatine[1], Y. R. Boisclair[2], and D. E. Bauman[2], *[1]Penn State University, University Park, [2]Cornell University, Ithaca, NY, [3]Santa Catarina State University, Lages, Santa Catarina, Brazil.*

Trans-10, *cis*-12 CLA decreases fat synthesis in mammary tissue and cell culture. We have previously observed that expressions of none of the 3 peroxisome proliferator-activated receptor (PPAR) isoforms were changed in mammary tissue during diet- and CLA-induced milk fat depression. However, PPARs are regulated at the level of ligand activation and specifically by some fatty acids (FA). The effect of PPARgamma (PPARg) on lipid synthesis and its role in the response to *trans*-10, *cis*-12 CLA was investigated using PPARg specific chemical agonist (Troglitazone, TG) and antagonist (T0070907). Bovine mammary epithelial cells (Mac-T) were treated with *trans*-10, *cis*-12 CLA (75 m*M*) complexed to BSA in serum free or growth media in the presence or absence of 9-*cis* retinoic acid (9cRA; retinoid X receptor agonist). Data was analyzed by ANOVA and protected LSD. Lipogenesis, measured as ^{14}C acetate incorporation into FA, was decreased 69.5 and 70.9% by CLA in serum free and growth media, respectively ($P < 0.05$). CLA also decreased expression of fatty acid synthase (FASN), sterol response element binding protein 1 (SREBP1), and thyroid hormone responsive spot 14 (S14), but not PPARg. PPARg agonist and antagonist did not change rates of lipogenesis. Additionally, neither PPAR agonist nor antagonist was able to inhibit CLA effects on lipogenesis (80 and 70% lower, respectively) or inhibit the reduction in expression of FASN, SREBP1, and S14. No interaction was observed between PPARg agonist or antagonist and 9cRA or growth media. Overall, there is no evidence for a role of PPARg in CLA inhibition of lipogenesis or downregulation of FASN, SREBP1 and S14.

Key Words: PPARg, conjugated linoleic acid, milk fat depression

W298 The inflammatory response of primary bovine mammary epithelial cells to *Staphylococcus aureus* strains reflects the molecular background of the bacteria. C. Zbinden[1,3], R. Stephan[2], S. Johler[2], RM Bruckmaier*[1], and O. Wellnitz[1], *[1]Veterinary Physiology Vetsuisse Faculty, University of Bern, Bern, Switzerland, [2]Institute for Food Safety and Hygiene, Vetsuisse Faculty, University of Zurich, Zurich, Switzerland, [3]Graduate School for Cellular and Biomedical Sciences, University of Bern, Bern, Switzerland.*

Using a latex agglutination-based diagnostic tool (Staphaurex test) we grouped bovine *S. aureus* strains into: Staphaurex-negative SLAT(−) and -positive SLAT(+) isolates. SLAT(−) strains belong to clonal complex (CC) 151, SLAT(+) strains can be assigned to various CC's. Genetic changes in spa, clfA and fnbpA genes and loss of the fnbpB gene (important virulence factors) were detected in SLAT(−) isolates. Recently we showed that microarray profiles of SLAT(−) isolates were highly similar but differed largely from those of SLAT(+) isolates. Based on these molecular data we postulate that SLAT(+) strains are more virulent than SLAT(−) strains. This study aimed to investigate if the immune response of the mammary gland to SLAT(−) and SLAT(+) strains differs, which could play a role in mastitis development. Primary bovine mammary epithelial cells in 4th passage were stimulated in sixtuplicates with 10 and 25 multiplicity of infection of inactivated suspensions of 3 SLAT(+) and 1 SLAT(−) strain isolated from bovine mastitis of different clinical severities. After 1, 6, and 24 h cells were harvested. At several time points the relative mRNA abundance (ΔΔCT) of selected immune factors was higher ($P < 0.05$) after stimulation with SLAT(+) compared to SLAT(−). Differences were highest after 6 h of incubation (1.3 to 2.5 threshold cycles [CT] for tumor necrosis factor alpha, 0.9 to 3.0 CT for interleukin-8, 1.5 to 3.6 CT for RANTES [Regulated And Normal T cell Expressed and Secreted] and 0.8 to 5.5 CT for serum amyloid A, respectively). The overall immune response was more pronounced with higher MOI. The mRNA expression of tight junction proteins zonula occludens-1 and occludin was not affected in both groups. These data are supported by an adhesion assay where the adherence of SLAT(−) to epithelial cells (Hep2) was lower than of SLAT(+) strains. The results indicate that *S. aureus* strains with varying virulence and different latex agglutination cause differences in the immune response of bMEC in vitro, which may reflect the severity of mastitis.

Key Words: *Staphylococcus aureus*, cow, mastitis

W299 Identification and characterization of microRNAs in a dairy cattle mammary gland epithelial cell line. X. M. Nan[1], D. P. Bu*[1], J. Q. Wang[1], J. J. Loor[2], and H. Hu[1], *[1]State Key Laboratory*

of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Mammalian NutriPhysioGenomics, Department of Animal Sciences and Division of Nutritional Sciences, University of Illinois, Urbana.

Our objective was to identify and characterize the microRNAs (miRNAs) expressed in bovine mammary gland epithelial cells (MEC) isolated by our laboratory. Cells were cultured and passaged in DMEM/F12 basic medium with 10% fetal bovine serum. For experimental assays, cells at 80% confluence were cultured in lactation medium (containing insulin, epidermal growth factor, transferring, hydrocortisone and progesterone) for 24 h. MicroRNAs of MEC were isolated using TRIzol reagent and PAGE. Subsequently, small RNAs were amplified and sequenced by PCR and Solexa sequencing technology. Novel miRNAs were identified by stem-loop RT-PCR and sequencing of PCR products. To confirm the tissue specificity, expression of novel miRNAs was measured in mammary gland, liver, adipose, ileum, spleen and kidney tissues from 3 lactating Holstein cows (L350 ± 40 d) by stem-loop RT-PCR and sequencing of PCR products. After bioinformatics analysis, a total of 12,323,451 reads were obtained by solexa sequencing and 11,979,706 were clean reads. Among clean reads, 9,428,122 reads belonged to miRNAs. Further analysis revealed that bta-mir-184 had the most abundant expression and 388 loci possessed the typical stem-loop structures matching the known miRNA hairpins, whereas 38 loci with novel hairpins were identified as novel miRNAs. One of novel miRNAs named as bta-U21 was tissue specific in lactating mammary gland. Seven novel miRNAs, including bta-U21, had tissue-restricted distribution. In conclusion, the study identified 388 known miRNAs and 38 novel miRNAs expressed in dairy cattle MEC and some of them had tissue specificity and/or tissue-restricted distribution.

Key Words: microRNA, mammary gland epithelial cell line

W300 Evaluation of udder development shortly before parturition. V. Bjerre-Harpøth*[1], E. C. Kessler[2], J. J. Gross[2], and R. M. Bruckmaier[2], *[1]Department of Animal Science, Aarhus University, Foulum, Tjele, Denmark, [2]Veterinary Physiology, Vetsuisse Faculty, University of Bern, Bern, Switzerland.*

Udder development shortly before parturition involves a final stage of mammogenesis and increasingly early stages of lactogenesis including colostrogenesis. Both, mammogenesis and lactogenesis contribute to an increased size of the udder in the period around parturition. The aim of the study was to investigate the udder development, and thereby the possibility of predicting the time of parturition. The observation technique for udder development should be a simple, on farm technique. Starting a week before expected parturition, 10 multiparous dairy cows were daily measured. Blood was sampled every 8 h until parturition and analyzed for progesterone. For determination of udder growth, the distance between 2 marks on the upper part and 2 marks on the lower part of the hindquarters was measured. Additionally, udder tension (scored: 1 = soft to 4 = hard) and the tension of the tail head ligaments (scored: 1 = hard to 3 = soft) was determined by manual palpation. A first index, Total Difference (TotDif) was calculated as the total difference in the upper and lower udder measurements per day. A second index, Tension in Udder and Ligament (TenUdLig) was the udder tension plus the tail head ligament scores. An exponential regression line depending on the time relative to parturition was used to describe prepartum udder growth expressed by TotDif and TenUdLig. Exponential growth of the udder already started before the drop of blood progesterone concentration. The equations were TotDif = $0.5838+9.8460 \times \exp(0.0002 \times x)$ and TenUdLig = $2.8446+3.1764 \times \exp(0.0002 \times x)$, x = the time in minutes before parturition. TenUdLig was the single best predictor of time to parturition. Alone, a TenUdLig score at minimum 5 could predict 20% chance of parturition within 24 h, 70% chance within 48 h, and 80% chance within 72 h. Cows with a combination of a TenUdLig score at minimum 5 and an increase in TotDif score on minimum 4 between 2 daily measurements calved within 24 h (100%). In conclusion, the prepartum udder development followed an exponential pattern, and in regards to prediction of parturition, the tension in the udder (combined with tension in the tail head ligament), was a better parameter than the growth of the udder.

Key Words: udder development, ligament

W301 Adiponectin receptor gene expression and adiponectin regulation of glucose uptake and cell growth in mammary epithelial cells. I. S. Yuh*[1,2] and L. G. Sheffield[3], *[1]Department of Animal Biotechnology, College of Animal Life Sciences, Kangwon National University, Chunchon, Republic of Korea, [2]Institute of Animal Resources, Kangwon National University, Chunchon, Republic of Korea, [3]Department of Dairy Science, University of Wisconsin, Madison.*

The objective of the research is to identify the presence of adiponectin receptors and to study adiponectin action on glucose uptake and growth in mouse mammary epithelial cells as an experimental model. In the real time RT-PCR analysis, these cells expressed both types of adiponectin receptors, AdipoR1 and AdipoR2, and the expression levels of these receptors were similar in the presence of 10% FBS. Some of lactogenic or growth factors, insulin (10 ng/mL) or IGF-I (10 ng/mL) alone or each of these in the presence of 1% FBS, did not alter AdipoR1 and AdipoR2 gene expression pattern for 0, 0.5, 1, 2, 4, 12 or 24 h incubation ($P > 0.05$). Prolactin (10 ng/mL) or EGF (10 ng/mL) alone or each of these in the presence of 1% FBS, did not affect the AdipoR1 and AdipoR2 mRNA induction ($P > 0.05$). In glucose uptake experiment, adiponectin plus pre-incubation of insulin for 2 h before adiponectin stimulation (1 mg/mL, 30 min) significantly increased 2-deoxy-D-glucose,[1,2-^{3}H] uptake compared with no treatment ($P < 0.01$)), but adiponectin alone or insulin alone (pre-incubation) did not. In a similar way, insulin alone for 30 min incubation or adiponectin for 2-h pre-incubation did not increase glucose uptake ($P > 0.01$) but insulin plus pre-incubation of adiponectin significantly increased glucose uptake compared with no treatment ($P < 0.01$). The interaction effects of these hormones were not significant when these hormones were pre-activated by the other side ($P > 0.05$) suggesting additive effect between these hormones in glucose uptake. In cell growth experiments, addition of 1 m*M* adiponectin in the presence of 1% FBS, significantly decreased DNA synthesis of mammary epithelial cells compared with control ($P < 0.01$). In addition, AICAR(100 or 200 μ*M*), AMPK activator and adiponectin signaling intermediate, significantly decreased mammary epithelial cell growth for 2 day and 4 day incubation periods in the presence of 2% FBS ($P < 0.05$). These results indicate that adiponectin has inhibitory effect on mammary epithelial cell growth.

Key Words: adiponectin receptor, glucose uptake, mammary growth inhibition

W302 Effect of rib fat thickness on meat quality attributes of Nellore young bulls. E. E. Dallantonia, J. F. Lage*, L. R. Simonetti, E. San Vito, E. A. Oliveira, M. Machado, L. M. Delevatti, M. B. Abra, and T. T. Berchielli, *Universidade Estadual Paulista, Jaboticabal, Sao Paulo, Brazil.*

The objective of this study was to evaluate the effect of rib fat thickness (RFT) on ultimate pH, lean and fat color, water-holding capacity (WHC), Warner-Bratzler shear force (WBSF), cook loss (CKL) of 14 young Nellore bulls. Bulls were housed in individual stalls and fed a diet containing 40% corn silage and 60% concentrate (grounded corn, soybean meal, urea/ammonium sulfate, mineral mixture). Bulls were slaughtered at 17 mo of age and carcasses chilled at 0°C for 24 h. Carcasses were ribbed between the 12 - 13th ribs and separated into 2 groups by RFT: 3 - 6 mm (7 carcasses) and 6.1 −10 mm (7 carcasses). Longissimus dorsi (LD) section (10 cm thick) was removed from the posterior end of the wholesale rib. LD samples and subcutaneous fat were individually vacuum-packaged and held at −20°C for analysis. The color reading was conducted on the surface of lean or fat, using the CIE L*a*b* system. The WHC was measured for the difference between the weights of the sample before and after it was subjected to a pressure of 10 kg for 5 min. Data were analyzed by the GLM procedure of SAS, and the Tukey test used considering 5% probability. The RFT did not affect the pH ($P = 0.91$). Similar lightness (L*; $P = 0.77$), redness (a*; $P = 0.99$) and yellowness (b*; $P = 0.81$) were observed for beef from carcasses with different rib fat thickness. Regards the subcutaneous fat color, similar L* ($P = 0.37$), a* ($P = 0.94$) and b* ($P = 0.47$) were observed from carcasses with different RFT. The carcasses with RFT (3 - 6 mm) had lower WHC ($P = 0.01$) than carcasses with RFT >6.1 mm. The RFT did not affect the WBSF ($P = 0.77$) and CKL ($P = 0.80$). Carcasses with rib fat thickness lower 6.1 mm have lower water holding capacity. The rib fat thickness over 3.0 mm did not affect the tenderness, pH, color or cook loss in carcasses from young Nellore bulls.

Key Words: beef, color, tenderness

W303 Fatty acid profile and sensory analysis of meat from Nellore steers fed with different levels of whole raw soybeans. N. R. B. Cônsolo*, A. S. C. Pereira, R. Gardinal, J. E. Freitas Junior, J. R. Gandra, C. S. Takiya, F. P. Rennó, and G. D. Calomeni, *Universidade de São Paulo, Pirassununga, São Paulo, Brazil.*

The aim of this work was to evaluate the fatty acid profile and sensory analysis of meat from Nellore steers treated with different concentrations of whole raw soybean (WRS) into their diet. Fifty-four animals with mean weight and age of 350 kg and 24 mo were fed for 84 d with 4 isoproteic diets of 15% crude protein as follows: T0, with 0% of WRS, T8, with 8% of WRS, T16, with 16% of WRS and T24, with 24% WRS. These diets contained 2.0, 3.5, 4.9 and 6.4% of fat content, respectively. Steers were allotted to 4 pens and assigned to a completely randomized design. Animals were slaughtered and 24 h later, samples of the Longissimus muscle were collected from the left half-carcass between the 12th and the 13th ribs. Two samples were collected from each animal. Samples were identified and vacuum stored in polyethylene bags and aged for 14 d with temperature varying between 0°C and 4°C for determination of fatty acid profile and sensory analysis. Fatty acids were extracted and quantified by chromatography (GC Shimadzu 2010). Sensory evaluation was assessed by a panel of 10 trained tasters (American Meat Science Association. 1995). The steaks were cooked until the internal temperature of meat reached 71°C then sliced and served to each member of the panel. Statistical analysis was conducted by SAS software. The results showed that fatty acids highest scores were C18:1 c9, C16:0 and C18:0. No difference ($P > 0.05$) was observed for the C18:2, C18:3 total fatty acids saturated, unsaturated and the unsaturated/saturated. However, the fatty acid C14:0 and C16:1 content presented an inverse correlation with WRS levels ($P = 0.05$ and $P = 0.006$). On the other hand, fatty acid C20:0 and C20:2 showed a positive correlation ($P = 0.039$ and $P = 0.001$). Regarding sensory analysis, no effect was observed ($P > 0.05$) for juiciness, flavor, characteristic flavor and off flavor. Interestingly, animals feed with 24% of WRS presented more tender meat than controls ($P < 0.05$). Including 24% of WRS in diet presented a slight improvement in the fatty acid profile and meat tenderness from Nellore steers

Key Words: protein source, meat quality, ruminant

W304 Using near-infrared reflectance spectroscopy to predict chemical composition with a wide range of variability in beef. H. W. Su*[1], K. Sha[1,2], L. Zhang[1,3], Q. Zhang[4], Y. L. Xu[1,3], R. Zhang[5], H. P. Li[1], and B. Z. Sun[1], *[1]Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]College of Food and Wine, Yantai Research Institute of China Agricultural University, Yantai, Shandong, China, [3]Department of Food Science and Engineering, Gansu Agricultural University, Lanzhou, Gansu, China, [4]Department of Animal Sciences, Purdue University, West Lafayette, IN, [5]Beijing Zhongnong Boya Technology Development Co. Ltd., Beijing, China.*

The objective of this study was to develop near infrared reflectance spectroscopy (NIRS) models for predicting the chemical composition with a wide range of variability in beef. In total, 182 samples (168 samples from specific carcass and additional 14 artificially mixed samples with high proportion of fat tissue) were minced and divided into calibration set (n = 140) and independent validation set (n = 42). Reference values had extremely wide ranges of fat (0.20–86.45%, mean 10.04%), protein (1.98–23.28%, mean 19.42%) and moisture (12.85–78.53%, mean 69.92%). Reflectance spectra (1000–1800 nm) were collected, and then calibration models were built using partial least squares regression (PLSR) on the calibration set of samples. Different mathematical pre-treatments were tested and either multiplicative scatter correction (MSC) or mean centering (MC) combined with the 1st derivative gave the best calibration models for different chemical composition. According to the selected calibration equations, both the coefficient of determination in calibration (R^2_C) and the coefficient of determination in prediction (R^2_P) was over 0.98 for all chemical composition, and the ratio performance deviation (RPD) was 17.37, 5.12 and 10.43 for fat, protein and moisture, respectively (Table 1). The results of the present study indicate the outstanding ability of NIRS to predict chemical composition in beef from different cattle breeds, which is probably due to the wide ranges of reference data and the homogeneity in minced beef samples. To our knowledge, performances of the calibration equations have never been so high to offer an alternative to analytical methods of the chemical composition in beef.

Table 1. Statistics of prediction models for chemical parameters in beef samples by NIRS[1]

Item	Mathematical treatment	No. of latent factors	Calibration set		Validation set		
			R^2C	SEC	R^2P	SEP	RPD
Fat	MC + 1st derivative	9	0.998	0.940	0.998	0.986	17.37
Protein	MSC + 1st derivative	10	0.984	0.654	0.981	0.746	5.12
Moisture	MC + 1st derivative	9	0.997	1.017	0.995	1.246	10.43

[1]SEC = standard error of calibration; SEP = standard error of validation.

Key Words: NIRS, beef, chemical composition

W305 Effects of anti-gonadotropin-releasing factor (GnRF) vaccine and band castration on carcass quality in beef cattle under North American management practices. S. Marti*[1,2], M. Devant[2], S. Amatayakul-Chantler[3], J. A. Jackson[4], E. D. Janzen[5], and K. S. Schwartzkopf-Genswein[1], *[1]Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada, [2]IRTA-Ruminant Production, Caldes de Montbui, Barcelona, Spain, [3]Veterinary Medicine R&D, Zoetis, Parkville, Victoria, Australia, [4]Veterinary Medicine R&D, Zoetis, Kalamazoo, MI, [5]University of Calgary Veterinary Medicine, Calgary, Alberta, Canada.*

Angus bulls (n = 60; 257 d of age; initial BW 358.8 ± 3.98 kg) were used to study the effect of an Anti-Gonadotropin-Releasing factor (anti-GnRF) vaccine and band castration on carcass quality. Cattle were randomly assigned to 1 of 3 treatments: Bulls, band-castrated animals without pain mitigation (castrated), and animals administered an anti-GnRF vaccine Bopriva (Zoetis, Parkville, Australia, vaccinated). Animals were randomly assigned to one of 6 pens (10 animals/pen). Three doses of 1 mL of anti-GnRF were administrated via subcutaneous injection on d −35, 0 and 90, and band-castration was performed on d 0. Animals were harvested at 514 ± 5.2 d of age, and hot carcass weight (HCW), average fat, ribeye area, marbling quality and percent saleable meat were measured. Data were analyzed using a mixed-effects model with treatment as the main and pen as a random effect. No differences ($P > 0.05$) were observed between castrated and vaccinated steers in final BW (680 ± 8.0 vs. 678 ± 8.0 kg, respectively) and carcass weight (400 ± 5.1 vs. 401 ± 5.1 kg, respectively), however, bulls had greater ($P < 0.001$) final BW and HCW (764 ± 8.0 and 469 ± 5.1 kg, respectively) than castrated and vaccinated animals. Ribeye area (100.9 ± 1.52, 84.2 ± 1.52, and 86.8 ± 1.52 cm^2, for bulls, castrated and vaccinated), and percent saleable meat (53.9 ± 0.79, 49.3 ± 0.79, and 50.2 ± 0.79%, for bulls, castrated and vaccinated) were greater in bulls than in castrated and vaccinated steers. However, average subcutaneous fat (16.7 ± 0.97, 21.1 ± 0.97, and 20.6 ± 0.97 mm, for bulls, castrated and vaccinated) and marbling were greater in castrated and vaccinated steers compared with bulls, with marbling levels numerically greater in vaccinated than castrated steers. These data suggest that an anti-GnRF vaccine (Bopriva) does not negatively affect growth performance or carcass quality making it a viable animal welfare-friendly alternative to traditional banded castration.

Key Words: carcass quality, anti-GnRF vaccine, band castration

W309 Meat characteristics of lambs fed fresh or dehydrated spineless cactus (*Opuntia ficus-indica*). **M. I. Aguilar-Yanez[1], O. Hernandez-Mendo[1], G. Aranda-Osorio*[2], I. Guerrero-Legarreta[3], and M. M. Crosby-Galvan[1],** *[1]Colegio de Postgraduados, Montecillo, Mexico, [2]Universidad Autonoma Chapingo, Texcoco, Mexico, [3]Universidad Autonoma Metropolitana, Iztapalapa, Mexico.*

The objective of this study was to evaluate meat characteristics and fatty acid profile from finishing lambs supplemented with fresh or dehydrated spineless cactus (*Opuntia ficus-indica*). Twenty-seven commercial crossbred male lambs were used, with an initial liveweight mean of 21.4 ± 3.8 kg. They were distributed homogeneously into 3 groups of 9 each, allocated in individual pens, and then randomly assigned to one of the following treatments: (T1) Control diet, (T2) Diet with 17% of dehydrated cactus (dry matter), and (T3) Diet with 17% of fresh cactus (dry matter). Crude protein, ash and fat content, color, shear force of raw and cooked meat, water activity (Aw), holding water capacity (HWC) and fatty acid profile were evaluated in the muscle Longissimus dorsi. A completely random design using Proc GLM was used, and when statistical differences were observed, a mean comparison was done using the Tukey test. There were differences in water-holding capacity ($P < 0.001$) and behenic fatty acid ($P < 0.005$), being lower and higher on T1 and T2, respectively. Meat chemical analysis, color and shear force, were not different ($P > 0.05$) among treatments, neither were the percentage of total fatty acids, saturated, monounsaturated and polyunsaturated. These results suggest that including cactus (fresh or dehydrated) into the lamb finishing diet at around 17% of the dry matter, had similar benefits on meat quality than that without cactus (a common finishing diet); or even in fatty acid profile, which makes cactus a viable feeding strategy. It seems that the level of cactus pear could be increased in the diet without affecting animal performance and to have a positive effect on sheep meat, in particular, enhancing the fatty acid profile.

Key Words: sheep, cactus pear, meat trait

W310 Effect of fat source addition on the profile of main fatty acids in the longissimus muscle and subcutaneous fat of feedlot steers. G. Fiorentini*[1,2], I. P. C. Carvalho[1,2], J. F. Lage[1,2], L. G. Rossi[1,2], L. Delevatti[1], C. S. Ribeiro Junior[1], and T. T. Berchielli[1,3], *[1]Universidade Estadual Paulista (UNESP) - FCAV, Jaboticabal, SP, Brazil, [2]Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP), São Paulo, SP, Brazil, [3]Instituto Nacional de Ciência e Tecnologia em Ciência Animal (INCT-CA), Brasília, DF, Brazil.*

The aim of this experiment was to evaluate the effect of addition of fat sources on fatty acid composition of the longissimus muscle and subcutaneous fat of steers. Forty-five Nellore steers with an initial average age of 15 mo and an initial body weight of 419 kg were used in this study. The diet was provided ad libitum with a forage (corn silage): concentrate ratio of 60:40. Five different concentrates were formulated for each treatment: without additional of a fat source (WF) (2.8% ether extract in the total diet) or with addition lipids of different fatty acid profiles: linseed oil (LO), palm oil (PO), soybeans (SG) and a commercial supplement with protected fat (Lactoplus) (PF) with 7.0% ether extract on a total dietary. The experimental period was 90 d and the experiment was set up as a completely randomized design. After slaughter, samples were taken from the longissimus muscle and subcutaneous fat (between the 12th and 13th rib) for the measurement of fatty acid concentration. The means were compared by the Tukey test at 5%. Palm oil diet increased the concentration of C14:0 in the muscle and subcutaneous fat ($P < 0.05$) when compared with the other diets (5.18 and 6.99%, respectively). The concentration of C16:0 in the muscle was higher in the diet WF (26.3%) and lower in animals fed with the diet with LO (22.2%). For subcutaneous fat, in addition to the treatment WF (24.1%), the treatments that contained PO (24.7%) and PF (23.5%) also showed higher C16:0 concentration when compared with LO (18.7%) ($P < 0.05$). The highest amount of oleic on the muscle

was obtained in WF (40.2%), whereas PO and PF showed lowest concentrations (34.0 and 33.8%, respectively). The highest level of linoleic was verified in animals fed PF (4.91%). Concentrations of linolenic and CLA were found at a higher percentage in the muscle and fat of animals fed with LO when compared with the others ($P < 0.05$). Diet with LO provided greater concentrations of CLA in the longissimus muscle and subcutaneous fat of Nellore cattle, improving beef quality. Using PO as a fat source elevated the amount of undesirable saturated fatty acids.

Key Words: linseed oil, meat quality, palm oil

W311 Fatty acid profile of meat from Nellore young bulls fed crude glycerin replacing energy sources on concentrate. J. F. Lage*, E. San Vito, A. F. Ribeiro, R. A. Silva, E. E. Dallantonia, L. R. Simonetti, L. M. Delevatti, R. A. Reis, and T. T. Berchielli, *Universidade Estadual Paulista, Jaboticabal, Sao Paulo, Brasil.*

This trial aimed to evaluate the effects of feeding crude glycerin (CG; 80% glycerol) included on 10% of DM diet, replacing corn (Cr) or soybean hulls (Sh) in different ratio of concentrate:roughage (60:40 or 40:60) on fatty acid profile of meat from young bulls. Sixty young bulls (Nellore), with 374.11 ± 24.77 kg initial BW were randomly assigned to 6 treatments, with 10 replicates. The diets were (1) without CG plus Cr; (2) combination of CG and Cr, (3) combination of CG plus Sh. These 3 diets were combined with 2 concentrate levels (CL; 60:40 or 40:60), resulting in 6 diets. The diets were isonitrogenous. Animals were slaughtered at 498.35 ± 33.55 kg BW and all carcasses were refrigerated at 0°C for approximately 24 h. A boneless longissimus muscle (LM) section 10 cm thick was removed from the posterior end of the wholesale rib. LM samples were individually vacuum-packaged and held at −20°C for analysis. The experiment was conducted according to a completely randomized design in a 2 × 3 factorial arrangement: 2 CL × 3 feeding regimens (FR). Data were analyzed by the GLM procedure of SAS, and the Tukey test used considering 5% probability. Meat from animals fed lower CL had greater ($P = 0.0184$) level of palmitic acid (C16:0), myristoleic acid ($P = 0.0218$) and palmitoleic acid ($P = 0.0026$) compared with meat from animals fed greater CL. Greater levels of stearic acid ($P = 0.0274$) and lower levels of oleic acid ($P = 0.0119$) were detected in meat from animals fed diets without CG. Lower level of linoleic acid ($P = 0.0442$) was observed in meat from animals fed lower CL. Animals fed diets without CG had the highest level ($P = 0.0246$) of linoleic acid, lower CLA (18:2 *cis*-9, *trans*-11) content ($P = 0.0001$) and lower values of monounsaturated fatty acids ($P = 0.0022$) compared with meat from animals fed CG. Animals fed high CL had higher linoleic acid meat content. The inclusion of crude glycerin in beef cattle diets as a substitute of corn or soybean hulls improves the fatty acid profile of meat by increasing the monounsaturated and linoleic acid contents.

Key Words: beef cattle, glycerol, linoleic acid

W312 Lipid oxidation and color of meat and subcutaneous fat from young bulls fed crude glycerin replacing energy sources on concentrate. J. F. Lage*, E. San Vito, R. A. Silva, A. F. Ribeiro, M. Machado, L. M. Delevatti, L. R. Simonetti, E. E. Dallantonia, R. A. Reis, and T. T. Berchielli, *Universidade Estadual Paulista, Jaboticabal, Sao Paulo, Brazil.*

This trial aimed to evaluate the effects of feeding crude glycerin (CG; 80% glycerol) included on 10% of DM diet, replacing corn or soybean hulls in different ratio of concentrate:roughage (60:40 or 40:60) on lipid oxidation (using thiobarbituric acid reactive substances - TBARS) and color of meat and subcutaneous fat (SF) from young bulls. Sixty young bulls (Nellore), with 374.11 ± 24.77 kg initial BW were randomly assigned to 6 treatments, with 10 replicates. The diets were: 1- without CG plus corn; 2- association of CG and corn, 3- association of CG plus soybean hulls. These 3 diets were combined with 2 concentrate level (CL; 60:40 or 40:60), resulting in 6 diets (isonitrogenous). Animals were slaughtered at 498.35 ± 33.55 kg BW and all carcasses were refrigerated at 0°C for 24 h. Longissimus muscle (LM) section 10 cm thick was removed from the posterior end of the wholesale rib. LM samples and SF were individually vacuum-packaged and held at −20°C for analysis. The color reading was conducted using the CIE L*a*b* system. The experiment was conducted according to a completely randomized design in a 2 × 3 factorial arrangement: 2 CL × 3 feeding regimens (FR). Data were analyzed by the GLM procedure of SAS, and the Tukey test used considering 5% probability. Similar values of lightness (L*; $P = 0.4090$), redness (a*; $P = 0.8282$) and yellowness (b*; $P = 0.7200$) were observed for beef from animals fed different CL. Regards to SF, animals fed lower CL had greater values of b* ($P = 0.0135$) than those fed higher CL whereas no differences were observed for L* ($P = 0.3416$) and a* ($P = 0.5075$) did not differ among animals fed different CL. FR did not affect the variables evaluated with regard to meat color L* ($P = 0.6284$), a* ($P = 0.7292$), and b* ($P = 0.4932$). No effects of CL ($P = 0.4464$) and FR ($P = 0.1868$) were observed for levels of TBARS. The level of inclusion of CG (10% DM) in the diets with different energy sources on concentrate was not enough to promote changes in beef color and lipid oxidation. Animals fed diets with greater proportion of roughage have more yellow subcutaneous fat.

Key Words: glycerol, Nellore, TBARS

W313 Effect of supplementation of an extract rich in flavonoids on meat quality in young Friesian bulls. M. M. Campo[1], B. A. Refat[2], A. R. Seradj[2], J. Crespo[3], and J. Balcells*[2], *[1]Dept. Animal Production and Food Science, University of Zaragoza, Zaragoza, Spain, [2]Dept. Animal Production, University of Lleida, Lleida, Spain, [3]Interquim, S.A. (Ferrer HealthTech), Barcelona, Spain.*

To assess the effect of flavonoids on meat quality acceptability, 32 young Friesian bulls were randomly divided into 4 pens, according to the dose of Bioflavex (Interquim, SA, Spain) supplemented in the concentrate: 0 (CTR), 150 mg/kg (FL1), 300 mg/kg (FL2) or 450 mg/kg (FL3). Bioflavex is a blend of naringine (200 g/kg) and *Citrus aurantium* extract (400 g/kg). The trial lasted 3 wk, with straw ad libitum, until animals reached the target slaughter weight (414.3 ± 10.7 kg). At 36 h postmortem, the loins between the 7th and 10th vertebrae were obtained, vacuum packaged and kept at 4°C. At 5 d post mortem, the longissimus thoracis was excised and 2-cm-thick steaks were sliced and placed either in polystyrene trays overwrapped with oxygen permeable film or packed with modify atmosphere (MAP; 80% O_2: 20% CO_2). Samples were displayed under simulated retail conditions at 4°C under light (700 lx) for 12 h a day during 14 d. A panel of 15 consumers was asked daily to assess the aspect of the meat on a 9-point scale (1 = non-desirable; 9 = very desirable) and to express their willingness to purchase and consume the meat. As expected, consumers preferred meat under MAP than under film conditions, due to color preservation. Consumers preferred the meat with FL from the 7th d of blooming ($P < 0.1$) when stored in film, although the scores were already fairly low (being 3.27 the highest for FL3 vs. 2.76 for CTR). In meat stored under MAP, no differences were found between treatments during the first 7 d of display. However, FL3 showed the best acceptability from there onwards, being the only treatment with a score over 5 (5.09) after 8 d of blooming. The percentage of willingness to purchase the meat stored in MAP remained over 50% till the 7th d of display decreasing afterward,

although the rate of decrease was lower in FL3 (40.3% of willingness) than in the other treatments, especially the CTR group (25.0% of willingness). In MAP, the inclusion of Bioflavex at a dose of 450 mg/kg allows to moderately increase the shelf life of meat (from 7 to 8 d), in terms of consumer purchase decision.

Key Words: beef cattle, flavonoid, meat quality

W314 Meat quality traits of young bulls finished in feedlot with sources of fiber and crude glycerin. M. Machado, A. F. Ribeiro*, L. R. Simonetti, E. E. Dallantonia, J. F. Lage, E. A. Oliveira, E. San Vito, R. A. Silva, A. J. Neto, and T. T. Berchielli, *São Paulo State University, Jaboticabal, SP, Brazil.*

The objective of this study was to evaluate the beef quality of young bulls fed crude glycerin, 80% of glycerol, with different sources of fiber. Ten percent of crude glycerin was used in replacement of corn on diet dry matter. Three sources of roughage: corn silage (T1), sugar cane (T2) and sugar cane bagass (T3) were used at the inclusion level on the diet dry matter of 28, 27 and 17%, respectively. Diets were adjusted to contain 15% of NDF from roughage. Thirty Nellore young bulls with 416 ± 24.68 kg initial BW were randomly assigned to 3 treatments, with 10 replicates during 90 d. Animals were slaughtered at average body weight of 550.50kg BW and all carcasses were chilled at 0°C for 24 h. Longissimus muscle (LM) section 10 cm thick was removed from the posterior end of the wholesale rib, individually vacuum-packaged and maintained under refrigeration at 0°C for 14 d post mortem. The color reading was conducted on the surface, using the CIE L*a*b* system. The water holding capacity (WHC) was measured for the difference between the weights of the sample before and after it was subjected to a pressure of 10 kg for 5 min. Data were analyzed by the GLM procedure of SAS, and the Tukey test used considering 5% probability. The diets did not affect the pH ($P = 0.1951$), WHC ($P = 0.7534$), Warner-Bratzler shear force ($P = 0.2778$) and cooking losses ($P = 0.2528$). Similar values of lightness (L*; $P = 0.2014$), redness (a*; $P = 0.1411$) and yellowness (b*; $P = 0.1506$) were observed on beef. Animals fed with crude glycerin (10% DM) in diets with different sources of fiber showed similar beef quality traits.

Key Words: glycerol, pH, tenderness

W315 Predicting percent empty body fat in calf-fed Holstein steers using carcass measurements. J. E. Hergenreder*[1], M. J. Anderson[1], L. D. Luque[2], P. D. Bass[3], W. Nichols[5], R. J. Delmore[2], J. L. Beckett[4], and B. J. Johnson[1], *[1]Animal and Food Science Department, Texas Tech University, Lubbock, [2]Animal Science Department, California Polytechnic State University, San Luis Obispo, [3]Certified Angus Beef, Wooster, OH, [4]Beckett Consulting Services, Fallbrook, CA, [5]Merck Animal Health, Summit, NJ.*

Current empty body fat (EBF) prediction equations using carcass measurements are not as accurate for calf-fed Holstein steers as compared with beef-type cattle. Our objective was to evaluate potential new methods to predict EBF of calf-fed Holstein steers using carcass measurements. Steers (n = 120; 127 ± 3 kg) were randomly assigned to a non-implanted control or implanted treatment (Syn C at d 0, Rev IS at d 120, and Rev S at d 240), fed a finishing ration for up to 420 d, and weighed at 30 d intervals. Steers (n = 8 to 12) from each treatment were harvested on d 0, 60, 120, 180, 240, 270, 300, 360, and 420. A 9 - 11 rib section was taken from the right side of each carcass to evaluate chemical carcass composition. The 9 - 11 rib section was dissected into eye, lean, and fat portions which were subsequently ground through 4-mm grinder. Chemical analysis was performed to determine EBF using the equation developed by Hankins and Howe (1946), which correlates EBF to the 9 - 11 rib section composition. The equation for predicting EBF in calf-fed Holsteins was developed by regressing carcass factors against the EBF predicted from Hankins and Howe's equation. Percent empty body fat was also calculated with the equation developed Guiroy et al. (2001) for beef-type cattle using carcass measurements, to see how the new equation and Guiroy's equation correlated to Hankins and Howe's equation. The new equation was more highly correlated to Hankins and Howe EBF than Guiroy's equation ($r^2 = 0.83$ and 0.27, respectively). The new equation was then validated against another population of calf-fed Holstein steers. The new equation was still more highly correlated to Hankins and Howe than Guiroy's equation ($r^2 = 0.43$ and 0.31, respectively). The newly developed equation is more accurate and correlated to Hankins and Howe's equation in predicting the empty body fat of calf-fed Holstein steers using typical carcass measurements.

Key Words: Holstein steer, implant, empty body fat

Dairy Foods: Microbiology II

W316 Preliminary study of bacteriocin production in tina bacterial biofilms. N. Fuca*[1], C. Pediliggieri[1], M.-N. Madec[2], V. Chuat[2], S. Lortal[2], F. Valence-Bertel[2], and G. Licitra[1], *[1]CoRFiLaC, Ragusa, Italy, [2]INRA UMR 1253 - Science et Technologie du Lait et de l'Oeuf, Rennes Cedex, France.*

Tina is the wooden vat used in the cheese making process of the Sicilian PDO Ragusano cheese. The existence of microorganisms (bacteria) consortia in tina samples has a profound implication both for milk colonization and its fermentation process. Tina biofilm is mainly constituted of lactic acid bacteria and it is free of pathogens. Different factors can explain this absence: nutritional competitiveness, low pH, temperature cycles during cheese making and the production of inhibitory bacteriocin-like substances by lactic acid bacteria. The aim of this work is the assessment of class II bacteriocins production by the microflora of tina biofilm. Biofilm samples were collected from 11 different farms of the Hyblean Region. The ability to produce bacteriocin was screened by microbiological, genetic, and confocal microscopy investigations. *Lactococcus lactis* ssp. *cremoris* (bacteriocin producer) and nisin were chosen as positive controls. The colonies of each biofilm, resulted positive to the microbiological test, were isolated and screened again for bacteriocin production by streaking each colony onto the surface of M17 and BHI agar plates, previously inoculated with the chosen sensitive strains. The spot-on-a-lawn method showed that nearly one-third of the 11 biofilm samples were active against *Listeria innocua* 20Li and that half of them were active against *Lactococcus lactis* CNRZ-117. PCR assay performed using class II bacteriocin specific primers revealed that amplification was obtained for 9 out of 11 biofilms. Confocal microscopy observations registered a decrease of *Lactococcus lactis* CNRZ-117 and *Listeria innocua* 20Li viability in the presence of the producer strains' supernatant, measured over time (between 3 and 48 h). Furthermore, the agar test by streaking of the isolated positive colonies confirmed their antagonistic activity against *Lactococcus lactis* CNRZ-117 and *Listeria innocua* 20Li, supporting their positive role in producing bacteriocin-like substances. This study highlights tina LAB ability to produce anti *Listeria* compounds, mantaining biofilm safety.

Key Words: bacteriocin, lactic acid bacteria, pathogen

W317 Effect of *Lactobacillus acidophilus* NS on plasma cholesterol level in diet-induced obese mice. M. Song*[1], S. Park[2], H. J. Lee[3], B. J. Min[3], S. U. Jung[3], S. H. Park[3], E. Kim[2], and S. Oh[1], *[1]Division of Animal Science, Chonnam National University, Gwangju, Republic of Korea, [2]Department of Biological Sciences, Chonnam National University, Gwangju, Republic of Korea, [3]Research & Business Development Center, Nong Shim Co., Ltd., Seoul, Republic of Korea.*

Reductions of plasma total and LDL cholesterol are major strategies to decrease the risk of cardiovascular diseases. Several studies have reported that administrations of probiotics and yogurt containing probiotics both induce resistance to diet-induced body weight gain and increase of plasma cholesterol and triglyceride levels. The objective of this study was to investigate whether *Lactobacillus acidophilus* NS effectively reduces plasma cholesterol level in high fat diet-fed mice. In addition, we also evaluated the probiotic properties of *L. acidophilus* NS such as acid resistance, bile tolerance, adherence onto HT-29 cells, and cholesterol-assimilation activity. In animal study, 7-wk-old male C57BL/6N mice were fed with a normal diet, a high-fat diet (HFD) or a HFD with *L. acidophilus* NS (~1.0×10^8 cfu) for 10 wk. Total cholesterol and LDL cholesterol levels were significantly lower in mice fed with a HFD with L. acidophilus NS than in those fed with a HFD only while HDL cholesterol level was similar in these 2 groups. To understand the mechanism of the cholesterol lowering effect of *L. acidophilus* NS on HFD-mediated increase of plasma cholesterol level, we determined mRNA levels of genes involved in cholesterol homeostasis in the liver. Expressions of SREBP-2 and LDLR in the liver were dramatically reduced in mice fed with a HFD as compared with those of mice fed with a normal diet. When *L. acidophilus* NS was administrated orally to mice fed with a HFD, a HFD-induced suppression of SREBP-2 and LDLR expression in the liver was abolished. These results suggest that the oral administration of *L. acidophilus* NS increased the expressions of SREBP and LDLR in the liver which were inhibited by high fat intake, leading to a decrease in plasma cholesterol level. *L. acidophilus* NS could be useful probiotics for cholesterol-lowering dairy products and the improvement of hyperlipidemia and hepatic lipid metabolism.

Key Words: probiotic, cholesterol, high-fat diet

W318 Comparative genome analysis of *Lactobacillus curvatus* strains isolated from cheese and fermented sausage. C. J. Oberg*[1,2], M. D. Culumber[1], T. S. Oberg[2], J. R. Broadbent[2], D. J. McMahon[2], and J. L. Steele[3], *[1]Weber State University, Ogden, UT, [2]Western Dairy Center, Utah State University, Logan, [3]University of Wisconsin, Madison.*

Recent studies of cheese microbiology have revealed that *Lactobacillus curvatus* is an increasingly common component of the nonstarter lactic acid bacteria (NSLAB) population in aged Cheddar cheese. We recently sequenced the genome of *L. curvatus* WSU01, an NSLAB isolated from aged Cheddar cheese manufactured at Utah State University. The WSU01 genome was sequenced using a whole-genome shotgun strategy on a 454 GS Titanium pyrosequencer. The sequence was assembled into a 1.98 Mb draft genome consisting of 131 contigs, and preliminary genome annotation was performed using the RAST algorithm (rast.nmpdr.org). To learn more about the role of *L. curvatus* in cheese ripening, we compared the WSU01 genome to the 1.83 Mb genome of *L. curvatus* CRL 705, a strain isolated from dried fermented sausage. Plasmid DNA is common among *L. curvatus*, and CRL 705 is known to contain 2 plasmids (12.3 kb and 18.6 kb). WSU01 appears to contain at least one extrachromosomal replicon that includes genes for conjugative mobilization. Overall, comparative genome analysis using a 90% amino acid identity threshold revealed there were 390 proteins in WSU01 that were absent in strain CRL 705, and 196 CRL 705 proteins that were not encoded in the WSU01 genome. Notable examples of proteins unique to WSU01, which could contribute to growth and flavor production by this organism in Cheddar cheese included those associated with propanediol metabolism, arginine utilization, bacteriocin production, and fatty acid biosynthesis.

Key Words: *Lactobacillus curvatus*, NSLAB, genome

W319 Genomic analysis of *Lactobacillus* WDC04, a novel species associated with late gas production in cheese. C. J. Oberg*[1,2], M. D. Culumber[1], T. S. Oberg[2], F. Ortakci[2], J. R. Broadbent[2], and D. J. McMahon[2], *[1]Weber State University, Ogden, UT, [2]Western Dairy Center, Utah State University, Logan.*

A new heterofermentative *Lactobacillus* species (WDC04), which may be associated with late gas production in Cheddar, was isolated from aged cheese following incubation on MRS agar at 6°C for 35 d. WDC04 had 97% 16S rRNA sequence identity with *Lactobacillus suebicus* strain CECT5917 (AJ575744) and *Lactobacillus vaccinostercus* (AB218793). This bacterium only fermented 2 of the 50 substrates tested, ribose and galactose, on API CH50 fermentation panels. To learn more about the metabolic capabilities of *Lactobacillus* sp. WDC04, total genomic DNA was sequenced using a whole-genome shotgun strategy on a 454 GS Titanium pyrosequencer. The sequence was assembled into a 1.90 Mb draft genome consisting of 105 contigs, and preliminary genome annotation was performed using the RAST algorithm (rast.nmpdr.org). Genome analysis confirmed the pathway for ribose metabolism as well as a glycerol fermentation pathway that are likely related to the oligotrophic nature of this organism. This is the first report on a genome from a previously unknown nonstarter lactic acid bacterium in aged Cheddar cheese. Further study of this novel bacterium may shed new insight on the phenomenon of late gas production in Cheddar.

Key Words: *Lactobacillus*, gas production, genome

W320 Comparative analysis of blp gene clusters in bacteriocin-producing strains of *Streptococcus thermophilus*. J. Renye* and G. Somkuti, *Agricultural Research Service, USDA, Wyndmoor, PA.*

Streptococcus thermophilus LMD-9 contains a gene cluster for the production of a bacteriocin-like peptide (Blp); yet expression depended on the exogenous addition of a quorum sensing induction peptide. In contrast, *S. thermophilus* ST110 naturally produces a bacteriocin with unique antipediococcal activity. PCR analysis of ST110 confirmed the presence of several components of the blp gene cluster. Inactivation of blpC, known to encode the quorum sensing induction peptide, resulted in impaired antipediococcal activity. Analysis of the blp gene cluster in ST110 by chromosomal walking revealed that it was 2 kb shorter and contained 9 fewer open reading frames (ORF) when compared with LMD-9. The nucleic acid sequence encoding components of the blp quorum sensing system (blpABC and blpHR) were identical between both strains, yet real-time PCR analysis showed the expression of BlpC was over 500-fold higher in ST110. In ST110, sequence analysis revealed 2 ORF, designated blpU and blpK, which may encode the bacteriocin based on the presence of a double glycine leader peptide. In the ST110 blpC knockout strain the expression of blpU and blpK was 21 and 39-fold lower when compared with the ST110 parent strain, suggesting they are needed for optimal expression of the bacteriocin. In LMD-9 blpD was shown to be essential for the strains antimicrobial activity; and its absence from the ST110 gene cluster further supports the possibility of either blpU or blpK encoding the actual bacteriocin. When compared with LMD-9, where BlpU serves as an accessory peptide to enhance BlpD activity, blpU expression was 174-fold higher in ST110 and 8-fold higher in the ST110 blpC knockout strain. Analysis of the promoter region of blpU in ST110 detected 2 direct repeats required for binding of the response regulator which were identical to those found within the blpD promoter of LMD-9, suggesting BlpU may have an essential role in the antipediococcal activity of ST110.

Key Words: *Streptococcus thermophilus*, bacteriocin

W321 Influence of phospholipids on the viability of *Streptococcus thermophilus* and *Lactobacillus delbrueckii* ssp. *bulgaricus* under acid stress. B. Chinnasamy*, S. Clark, and A. Mendonca, *Iowa State University, Ames.*

Improved extraction methods of phospholipids (PLs) from by-products such as buttermilk and whey and their potential health benefits have opened new avenues for dairy PLs applications in foods; one such application is fortification of yogurt. However, it is critical to evaluate the influence of PLs on the viability of common lactic acid bacteria (LAB) before application in yogurt. As post acidification is a limiting factor for viability of LAB, the objective of this study was to investigate the influence of PLs on viability of *Streptococcus thermophilus* (ST) and *Lactobacillus delbrueckii* ssp. *bulgaricus* (LB) under normal and acid stressed conditions (pH of 4.5 and 4.2, respectively). Yogurt cultures, ST and LB, were grown individually in M17 and MRS broths and later inoculated in broths fortified with one of 3 PLs: phosphatidylcholine (PC), phosphatidylethanolamine (PE) and phosphatidylserine (PS); the PLs were fortified at the rate of 0.01% w/v. The pH in the broths were adjusted to 4.5 and 4.2 before inoculation and stored at refrigeration temperature for 20 d to mimic yogurt storage conditions. The LAB were enumerated on d 0, 5, 10 and 20 using the pour plate technique; 3 replications were completed. ST showed varied response in the presence of PLs; improved viability with PC, a slow decline with PE and decreased viability with PS was noted in comparison to control (without PLs) at pH 4.5. While decreased viability was observed in the presence of PE and PS at pH 4.2, ST showed improved viability in the presence of PC by the end of the storage period. Generally, viability of LB declined during the study period, but the decline was slower in the presence of PE (pH 4.5 and 4.2) and PC (at pH 4.2) than without PLs. The results suggest that individual PLs do not have profound beneficial or inhibitory influences on ST and LB under acid stress conditions. For practical applications in yogurt, influence of additional PLs and combined PLs on LAB is currently being investigated.

Key Words: phospholipid, *Streptococcus thermophilus*, *Lactobacillus delbrueckii* ssp. *bulgaricus*

W322 Influence of the tina wooden vats biofilm composition on milk microbial growth under Ragusano cheese-making conditions. S. Carpino*[1], I. Schadt[1], V. Giummarra[1], and G. Licitra[1,2], *[1]CoRFiLaC, Regione Siciliana, Ragusa, Italy, [2]DISPA, Catania University, Catania, Italy.*

Ragusano cheese is a brine-salted pasta filata raw-milk cheese. The raw milk is placed in the traditional tina for cheese making. Starters are not added, but the tina biofilm and the natural milk flora are responsible for the milk acidification. The aim of the present study was to investigate the influence of the tina biofilm on the microbial composition of milk which has undergone the usual cheese-making procedure except for the rennet addition step. Biofilm samples were obtained from the inner surface area of 100 cm^2 of 11 wooden tinas using sterile swabs which were then suspended in peptone water. Aliquots of a UHT milk sample were inoculated (InoMB) with the biofilm samples. Tina surface area per volume milk was 1.5 times the usual exposure conditions. Inoculated milk samples were then incubated (Inc.MC) under Ragusano cheese-making conditions: 65 min at 35°C, 45 min at 40°C (first cooking), 120 min at 45°C (second cooking), 24 h at 15°C (time before brining). Biofilm, inoculated and incubated samples were analyzed for TBC, for counts of mesophilic lactobacilli (ME_LB), mesophilic lactococci (ME_LC), thermophilic lactobacilli (TH_LB), thermophilic lactococci (TH_LC) and enterococci (EC). A linear model was used to test the effects of log-transformed biofilm counts on log-transformed counts of inoculated and incubated milk samples. Biofilm samples had highest variations in TH_LC and ME_LC ($1 – 5.5 \times 10^3$ and $1 – 1.3 \times 10^3$ cfu/cm^2, respectively), followed by TH_LB and ME_LB ($1 – 7 \times 10^2$ and $1 – 3.8 \times 10^3$ cfu/cm^2, respectively) and by EC ($1 – 6.4 \times 10^1$ cfu/

cm^2). Biofilm TBC ($P < 0.01$), ME_LB ($P < 0.01$), ME_LC ($P < 0.01$), TH_LB ($P < 0.01$), and TH_LC ($P < 0.05$) counts were highly associated with counts of the inoculated milk samples. Moreover, biofilm EC ($P < 0.05$), ME_LC ($P = 0.05$), and TH_LB ($P < 0.05$) were associated with counts of the incubated milk. The counts of respective Inc.MC samples were estimated to vary by 2.80×10^6 cfu/mL EC, by 1.75×10^8 cfu/mL MESO_LC and by 1.42×10^3 cfu/mL TH_LB. Considering equal levels of all biofilm bacteria, the EC growth was most abundant during incubation.

Key Words: Ragusano, cheese, biofilm

W323 Growth of specific lactic acid bacteria (PCR-DGGE) in relation to volatile compounds (SMart Nose and GC/MS) in biofilm inoculated milk under Ragusano cheese-making conditions. S. Carpino*[1], I. Schadt[1], T. Rapisarda[1], C. Randazzo[2], and G. Licitra[1,3], *[1]CoRFiLaC, Regione Siciliana, Ragusa, Italy, [2]DiGeSA, Catania University, Catania, Italy, [3]DISPA, Catania University, Catania, Italy.*

Ragusano cheese is a brine-salted pasta filata raw-milk cheese. Starters are not added, but the biofilm of the wooden vat (tina) and the natural milk flora are responsible for the milk acidification. The aim of the present study was to investigate the growth of specific LAB species in relation to the development of volatile compounds in milk which has been inoculated with biofilm from different tinas and which has undergone the usual cheese-making procedure except for the rennet addition step. Biofilm samples were obtained from the inner surface of 11 wooden tinas (A-K) with sterile swabs suspended in peptone water. Aliquots of a UHT milk sample were inoculated with the biofilm samples. Tina surface area per volume milk was 1.5 times the usual exposure conditions. Incubated samples were analyzed by PCR-DGGE to determine LAB species, with SMart Nose and by GC/MS. The following LAB species were identified: *Lb. plantarum* and *Lb. paracasei* (mesophilic lactobacilli), *Lc. lactis* and *Lc. mesenteroides* (mesophilic lactococci), *Lb. delbrueckii* and *Lb. helveticus* (thermophilic lactobacilli), *S. thermophilus* (thermophilic lactococcus) and *E. faecalis* (enterococcus). Data were evaluated with principal component analysis (PC1: 23%; PC2: 14%). Four (B, E, F, J) represented the greatest volatiles' variation. Samples E and F were similar in profile, but different from B and J. Profiles of B and J differed also. *Lb. paracasei* was associated to hexane 2,3,4-trimethyl and heptane-2,2,4,6,6-pentamethyl, *E. faecalis* and *Lb. delbrueckii* to tetradecanal, *Lb. plantarum* to nonanoic acid and benzeneacetaldehyde, *Lc. lactis* to octanal. Differences in volatile compounds were most related to *Lc. mesenteroides* and *Lb. paracasei* which separated B from E and F samples, but not to *Lb. plantarum*, *S. thermophilus* and *Lb. delbrueckii*. Sample J was distinguished from the others by 2-dodecanone. Further studies are still needed to better understand the relationship between individual LAB species and flavor production in cheese.

Key Words: Ragusano, cheese, biofilm

W324 Influence of different concentrations of lactose on the growth of *Lactobacillus delbrueckii* ssp. *bulgaricus* LB-12 and *Streptococcus thermophilus* ST-M5. B. Mena*[1] and K. Aryana[1,2], *[1]School of Animal Sciences, Louisiana State University Agricultural Center, Baton Rouge, [2]Department of Food Science, Louisiana State University Agricultural Center, Baton Rouge.*

Lactic acid bacteria ferment lactose. The objective of this study was to evaluate the effect of various concentrations of lactose on the growth of yogurt culture bacteria *Lactobacillus bulgaricus* and *Streptococcus thermophilus*. Sterile MRS broth was inoculated separately with freshly thawed *Lactobacillus bulgaricus* LB-12 and *Streptococcus thermophilus* ST-M5 and different amounts of lactose (1, 2, 3, 4, and 5% w/v) were added. No added lactose was used as control. Growth was determined by plating in duplicate at 0, 4, 10, 12, 24, 36, 48 and 60 h of incubation period for both microorganisms. Growth of *L. bulgaricus* was determine by pour plating using MRS agar pH 5.2 and anaerobically incubation at 43°C for 72 h. Growth for S. thermophilus was determine by pour plating using *Streptococcus thermophilus* agar and aerobically incubation at 37°C for 24 h. Data were analyzed using ANOVA of SAS with Duncan adjustment. Three replications were conducted. At hours 36, 48 and 60, use of 5% lactose (w/v) resulted in significantly highest log cfu/mL of *S. thermophilus*, while only 4% lactose (w/v) resulted in significantly highest log cfu/mL of *L. bulgaricus*. It is concluded that both these lactic acid bacteria had a slightly different lactose optimum for growth.

Key Words: lactose, yogurt, bacteria

W325 Influence of whey protein isolate on growth of *Streptococcus thermophilus* ST-M5. L. Vargas*[1] and K. Aryana[1,2], *[1]School of Animal Sciences, Louisiana State University Agricultural Center, Baton Rouge, [2]Department of Food Science, Louisiana State University Agricultural Center, Baton Rouge.*

Whey protein is used in manufacture of some dairy products to increase protein content and as a replacement of solids. The objective was to study the effect of whey protein isolate (WPI) on the growth of *Streptococcus thermophilus* ST-M5. Sterile MRS broth was inoculated with freshly thawed *S. thermophilus* and WPI was added in different amounts namely, 0 (control), 1, 2, 3, 4, and 5% w/v. The MRS broth containing WPI was incubated at 37°C for up to 60 h. Growth was determined by pour plating using *Streptococcus thermophilus* agar followed by aerobic incubation at 37°C for 24 h. Data were analyzed using ANOVA of SAS. Three replications were conducted. At 24 and 60 h, significantly lower counts were observed for control compared with WPI use. With the use of 5% WPI the *Streptococcus thermophilus* ST-M5 counts were 2 log cfu/mL higher than the control. Use of WPI improved growth of *Streptococcus thermophilus* ST-M5.

Key Words: yogurt, whey, culture bacteria

W326 Effect of several health beneficial spices on the bile tolerance of *Lactobacillus bulgaricus* LB-12. M. Sanchez-Vega*[1] and Kayanush Aryana[1,2], *[1]School of Animal Sciences, Louisiana State University Agricultural Center, Baton Rouge, [2]Department of Food Science, Louisiana State University Agricultural Center, Baton Rouge.*

Functional foods have become an important and rapidly expanding market. Spices such as garlic and ginger are widely used for their antibacterial properties and as a preventative for cardiovascular diseases. Onion and turmeric have been studied for its potential use in decreasing the risk of developing diabetes and along with garlic, they have been researched for their anticancer properties. *Lactobacillus bulgaricus* is a culture bacterium with some health benefits. Bile tolerance is an important probiotic characteristic. Influence of pure spice juice on the bile tolerance of culture bacteria is not known. Objective was to elucidate the effect of garlic, ginger, onion and turmeric on bile tolerance of *Lactobacillus bulgaricus* LB-12. Bile tolerance of *L. bulgaricus* was analyzed in MRS-THIO broth supplemented with 0.3% (w/v) oxgall and 0.2% (w/v) sodium thioglycolate, and 1% (v/v) of freshly extracted spice juice. Sample without spice juice were the control. Samples were incubated at 43°C for 5 h, but removed hourly

for plating. Growth was determined by pour plating using MRS agar pH 5.2. Plates were incubated anaerobically at 43°C for 72 h. Data were analyzed using Proc Mixed model with a Tukey adjustment of SAS. Experiments were conducted in triplicate. At 0 h of incubation (8.4 log cfu/mL), ginger showed a significant higher count with a difference of 0.5 log cfu/mL when compared with control. Garlic and onion showed significantly lower counts after 2 h of incubation with a difference of 1 log cfu/mL when compared with control. After 3 h of incubation, garlic and ginger showed significantly lower counts with a difference of 1 log cfu/mL when compared with control. After 4 and 5 h, all spices showed significantly lower counts with a minimum difference of 1.5 log cfu/mL for garlic and a maximum of 3 log cfu/mL for turmeric, when compared with control. Even though these spices showed significantly lower counts, *L. bulgaricus* was still viable, indicating that these spices can be used in combination with this bacterium allowing health benefits from both bacteria and spices.

Key Words: spice, bile, probiotic

W327 Evaluation of coated and powder sodium butyrate in diets for broilers reared with reused litter during a commercial production cycle. J. Hernandez*[1], G. Afanador[1], C. Ariza-Nieto[2], and Y. Avellaneda[2,1], *[1]Universidad Nacional de Colombia, Bogota Colombia, [2]Corpoica, Mosquera Colombia.*

Short-chain fatty acids have been widely used as feed additives, but data on the use of sodium butyrate in broilers are lacking. This study was carried out to evaluate the use of powder (99%) and coated sodium butyrate(30%) and its effects on the performance of broilers reared with reused litter during a commercial production cycle of 41 d. 720 one-day-old Avian cobb male chicks were fed with isocaloric and isoproteic commercial type diets: starter phase (1–20 d) and finisher phase (20–41 d). Broilers were located on reused litters and randomly assigned to 1 of the 4 dietary treatment groups: (1) Control diet without supplementation (C); (2) zinc bacitracin (15%) diet 500 g/ton (CP); (3) sodium butyrate: free 98% (FB); and (4) coated 30% (CB) at a dosage of 500 g/ton in both diets (FB, CB). Data were analyzed as a completely randomized design with 6 replicates (30 birds/replicate) using GLM procedures of SAS software package. Tukey method was used to compare means ($P < 0.05$). Each replicate of birds was weighted weekly and feed residuals were used to calculate daily feed intake and feed conversion. Results showed a positive effect ($P < 0.05$) of FB and CB supplementation on productive performance compared with C group and similar ($P > 0.05$) results with CP. FB group presented the highest weight gain/day (51.6 g ± 1.76) compared with group C (48.1 g ± 2.36) ($P < 0.05$), but similar to CB group (50.5 g ± 1.96) and CP (49.4 g ± 1.75). Feed conversion showed a better result in CB (1.65 ± 0.040) and CP (1.62 ± 0.034) groups compared with C (1.76 ± 0.090) group, while FB (1.66 ± 0.026) group did not differ to all the groups ($P > 0.05$). Despite the fact that butyrate groups received different concentrations of sodium butyrate per kg feed, CB was no different to FB in the commercial performance of broilers, but sodium butyrate can be used as an alternative additive to antibiotic growth promoters.

Key Words: sodium butyrate, performance, reused litter

W328 Effect of oregano essential oils (*Lippia origanoides* Kunth) on lipid peroxidation in eggs enriched with n-3 fatty acids during storage. R. E. Ortiz*[1,2], G. Afanador[1], Y. Avellaneda[1,2], D. Vasquez[2], and C. Ariza-Nieto[2], *[1]Universidad Nacional de Colombia, Bogotá, Colombia, [2]Corpoica, Bogotá, Colombia*.

Higher PUFA content in eggs provides a functional food, but it leads to greater susceptibility to lipid peroxidation. A natural way to increase the intrinsic antioxidant concentration is through dietary supplementation with natural antioxidants, such as oregano essential oils (OEO). There is an inverse relationship between malondialdehyde (MDA), an indicator of lipid peroxidation, and dietary antioxidant level in poultry products. A feeding study was carried out to evaluate the effects of OEO native to Colombia on oxidative stability of enriched eggs during storage. A total of one hundred eighty 48-wk-old Babcock Brown laying hens were randomly assigned to 1 of the 5 treatments: (1) Control (CONT) without supplementation; (2) vitamin E 200 g/ton (VITE); (3) OEO 100 g/ton (O100); (4) OEO 150 g/ton (O150); (5) OEO 200 g/ton (O200). Hens were individually placed in 30 cages during 8 weeks. At the end of the period, 8 freshly collected eggs from each replicate, totaling 48 eggs from each treatment were refrigerated at 4°C and analyzed for MDA levels in yolk at 0, 15, 30 and 60 d of storage. Data were analyzed as a completely randomized design with a factorial arrangement of treatments (5 × 4). Tukey method was used to compare means ($P < 0.05$). Results showed that the extent of lipid oxidation, as measured by MDA formation differed ($P < 0.0001$) between dietary treatments and storage time with no interaction ($P > 0.05$). During storage significant changes occurred in egg yolk MDA value ($P < 0.001$). Fresh eggs showed 36.1 mg/g of MDA, while in eggs stored at 4°C during 60 d the MDA value increased in 32% (47.9 mg/g). The control group exhibited the higher MDA values (48.4 mg/g) comparable ($P > 0.05$) to O100 (45.4 mg/g), but different ($P < 0.0001$) than O150, VITE, and O200 (39.9, 38.4, 36.2 mg/g, respectively). There was an inverse relationship between OEO in the diet (ppm) and MDA concentration in the egg yolk (Y = 60.69–0.0839 OEO, R^2: 0.74, $P < 0.0001$). It can be concluded that there is a clear oxidative stability effect of OEO supplementation in n-3 fatty acids enriched eggs during storage.

Key Words: oregano essential oil, enriched egg, yolk stability

W329 Evaluation of Optifeed Poultry in the diet of female broiler chickens. V. Noirot*, M. Champagnac, P. Etienne, and D. Éclache, *Laboratoires Phodé, Terssac, France.*

The objective of this trial was to evaluate the effect of Optifeed Poultry (OP, Laboratoires Phodé, France) based on plant extracts and designed to stimulate animal voluntary feed intake. The trial was conducted in the experimental aviary Farm School of State University of Londrina (Brazil). Four hundred and forty one-day-old Cobb female broiler chickens were divided following a completely randomized design in 5 homogeneous groups of 4 replicate pens. Each pen contained 22 birds. They were slaughtered at 48 d. The birds were given pre-starter feed for 1–7 d (22% CP, 3000 kcal/kg ME), starter for 8–21 d (20% CP, 3100 kcal/kg ME), grower for 22–42 d (19% CP, 3190 kcal/kg ME) and finisher for 43–48 d (17.5% CP, 3210 kcal/kg ME).The 5 treatments consisted in providing OP (500g/t) according to different programs: for treatment 1 only from 1 to 7 d, for treatment 2 only from 1 to 21 d, for treatment 3 during the whole experimental period, for treatment 4 OP from 1 to 7 d, no OP from 8 to 41 d and OP from 42 to 48 d, and for treatment 5 (control) no OP. The chickens were weighed weekly. Feed intake and feed conversion were evaluated for each pen and each group at weighing time. Dead birds were recorded daily. Results were submitted to ANOVA followed by Tukey test, except viability that was analyzed using chi-squared test. Feed intake between 1 and 42 d was improved with treatment 3 (4.795 kg/bird) compared with the control group (4.529 kg/bird) and compared with the other treatments ($P < 0.05$). Treatment 3 increased feed conversion measured between 1 and 21 d, 1 and 42 d, and 1 and 48 d compared with control ($P < 0.05$).OP increased live weights at 7 d with treatments 1 (196 g), 2 (196 g), 3 (200 g) and 4 (202 g) compared with control group (188 g, $P < 0.05$), without any effect on feed conversion between 1 and 7 d ($P > 0.05$). Weights at 21 d were improved only for treatment 4 (0.903 kg vs. 0.854 kg for control, $P < 0.05$). Weight at 48 d and viability were not modified by treatments ($P > 0.05$). In this trial, OP allowed to improve performances of female broiler chicken during the first week.

Key Words: female broiler chicken, feed intake stimulation, plant extract

W330 Effect of a blend of plant extracts with controlled release on the performances of heat stressed broiler. V. Noirot*, M. Champagnac, P. Etienne, and D. Éclache, *Laboratoires Phodé, Terssac, France.*

A blend of antioxidant and anti-inflammatory ingredients among which curcumin, formulated to be released in the intestine (Force 6 Poultry, Laboratoires Phodé, France), was tested on 2 groups (0 and 50 ppm doses in feed) of 6 replicate pens each containing 25 Ross x Ross broiler chickens, slaughtered at 35 d. A moderate heat stress was applied to induce an oxidative stress: temperature was increased beginning d 10 to 21 and d 29 to 34 from 3 to 6°C above Ross recommendations (during 12 h per day, see table). Birds were individually weighed at 21, 28, and 35 d. Feed conversion was evaluated per pen at each weighing and mortality was recorded daily. Liver glutathione peroxidase (GPx) activity was measured on 2 sacrificed birds per pen, chosen to be representative of the pen average weight, at 35 d of age ("Glutathione Peroxydase Assay Kit," Cayman chemical, Michican, USA, method adapted from Paglia and Valentine, 1967). Performance data were subjected to mixed model procedure with treatment as fixed factor and pen in treatment as random factor, and chi-squared tests were performed on mortality rates (SAS v. 9.1, Cary, N.C.). Live weights at 28 and 35 d were improved ($P < 0.05$) in treated group (D28: 1883 g, D35: 2582 g) compared with control (D28: 1802 g, D35: 2509 g). Average daily weight gain was increased in treated group between 22 and 28 d (121.48 g/d vs 111.56 g/d for the control, $P < 0.05$). GPx activity was increased in treated group (94.14 vs 74.73 U/mg protein for control group, $P < 0.05$). Treatment has no significant effect on the other parameters ($P > 0.05$). In this trial, during a moderate heat stress, the product Force 6 Poultry improved chickens growth performances compared with a nonsupplemented control.

Table 1. Temperatures recommended (R) and applied in this trial (T); temperatures in bold indicate heat stress period

Temp,	Age, d															
°C	1-4	5-6	7-9	10	11-15	16-17	18-21	22-23	24-25	26-27	28	29	30-31	32	33-34	35
R	31	30	29	29	28	27	26	25	24	23	22	22	21	20	19	19
T	31	30	29	32	32	31	30	25	24	23	22	27	26	26	25	19

Key Words: broiler, antioxidant

W331 Effect of two chemotypes of oregano essential oil on growth performance and nutrient balance of broilers. C. Ariza-Nieto[1], W. Marquez[1], G. Afanador*[2], J. S. Knott[3], and R. W. Fent[3], *[1]CORPOICA, Bogota, Colombia, [2]Universidad Nacional, Bogota, Colombia, [3]Ralco Nutrition Inc., Marshall, MN.*

One alternative to feed-based antibiotics is oregano essential oil (OEO); however, there are many varieties and species of OEO. Two species of OEO were evaluated in this trial, a European strain (*Origanum vulgare* Hirtum) and a South American strain (*Lippia origanoides*). A 42-d experiment was conducted to evaluate growth performance using 2,000 one-day-old Ross male broilers housed in 40 pens. A separate trial was conducted using 200 broilers to determine organic matter, energy and nitrogen balance. The sources of OEO are the South American Lippia Origanoides (LO) and a commercially available oregano essential oil product Synergy Essence (SE; Ralco Nutrition Inc., Marshall, MN USA). For both experiments, experimental units were randomly assigned to 1 of 8 dietary treatments: (1) Basal diet (BD) without OEO or antibiotic; (2) BD+AGP (bacitracin 50 g/ton); (3) BD+LO125 (125 g/ton); (4) BD+LO250 (250 g/ton); (5) BD+LO500 (500 g/ton); (6) BD+SE125 (125 g/ton); (7) BD+SE250 (250 g/ton); (8) BD+SE500 (500 g/ton). Data were analyzed by ANOVA as a completely randomized design. Each pen served as experimental unit. Tukey method was used to compare means ($P < 0.05$), and orthogonal single degree-of-freedom contrasts were used to compare means. Broilers fed SE250 had greater ($P < 0.05$) final body weight (2,295 g vs. 1,985 g) and greater ($P < 0.05$) ADG compared with the BD (53.9 g/d vs. 46.5 g/d). There were no differences ($P > 0.10$) among the LO, SE or AGP fed birds for ADG, ADFI, or gain:feed. Broilers consuming the AGP diet tended ($P < 0.10$) to have lower ADFI compared with the other dietary treatments. Broilers fed LO500 had greater ($P < 0.05$) organic matter digestibility than BD. There were no differences in organic matter, energy, or nitrogen digestibility among AGP, LO, or SE-fed birds. There was a tendency ($P < 0.10$) for BD-fed birds to have lower ME/GE compared with birds fed the AGP or OEO treatments. These data indicate that birds fed diets containing OEO grow faster than those fed a basal diet and similar to birds fed AGP with some of this response being possibly explained by increased digestibility and energy utilization.

Key Words: broiler performance, *Lippia origanoides*, *Origanum vulgare*

W332 An intimate combination of a high intensity sweetener and a phytonutrient improves performance of weaned piglets. C. Oguey[1], A. L. Wagner[2], and C. Bruneau*[1], *[1]Pancosma S.A., Le Grand Saconnex, Geneva, Switzerland, [2]Cooperative Research Farms, Richmond, VA.*

Dietary levels of a high intensity sweetener based on saccharin are known to improve glucose absorption. Anethole was shown to enhance gut immunity and minimize local inflammation leading to optimal gut health. The objective of this trial was to evaluate the effects of an intimate combination of these 2 components (TT, TakTik X-In, Pancosma) on piglet's performance. Three hundred sixty weanling pigs (20 d of age, 5.5 ± 0.2 kg BW) were blocked based on weight and sex, and allocated to 36 pens for 6 weeks. Diets were supplemented with 264 ppm Cu, 2000 ppm Zn and antibiotics. During wk 1 to 3, pens were assigned to 2 treatments: a control (CT) unsupplemented basal diet (n = 12) or the basal diet + 150 ppm TT (TT; n = 24). During wk 4 to 6, the CT pens continued to receive CT, but the TT pens were split (n = 12) into 0 ppm TT (TT-S) or 150 ppm TT groups (TT-SG). Performance (ADFI, ADG, G:F) was recorded per pen and per phase and analyzed using PROC Mixed in SAS. From week 1 to 3 and compared to CT, TT increased ADFI (respectively 326.5 and 348.7 g/d, $P < 0.01$) and ADG (respectively 319.3 and 329.0 g/d, P = 0.09). During week 1, ADFI and ADG were similar among treatments ($P > 0.4$). However in weeks 2-3, TT increased ADFI by 7.6% ($P < 0.01$) and ADG by 3.1% ($P = 0.08$). These results suggest that TT does not target immediate performance, but improves intake and growth after enhancing gut development. During weeks 4-6, TT-SG improved ADG and G:F respectively by 4.9% and 4.5% compared to CT ($P < 0.05$) but did not affect ADFI (mean 858.0 g/d, $P = 0.78$). TT-S and CT exhibited similar ADFI, ADG and G:F in this phase ($P > 0.21$). This shows that a continuous TT supplementation improves piglets' performance during this period. On the overall, compared to CT, TT-SG did not affect ADFI (mean 585.05, $P = 0.34$) but enhanced ADG (respectively 453.7 and 472.9 g/d, $P = 0.01$) and G:F (respectively 784.8 and 800.0 g/kg, $P = 0.02$). These results show that TT improve performance of weaning piglets, through a better feed intake during the starter period, then via an increased feed efficiency during the grower phase.

Key Words: anethole, piglet performance, sweetener

W333 Effects of lactulose supplementation on production performance in sows and piglets. S. C. Kim, K. H. Kim, and I. H. Kim*, *Department of Animal Resource & Science, Dankook University, Cheonan, Choognam, South Korea.*

A total of 18 sows (Landrace × Yorkshire) and their litters were used in this study to evaluate the effects of lactulose supplementation on performance in sows and piglets. On d 107 of gestation, all sows were relocated to farrowing crates in an environmentally regulated farrowing house, and allotted to 1 of 3 dietary treatment groups. Dietary treatments included (1) CON, control diet; (2) L1, CON + 0.1% lactulose; (3) L2, CON + 0.2% lactulose. All diets were provided in mash form, and sows were provided with free access to water throughout the experimental period. Individual piglet BW was assessed on d 0, 7, 14 and 21(weaning), and 7 d after weaning to calculate ADG. Fecal *Lactobacillus* and *E. coli* shedding were measured by using MacConkey agar plates and lactobacilli medium III agar plates. The individual sow or litter of piglets was used as the experimental unit. All data in this experiment were analyzed in accordance with a completely randomized design using the GLM procedure (1996). Differences among treatment means were determined via Duncan multiple range test, and a probability level of $P < 0.05$ was regarded as statistically significant. At the weanling day (21 d), higher ($P < 0.05$) fecal *Lactobacillus* population of sows was observed in L2 treatment compared with CON treatment. In conclusion, our results suggested that dietary inclusion of lactulose at the level of 0.2% could increase the fecal *Lactobacillus* concentration in sows, but no beneficial effects were observed on the production performance either in sows or piglets.

Table 1. Effect of supplementation lactulose in lactating sows and piglets

Item	CON	L1	L2	SE
Sow BW, kg				
Before farrowing	234.6	235.7	239.2	15.1
After farrowing	214.1	217.9	219.2	12.9
Weaning	207.8	206.7	212.9	13.8
BW loss	6.3	11.2	6.3	3.6
Piglets				
Birth weight, kg	18.3	18.5	18.5	1.2
Weaning weight	59.2	65.7	67.2	5.0
ADG, g	211	217	225	13.8
Weaning Lactobacillus, log10 cfu/g	6.45[b]	6.88[ab]	7.02[a]	0.17

[a,b]Means in the same row with different superscripts differ ($P < 0.05$).

Key Words: lactulose, piglet, sow

W334 Effect of propolis on the growth performance, nutrient digestibility, blood profiles, fecal microflora, fecal score, and intestinal morphology in weanling pigs. B. R. Lee, J. Li, and I. H. Kim*, *Department of Animal Resource & Science, Dankook University, Cheonan, Choognam, South Korea.*

A total of 125 pigs [(Yorkshire × Landrace) × Duroc] with an average initial BW of 6.68 ± 1.03 kg were used to investigate the effects of propolis on growth performance, nutrient digestibility, blood profiles, fecal microflora, fecal score, and intestinal morphology in weanling pigs in this 5-wk trial. Pigs were randomly allocated into 1 of 5 dietary treatments on the basis of BW and sex [5 replicate pens per treatment with 5 pigs (2 gilts and 3 barrows) per pen]. Propolis feed additive contained more than 60% propolis and 6% of total flavonoid in powder form. Dietary treatments were (1) NC, negative control (free antibiotics); (2) PC, NC + 33 ppm tiamulin; (3) PRO1, NC + 0.05% propolis; (4) PRO2, NC + 0.10% propolis; (5) PRO3, NC + 0.20% propolis. At the end of wk 2 and wk 5, individual pig BW and feed consumption was recorded on a pen basis to calculate growth performance, nutrient digestibility was measured following the procedures by the AOAC (2000), blood profiles and fecal microflora were analyzed. All data were subjected to the GLM procedures of SAS (1996) as a randomized complete block design, with pen as the experimental unit. Pigs fed PRO1, PRO2 and PRO3 diets had higher (378, 382 and 389 vs. 352 g; $P < 0.05$) ADG than pigs fed NC diet during wk 0 to 2. During d 0 to 35, the ADG in PRO2 and PRO3 was higher (492 vs. 459 g; $P < 0.05$) than NC, the gain/feed in PRO3 was higher (0.849 vs. 0.765; $P < 0.05$) than NC. Apparent total tract digestibility (ATTD) of DM and N of NC was lower (DM: 80.78 vs. 83.65%; N: 79.14 vs. 82.46%; $P < 0.05$) than other treatments at wk 2. PRO1, PRO2 and PRO3 treatments had higher (84.17 vs. 80.02%; $P < 0.05$) ATTD of energy compared with NC treatment at 2 wk. The concentration of IgG in PRO2 was higher (381 vs. 319 mg/dL; $P < 0.05$) than NC at 5 wk. Fecal score in NC and PC treatments were higher (4.0 vs. 3.4; $P < 0.05$) than in PRO2 treatment at 1wk. In conclusion, inclusion of propolis at a level of 0.10% could increase growth performance, nutrient digestibility, IgG, and had positive effect on fecal score in weanling pigs.

Key Words: growth performance, propolis, weanling pig

W335 Effect of phytogenics on growth performance, calcium and phosphorus digestibility, and bone calcium and phosphorus contents in broilers. Z. F. Zhang, B. R. Lee, and I. H. Kim*, *Department of Animal Resource & Science, Dankook University, Cheonan, Choognam, South Korea.*

A total of 756 day-old broilers (40 ± 0.2 g) were used in a 28-d feeding trial to evaluate the effects of phytogenics on calcium (Ca) and phosphorus (P) digestibility, and bone Ca and P contents which affected the bone strength and growth performance. Broilers were randomly distributed into 1 of 7 treatments on the basis of BW (6 replicate pens per treatment with 18 broilers per pen). Phytogenics (Biostrong 510, Delacon, Austria) contains 30% Quilaja, 20% Anise and 17% Thyme. Dietary treatments were: T1, negative control (without antibiotic); T2, CP 0.5% reduced; T3, CP 0.5% reduced + 0.015% phytogenics; T4, Ca 0.07% reduced + P 0.065% reduced; T5, Ca 0.07% reduced + P 0.065% reduced + 0.015% phytogenics; T6, T1 + 0.015% phytogenics; T7, T1 + 0.2% mixed organic acids (20% formic acid, 20% lactic acid, 10% citric acid and 10% fumaric acid). The broilers were weighed and feed intake were recorded on d 1, 7, 21 and 28 for calculating BW gain (BWG), ADFI, and feed conversion ratio (FCR). At d 28, fresh excreta samples were collected from each pen for the measurement of nutrient digestibility according to the procedures of AOAC (2003). All data were subjected to GLM procedures of SAS (1996) as a randomized complete block design, with pen as the experimental unit. Differences among treatments were separated by Duncan's multiple range test; $P < 0.05$ was considered statistically significant. There was no difference ($P > 0.05$) in BWG, ADFI and FCR among treatments. The apparent total tract digestibility (ATTD) of Ca in T7 treatment was higher ($P < 0.05$) than in T1, T2 and T3 (0.58 vs. 0.52, 0.53 and 0.52). Broilers fed the T2 diet had a lower ($P < 0.05$) ATTD of P than T1, T3, T5, T6, and T7 (0.47 vs. 0.55, 0.55, 0.54, 0.55 and 0.55). At wk 4, bone Ca in T6 was increased (10.76 vs. 9.71 g/100g DM; $P < 0.05$) compared with T4, bone P of T5, T6 and T7 increased ($P < 0.05$) compared with T4 (5.29, 5.30 and 5.29 vs. 5.13 g/100g DM). In conclusion, phytogenics could improve bone calcium and phosphorus of broilers. Mixed organic acids improve the ATTD of Ca and P, and increased bone phosphorus in broilers.

Key Words: bone calcium and phosphorus, broiler, phytogenics

W336 Effects of microencapsulated organic acids and pure botanicals (Aviplus-S) supplementation on reproductive performance, nutrient digestibility, and fecal scores in lactating sows and piglets. J. H. Cho, H. Y. Beak, and I. H. Kim*, *Department of Animal Resource & Science, Dankook University, Cheonan, Choognam, South Korea.*

A total of 21 crossbred (Yorkshire × Landrace) sows were used to determine the effects of microencapsulated organic acids and pure botanicals (Aviplus-S) supplementation on reproductive performance, nutrient digestibility, and fecal scores in lactating sows and piglets. Microencapsulated feed additive (Aviplus-S, VetAgro SpA, Reggio Emilia, Italy) contains 25% citric acid, 16.7% sorbic acids, 1.7% thymol and 1.0% vanillin. Sows were randomly allotted into 1 of 3 dietary treatments. Treatments were (1) CON, control diet; (2) Avi1, CON + 0.05% Aviplus-S; (3) Avi2, CON + 0.10% Aviplus-S. Experimental stage was from 2 weeks before farrowing to weaning (weaning period 25 d). Fresh fecal grab samples collected from each sow on d 25 after farrowing were mixed and pooled, and analyzed for nutrient digestibility of DM, gross energy and nitrogen following the procedures of AOAC (2000). Fecal consistence was monitored twice daily during d 5 to d 25 after farrowing and quantified using a scale ranging from 0 to 5. When the scoring was bigger than 3, the piglet was considered to have diarrhea. Data will be analyzed using a randomized complete block design following GLM procedures of SAS (1996), with each sow being used as the experimental unit. Sows fed Avi2 diet had higher ($P < 0.05$) BW a few hours before farrowing, a few hours after farrowing and at the day of weanling compared with sows fed CON and Avi1 diets. No significant difference ($P > 0.05$) was observed in nutrient digestibility among treatments. During d 5 to 8, d 16, fecal score were decreased ($P < 0.05$) in treatment Avi1 compared with CON treatment. Avi1 and Avi2 diets had lower ($P < 0.05$) fecal score than CON diet from d 20 to 22. The number of diarrhea piglets was decreased ($P < 0.05$) when sows were supplemented with 0.10% Aviplus-S compared with CON treatment at d 15. In conclusion, this study indicates that administration of 0.10% Aviplus-S could decrease the BW loss after farrowing, and dietary inclusion of 0.05 or 0.10% Aviplus-S could improve the fecal score in piglets.

Key Words: organic acid, pure botanical, sow

W337 Evaluation of Flavomycin 4 (bambermycins) and Stafac 20 (virginiamycin) in growing-finishing pigs' growth performance and carcass characteristics under different environmental temperatures. S. K. Baidoo*[1], J. A. Jendza[1], and R. Cabrera[2], *[1]University of Minnesota, Southern Research and Outreach Center, Waseca, [2]Huvepharma Inc., Chapel Hill, NC.*

Two feed additives, Flavomycin (FLAV) and Stafac (STAF), were evaluated in growing-finishing pigs under different environmental temperatures in a 49-d growth performance study. Growing-finishing pigs (n = 397, 87.9 ± 7.2 kg) were allotted to 3 × 2 factorial arrangement with 3 dietary treatments (CON; FLAV (250ppm), STAF (250 ppm) and 2 environmental temperatures (Normal Temp (N) = 18°C and High Temp (H) = 30°C). Forty-eight pens of growing-finishing pigs (7 to 8 pigs per pen) divided evenly between 3 rooms with 2 designated as H Temp rooms and one as N Temp room. Pen BW was used to assign pens to treatments in a randomized incomplete block design. A basal diet was formulated using 54% corn, 30% corn-derived DDGS and 10% SBM to contain 3,124 kcal ME/kg, 0.96% SID Lys, 0.65% Ca and 0.38% available P. Pigs were weighed and blood samples (for BUN and IgG analyses) collected on d 0, 28 and 49 of the study. Carcass traits were measured at slaughter. Statistical analysis was for a randomized incomplete block design with block nested within temp. Statistical significance was set at $P < 0.05$. Heat stress (H) reduced ($P < 0.01$) BW, ADFI and ADG at all time points but improved ($P < 0.01$) feed efficiency d0 to d28. Dietary treatment did not interact with environmental temperature, or exert an independent effect on growth performance measures. Blood urea nitrogen was not affected by any treatment, but increased ($P < 0.05$) with time. Plasma IgG was not affected by diet, but was increased by high environmental temperature on d 28 ($P < 0.05$) but not on d 49 and was reduced with time ($P < 0.01$). For carcass characteristics, H Temp reduced HCW yield ((107 ± 0.04 kg vs. 95 ± 0.59 kg; $P < 0.01$), back fat depth ((19.8 ± 0.25 mm vs. 23.1 ± 0.50 mm; $P < 0.01$) and loin depth (72.9 ± 0.51mm vs. 74.4 ± 0.5; $P < 0.04$) but increased ((55.1 ± 0.13 vs. 54.9 ± 0.18; $P < 0.05$) percent lean yield. Dietary supplementation with either FLAV or STAF did not mitigate the heat stress related feed suppression and there was no interaction between diet and temperature.

Key Words: environmental temperature, pig, Flavomycin

W338 Effect of antimicrobials on energy and phosphorus utilization in pigs. K. McCormick* and O. Adeola, *Purdue University, West Lafayette, IN.*

The improvement in energy and nutrient utilization may be a contributing factor in the growth- promoting benefits of antimicrobials. The current study evaluated the effect of 3 antimicrobials (carbadox, tylosin, or virginiamycin) on total tract utilization of energy and P in 17-kg pigs fed a P-deficient corn-soybean meal-based diet. Twenty-four barrows blocked by weight (17.5 ± 0.41 kg) and housed in metabolism crates were assigned in randomized complete block design to dietary treatments that included (1) negative control (NC), (2) NC plus 55g/T carbadox, (3) NC plus 44 g/T tylosin, and (4) NC plus 11 g/T virginiamycin. The NC diet contained 0.7% Ca, and 0.4% total P. Pigs were fed twice daily at an allowance of 4% of BW. A 5-d adaptation period preceded a 5-d total collection period, with chromic oxide as a marker to determine initiation and termination of fecal collection. The results show that the supplementation of antimicrobials did not affect DM digestibility (87.1%, 88.5%, 87.0%, and 87.7%, respectively), P absorption (35.1%, 34.0%, 31.5%, and 38.3%, respectively), DM retention (81.8%, 82.9%, 80.7%, and 82.7%, respectively), or P retention (34.8%, 33.7%, 31.0%, and 38.0%, respectively). There was an increase in energy digestibility ($P = 0.02$, 86.5% and 88.1%) and retention ($P = 0.03$, 83.4% and 84.9%) with supplementation of carbadox relative to pigs fed the NC diet. Furthermore, supplementation of virginiamycin showed a tendency to improve energy retention relative to the NC diet ($P = 0.10$, 83.4% and 84.5%). Results from the current study show that supplementation of carbadox improved energy utilization, whereas virginiamycin improved energy retention, although there were no changes in DM and P utilization.

Key Words: antimicrobial, phosphorus digestibility, pig

W339 Effects of turmeric and curcumin addition to diets on growth performance and immune response of nursery pigs. M. R. Bible*, S. D. Carter, K. F. Coble, H. J. Kim, and T. M. Walraven, *Oklahoma State University, Stillwater.*

Curcumin is an active component in turmeric that has antimicrobial and anti-inflammatory properties, which may aid in improving growth performance of nursery pigs. Thus, 216 (5.8 kg; 8 reps/trt) crossbred [D × (L × Y)] pigs were used to determine the effects of curcumin on growth performance and immune response of nursery pigs. Pigs were weaned at 20 d of age, blocked by BW and ancestry, and allotted randomly to

4 dietary treatments in a randomized complete block design (RCBD). Standard corn-soybean meal-based diets were fed in meal form in a 4-phase feeding program (SID Lys 1.56, 1.51, 1.31, 1.25%). Diets were a negative control (no antibiotic; CNT), a positive control (mecadox, 55 mg/kg; AB), CNT + 2 g/kg of turmeric powder (TUM), and CNT + 80 mg/kg of curcumin powder (CUR). AB, TUM, and CUR replaced corn in the diets. ADG), ADFI, and G:F were calculated for d 0–21 and 0–42. On d 20, 1 pig/pen was challenged with *E. coli* lipopolysaccharide (LPS; 25 μg/kg BW intraperitoneal). Rectal temperatures (RT) were measured and blood collected for analysis of tumor necrosis factor-α (TNF-α) at 0, 3, 6, 12, and 24 h post-injection (PI). Growth data were analyzed as a RCBD using a general linear model; immune response analysis used a mixed model with repeated measures. For d 0–21, ADG for pigs fed AB (324 g) was greater ($P < 0.05$) compared with pigs fed CNT (294 g) or TUM (293 g), with pigs fed CUR (317 g) intermediate. There was a tendency ($P < 0.10$) for ADFI to be lower for pigs fed TUM (453 g) than pigs fed AB (489 g), with pigs fed CNT (466 g) and CUR (468 g) intermediate. Pigs fed CUR (0.68) had greater ($P < 0.05$) G:F than pigs fed CNT (0.63), with G:F similar for pigs fed AB (0.66) and TUM (0.64). Results for d 0–42 were similar to d 0–21, but there were no effects on ADFI. RT and TNF-α increased ($P < 0.01$) from hr 0, peaked at 3 h, and returned to normal by 24 h PI of LPS. For TNF-α (ng/mL), pigs fed CUR (2.8) had the smallest increase ($P < 0.01$) at hr 3 PI, followed by AB (3.8), CNT (5.1), and finally, TUM (5.3). In conclusion, pigs fed CUR had similar growth performance to AB and CUR blunted the response to a LPS challenge.

Key Words: pig, curcumin, turmeric

W340 Effect of supplementing a nucleotide-rich yeast extract without or with in-feed antibiotics on performance and total-tract nutrient digestibilities in weaned piglets. S. M. Waititu*[1], J. M. Heo[1], R. Patterson[1,2], and C. M. Nyachoti[1], *[1]University of Manitoba, Winnipeg, MB, Canada, [2]Canadian Bio-Systems Inc., Calgary, AB, Canada.*

Dietary nucleotides are bioactive compounds with the potential to mitigate weaning-associated challenges in piglets. Two experiments were carried out to determine the effect of supplementing a nucleotide-rich yeast extract (NRYE) in a piglet diet with or without an antimicrobial growth promoter (AGP) on performance and apparent total tract digestibility (ATTD) of DM, CP and GE. In Exp. 1, ninety 21-d-old piglets (initial BW 6.79 ± 0.5 kg; mean ± SD) were randomly assigned to 6 dietary treatments consisting of a basal corn-soybean meal-based diet containing 0, 0.1, or 0.2% NRYE each fed with or without AGP (55 mg of Aueromycin and 31.2 mg of Tiamulin per kg of diet) in a 3 × 2 factorial arrangement for a 21-d period. In Exp. 2, 6 corn-soybean meal-based diets formulated to contain 0% NRYE or 0.1% NRYE with 0, 25, 50, 75 or 100% of the recommended AGP dosage were fed to 108, 21-d-old piglets (initial BW 7.11 ± 0.9 kg; mean ± SD) for 28 d. Dietary treatment did not influence growth performance in both experiments. In Exp. 1, supplementing 0.1% NRYE reduced ($P < 0.05$) occurrence of loose feces compared with 0.2% NRYE, and AGP supplementation with 0.2% NRYE reduced ($P < 0.05$) the ATTD of DM, CP and GE. In Exp. 2, supplementing 50% AGP with 0.1% NRYE reduced ($P < 0.05$) occurrence of loose feces and increased ($P < 0.05$) the ATTD of CP and DM in wk 3. Increasing AGP concentration linearly ($P < 0.05$) decreased and increased ADFI and G:F in wk 3, respectively, increased ADG in wk 4, and quadratically ($P < 0.05$) reduced occurrence of loose feces from wk 2 to 4 and overall. The results show that supplementing 0.1% NRYE with 50% AGP would have beneficial effects in reducing occurrence of loose feces in piglets and increasing ATTD of DM and CP but further research is needed to explain the lack of response in growth performance.

Key Words: antimicrobial growth promoter, nucleotide-rich yeast extract, performance

W341 Effect of two chemotypes of oregano essential oils on lipid peroxidation of broiler breast meat during storage. C. Ariza-Nieto*[1], D. Vasquez[1], G. Afanador[2], J. S. Knott[3], and R. W. Fent[3], *[1]CORPOICA, Bogota, Colombia, [2]Universidad Nacional, Bogota, Colombia, [3]Ralco Nutrition Inc., Marshall, MN.*

Oregano essential oil (OEO) is powerful natural antioxidant. A feeding study was conducted to evaluate the effects of 2 chemotypes of OEO on oxidative stability of breast meat. The sources of OEO are the South American *Lippia origanoides* (LO) and a commercially available oregano essential oil product Synergy Essence (SE; Ralco Nutrition, Inc. Marshall, MN USA). One-day-old Ross broilers were randomly assigned to 1 of 8 dietary treatments: (1) Basal diet (BD) without OEO or antibiotic; (2) BD+AGP (bacitracin 50 g/ton); (3) BD+LO125 (125 g/ton); (4) BD+LO250 (250 g/ton); (5) BD+LO500 (500 g/ton); (6) BD+SE125 (125 g/ton); (7) BD+SE250 (250 g/ton); (8) BD+SE500 (500 g/ton). At the time of slaughter (42 d of age), 5 birds per treatment were selected and slaughtered. A portion of the breast was minced with a conventional meat grinder. Three subsamples were wrapped in an oxygen-permeable polyethylene film and stored at −4°C for 3, 6, and 9 d, then were vacuum-packed at and stored at −20°C until analysis. Lipid peroxidation was determined by measuring malondialdehyde (MDA) concentration in samples from each day. Data were analyzed by ANOVA as a completely randomized design with a factorial arrangement of treatments (8 × 4) with 4 replicates. Tukey method was used to compare means ($P < 0.05$). As day of storage increased (0, 3, 6, 9), MDA concentration increased ($P < 0.05$) from 49.3 to 116.2 ng/g MDA. Broilers fed SE500 had lower ($P < 0.05$) MDA concentration than BD and AGP fed birds. Within OEO supplementation chemotypes at all levels, no differences in MDA ($P > 0.10$) were observed. This study illustrates that providing OEO from SE at 500g/ton in the diet of broilers results in lower lipid peroxidation in ground breast meat throughout the time of storage tested.

Key Words: breast meat, lipid stability, oregano essential oil

W342 Do phytogenics interact with exogenous xylanase when fed to broiler chicks? V. Pirgozliev[1,3], D. M. Bravo*[2], and S. P. Rose[3], *[1]Avian Science Research Centre, Scottish Agricultural College, Ayr, UK, [2]Pancosma, Geneva, Switzerland, [3]National Institute of Poultry Husbandry, Harper Adams University College, Newport, UK.*

The aim of the study was to investigate the effects of dietary supplementation of a mixture of carvacrol, cinnamaldehyde and capsaicin (XT, Pancosma S.A.) alone or combination of XT and xylanase (XYL; a commercial xylanase preparation) on N-corrected dietary apparent metabolizable energy (AMEn) and bird growth performance. A total of three hundred male day-old Ross 308 chicks reared in floor pens from day old to 21 d age, and were fed 1 of 3 diets. A basal diet was prepared that had major ingredients of 546.8 g/kg wheat and 274.9 g/kg soybean meal, and contained 215 g/kg crude protein and 12.12 MJ/kg. The basal diet was then split on 3 batches and supplemented with either no additive (control diet), or 100 g/t of XT (XT diet), or combination of XT and XYL at the rate of 100 g and 2000 units of xylanase/kg (XYL diet). The treatments were allocated in a randomized complete block design with each treatment having 10 replicate floor pens with 10 birds

per pen. Birds fed XT and XYL diets grew 18.5 and 10.7%, respectively, faster ($P < 0.05$), and converted about 9.5% more efficiently the feed to gain, when compared with control fed birds only. There was no difference ($P > 0.05$) in weight gain and feed efficiency between birds fed XT and XYL based diets. Experimental diets did not differ in AMEn ($P > 0.05$), but birds fed XT alone had 10 and 5.5%, respectively, higher daily metabolizable energy intake ($P < 0.05$) than birds fed control and XYL diets. For each gram of weight gain, birds fed XT and XYL diets on average consumed 6.1% less AMEn ($P < 0.05$) than birds fed the control diet only, resulting in proportionately more dietary metabolizable energy intake being available for production as opposed to maintenance. It can be concluded that there were no negative interactions between XT and xylanase when added to a wheat soybean diet and fed to broilers.

Key Words: phytonutrient, xylanase, metabolizable energy

W343 Effects of Healthy Edge technology on sow and litter performance. S. D. Carter*[1], B. de Rodas[2], K. F. Coble[1], H. J. Kim[1], M. R. Bible[1], and G. Willis[2], *[1]Oklahoma State University, Stillwater, [2]Purina Animal Nutrition Center, Gray Summit, MO.*

A cooperative study, utilizing 315 primi- and multiparous crossbred sows from 2 stations (OSU, Purina Animal Nutrition Center), was conducted to determine the effects of inclusion of Healthy Edge in corn-soybean meal diets during the last 6 weeks of gestation through lactation on sow and litter performance. Sows were allotted, based on weight and parity within station, 6 weeks before farrowing to 2 dietary treatments. The control (C) diet was a fortified corn, soybean meal diet (n = 155 sows). Healthy Edge (HE) was added to the control diet at 0.05% at the expense of corn to formulate the test diet (n = 160 sows). The HE contained a select combination of immune-modulating compounds. The gestation and lactation diets were formulated to 0.5 and 0.95% standardized ileal digestible Lys, respectively. Both the gestation and lactation diets contained 0.85% Ca and 0.39% available P. Sows were fed 2.2 kg/d in gestation and allowed ad libitum access to feed in lactation. Sows were weighed at d 109 of gestation, within 24 h after farrowing, and at weaning. Data were analyzed as a mixed model with station, trt, and interactions tested. Sow (litter) served as the experimental unit. Litters were weighed within 24 h of parturition and at weaning. Average sow parity (3.0), lactation days (19.4 d), ADFI (6.0 kg), sow weight post-farrowing (224 kg) and weaning (239 kg), and sow weight change (−4.4 kg) were similar ($P > 0.10$) for both diets. However, number born (11.5 vs. 12.7), number born alive (10.1 vs. 11.4), and number weaned (9.3 vs. 10.0) were increased ($P < 0.004$) for sows fed HE compared with C. Pig weight at birth and weaning were not affected ($P > 0.10$) by diet, but because of greater no. of pigs, litter weights at birth (16.8 vs. 17.7 kg) and weaning (59.2 vs. 63.6 kg), and litter weight gain (42.7 vs. 46.2 kg) were increased ($P < 0.02$) for sows fed HE. Also, sows fed HE returned to estrus sooner ($P < 0.01$) compared with C sows. There were no station × treatment interactions ($P > 0.10$). These results indicate that HE increased number of pigs born alive and weaned, increased litter weight gain, and reduced days to return to estrus.

Key Words: sow, diet, lactation

W344 Effect of glutamic acid plus glutamine on the intestinal morphology of piglets. D. Lescano[1], L. Albino[1], M. Hannas[1], S. Salguero[1], M. Kutschenko[2], E. Nogueira[2], and H. Rostagno*[1], *[1]Federal University of Viçosa, Viçosa, MG, Brazil, [2]Ajinomoto of Brazil Ajinomoto Animal Nutrition, São Paulo, SP, Brazil.*

Weaning of piglets affects intestinal morphology directly and indirectly. Glutamine has synergistic effect with glutamic acid, play key roles for the maintenance of the functional structure of the small intestine. A study was conducted to evaluate the utilization of 4 dietary levels of a commercial product containing glutamic acid plus glutamine (min 95%) in diets for weanling pigs from (18 d) to 25 d old. A total of 24 piglets were used and euthanized 7 d after weaning for sampling. The animals were randomly assigned in a completely randomized design into 4 treatments, 6 replicates and 1 animal per experimental unit. The treatments were: T1- 0.0%; T2- 0.4%; T3- 0.8% and T4- 1.2% glutamic acid (Glu) plus glutamine (Gln). Diets were based on corn, soybean meal, precooked corn, dairy products, blood plasma, L-lysine, L-threonine and DL-methionine. Small intestine histological parameters were measured such as villi height, crypt depth and villous: crypt ratio. The addition of Glu plus Gln improved linearly ($P < 0.05$) duodenum villus height (DV), ileum villus height (IV) and the villus height: crypt depth ratio in the duodenum (DV: DC), jejunum (JV: JC) and ileum (IV: IC). There were also linear and quadratic effects ($P < 0.05$) in duodenal crypt depth (CD) (Table 1). It is concluded that the dietary utilization of 1.2% Glu plus Gln is beneficial to ameliorate the detrimental effects of weaning on morphological parameters in the small intestine of weanling piglets from 18 to 25 d of age.

Table 1. Mean of the intestinal histological parameters of piglets at 25 days of age

	Glu plus Gln (%)				Regression		
Parameter	0.0	0.4	0.8	1.2	Linear	Quadratic	CV (%)
DV (µm)	376	372	418	462	<0.01	NS	14.6
DC (µm)	254	171	175	166	<0.0003	<0.009	16.0
DV: DC	1.7	3	3.1	3.8	<0.0002	NS	24.0
JV (µm)	339	353	321	365	NS	NS	19.2
JC (µm)	183	177	189	157	NS	NS	11.4
JV: JC	2	2.3	1.8	2.8	<0.04	NS	22.1
IV (µm)	240	299	313	367	<0.0001	NS	13.6
IC (µm)	199	197	188	200	NS	NS	7.8
IV: IC	1.3	1.7	1.8	2	<0.00001	NS	11.9

Key Words: piglet, intestinal histology, glutamic acid plus glutamine

W345 Intestinal health of weaned piglets fed diets containing purified cellulose. M. V. Marujo, M. C. Thomaz, V. V. Almeida*, M. M. Lima, E. Daniel, D. J. Rodrigues, F. R. Castelini, M. S. F. Oliveira, and Y. V. S. Guillen, *FCAV/UNESP, Jaboticabal, SP, Brazil.*

The study was conducted to evaluate the effects of purified cellulose inclusion in the diets of newly weaned piglets on intestinal morphology and bacterial enumeration. Thirty-two barrows weaned at 21 d of age were blocked by initial BW (6.68 ± 1.79 kg) and randomly allotted to 1 of 4 treatments, with 8 replicates per treatment and 1 pig per pen. Treatments consisted of corn-soybean meal-based diets formulated to contain 0.0, 1.5, 3.0, or 4.5% purified cellulose. Lactose was added to all diets as an energy source. On d 14 and d 29 post-weaning, piglets were slaughtered and tissues samples were collected from duodenum and jejunum to determine villus height (VH), crypt depth (CD), villus-to-crypt ratio (VH:CD), and number of goblet cells (GC). *Lactobacillus* spp., *E. coli*, and *Clostridium perfringens* counts were determined in digesta samples from the distal portion of the small intestine using plate counts. Statistical analyses were performed using the GLM procedure of SAS. On d 14 post-weaning, increasing purified cellulose level had no effect on duodenal VH, CD, and GC, but resulted in a linear increase in duodenal VH:CD (1.05, 1.09, 1.04, and 1.27 ± 0.28 ; $P < 0.05$) and in a quadratic response in VH (311.99, 293.35, 318.78, and 339.12 ± 0.29 µm; $P < 0.01$) and VH:CD (1.21, 1.06, 1.05, and 1.21 ± 0.27; $P < 0.01$) in the jejunum. On d 29 post-weaning, increasing dietary fiber level had no effect on duodenal morphology, but resulted in a quadratic effect on VH (339.88, 332.06, 308.80, and 380.79 ± 0.27 µm; $P < 0.05$), CD (306.41, 325.89, 295.26, and 270.64 ± 0.27 µm; $P < 0.05$), and VH:CD (1.12, 1.02, 1.05, and 1.42 ± 0.29; $P < 0.05$) in the jejunum. There was a quadratic effect of purified cellulose inclusion on *Lactobacillus* spp. population (7.92, 7.39, 7.30, and 8.09 ± 0.28 log UFC/g; $P < 0.05$) only on d 29 after weaning. Counts of *E. coli* and *Clostridium perfringens* were not affected by treatments on d 14 or 29 post-weaning. In conclusion, adding 4.5% of purified cellulose to the diets of newly weaned piglets improved intestinal health by increasing mucosal membrane integrity and Lactobacillus spp. counts.

Key Words: dietary fiber, piglet, weaning

W346 Effects of nucleotides on growth performance, blood profiles, and fecal microflora in weanling pigs. Z. F. Zhang[1], A. V. Rolando[2], and I. H. Kim*[1], *[1]Department of Animal Resource & Science, Dankook University, Cheonan, Choognam, South Korea, [2]DSM Nutritional Products Philippines Inc., Bonifacio Global City, Taguig, Philippines.*

A total of 140 weanling pigs [(Landrace × Yorkshire) × Duroc; BW = 7.50 ± 0.71 kg; 21 d of age] were used in this 42-d feeding trial to evaluate the effect of nucleotides (NU) as an alternative of antibiotics on growth performance, blood profiles, and fecal microflora which related to post-weaning applicability in weanling pigs. Pigs were randomly distributed into 1 of 4 treatments on the basis of BW and litter (7 replicate pens per treatment with 5 pigs per pen). Dietary treatments were (1) T1, control diet; (2) T2, T1 + 150 g/ton NU; (3) T3, T1 + 220 g/ton NU; (4) T4, T1 + 275 g/ton NU. NU (Rovimax NX) contains at least 80% nucleotides, half of which are free NU. At d 1, 14, 28, 42, BW and feed intake were recorded to calculate the ADG, ADFI and G:F, 2 pigs were randomly chosen from each pen and bled via jugular venipuncture to obtain blood samples, then, fecal *Lactobacillus* and *E. coli* shedding were measured by using MacConkey agar plates and lactobacilli medium III agar plates. All data were subjected to the GLM procedures of SAS (1996) as a randomized complete block design, with pen as the experimental unit. During d 1 to 14, pigs fed T3 diet had higher ($P < 0.05$) ADG than pigs fed T1 diet. During d 29 to 42, pigs fed the T3 diet increased ($P < 0.05$) ADG and G:F compared with pigs fed the T1 diet. During d 15 to 28 ADG and G:F of pigs fed the T2, T3 and T4 diets was higher ($P < 0.05$) than those fed the T1 diet. During d 1 to 42, ADG and G:F of pigs fed the T2, T3 and T4 diets was higher ($P < 0.05$) than those fed the T1 diet. The IgG concentration in T3 and T4 was increased ($P < 0.05$) compared with T1 at d 28 and 42. The fecal Lactobacillus counts in T2, T3 and T4 was higher ($P < 0.05$) than that in T1 at d 28 and 42. In conclusion, dietary supplementation with 150,

220, and 275 g/ton NU could improve growth performance and increase fecal *Lactobacillus* population, moreover, inclusion of 220 and 275 g/ton NU could increase blood IgG centration in weanling pigs.

Key Words: growth performance, nucleotides, weanling pig

W347 Dietary supplementation with a novel *Lactobacillus acidophilus* fermentation prototype improved nursery pig performance and gut health. J. W. Frank*, A. Brainard, M. Wright, and M. Scott, *Diamond V, Cedar Rapids, IA.*

Two experiments were conducted to evaluate the effects of a novel Lactobacillus acidophilus fermentation prototype (SGX; SynGenX, Diamond V) on nursery pig growth and health. In experiment 1, 180 pigs weaned at 19 d of age and weighing 6.7 kg were fed 1 of 6 treatments for 30 d. Pigs were housed 2/pen with 15 replicates/treatment. Treatments were control (CON), XPC (1 g/kg; Original XPC, Diamond V), and SGX at 0.5, 1, 1.5, and 2 g/kg. The control diet contained antibiotics and pharmacological levels of copper and zinc with XPC and SGX treatments added to the control diet. Pig BW and feed intake were recorded, as well as number of injectable medications administered to the pigs to treat health problems. Pigs supplemented with XPC or SGX had improved G:F compared with CON ($P = 0.04$). Final BW of CON, XPC, and the 4 levels of SGX were 15.9, 16.6, 16.7, 17.1, 17.3, and 17.3 kg, respectively ($P = 0.57$). The total number of medications administered to the pigs were 33, 34, 28, 24, 13, and 5 for CON, XPC, and the 4 levels of SGX, respectively ($P = 0.12$). In experiment 2, 1040 pigs weaned at 19–21 d of age and weighing 6.4 kg were fed 1 of 4 treatments for 22 d. Treatments were control (CON) or 1, 2, and 3 g/kg of SGX. The control diet contained antibiotics and pharmacological levels of copper and zinc with SGX treatments added to the control diet. Pigs were housed 26/pen with 10 replicates/treatment. Pig BW and feed intake were recorded. Composite fecal samples were collected from each pen on d 8 to measure Bifidobacteria and Lactobacillus levels using quantitative PCR. Fecal Bifidobacteria ($P = 0.05$) and Lactobacillus ($P = 0.02$) levels were greater in pigs fed SGX at 2 g/kg compared with CON. Final BW for CON and 1, 2, and 3 g/kg of SGX were 11.7, 11.9, 12.4, and 11.9 kg, respectively ($P = 0.25$). The results of these experiments demonstrate that feeding SynGenX, a novel *Lactobacillus acidophilus* fermentation prototype, can improve growth performance and increase the presence of beneficial bacteria in the gut of pigs.

Key Words: pig, lactobacillus, growth

W348 Eugenol affects the integrity of the mucus layer and susceptibility to enteric pathogens. M. Wlodarska[1,2], B. B. Finlay[1,2], and D. M. Bravo*[3], *[1]Michael Smith Laboratories, University of British Columbia, Vancouver, BC, Canada, [2]Department of Microbiology and Immunology, University of British Columbia, Vancouver, BC, Canada, [3]Pancosma, Geneva, Switzerland.*

Phytonutrients are gaining interest for their use as health promoting feed additives in animal production however their ability to alter mucosal immune response in the intestine is still unknown. Due to its potential beneficial use in the feed industry, we characterized the immunomodulatory function of eugenol, a phytonutrient extracted from cloves. Eugenol is a phenolic compound with previously described functions as an antimicrobial and anti-inflammatory agent when used at high concentrations. We explored the effect of eugenol on the large intestine in terms of changes to the microbial ecosystem, mucosal defenses, and stimulation of innate immunity. Mucus secretion and thickness is thought to play a major role in both health and disease by providing a protective yet permeable barrier between intestinal contents and host tissue. The mucus layer in the large intestine consists of 2 stratified layers, mainly composed of the secreted mucin, Muc2. The inner layer is of dense composition and devoid of commensal bacteria, while the outer layer is built as a loose matrix housing commensal bacteria. Eugenol was evaluated in C57Bl/6 mice for its effect on the mucus layer, microbial composition, and colitis induced by enteric pathogens, including *Citrobacter rodentium* (*C. rodentium*), *Salmonella typhimurium*, and *Trichuris muris*. Eugenol was given to mice through their drinking water for 7 d. Eugenol-fed mice were found to have increased Muc2 expression ($P = 0.06$) and a significantly thicker inner mucus layer ($P = 0.02$) in the large intestine compared with untreated mice. We hypothesize that the thickening of the inner mucus layer mediated by eugenol treatment is dependent on the activation of specific immune signaling pathways. Further, we show that eugenol-fed mice were less susceptible to initial *C. rodentium* colonization in the large intestine 3 d post infection ($P = 0.0341$). These results suggest that eugenol acts to strengthen the mucosal barrier by increasing the thickness of the inner mucus layer, which protects against invading pathogens and intestinal inflammation.

Key Words: phytonutrient, enteric disease, mucus

W349 Effect of dietary resistant starch content on nutrient digestibility, fecal microbial diversity and body weight in piglets. H. Lu*[1], H. Yan[1], R. Potu[1], M. G. Ward[1], C. C. Pelkman[2], C. H. Nakatsu[1], O. Adeola[1], and K. M. Ajuwon[1], *[1]Purdue University, West Lafayette, IN, [2]Ingredion Incorporated, Bridgewater, NJ.*

Resistant starch (RS), a major component of amylose corn, is considered a prebiotic. The utilization of RS rich substrates leads to enrichment of the hind gut with beneficial bacteria and increased production of short chain fatty acids (SCFA). The effect of consuming diets with different amounts of RS during gestation and lactation on birth and weaning weights, concentrations of maternal blood metabolites such as triglycerides (TG), glucose and free fatty acids (FFA) and hormones (IGF-1 and insulin) and milk composition (ether fat, protein, ash and total solids) was evaluated. Two corn-soybean diets (65.8% of control corn or high amylose corn) were fed to 16 sows (8 sows per diet) from D 60 of gestation to farrowing (D 114) and during the lactation period (up to 21 d after farrowing). The control and amylose corn diets had RS contents of 23.5 and 54.5%, respectively. Fecal microbial composition of sows on the 2 diets was determined by PCR-DGGE analysis. Ileal digestibility and total tract nutrient utilization were also determined in ileal-cannulated pigs, (35 kg BW, 5 per diet) in a 7-d digestibility trial. Feeding amylose corn during gestation diet tended ($P < 0.1$) to result in piglets with lower birth weight than control (1.5 vs. 1.7 kg) but with similar weaning weights (6.5 ± 0.2 vs. 6.6 ± 0.2 kg). Serum hormone and metabolite concentrations were not different ($P > 0.05$). Milk from sows on amylose corn diet had higher ($P < 0.05$) total solids (20.6 vs.18.9%) and tended ($P < 0.09$) to have a higher ether fat (9.3 vs.7.8%) than those on the control corn diet. Apparent ileal digestibility of DM, N, energy, Ca and P were not different. Hind gut digestibility was higher ($P < 0.05$) in the amylose vs. control diet for DM (0.56 vs. 0.42) and energy (0.49 vs. 0.36). Amylose diet also resulted in higher ($P < 0.05$) total SCFA concentration than control (142.5 vs. 96.7 m*M*). Analysis of DGGE band profile showed greater microbial diversity in the amylose corn diet than control. Consumption of amylose corn rich diet may be a strategy to enhance sow milk lipid concentration and increase hindgut microbial diversity.

Key Words: maternal, amylose, piglet

W350 Influence of whole wheat feeding on the development of coccidiosis in broilers. Y. Singh, T.J. Wester, A. L. Molan, G. Ravindran, and V. Ravindran*, *Massey University, Palmerston North, New Zealand.*

A study was conducted to assess the effect of whole wheat (WW) feeding on performance, gizzard development, oocyst yield and intestinal lesion score of male broilers (Ross 308) experimentally challenged with *Eimeria acervulina*, *E. maxima*, and *E. tenella*, and to test the hypothesis that the inclusion of whole grain in the diet will reduce the severity of coccidial infection. Diets (finely ground wheat (GW) and 300g/kg WW replacing GW either before or after pelleting) were offered ad libitum from d 1 to d 28 post-hatching. At 21 d of age, each dietary treatment was divided into 2 groups, one unchallenged control and the other inoculated with mixed species of coccidia. No differences ($P > 0.05$) between dietary treatments were observed in weight gain and feed per gain during the pre-challenge period (1 to 21 d), but feed intake was lower ($P < 0.05$) in WW fed birds. After the inoculation (21 to 28 d), challenged birds had reduced ($P < 0.05$) weight gain and feed intake, and higher ($P < 0.05$) feed per gain compared with unchallenged birds. Mortality in challenged birds was highest in those fed diets with WW post-pelleting, followed by pre-pelleted WW and GW (58, 35, and 17%, respectively; $P < 0.05$). Relative gizzard weights were heavier ($P < 0.05$) in WW fed birds, irrespective of the method of inclusion, compared with those fed GW in both challenged and unchallenged groups. Total lesion scores of challenged birds were not influenced ($P > 0.05$) by dietary treatments. Lesion scores were, however, lower ($P < 0.05$) in the duodenum and jejunum, and higher ($P < 0.05$) in the ceca in WW fed birds, irrespective of the method of inclusion. Total oocyst counts in the excreta of challenged birds were higher ($P < 0.05$) in birds fed WW, irrespective of the method of inclusion. No mortality, intestinal lesion and excreta oocyst shedding were observed in unchallenged treatments. Based on increased mortality, it can be concluded that WW feeding exacerbated the severity of coccidiosis infection, possibly via a mechanism involving enhanced gizzard development.

Key Words: whole wheat, coccidiosis, broiler

W351 Effects of whey protein on intestinal integrity in heat-stressed growing pigs. M. V. Sanz-Fernandez*[1], S. C. Pearce[1], V. Mani[1], N. K. Gabler[1], D. C. Beitz[1], L. Metzger[2], J. F. Patience[1], R.P. Rhoads[3], and L. H. Baumgard[1], *[1]Iowa State University, Ames, [2]South Dakota State University, Brookings, [3]Virginia Polytechnic Institute and State University, Blacksburg.*

Heat stress (HS) decreases livestock productivity and this may in part be mediated by reduced intestinal integrity or "leaky gut." Dairy products improve intestinal integrity in a variety of human and small animal models. Consequently, we hypothesized that dietary bovine colostrum (CL) and whey protein (WP) would mitigate HS-induced leaky gut in pigs. Crossbred gilts (39 ± 3 kg BW) were ad libitum fed 1 of 4 dietary treatments (n = 8 pigs/treatment): (1) control (CT), (2) diet A, containing test product A (98% WP, 2% CL); (3) diet B, containing test product B (80% WP, 20% CL); and (4) diet C, containing test product C (100% WP). Diets were formulated to provide 100 g/d of protein from the test products. After 7d (Period 1, P1) on experimental diets, all pigs were exposed to constant HS conditions for 24 h (P2; 32°C, ≈26% relative humidity). Production parameters and body temperature indices were recorded throughout the experiment, and P2 measurements were compared with P1. At the end of the study, pigs were euthanized and fresh ileum and colon sections were isolated and mounted into modified Ussing chambers for ex vivo assessment of intestinal integrity. There were no differences in growth or feed efficiency during P1. Prior to HS, diet C-fed pigs had a slightly increased ($P < 0.05$; 0.1°C) rectal temperature (Tr), but respiration rates (RR) were not different between treatments. As expected, during P2, both Tr ($P < 0.01$; 40.29 vs. 39.43°C) and RR ($P < 0.01$; 116 vs. 40 breath/min) increased, but no treatment differences were detected. Heat stress markedly reduced feed intake ($P < 0.01$; 44%), and none of the treatments ameliorated this decrease. After 24 h of HS, pigs in all treatments lost a similar amount of BW (−0.5 kg). When compared with CT, ileal transepithelial electrical resistance was decreased ($P = 0.02$; 37%) and tended to be decreased ($P = 0.10$; 27%) in B and C diet-fed pigs, respectively. No differences were detected in any of the remaining intestinal integrity variables. These data demonstrate that supplementing CL and WP in the proportions present in the test products augmented HS-induced leaky gut in pigs.

Key Words: heat stress, whey protein

Physiology and Endocrinology II

W352 Heat stress affects the intestinal temperature in growing pigs. N. Arce, M. Cota, B. A. Araiza, M. Cervantes, and A. Morales*, *Instituto de Ciencias Agrícolas, UABC, Mexicali, BC, México.*

High ambient temperature (°T) may increase the intestinal °T, which might affect the digestive and absorptive functions of the small intestine. This experiment was conducted to analyze the °T in duodenum and jejunum of pigs exposed to practical daily variations in ambient °T (22 to 41°C) and fed a commercial diet. Two pigs (19 ± 1.8 kg BW) were surgically implanted with thermographs in duodenum and jejunum. Pigs were individually housed in 1.2 × 1.2 m^2 raised-floor pens, under heat stress (HS) in a room with no climate control during 4 d, followed by other 4 d in a room with a thermostat set up at 22 ± 2°C (Comfort). Intestinal °T was recorded at each intestinal segment every 15 min for 4 d (24 h-periods) under HS or Comfort; room °T was recorded with the same frequency. Feed was equally provided 6 times daily at 0600, 0900, 1200, 1500, 1800 y 2100 h. Purified water (31.4°C and 23.9°C for HS and Comfort room) was freely available. Average feed intake was 930 and 1,070 g/d for HS and Comfort pigs, respectively. Correlation analyses between ambient and intestinal °T were performed. Minimum, average, and maximum °T in the HS room were 26.1, 31.2, and 37.1°C, respectively; the average Comfort room °T was 24.3°C. Lowest and highest intestinal °T were: HS: duodenum, 39.0, 40.3; jejunum, 39.1, 40.5; Comfort: duodenum, 38.5, 39.3; jejunum, 38.6, 39.4°C, respectively. Correlation coefficients for room and duodenal or jejunal °T at each 24-h period (P) in HS pigs were: Duodenum, P1, 0.81 ($P < 0.01$); P2, 0.80 ($P < 0.01$); P3, 0.83 ($P < 0.01$); P4, 0.75 ($P < 0.01$); Jejunum, P1, 0.75 ($P < 0.01$); P2, 0.79 ($P < 0.01$); P3, 0.88 ($P < 0.01$); P4, 0.79 ($P < 0.01$). In HS pigs, the °T in duodenum was highly correlated (r = 0.91) with that in jejunum ($P < 0.01$). There was a positive correlation between room and duodenal (r = 0.81) or jejunal (r = 0.76) °T ($P < 0.01$) of HS pigs. Room °T of HS pigs showed an S-type curve with the lowest value between 0500 and 0700, and the highest between 1400 and 2000 h, which was mirrored by the °T recorded in both duodenum and jejunum. In conclusion, high ambient °T increases the °T in the small intestine, which in turn may affect the digestive and absorptive functions of HS pigs

Key Words: pig, heat-stress

W353 Energy supplementation effect on follicular population and gonadotropin plasma concentration in prepubertal Nellore heifers. M. C. Miguel*, H. Costa, J. Souza, R. Cipriano, J. L. Delfino, D. Giraldo, N. Romanello, D. Oliveira, M. A. Maioli, S. P. Gobbo, D. Pinheiro, and G. Nogueira, *Sao Paulo State University (UNESP), Aracatuba, Sao Paulo, Brazil.*

The objectives were to study nutritional influences on follicle population and gonadotropin concentration in prepubertal Nellore heifers. Calves at 5 d of age were assigned to 2 diets, 3% of body weight as ground corn (n = 8) or control with no supplement (n = 8). Ground corn was offered daily until weaning. Every 4 d, from 15 d of age until weaning, the diameter of the largest follicle and number of follicles were evaluated and venous blood sample collected. Data were analyzed by ANOVA with the mixed procedure of SAS for repeated measures. The diameter of the largest follicle increased ($P < 0.0001$) from 1 to 5 mo of age in both corn supplemented (2.2 ± 1.6 mm to 6.1 ± 1.5 mm) and control heifers (1.5 ± 0.9 mm to 5.3 ± 0.7 mm). Heifers supplemented with corn had greater larger follicle diameter ($P = 0.006$; 5.1 ± 2.2 mm vs. 4.1 ± 1.9 mm) and larger number of follicles than controls ($P = 0.0461$, 30.3 ± 9.2 vs. 29.6 ± 8.7). Corn supplementation increased average concentration of LH ($P = 0.06$, 0.43 ± 0.33 ng/mL vs. 0.35 ± 0.29 ng/mL). In both treatments, LH increased according to age and concentrations were greatest on the mo 2, 4, and 5 of age. In control heifers, FSH concentration was greater at mo 1 and 2 of age, whereas in heifers supplemented with corn, concentrations of FSH were greater on mo 4 and 5 of age. Young prepubertal heifers can be used as a model to study follicle population, and supplementation with ground corn influenced concentrations of LH and FSH and enhanced follicle growth in Nellore heifers in the first 5 mo of age.

Key Words: prepubertal Nellore calf, largest follicle diameter, feed supplementation

W354 Calf fetal nutrition in grasslands: Muscle fiber characteristics and gene expression at birth. M. Carriquiry*, V. Guiterrez, P. Machado, A. L. Astessiano, and A. C. Espasandin, *Facultad de Agronomia, UDELAR, Montevideo, Uruguay.*

The aim of this study was to determine the effect of nutrition during fetal life and dam genotype on calf BW, plasma IGF-I, and muscle characteristics and gene expression at birth. Forty crossbred calves and their dams (purebred-PU: Hereford and Angus, and crossbred-CR: F1) were used in a randomized block design with a factorial arrangement of herbage allowance of native pastures (High: Hi-HA and Low; Lo-HA, 4 vs. 2.5 kg dry matter/kg BW) and dam genotype (PU vs. CR). Blood and Semitendinous muscle samples were collected at birth to measure gene expression by SYBR-Green real time PCR using ACTB and HPRT as internal control genes. Data were analyzed with a mixed model including herbage allowance, dam genotype, their interaction and calf sex as fixed effects and block as a random effect. Calf BW at birth (39.8 ± 2.6 kg) and Semitendinous muscle fiber diameter (43.7 ± 1.7 μm) did not differ due to herbage allowance or dam genotype but muscle fiber density was less ($P < 0.05$) in Lo-CR offspring than other calf groups (5.5×10^{-4}, 5.6×10^{-4}, 6.0×10^{-4} and $4.2 \times 10^{-4} \pm 0.7 \times 10^{-4}$ fiber/μm^2 for Hi-PU, Lo-PU, Hi-CR, Lo-CR, respectively). Plasma IGF-I (165 vs. 145 ± 11 ng/mL) and muscle IGF1 mRNA were greater ($P \leq 0.04$) in Hi-HA than Lo-HA offspring (1.20 vs. 0.66 ± 0.06). Muscle expression of IGFBP3, IGFBP5 and IGF1R mRNA tended ($P < 0.09$) to be greater in CR than PU offspring (1.0 vs 0.52 ± 0.20, 0.98 vs. 0.64 ± 0.19, 1.0 vs. 0.66 ± 0.12, respectively). Muscle expression of PPARγ mRNA was greater ($P = 0.02$) in Hi-HA than Lo-HA offspring (0.54 vs. 0.34 ± 0.08) but SREBF1 mRNA did not differ among calves. High herbage allowance of native pastures offered to beef dams during gestation would increase calf plasma IGF-I and muscle IGF1 and PPARγ mRNA expression at birth, which could increase growth and muscle adipogenesis potential. In addition, CR offspring had an increased mRNA expression of IGF system components in muscle.

Key Words: fetal programming, beef cattle, grazing

W355 Changes in plasma leptin in newborn and postnatal beef calves. N. M. Long*[1] and D. W. Schafer[2], *[1]Department of Animal and Veterinary Science, Clemson University, Clemson, SC, [2]Department of Animal Science, University of Arizona, Tucson.*

Changes in neonatal plasma leptin play a central role in regulating development of the hypothalamic appetite control centers in rodents. A postnatal leptin surge has been shown in lambs. Maternal obesity and overfeeding initiated before conception and maintained throughout

gestation blocks this leptin surge in newborn lambs. The presence, timing and duration of a neonatal leptin peak have not been established in bovine neonates. To investigate this, 12 nulliparous cows giving birth to 6 bull and 6 heifer calves with no assistance or complication during parturition were chosen for this study. A BCS was determined at calving on all cows. Calves were bled via jugular venipuncture within 2 h of birth and then daily until d 8 and every other day until d 18 of age at 0700 h. Plasma was collected and analyzed for glucose, insulin, cortisol and leptin concentrations via validated colorimetric and radioimmunoassay procedures. Plasma hormone and metabolite values were analyzed as repeated measures using PROC Mixed of SAS. Cow BCS and calf birth weight were analyzed using the PROC GLM of SAS. Cows having bull or heifer calves had a similar BCS at parturition (4.8 ± 0.1; $P = 0.36$). Calf birth weight was similar ($P = 0.90$) between sexes and averaged 31.6 ± 1 kg. Bull calves exhibited elevated plasma leptin concentrations compared with heifers ($P = 0.01$). Further, plasma leptin concentrations increased from birth until d 2 then decreased by d 16 of age ($P < 0.0001$). Plasma cortisol was elevated ($P < 0.0001$) at birth and then decreased over the next 5 d. Bull calves had greater ($P = 0.0431$) plasma insulin than heifer calves. We conclude that there is a postnatal change in plasma leptin that shows clear sex effects with bulls having a greater plasma leptin secretion during the initial neonatal period. These changes in plasma leptin may affect the appetite centers of the hypothalamus and could influence appetite and weight gain in later life and could be a mechanism through which fetal programming acts.

Key Words: postnatal calf, plasma leptin, cortisol

W356 Use of eCG and a progesterone to induce reproductive activity in anestrous goats. V. Contreras-Villarreal[1], O. Angel-Garcia[1], J. M. Guillen-Muñoz[1], P. A. Robles-Trillo[1], M. A. De Santiago-Miramontez[1], G. Arellano-Rodriguez[1], R. Rodriguez-Martinez[1], M. Mellado[1], C. A. Meza-Herrera[2], and F. G. Veliz*[1], *[1]Universidad Autonoma Agraria Antonio Narro, Toreon, Coahuila, Mexico, [2]URUZA-UACh, Bermejillo, Durango.*

The aim of this study was to evaluate the use of eCG and progesterone as inductors of reproductive activity in anestrous goats. Mixed-breed anovulatory adult goats (n = 16) homogeneous regarding body condition score and body weight were divided into 2 experimental groups (n = 8 each), while 4 mixed-breed bucks were also used. Goats grazed during 7 h daily. Group 1 (IM+eCG) received 25 mg i.m. progesterone and 24h later received 250 IU eCG i.m. Group 2 (Esp+eCG) were treated during 7d with an intravaginal sponge impregnated with 20 mg cronolone (a progestin); at the time of sponge removal, goats received 250 IU eCG i.m. At the time of eCG administration, females were penned during 5d, and were fed with alfalfa hay ad libitum. Estrus activity was evaluated by introducing a male in each group of females during 15 min (morning and afternoon). Females displaying estrus activity were placed in a different pen with 2 males. Follicular activity was evaluated by transrectal ultrasonographic scanning (TUS) from −7d up to +7d regarding eCG administration. Forty-five days after estrus detection, goats were evaluated for pregnancy by TUS. Number and size of ovulatory follicles and size of corpus luteum for each group were compared with a Student *t*-test, while percentage of females displaying estrus, ovulation and pregnancy were compared with a chi^2. Reproductive response for both experimental groups is on Table 1. Anestrous mixed-breed goats from northern Mexico (26°N) positively responded to the estrus activity induction with eCG and progesterone, regardless of the administration method (injection or intravaginal sponge), with the use of intravaginal sponge generating an increased corpus luteum size.

Table 1. Reproductive response of mixed-breed anestrous goats receiving either i.m. progesterone or intravaginal sponges impregnated with progesterone and eCG.

	Treatment	
Sexual response	IM+eCG	Esp+eCG
Estrus (no.)	8/8[a]	8/8[a]
Ovulation (no.)	8/8[a]	8/8[a]
Pregnancy (no.)	7/8[a]	8/8[a]
Ovarian follicles (no.)	1.3 ± 0.07[a]	1.6 ± 0.02[a]
Ovarian follicles size (mm)	0.75 ± 0.25[a]	0.82 ± 0.17[a]
Corpus luteum size (mm)	0.89 ± 0.10[a]	1.20 ± 0.02[b]

[a,b]Values with different superscript within a row denote differences ($P \leq 0.05$).

Key Words: eCG, reproductive activity, goat

W357 Impact of low body condition score and the time of exposure on the sexual response of female goats to "male effect." L. I. Vélez[1], J. J. A. Maldonado[1], A. U. Chavez[1], G. J. C. López[2], F. G. Véliz*[3], C. A. Meza-Herrera[4], R. Rodríguez Martínez[3], and G. H. Salinas[1], *[1]INIFAP Laguna, Matamoros, Coahuila México, [2]INIFAP Zacatecas, Calera, Zacatecas México, [3]Universidad Autónoma Agraria Antonio Narro Unidad Laguna, Torreon, Coahuila México, [4]Universidad Autónoma Chapingo Unidad Regional Universitaria de Zonas Aridas, Bermejillo, Durango México.*

The aim of this study was to determine the effect of low body condition score and timing of male exposure on the reproductive response of seasonally anestrous female goats in Comarca Lagunera, Mexico (26°N). Mixed-breed female goats (n = 68) under marginal-range conditions and browsing from 0800 h to 1800 h, were exposed to 8 sexually-active males exposed to an artificial lighting treatment of 2.5 mo of long days, beginning at April 30, 2012. Goats were divided in 2 main groups according to their body condition score (BCS; 1 = emaciated to 4 = very fat). One group of females with a low BCS (1 ± 1) was subdivided as G1 (C1–24; n = 17) and placed in contact with 2 males for 24 h while G2 (C1–14; n = 17) was placed in contact with 2 males only 14 h. Another group depicting regular BCS (2 ± 1) was also subdivided as G3 (C2–24; n = 17) and placed in contact with 2 males for 24 h, while G4 (C2–14; n = 17) was placed in contact with 2 males only 14 h. All groups were 500 m apart from each other in pens of 8 × 4 m. Estrus activity was measured during 15-d. Pregnancy was determined at 40-d from estrus by means of a transrectal ultrasonographic scanning; kidding rate and prolificacy were measured. Percentages of estrus and pregnancy rates were analyzed with chi^2, while latency of estrus and prolificacy were determined with a "t" student test (MYSTAL v.10, 2007). Female response with different body condition score and different time of exposure to sexually active bucks is shown in Table 1. While low body condition score decreased the female response to the male effect, a decreased exposure time to males lowered the intensity of estrus in female goats during seasonal anestrous in the Comarca Lagunera.

Table 1. Response of females with different body condition score and time of exposure

	CC	Weight	Estrous	Short-cycle	Latency	Pregnancy	Kidding	Prolificacy
C1-24	1.1[b]	35.6[b]	13[b]	3[b]	148.3 ± 15.2[b]	9[b]	9[b]	1.2 ± 0.1[a]
C1-14	1.1[b]	33.1[b]	4[b]	0[b]	243.0 ± 11.5[c]	0[c]	0[c]	0[b]
C2-24	2.0[a]	39.0[a]	17a	13[a]	94.6 ± 7.1[a]	17[a]	16[a]	1.6 ± 0.1[a]
C2-14	2.0[a]	41.6[a]	17a	9[a]	94.6 ± 13.5[a]	15[a]	12[ab]	1.3 ± 0.1[a]

[a–c]Values with different superscripts within variables denote differences ($P < 0.01$).

Key Words: male effect, body condition, goat

W358 Reproductive performance of Holstein cows with retained fetal membranes treated with ceftiofur hydrochloride, 17-β-estradiol, and oxytocin. R. Solano-Gurza*, M. Mellado, F. G. Veliz, M. A. de Santiago-Miramontes, and J. E. Garcia, *Universidad Autonoma Agraria Antonio Narro, Torreon Coahuila, México.*

Reproductive performance of Holstein cows with retained fetal membranes and subjected to 2 protocols during 3 or 6 consecutive days for the treatment of this disorder was evaluated in a field trial in a dairy operation in a hot environment. A total of 293 pluriparous cows were used. 231 cows diagnosed as having retained placenta (fetal membranes retained for more than 10 h) were assigned to 4 treatment groups. One group received 2.0 mg/kg ceftiofur clorhydrate, 50 mg 17-β-estradiol and 100 IU oxytocin I.M. for 3 consecutive days (CEO-3; n = 63). The second group received the same treatment during 6 consecutive days (CEO-6; n = 48). A third group was treated with ceftiofur clorhydrate and oxytocin for 3 consecutive days (CO-3; n = 68). A 4 group was subjected to the previous treatment during 6 consecutive days (n = 52). The control group (n = 62) was established with cows without retained placenta and consequently with no drugs applied after parturition. Cows were inseminated multiple times, therefore the entire experimental population received 1,098 services (artificial inseminations, and not cow, were the experimental unit). Cow in the CEO-6 group had the lowest ($P < 0.05$) pregnancy per artificial insemination (P/AI; 11.6 (23/199). P/AI for CEO-3, CO-3, CO-6 and control were 18.5 (41/222), 15.4 (39/253), 13.6 (28/206) and 18.8 (41/218), respectively, with no difference among these groups. Services per pregnancy were 3.2 ± 1.9, 4.4 ± 2.3, 3.2 ± 2.3, 4.5 ± 1.9 and 3.6 ± 1.8 (mean ± SD) for CEO-3, CEO-6, CO-3, CO-6 and control, respectively, without differences among groups. Interval between calving and conception (range 132 to 158 d) did not differ among treatments. Results indicate that prolonged (6-d) application of 17-β-estradiol with oxytocin and ceftiofur clorhydrate decreased P/AI. On the other hand, fertility of cows with retained placenta treated with short-term (3-d) application of 17-β-estradiol in combination with oxytocin and ceftiofur clorhydrate was not impaired.

Key Words: pregnancy per AI, services per pregnancy, interval calving conception

W359 Incorporation of sexed semen into reproductive management of range cow-calf operations. R. F. Cooke*[1], D. W. Bohnert[1], B. I. Cappellozza[1], T. DelCurto[2], and C. J. Mueller[2], *[1]Oregon State University–Eastern Oregon Agricultural Research Center, Burns, [2]Oregon State University–Eastern Oregon Agricultural Research Center, Union.*

The objective was to evaluate pregnancy per AI of lactating beef cows reared in extensive systems and assigned to AI with sexed or conventional semen. Over 2 consecutive years, 896 cows originated from the Oregon State University–Eastern Oregon Agricultural Research Station (Burns location, n = 491 cows, Union location n = 405 cows) received a 100-μg treatment of GnRH and a controlled internal drug releasing device containing 1.38 g of progesterone (CIDR) on d 0 of the study, $PGF_{2\alpha}$ treatment (25 mg) and CIDR removal on d 7, and a second GnRH treatment (100 μg) and fixed-time AI 66 h after the $PGF_{2\alpha}$ treatment. At the Union station, estrus behavior was evaluated between CIDR removal and the second GnRH, and cows were inseminated 12 h after onset of estrus. At the time of AI, cows were assigned to be inseminated with: A) conventional semen (CON; n = 456); and 2) GenChoice 90 sorted for male calves (SEXED; n = 440). Blood samples were collected at AI and 7 d later to determine concentrations of progesterone and assess cow response to the estrus synchronization protocol. Cows that had progesterone concentrations <1 ng/mL at AI and >1 ng/mL 7 d after AI were considered synchronized. Pregnancy status to AI was determined via transrectal ultrasonography at least 45 d after AI. Data were analyzed with the PROC GLIMMIX of SAS. No treatment effects detected ($P = 0.97$) for synchronization rate (82.8 vs. 82.7% for CON and SEXED cows, respectively; SEM = 1.8). Across both locations, SEXED cows had reduced ($P < 0.01$) pregnancy per AI compared with CON (31.5 vs. 46.3%, respectively; SEM = 2.2). However, within cows inseminated after estrus detection at the Union location, SEXED cows had similar ($P = 0.99$) pregnancy per AI compared with CON (55.8 vs. 55.7%, respectively; SEM = 6.7). Within cows timed-inseminated at the Union location, SEXED cows had reduced ($P = 0.02$) pregnancy per AI compared with CON (35.0 vs. 47.8%, respectively; SEM = 4.0). In summary, cows timed-inseminated with sexed semen had reduced pregnancy per AI compared with cows inseminated with conventional semen, whereas the same outcome was not observed in cows inseminated upon estrus detection.

Key Words: AI, beef cow, sexed semen

W360 Use of a single injection of long-acting recombinant bovine FSH to superovulate Holstein heifers. P. D. Carvalho*, K. S. Hackbart, R. W. Bender, A. R. Dresch, G. M. Baez, J. N. Guenther, A. H. Souza, and P. M. Fricke, *Department of Dairy Science, University of Wisconsin-Madison, Madison.*

Our objective was to compare the efficacy of a single injection of 2 different preparations of a long-acting recombinant bovine FSH (rbFSH; type A and B) to a porcine pituitary-derived FSH (Folltropin) to superovulate heifers. Nonlactating, non-pregnant Holstein heifers (n = 56) from 12 to 15 mo of age were randomly assigned to 1 of 4 superstimulatory treatments (n = 14/trt). Beginning at a random stage of the estrous cycle, all follicles > 5mm were aspirated, and 36 h later superstimulatory treatments were initiated and a CIDR device was inserted. Treatments were (1) a single injection of 50 μg of A-rbFSH; (2) a single injection of 100 μg of A-rbFSH; (3) 300 mg of pFSH administered in 8 decreasing doses over 4 d; and (4) a single injection of 50 μg of B-rbFSH. All heifers received 25 mg $PGF_{2\alpha}$ at the 5th and 7th FSH injections (in relation to treatment 3). Concurrent with the last FSH injection in treatment 3, CIDRs were removed and ovulation was induced with hCG (2,500 IU) administered 24 h after CIDR removal. Heifers received AI 12 and 24 h after hCG treatment. Number of ovulatory follicles and corpora lutea were evaluated by ultrasound, and embryos were recovered using a nonsurgical flushing procedure 7 d after hCG treatment. Data were analyzed using PROC MIXED of SAS. Superovulatory response and embryo production differed among treatments (see table), but not AMH. In conclusion, a single dose of long-acting rbFSH (either 100 μg of A-rbFSH or 50 μg of B-rbFSH but not 50 μg of A-rbFSH) induced superovulation and produced the same quantity of good-quality embryos compared with pituitary-derived FSH. Supported by CEVA Animal Health.

Table 1.

	1	2	3	4
Follicles (no.)	5.9 ± 0.9^{c}	16.6 ± 3.1^{b}	25.7 ± 3.2^{a}	18.9 ± 3.2^{ab}
CL (no.)	2.6 ± 0.9^{b}	15.9 ± 2.9^{a}	19.1 ± 2.4^{a}	16.1 ± 3.0^{a}
Heifers superovulated (no.)	4^{b}	12^{a}	14^{a}	13^{a}
Total ova/embryos recovered (no.)	4.3 ± 2.4	8.4 ± 2.3	8.5 ± 2.2	10.1 ± 2.4
Fertilized ova (no.)	2.0 ± 0.7^{b}	6.4 ± 2.1^{ab}	8.0 ± 2.1^{ab}	9.5 ± 2.3^{a}
Fertilized ova (%)	71.6 ± 16.6^{ab}	63.8 ± 14.3^{b}	94.5 ± 2.2^{a}	94.5 ± 2.0^{a}
Transferable embryos (no.)	0.8 ± 0.5^{b}	4.3 ± 1.5^{ab}	6.5 ± 1.7^{a}	7.6 ± 2.4^{a}
Transferable embryos (%)	37.5 ± 23.9^{b}	44.7 ± 12.2^{ab}	78.0 ± 7.3^{a}	66.1 ± 10.6^{ab}
Degenerate embryos (no.)	1.3 ± 0.9	2.1 ± 0.8	1.5 ± 0.6	1.8 ± 0.5
Degenerate of fertilized (%)	50.0 ± 28.9	31.6 ± 8.7	18.8 ± 6.7	30.5 ± 10.8

Key Words: superovulation, rbFSH, dairy heifer

W361 Characterization of follicular fluid adiponectin and its relationship with blood adiponectin during estrous cycle in cattle. S. P. Singh*[1], S. Häussler[1], D. Tesfaye[2], M. Hölker[2], K. Schellander[2], and H. Sauerwein[1], *[1]Institute of Animal Science, Physiology and Hygiene Group, University of Bonn, Bonn, Germany, [2]Institute of Animal Science, Animal Breeding and Husbandry Group, University of Bonn, Bonn, Germany.*

In humans, adiponectin (Aq) exerts direct effects on folliculogenesis and peri-ovulatory changes in ovarian follicles, while it also known that follicular growth is correlated with Aq gene expression in bovine granulosa and theca cells. The objectives of the present study were to quantify Aq in follicular fluid (FF) and to determine the relationship of Aq levels in FF and serum during estrous cycle (EC) in cattle. Simmental heifers (n = 14; 15–20 mo old) were synchronized by intramuscular (i.m.) administration of 500 mg cloprostenol (PGF2α) twice within 11 d. Two d after each PGF2α treatment, animals received 10 mg GnRH (i.m.). Blood samples and ovaries were collected from animals slaughtered at d 3 (n = 6), 7 (n = 3) or 19 (n = 5) after onset of estrus. FF was collected from the single leading follicle (8–12 mm) from each animal. FF and serum Aq were measured by ELISA (Mielenz et al., 2013). Assay accuracy was confirmed by linearity of serial samples dilutions. Data sets (means ± SEM) were analyzed by mixed model procedure in SPSS. Aq concentrations (µg/mL) in serum and FF, and there ratios were unchanged during EC ($P > 0.05$). Mean FF Aq concentrations (19.4 ± 1.4 µg/mL) were about 60% of mean levels found in serum (31.8 ± 1.5 µg/mL); data and relationships are presented in Table 1. Using the ELISA, Aq could be reliably quantified in FF. The FF:serum Aq ratio was higher than the values reported for women (~0.26 µg/mL). From the results of this study it can be postulated that any effects of Aq on oocyte and/or follicle development in the EC are likely due to changes in regulation of Aq receptor expression or activity.

Table 1. Adiponectin (Aq) concentrations (µg/mL) in follicular fluid (FF), serum and their ratio during luteal phase (LP) and follicular phase (FP) of estrous cycle (EC)

Phase/Days of EC	FF	Serum	FF:serum Aq
LP (d 3)	20.4 ± 0.4	32.7 ± 0.8	0.63 ± 0.02
LP (d 7)	20.0 ± 1.4	32.5 ± 1.0	0.62 ± 0.05
FP (d 19)	17.9 ± 2.4	30.2 ± 2.8	0.63 ± 0.13

Key Words: follicular fluid, adiponectin, estrous cycle

W362 Effects of excessive energy intake and supplementation with chromium propionate on serum glucose and insulin concentrations of non-lactating dairy cows. T. Leiva[1], R. F. Cooke[2], A. Aboin[1], D. B. Araujo[3], and J. L. M. Vasconcelos*[1], *[1]UNESP - Faculdade de Medicina Veterinária e Zootecnia, Botucatu, São Paulo, Brazil, [2]Oregon State University–Eastern Oregon Agricultural Research Center, Burns, OR, USA, [3]Kemin Agrifoods South America, Indaiatuba, São Paulo, Brazil.*

The objective was to determine if excessive energy intake affects serum concentrations of insulin and glucose in nonlactating dairy cows, and if supplementation with Cr propionate modulates this response. Thirteen multiparous, nonlactating Gir × Holstein cows were ranked by BCS, and randomly assigned to 1 of 3 dietary treatments on d 0: 1) diet to meet their ME requirements without Cr supplementation (CON; n = 4), 2) diet to exceed in 70% their ME requirements without Cr supplementation (HIGH; n = 4), and 3) diet to exceed in 70% their ME requirements with 2.5 g of Cr propionate (HICR; n = 5). Diets were offered twice daily via individual self-locking head gates during the experiment (d 0 to 88). Cow BCS was assessed on d 0, 15, 38, and 70. Blood samples were collected before and 2 h after the morning feeding every 4 d. Glucose tolerance tests (GTT) were performed on d 32 and 88. During each GTT, cows were infused (i.v.) with 0.5 g of dextrose/kg of BW. Blood samples were collected at −15, 0, 10, 20, 30, 45, 60, and 90 min relative to infusion, and analyzed for serum glucose and insulin concentrations. Data were analyzed with the PROC MIXED of SAS. A treatment x day interaction was detected ($P = 0.05$) for BCS. During the experiment, BCS increased for HIGH and HICR (0.25 change in BCS for both treatments; SEM = 0.17), and decreased for CON (−0.12 change in BCS, SEM = 0.18). A treatment x day interaction was detected ($P \leq 0.05$) for serum insulin concentrations in samples collected every 4 d and during the GTT. Beginning on d 7, serum insulin concentrations were greater for HIGH vs. CON ($P = 0.09$) and HICR ($P = 0.03$), but similar ($P = 0.39$) between CON and HICR (10.3, 7.3, and 5.7 µIU/mL, respectively; SEM = 1.3). During the GTT, serum insulin concentrations were greater ($P < 0.05$) for HIGH vs. CON and HICR at 10, 20, 60, and 90 min, and greater ($P < 0.05$) for HIGH and CON vs. HICR at 30 and 45 min. In conclusion, Cr propionate supplementation prevented the increase in circulating insulin concentration caused by excessive energy intake in nonlactating dairy cows.

Key Words: chromium propionate, dairy cow, energy intake

W363 Effect of time of insemination relative to ovulation on pregnancy rate of Nelore cows submitted to TAI protocols. M. M. Filho, J. R. Naves*, R. G. Rezende, T. Santin, T. K. Nishimura, V. B. Nunes, and E. H. Madureira, *São Paulo University, São Paulo, Brazil.*

The economic success in reproduction is related to bovine calf production. The time of insemination relative to ovulation is an important factor in conception rate due to 2 physiological factors, time required for sperm capacitation in the female genital tract and survival of both gametes (spermatozoa and oocyte). The present study aimed to evaluate the influence of time of artificial insemination (AI) on pregnancy rate. The experiment was conducted on the campus of University of São Paulo (USP) Pirassununga, College of Veterinary Medicine and Animal Science (FMVZ). We used 665 Nelore cows submitted to timed artificial insemination protocol. The protocol consisted TAI Day 0 - inserting a device CIDR progesterone (1 mg) intravaginal release in a random stage of the estrous cycle, and an injection of 2.0 mg of estradiol benzoate (EB). On Day 8, the implants of progesterone were removed and the cows received an injection of 0.150 mg of PGF2α and 300 IU of equine chorionic gonadotropin (eCG). On Day 9, they received an injection of 1.0 mg of EB. AI was performed at 10 d with time of ovulation at 7:00 p.m. The cows were randomly divided into 3 experimental groups, according to the time of insemination, being performed using semen of 2 Nelore bulls: Group 1 (G1) inseminated between 1:30 and 2:50 p.m., Group 2 (G2) between 2:51 and 4:10 p.m. and Group 3 (G3) between 4:11 and 5:30 p.m. Pregnancy rate was obtained after 30 d using ultrasound Aloka SSD 500, using linear probe. After ANOVA, G1, G2 and G3 were compared by Teste F and the pregnancy rate obtained in 63.8, 75.4 and 54.7% respectively. The semen of 2 bulls used to AI, was distributed in a balanced form among the groups, however, there was no difference in pregnancy among them. The time of AI influenced ($P < 0.05$) fertility, was observed that the best time to perform the AI is between 6 and 4 h before the expected ovulation.

Key Words: Nelore cow, TAI, ovulation

W364 Enhancing peri-compaction bovine embryo glucose metabolism in vitro in preparation for a hypoxic uterine environment. V. A. Absalón-Medina*, S. H. Cheong, R. O. Gilbert, and W. R. Butler, *Cornell University, Ithaca, NY.*

The metabolic adjustment from low to high glucose requirements at the onset of the morula stage is a natural event in the oviduct when the embryo is migrating to the uterus. Metabolic regulators (MR) such as 2,4-dinitrophenol (DNP) and phenazine ethosulfate (PES) can improve glucose metabolism of in vitro produced embryos (IVP) via 2 different pathways i.e., glycolysis and pentose phosphate pathways to ensure the metabolic switch. The objective of this study was to evaluate the effects of MR when supplemented to embryos obtained by IVP procedures. A total of 2496 oocytes were used in this project. Statistical analyses utilized ANOVA (JMP) with group as the experimental unit. MR were supplied from d 5 to d 8 post insemination. In experiment 1 (EXP1) embryos were supplemented with PES (0.3 μM), DNP (10 μM), or PES + DNP for comparison to control. In EXP2 embryos were supplemented with lower PES (0.15 μM; based on EXP1 results) in combination with DNP (5, 10 and 30 μM). Two quality control groups were included: control (no MR) and DNP 10 μM + PES 0.3 μM (best treatment from EXP1; control+). In EXP1, control+ resulted in higher embryo development to blastocysts when compared with others (43 ± 3% vs. 33 ± 3%; $P < 0.05$). Mean pixel intensity (MPI) values of embryos stained with Nile Red (indicator of triglyceride content) were reduced in MR compared with control (556 ± 76 vs. 650 ± 75, respectively; $P < 0.05$). PES and DNP alone reduced MPI by 20% relative to control group. There was a positive effect of MR on blastomere counts when compared with control (142 ± 7 vs. 135 ± 7; $P < 0.05$). However, PES alone resulted in embryos with a significantly reduced number of blastomeres (126 ± 7; $P < 0.05$). In EXP2 we observed reduced blastomere counts with any treatment combination different from control groups. In conclusion, addition of MR showed a significant improvement on overall blastocyst rates and reduced MPI values, but most importantly about twice as many embryos reached the expanded stage at d 8 post IVF when MR (control+) were supplied compared all other groups (28 ± 2% vs. 15 ± 2%, respectively; $P < 0.05$).

Key Words: bovine embryo, IVF, metabolic regulator

W365 Conjugated linoleic acid (CLA) does not improve post-thaw performance of expanded-stage in vitro produced bovine embryos. V. A. Absalón-Medina*, S. H. Cheong, R. O. Gilbert, and W. R. Butler, *Cornell University, Ithaca, NY.*

Conjugated linoleic acid isomers (CLA) can alter the lipid membrane configuration of cells. Our previous work indicated inclusion of CLA (100 μ*M* c9,t11) before vitrification improved post-thaw survival and embryo development. However, CLA was added from morula to early blastocyst stages; i.e., from d 5 to 6.5 post-IVF. For practical purposes we decided to work with later stage embryos suitable for embryo transfers i.e., d 7.5 post-IVF. Our current work on metabolic regulators (MR) indicated a beneficial effect on embryo development and we were interested in additional effects of providing CLA for membrane protection. The objective of this study was to evaluate the effect of CLA *cis*-9 *trans*-11 in combination with MR (2, 4-dinitrophenol [DNP] and phenazine ethosulfate [PES]) on embryos that were subsequently vitrified. MR were supplied from d 5 to d 8 post IVF. CLA was supplied at d 6 for the subsequent 36 h before vitrification. In 3 replicates a total of 620 oocytes were distributed across 4 treatment groups and analyzed by ANOVA (JMP) using group as the experimental unit. Groups were control (BSA), and MR combination (DNP 10 μ*M* + PES 0.3 μ*M*) supplemented without or with BSA-CLA (50 or 100 μ*M cis*-9 *trans*-11) complex. Among all groups, MR-treated embryos resulted in numerically higher re-expansion rates when compared with control after embryos were thawed (71 ± 12% vs. 60 ± 12%). However, CLA treated embryos showed the lowest re-expansion rates and this was more evident with the highest dose (CLA 50 μ*M* = 51 ± 12% vs. CLA 100 μ*M* = 32 ± 12%; $P < 0.05$). Embryos treated with MR and CLA resulted in higher blastomere counts when compared with control (130 ± 5 vs. 114 ± 6; $P < 0.05$). The distribution of cytoskeleton integrity, reflected by F-actin filament staining, remained similar among groups. In conclusion, when providing MR alone, embryos showed good ability to withstand the stressful procedures of vitrification similar to the control group. However, CLA treatment did not result in a further additive effect on blastocyst rates or benefits after vitrification.

Key Words: metabolic regulator, CLA, bovine embryo and vitrification

W366 Excess dietary protein rich in RUP alters ovulatory ovarian follicle growth and circulating steroid hormone concentrations in nonpregnant, nonlactating beef cows. P. J. Gunn*[1], R. P. Lemenager[2], E. G. Taylor[2], and G. A. Bridges[3], *[1]Department of Animal Science, Iowa State University, Ames, [2]Department of Animal Sciences, Purdue University, West Lafayette, IN, [3]North Central Research and Outreach Center, University of Minnesota, Grand Rapids.*

The objective was to determine if excess dietary CP abundant in RUP would affect follicular dynamics and circulating steroid hormone concentrations. Non-pregnant, nonlactating Angus-cross beef cows (n = 20) were stratified by age, BCS, and BW to 1 of 2 diets designed to meet or exceed NRC (2000) requirements and deliver similar NE_g per d. Diets included corn stover with: supplemental corn silage and corn gluten meal to meet CP requirements (CON) or supplemental corn gluten meal so that daily CP and MP was 150% of CON (PRO). After a 19-d dietary adaptation period, cows were pre-synchronized using the 5 d CO-Synch + CIDR protocol (5D). Ten d after 5D completion, follicular growth was reset with 2.5 mg of estradiol benzoate (EB). Starting at EB and daily thereafter until ovulation, follicular waves were mapped via ultrasonography and blood samples were collected. Corpora lutea (CL) parameters were assessed and diets were concluded 7 d after visual detection of estrus. Data were analyzed using the MIXED procedure of SAS. Treatment did not affect BW or BCS ($P \geq 0.77$). Plasma urea N concentrations were greater ($P < 0.001$) in PRO (9.56 ± 1.34 mg/dL) than CON (4.47 ± 1.34 mg/dL) at EB. Follicular wavelength, follicle size at dominance, and duration of dominance did not differ ($P \geq 0.17$). However, ovulatory follicle diameter the d before ovulation was greater ($P = 0.004$; 15.53 vs. 12.91 ± 0.51 mm) and average daily antral follicle count tended to be greater ($P = 0.06$; 27.9 vs. 23.9 ± 1.31) in PRO than CON, respectively. Peak estradiol concentrations tended ($P = 0.10$) to be greater in PRO (11.7 ± 0.53 pg/mL) than CON (10.3 ± 0.53 pg/mL). Volume of CL did not differ ($P = 0.34$), but progesterone concentrations tended ($P = 0.10$) to be less in PRO (3.29 ± 0.38 ng/mL) than CON (4.25 ± 0.38 ng/mL) 7 d after estrus. In summary, excess CP derived from a RUP-rich feedstuff increased ovulatory follicle diameter and preovulatory estradiol concentrations, but reduced progesterone concentrations in the subsequent estrous cycle of beef cows.

Key Words: beef cow, crude protein, ovarian follicle

W367 Sexual stimulation of male goats with high and low testosterone doses during natural sexual resting periods. O. Ángel-García[1], C. A. Meza-Herrera[2], J. M. Guillen-Muñoz[1], P. A. Robles-Trillo[1], C. Leyva[1], R. Rodríguez-Martínez[1], F. G. Véliz[1], and G. Arellano-Rodríguez*[1], *[1]Universidad Autónoma Agraria Antonio Narro, Torreón, Coahuila, México, [2]URUZA-Universidad Autónoma Chapingo, Bermejillo, Durango.*

The aim of this study was to evaluate the effect of exogenous testosterone propionate (T) upon sexual behavior in bucks from northern Mexico (26°N) during their natural sexual resting season. Mixed dairy goats bucks received alfalfa hay ad libitum and 200 g animal/day of a commercial concentrate (14% CP). The 3 groups (n = 4 each) were homogeneous regarding body weight and condition score, scrotal circumference and odor score. (1) Group 1 (LD) was treated with 25 mg/d i.m. T per animal, (2) Group 2 (HD) received 50 mg/d i.m. T per animal; both groups received T every third day/3 weeks, and (3) Group 3 (Control) was treated with 1 mL saline every third day/3 weeks. Odor intensity (0–4, 0 = equals female odor, 4 = very active male odor) was registered for each male. Thereafter, male were exposed to 30 anovulatory females for an hour. Differences between the different groups in the frequencies of sexual behaviors were analyzed using a chi-squared test for goodness of fit, with a null hypothesis of equal repartition of behavioral frequencies in 2 groups. The odor was compared by "t" test. T-treated groups displayed more sexual behavior and greater odor intensities ($P < 0.05$) in comparisons to controls (Table 1). Increased testosterone doses (50 mg/d) administrated to bucks during the sexual resting season stimulated sexual behavior. Therefore, such reproductive strategy increases the possibilities to stimulate both sexual and reproductive activity of anestrous female goats during the seasonal anestrous throughout the use of the "male effect" with T-treated bucks.

Table 1. Sexual behavior test of male goats treated with low (LD, 25 mg/d/goat) or high (HD, 50 mg/d/goat) dose of testosterone or (Control) and exposed to anovulatory females for an hour for two days in northern Mexico

Group	Flehmen (no.)	Ano-genital smelling (no.)	Approximations (no.)	Odor (mean ± SEM)	
				Initial	Final
Control	0	23[a]	0	0.3 ± 0.03[a]	0.3 ± 0.03[a]
LD	32[a]	41[a]	21[a]	0.5 ± 0.2[a]	1.2 ± 0.22[b]
HD	68[b]	36[b]	79[b]	0.5 ± 0.2[a]	1.1 ± 0.16[b]

[a,b]Columns with different superscripts between variables denote statistical differences ($P < 0.05$).

Key Words: sexual stimulation, goat, testosterone

W368 Sexual behavior of bucks treated with testosterone with different male:female ratios is not affected by environmental variables. O. Ángel-García[1], C. A. Meza-Herrera[2], J. M. Guillen-Muñoz[1], C. Leyva[1], M. Mellado[1], R. Rodríguez-Martínez[1], J. R. Luna-Orozco[3], F. G. Véliz[1], and G. Arellano-Rodríguez*[1], *[1]Universidad Autónoma Agraria Antonio Narro, Torreón, Coahuila, México, [2]URUZA-Universidad Autónoma de Chapingo, Bermejillo, Durango, México, [3]CBTa # 1, Torreón, Coahuila, México.*

The aim of this study was to evaluate the possible relationship of male goat sexual behavior to environmental variables. The study considered different male:female ratios using bucks in reproductive arrest during spring (26°N) and treated with testosterone propionate (25 mg/im, every 3 d during 3 wk); 2 mating loads were evaluated. Multiparous mixed-breed anestrous goats (n = 30) were randomly assigned to 1 of 2 treatment groups with different male:female ratios: (1) G20/1:10 with 20 goats exposed to 2 active bucks, and (2) G10/1:5 with 10 goats exposed to 2 bucks. Response variables considered attempted mounts, complete mounts and mounts with ejaculation, which were registered with a closed-circuit TV system throughout 24 h per day. Hourly differences in number of mount intents, full mounts and mounts with ejaculate were analyzed by Chi-squared test. In addition, correlation analyses were performed to determine the relationship between environmental temperature, relative humidity and THI index regarding buck sexual behavior. No differences ($P > 0.05$) were observed between groups regarding the number of mounts with ejaculation (G1:5 = 40 vs. G1:10 = 62). The effect of environmental variable upon sexual behavior of both groups is shown in Table 1. While intents of mounts were similar (G1:5 = 96; vs. G1:10 = 107; $P < 0.05$), completed mounts was affected by male:female ratio (1:5 = 179 vs. 1:10 = 249; $P < 0.05$). Results indicate that male:female ratios, either 1:5 or 1:10, did not promote any difference between experimental groups except for the number of mounts with ejaculation. In addition, environmental variables do not modified the sexual behavior of testosterone-treated bucks with different male:female ratios during the resting reproductive season at this latitude.

Table 1. Observed correlations between sexual behavior of testosterone-treated bucks and environmental variables

	Temperature		Relative humidity		THI	
	Correlation	P-value	Correlation	P-value	Correlation	P-value
Mounts completed	0.116	0.588	0.068	0.752	0.152	0.961
Mounts with ejaculation	−0.028	0.895	0.28	0.184	0.011	0.478
Attempted mounts	0.134	0.531	−0.017	0.936	0.170	0.427

Key Words: sexual behavior, buck, testosterone

W369 Effects of progesterone concentration and FSH administration on follicle number and oocyte competence. S. G. Kruse*[1], B. J. Funnell[1], S. L. Bird[1], H. P. Dias[2], M. L. Day[3], and G. A. Bridges[1], *[1]North Central Research and Outreach Center, University of Minnesota, Grand Rapids, [2]São Paulo State University, Botucatu, São Paulo, Brazil, [3]The Ohio State University, Columbus.*

The objective was to determine the effect of progesterone (P4) concentration and FSH administration on follicle number and oocyte competence, assessed by in vitro blastocyst production (IVP), after collection via ultrasound-guided oocyte pick-up (OPU). Estrus of mature Angus cows was synchronized (estrus = d 0). On d 5.5, follicles were ablated and cows received a used CIDR and 2, 25 mg doses of PG to decrease P4 (L; n = 57) or a new CIDR and no PG to maintain elevated P4 (H; n = 50). On d 7.5, 8, 8.5, and 9 FSH was administered preceding OPU of all visible follicles on d 10.5. After OPU, new or used CIDRs were replaced, cows were not given FSH, and OPU conducted on d 14.5. The experimental design was a 2 × 2 factorial experiment with main effects of P4 (L/H) and FSH (Yes [Y] vs. No [N]). The experiment was conducted in 3 replicates. On d 5.5, 6.5, 8.5, 10.5, 11.5, 12.5, and 14.5, P4 was assessed and follicle number evaluated at OPU. Oocytes were graded (1–6; 1 = ≥5 layers compact cumulus/homogeneous cytoplasm, 6 = denuded) and pooled by treatment for IVP regardless of grade. Cleavage and blastocyst rate, embryo quality, and number of total and dead cells of blastocysts were assessed. Concentration of P4 was decreased ($P < 0.01$) in the L treatment but not affected by FSH. Follicle number was affected ($P < 0.05$) by P4 (H = 19.0 ± 1.4; L = 23.2 ± 1.3) and FSH (Y = 25.1 ± 1.3; n = 16.9 ± 1.3). FSH increased oocytes recovered ($P < 0.01$), and grade 1–3 oocytes ($P < 0.01$) and tended ($P = 0.06$) to increase the percentage of grade 1–3 oocytes. Neither P4 nor FSH treatment affected cleavage or blastocyst rate (H, n = 430, 56.7%, 19.3%; L, n = 544, 61.9%, 22.1%; Y, n = 631, 60.2%, 22.2%; N, n = 343, 58.6%, 18.4%). However, blastocysts from cows in the L treatment were advanced in stage ($P < 0.05$; 5.5 ± 0.2) and tended to have more total cells ($P = 0.08$; 94.7 ± 3.3) than the H treatment (5.1 ± 0.2; 78.6 ± 3.6). In summary, P4 concentrations and FSH administration affected follicle number at OPU and oocytes from cows with low P4 yielded

embryos that were more advanced in stage progression and tended to contain more cells.

Key Words: progesterone, oocyte pick-up, FSH

W370 Gestational form of supplemental selenium affects gene expression in the newborn calf testis. I. Steroidogenesis. S. R. Garbacik*, J. C. Matthews, K. L. Cerny, and P. J. Bridges, *Department of Animal and Food Sciences, University of Kentucky, Lexington*

A selenium (Se) deficiency in soil necessitates supplementation of cattle feed with this trace element. A requirement of Se for fertility is known, however the effect of Se form consumed during gestation on the steroidogenic capacity of the bull testis remains unknown. Our objective was to determine the effect of inorganic versus organic form of maternal supplemental Se on the expression of genes regulating steroidogenesis in the newborn calf testis. Twenty-four Angus-cross cows, managed under a forage-based cow-calf production regimen, were assigned randomly (n = 8) to individual ad libitum access to a common mineral mix containing 35 ppm of Se supplied as sodium selenite (inorganic, ISe; Prince Se), Sel-Plex (organic, OSe; Sel-Plex, Alltech) or a 50/50 mix of ISe/OSe (Mix) for 4 mo before breeding and through gestation. Thirteen bull calves were born (ISe n = 5; OSe n = 4; Mix n = 4) and castrated within 2 d. Total RNA was extracted from small pieces of whole testis and subjected to microarray analysis using the bovine 1.0 ST arrays (Affymetrix). The effect of cow Se form was evaluated by one-way ANOVA. Overall, 1112 genes were differentially-expressed ($P < 0.05$). Treatment means were separated using a post-hoc pairwise comparison (*t*-test) and 7 mRNA involved in steroidogenesis and steroid hormone receptor binding were identified. When compared with ISe (the standard supplementation regimen) mRNA for: Hsd17b7 was increased in testis from OSe dams and decreased in Mix testis ($P < 0.01$); Hsd17b4 and Akr1c4 was similar in OSe testis and decreased in Mix testis ($P < 0.05$); Sult1e1 was similar in OSe testis and increased in Mix testis ($P < 0.05$); Cyp2s1 did not differ in OSe and Mix testis, however tended ($P = 0.054$) to be higher in Mix than OSe testis; Cyp2c18 was increased in OSe and Mix testis ($P < 0.02$); Cyp2J2 was increased in OSe but not Mix testis ($P < 0.02$). These results demonstrate that maternal source of Se affects development of the steroidogenic gene expression profile in the calf testis. Whether changes beget alteration to adult testosterone production awaits elucidation.

Key Words: RNA, selenium, steroidogenesis

W371 Factors affecting ovulation within three weeks postpartum in dairy cows. M. M. Vercouteren[3], J. H. Bittar[1], L. I. Barbia[1], M. Gobikrushanth[1], C. A. Risco[1], J. E. Santos[1], A. Vieira-Neto[2], and K. N. Galvão*[1], *[1]University of Florida, Gainesville, [2]Universidade do Estado de Santa Catarina, Lages, SC, Brazil, [3]Utrecht University, Utrecht, the Netherlands.*

Virtually, all dairy cows have their first follicular wave within 2 weeks postpartum; however, only 25–30% ovulate within 3 weeks postpartum. The objective was to evaluate factors affecting ovulation within 21 DIM in dairy cows. Cows (n = 768) from 2 herds had their ovaries scanned by ultrasonography (US) twice a week starting at 17 ± 3 DIM for a total of 4 US. Ovulation was characterized by the presence of a corpus luteum (CL) ≥ 20mm in any US or when a CL < 20mm appeared in 2 consecutive US. The following information was collected: calving season (CS; summer or fall vs. winter or spring), dry period length (DPL; ≤ 70 or > 70d), parity, dystocia, twins, stillbirths, abortions, retained placenta (RP), metabolic problems (ketosis or hypocalcemia), body condition score at enrollment (BCS), and metritis, mastitis, digestive problems [indigestion or displaced abomasum (DA)], lameness, body weight loss (BWL; ≤28 or >28 kg) and daily milk yield in the first 14 DIM. Data were analyzed using the GLIMMIX procedure of SAS. Three models were constructed: 1 – excluding both DPL (not available for primiparous) and BWL (only available for 456 cows); 2 – including DPL; 3 – including BWL. Only variables with $P \leq 0.2$ were included in each model. Herd was included as random. In model 1, cows with metabolic problems (20.7 vs. 33.9%; $P = 0.003$), digestive problems (19.4 vs. 32.2; $P = 0.05$), or that calved in the winter or spring (23.5 vs. 33.1; $P = 0.02$) had decreased ovulation. Dystocia tended to decrease (24.1 vs. 32.9; $P = 0.06$) ovulation. In model 2, cows with metabolic problems (22.0 vs. 38.6; $P = 0.02$) and metritis (17.3 vs. 35.8; $P = 0.05$) had decreased ovulation. Cows with > 70d DPL tended to have decreased (23.9 vs. 36.2; $P = 0.07$) ovulation. In model 3, cows with metritis (21.2 vs. 34.7%; $P = 0.03$), digestive problems (20.0 vs. 33.4%; $P = 0.05$), calved in the winter or spring (24.1 vs. 35.2; $P = 0.01$), or lost >28 kg BW (27.7 vs. 38.5; $P = 0.04$) had decreased ovulation. In conclusion, cows that had metabolic problems, digestive problems, dystocia, metritis, long DPL, calved in the winter or spring or lost >28 kg BW in the first 14 DIM had decreased ovulation within 21 DIM.

Key Words: ovulation, first follicular wave, dairy cow

W372 Physiological and transcriptional adaptations in skeletal muscle of Holstein cows in response to plane of dietary protein during early lactation. P. Ji*[1], J. J. Loor[2], H. M. Gauthier[1], S. Y. Morrison[1], F. T. da Rosa[3], and H. M. Dann[1], *[1]The William H. Miner Agricultural Research Institute, Chazy, NY, [2]University of Illinois at Urbana-Champaign, Urbana, [3]Federal University of Pelotas, RS, Brazil.*

To study the effect of dietary crude protein (CP) on skeletal muscle metabolism in early lactation, 31 multiparous Holstein cows were randomly assigned at calving to: 1) a high protein diet (H, 17.0% CP) until 21 d in milk (DIM) and a low protein diet (L, 15.3% CP) until 63 DIM (HL, n = 11); 2) H diet until 21 DIM and a moderate protein diet (M, 16.2% CP) until 63 DIM (HM, n = 11); or 3) L diet until 63 DIM (LL, n = 9). Dry matter intake (DMI) and milk yield were recorded daily and milk composition measured weekly starting at wk 2. Plasma 3-methylhistidine (3MH) and serum creatinine (CRE) were analyzed at 1, 7, 13, 19, 26, 40, 54 and 68 DIM. Semitendinosus muscle was biopsied at 2, 11 and 62 DIM for RNA extraction. The mRNA expression of 30 genes was determined through RT-qPCR and normalized using geometric mean of internal control genes (ERC1, MRPL39, and UXT). Data were analyzed as a completely randomized design using MIXED procedure of SAS. Treatments did not affect ($P > 0.05$) DMI (25.7 ± 0.8 kg/d), milk yield (49.9 ± 2.7 kg/d), composition, and the ratio of 3MH/CRE (297.2 ± 21.7 nmol/mg). Intake of CP was 3.79, 3.95, and 4.20 (±0.12) kg/d for LL, HL, and HM ($P = 0.06$). The expression of OXCT1, involved in ketone body (KB) utilization, was increased in LL and decreased in HM from 2 to 62 DIM ($P = 0.01$). A time effect ($P < 0.05$) was found in genes encoding E3 ubiquitin-protein ligases (FBXO32 and TRIM63), enzymes facilitating β-oxidation and sparing glucose (ACADVL, ACOX1, FABP3, CPT1B, and PDK4), translation repressor protein (EIF4EBP1), transcription factor (FOXO1 and PPARD), insulin (INSR) and mTOR pathway (RHEB) with higher expression on 2 over 62 DIM, whereas CAPN3, encoding a calcium-dependent protease, exhibited the opposite expression pattern ($P < 0.05$). Moderate reduction of CP during early lactation did not affect performance, muscle proteolysis and metabolism at mRNA level with the exception of KB utilization, which warrants further research. Initiation of lactation

orchestrated transcriptional adaptation of muscle in favor of utilizing fatty acid, conserving glucose and increasing proteolysis.

Key Words: cow, dietary protein, muscle

W373 Hepatic purinergic signaling gene network expression in dairy cattle during the peripartal period. J. Seo, J. S. Osorio*, and J. J. Loor, *University of Illinois, Urbana.*

The liver plays a central role in allowing dairy cattle to make a successful transition into lactation. In liver, as in other tissues, extracellular nucleotides and nucleosides trigger cellular responses through adenosine (P1) and ATP (P2) receptors. ATP and certain nucleotides serve as distress signals and are involved in heightened purinergic receptor activation in several pathologic processes. We evaluated the mRNA expression of genes associated with the purinergic signaling network in liver tissue during the peripartal period. Seven multiparous Holstein cows were dried off at d −50 relative to expected parturition and fed a controlled-energy diet (NEL = 1.24 Mcal/kg of DM) at intakes to meet and not greatly exceed 100% of NRC requirements during the entire dry period. All cows were fed a common lactation diet after calving. Liver tissue was harvested at −10, 3, and 21 d for mRNA expression of 9 purinergic receptors, 7 ATP and adenosine receptors, and 10 enzymes associated with ATP hydrolysis. The ANOVA model had day as the fixed effect and cow as the random effect. Differences between days were significant at a $P < 0.05$. The expression of some P2 receptors (P2RX4, P2RX7, P2RY1), ATP release channels (GJB1), and adenosine uptake (SLC29A1) increased ~2-fold between −10 and 3 d and remained elevated at 21 d. In contrast, expression of P1 receptors (ADORA2A and ADORA3) and several nucleoside hydrolases (ENTPD7, ENPP2, ENPP3, ADA) decreased ~2-fold between −10 and 3 d and remained downregulated at 21 d. Results suggested that alterations in hepatic purinergic signaling after calving could be functionally important because of their known role in bile formation, glucose metabolism, cholesterol uptake, steatosis, and inflammation.

Key Words: liver, inflammation, transition cow

W374 Five-day Resynch programs in dairy cows including the CIDR at two stages post-artificial insemination. S. L. Pulley*, S. L. Hill, and J. S. Stevenson, *Kansas State University, Manhattan.*

Two experiments were conducted to assess pregnancy outcomes after a 5-d Ovsynch-56 Resynch (RES; GnRH injection 5 d before [G-1; d 0] and 56 h (G-2) after $PGF_{2\alpha}$ [PG] injections on d 5 and 6, timed AI [TAI] on d 8) with and without a progesterone-releasing intravaginal controlled internal drug release (CIDR) 5-d insert. In Exp. 1, nonpregnant cows were enrolled on d 34 post-AI: d 34 RES-CON (n = 528) or d 34 RES-CIDR (n = 503). Blood was collected for progesterone (P4) assay. Pregnancy per AI (P/AI) was diagnosed by palpation per rectum at 34 and 69-d post-TAI. Only 76% of 1,031 cows had high P4 (≥1 ng/mL) at d 34 nonpregnant diagnosis (NPD). The d 34 RES-CIDR cows with low (<1 ng/mL) P4 had greater ($P = 0.036$) P/AI than d 34 RES-CON (37.7 vs. 29.4%), whereas d 34 RES-CIDR cows with high P4 had lesser P/AI than d 34 RES-CON (27.4 vs. 34.3%). In Exp. 2, cows were enrolled on d 31 post-AI (NPD): (1) d 31 PG3G (n = 102): Pre-PG on d 31, Pre-GnRH on d 34, and RES on d 41 (n = 102); (2) d 41 RES-CON (n = 108) as Exp. 1 but on d 41; and (3) d 41 RES-CIDR (n = 101) as Exp. 2 but on d 41. Blood was collected for P4 assay and ovarian structures were mapped by ultrasonography on d 31, 34, 41, 46, and 48. Pregnancy was diagnosed by ultrasonography on 31 and 59 d post-TAI. Proportion of cows with high P4 on d 31 was 70.6%. More ($P < 0.001$) cows ovulated after Pre-GnRH of d 31 PG3G (60.4%) than for d 41 RES-CON (12.5%) or d 41 RES-CIDR (17.1%). More ($P < 0.001$) PG3G cows had luteolysis after Pre-PG on d 31 than other treatments (73.7 vs. < 11%). Proportion of cows with high P4 on d 41 at G-1 tended ($P = 0.10$) to be greater for PG3G (75.6%) than for other treatments (65 to 70%). The P/AI was greater in cows starting RES on d 41 when P4 was low (44%) than high (33%), but no treatment differences were detected at 31 d after TAI (PG3G = 33.3%; d 41 RES-CON = 38.9%; d 41 RES-CIDR = 35.6%). We conclude that use of the CIDR insert is progesterone-dependent for cows initiating RES on d 34. Although d 31 PG3G increased luteolysis and greater ovulation rates before RES, no increase in P/AI compared with RES started on d 41 with or without a CIDR insert.

Key Words: Resynch, CIDR, pregnancy

W375 Effect of early or late resynchronization on reproductive performance of dairy cows observed for estrus. L. D. P. Sinedino*[1], F. S. Lima[1], R. L. A. Cerri[2], and J. E. P. Santos[1], *[1]University of Florida, Gainesville, [2]Unviersity of British Columbia, Vancouver, BC, Canada.*

The objective was to evaluate reproductive performance of dairy cows subjected to early (ER) or late (LR) resynchronization after nonpregnancy diagnosis. Holstein cows (n = 972) had their estrous cycle presynchronized and were then subjected to the Ovsynch protocol (d0 GnRH, d7 PGF, d9 GnRH, d10 AI) for first AI at 68 DIM. Weekly cohorts of cows were blocked by parity and assigned randomly to ER, based on nonpregnancy diagnosis using pregnancy associated glycoprotein (PAG) in blood, or LR based on palpation. ER cows received GnRH 2 d before PAG testing between 27 and 33 d after the previous AI, and not reinseminated nonpregnant cows continued on the Ovsynch for timed AI. LR cows had pregnancy diagnosed between 36 and 49 d after AI and those not reinseminated nonpregnant were resynchronized with the Ovsynch starting on the day of nonpregnancy diagnosis. After first AI, all cows were observed for estrus based on removal of tail chalk and those in estrus were inseminated on the same day. The study lasted 70 d for ER and 112 d for LR to allow a maximum of 2 resynchronized timed AI for each treatment in cows not observed in estrus. Pregnancy was based on palpation 36 to 49 d after AI. Data were analyzed with the GLIMMIX and PHREG procedures of SAS. The sensitivity and specificity PAG diagnoses were calculated. Pregnancy per AI (P/AI) at first AI did not differ between treatments and averaged 28.9%. Cows in ER tended ($P = 0.09$) to become pregnant faster after the first AI than LR cows (AHR = 1.25; 95% CI = 0.96–1.65), resulting in median days open of 133 and 141 for ER and LR, respectively. The proportion of cows not pregnant to first AI resynchronized with timed AI was greater ($P < 0.01$) for ER than LR (29.9 vs. 8.5%). P/AI after the first AI tended ($P = 0.09$) to be greater for cows reinseminated on estrus than resynchronized with timed AI for both ER (18.3 and 14.0%) and LR (15.7 and 10.4%). Sensitivity of PAG to diagnose a pregnant cow on d 27–33 after AI was 95.7% and on d 36–49 was 94.4%. Early diagnosis of nonpregnancy based on PAG with ER increased submission to timed AI, but tended to reduce interval to pregnancy in cows observed for estrus.

Key Words: dairy cow, resynchronization, PAG

W376 Increasing proestrus decreases pregnancy loss in lactating dairy cows submitted to E2/P4 timed artificial insemination programs. M. H. C. Pereira[1], A. D. P. Rodrigues[1], L. F. S. P. Barbosa[1], M. C. Wiltbank[2], and J. L. M. Vasconcelos*[3], *[1]Aluno do Programa de Pos-Graduacao em Zootecnia da FMVZ/UNESP, Botucatu, Sao Paulo, Brazil, [2]Department of Dairy Science, University of*

Wisconsin-Madison, Madison, [3]DPA/FMVZ/UNESP, Botucatu, Sao Paulo, Brazil.

The hypothesis of this study was that increasing proestrus would improve fertility to the timed artificial insemination (TAI). Lactating Holstein cows (759) yielding 30.5 ± 8kg of milk, with a detectable Corpus luteum (CL) at d-11 were randomly assigned to receive either one of the following treatments: (3d) d-10 = controlled internal drug release (CIDR, 1.9g) +2mg of estradiol benzoate (EB), d-3 = $PGF_2\alpha$ (25mg dinoprost tromethamine), d-2 = CIDR removal+1mg of estradiol cipionate (ECP); d0 = TAI; (4d) d-11 = CIDR+EB, d-4 = $PGF_2\alpha$, d-2 CIDR removal+ECP; d0 TAI. Cows were considered to be synchronized when a CL was detected on d7. Binomial variables were analyzed using PROC GLIMMIX and continuous using MIXED, in SAS. The 4d program tended ($P = 0.06$) to have higher progesterone (P4) at d7 in synchronized cows (3.14 ± 0.2 × 3.05 ± 0.2 ng/mL) than the 3d program. Although the pregnancy per artificial insemination (P/AI) at d32 (3d = 45%[175/385] × 4d = 43.9%[166/377]) and at d60 (3d = 38.1%[150/385] × 4d = 40.0%[154/377]) was not different, the 4d program had lower ($P = 0.04$) pregnancy losses (7.6%[12/166]) than the 3d program (14.7%[25/175]). P/AI at 60d was reduced ($P < 0.01$) for cows that ovulated smaller follicle (<11 = 37.2%[22/66]) or a larger follicle (>17 = 29.3%[39/128]), compared with follicles between 11 to 17mm (49.1%[197/395]). The cows in the 4d program were more likely ($P < 0.01$) to be detected in estrus (73.0%[269/374]) compared with 3d program (63.4%[240/385]). Expression of estrus improved ($P < 0.01$) synchronization (97.4%[489/501] × 81%[202/248]). In synchronized cows, the estrus detection improve P4 at d7 (3.22 ± 0.16 × 2.77 ± 0.17ng/mL), P/AI at 32d (51.2%[252/489] × 39.4%[81/202]), P/AI at 60d (46.3%[230/489] × 31.1%[66/202]) and reduce ($P < 0.01$) the pregnancy loss (9.3%[22/252] × 19.8%[15/51]), compared with cows that did not show estrus. In cows not detected on estrus within small (<11) or large follicles (>17) had higher pregnancy loss ($P = 0.01$), but, in cows detected on estrus the follicle diameter did not had effect on pregnancy loss. In conclusion, increasing proestrus increased estrous detection and reduced pregnancy loss.

Key Words: proestrus, estrus, pregnancy loss

W377 Effect of milk ingestion on LH and leptin plasma concentration in preweaning Nellore calves. G. Nogueira*, M. C. Miguel, H. Costa, J. Souza, R. Cipriano, J. L. Delfino, D. Giraldo, N. Romanello, D. Oliveira, M. A. Maioli, S. P. Gobbo, and D. Pinheiro, *Sao Paulo State University (UNESP), Aracatuba, Sao Paulo, Brazil.*

The aim of this study was to correlate the amount of milk ingested in nursling Nellore calves with live weight, LH and leptin plasmatic concentration from birth until weaning (at 5 mo). Once a month, 16 Nellore heifers were fasted for 12 h, weighed, allowed to suckle for 15 min, and weighed again. Last, a blood sample was collect for LH and leptin quantification after suckling. During the 5-mo period calves ingested on average 3.5kg, but the percent of live weight decreased from the 1st-5th month of age (8.22, 6.67, 3.85, 2.63, 2.63%). From suckling weight (16 × 5 = 80) calves were sorted into high ingestion (HI, ≥ 3.5 kg, n = 34) or low ingestion (LI, ≤ 3.4kg, n = 43) groups. In HI group as live weight increased, suckling weight decreased ($P = 0.043$; $r = -0.35$) and live weight was inversely related to leptin concentration ($P = 0.001$; $r = -0.56$). The increase in leptin concentration was related to greater LH concentration ($P = 0.03$; $r = 0.37$), but neither live weight ($P = 0.1$) nor suckling weight ($P = 0.3$) were correlated to LH concentration. In the LI group there were not similar correlations. When all the calves were considered (both groups combined) there was no correlation between milk ingestion and live weight ($P = 0.17$), but the amount of ingested milk positively increase LH ($P = 0.04$; $r = 0.23$) and leptin concentration ($P = 0.03$; $r = 0.24$). During the 5-mo period live weight was inversely related to LH ($P = 0.05$; $r = -0.22$) and leptin ($P = 0.01$; $r = -0.29$) but leptin was positively correlated to LH ($P = 0.005$; $r = 0.32$). During the calves first 5 mo of age, milk ingestion decreases as live weight increases, and live weight is not related to leptin concentration, probably due to decreased fat mass deposition during this period of time. This observation is coincident with the lack of positive correlation between live weight and LH concentration. But there was correlation between milk ingestion with leptin and LH. Leptin but not live weight was important to increase LH secretion during the preweaning phase in Nellore calves.

Key Words: *Bos indicus*, luteinizing hormone, suckling

W378 Prepartum insulin resistance in dairy cows increases offspring birth weight and insulin concentrations. L. H. Dauten*, B. E. Sullivan, and H. M. White, *University of Connecticut, Storrs.*

Selection of dairy cattle based on milk production has resulted in cows with increased insulin resistance. Transgenerational selection of heifers born to high-producing cows may exacerbate this trend through in utero effects on the developing fetus. The objective of this study was to determine the effect of maternal insulin resistance on calf birth weight and insulin responsiveness. Ten Holstein cows from the University of Connecticut dairy herd were selected based on anticipated calving date and fed the herd TMR, without nutritional intervention. At 7 d before anticipated calving and 7 d post-calving, BW and BCS were recorded and a 2-h glucose tolerance test was performed using a 0.25 g/kg BW, 50% dextrose bolus delivered via a jugular catheter. Calves were weighed 24h after birth. After 2 colostrum feedings, a meal test was performed, approximately 18 to 24h after birth. A serum sample was collected, one liter of milk fed, and a second serum sample collected at 1h post-feeding. Data (mean ± SE) were analyzed using MIXED procedure of SAS. Cow data were stratified into insulin sensitive and insulin resistant groups, with insulin resistant cows (n = 6) having greater ($P < 0.05$) glucose AUC than insulin sensitive cows (n = 4; 18493 vs. 13410 ± 1140 arbitrary units). There was no effect ($P \geq 0.1$) of parity, body weight, or BCS on maternal insulin resistance. Calves born to insulin resistant dams were heavier ($P < 0.05$) than those born to insulin sensitive dams (51 vs. 40 ± 2 kg). There was no difference ($P \geq 0.1$) in either baseline or 1 h glucose concentrations in calves during meal test; however, the relative change in glucose concentration at 1 h compared with baseline, was greater ($P < 0.05$) in calves born to insulin sensitive dams (153 vs. 117 ± 8%). Insulin concentrations before, but not after, meal test tended to be greater ($P = 0.09$) in calves born to insulin resistant dams (0.17 vs. 0.06 ± 0.04 ng/mL). Increased birth weight and insulin concentration in calves born to insulin resistant cows suggests that maternal insulin resistance, independent of other factors, may alter offspring glucose metabolism.

Key Words: insulin resistance, transition, glucose metabolism

W379 The influence of bPL and IGF-1 on the negative energy balance during the pre-parturition period of dairy cows. M. M. Weschenfelder[1], P. Montagner[1], A. R. Krause[1], E. Schwegler[1], F. A. B. Del Pino[1], E. G. Xavier[3], F. T. Rosa[1], E. Schmitt[2], A. Schneider[1], C. C. Brauner[1], and M. N. Correa*[1], *[1]Federal University of Pelotas - NUPEEC - Department of Veterinary Clinics, Pelotas, Rio Grande do Sul, Brazil, [2]EMBRAPA, Porto Velho, Rondonia, Brazil, [3]Granja 4 Irmaos, Pelotas, Rio Grande do Sul, Brazil.*

The increase in energy demand that occurs in late pregnancy is due, among other factors, to the histiotrophic distribution of nutrients caused by bovine placental lactogen (bPL), which acts by directing necessary nutrients to the placenta and fetal tissues, thus contributing to the occurrence of pre-parturition negative energy balance (NEB). Cows that have NEB during peripartum also show higher growth hormone (GH) and nonesterified fatty acid (NEFA) concentrations, as well as lower insulin-like growth factor I (IGF-I). Therefore, this study aimed to determine whether bPL is related to NEB occurrence during pregnancy and influences IGF-I concentrations during this period, as well as it acts as an indirect IGF-I concentration regulator. The body condition score (BCS) was assessed weekly, and bPL, IGF-I and NEFA plasma concentrations were assessed between d −21 and calving. Three groups (UP, MED and LOW) were formed according to bPL concentrations (UP >2.51 ng/mL; n = 7; MED >2.3 ng/mL and <2.5 ng/mL, n = 7; LOW <2.29 ng/mL, n = 6). The 5.0 Prism software was used for normalization of data, which were then submitted to MIXED MODELS for the ANOVA; finally, means were compared by the Tukey test through SAS software. Pearson correlation analyses between bPL × IGF-I, bPL × NEFA and NEFA × IGF-I variables were performed. The 3 groups compared differed as to bPL concentrations (UP = 2.91 ± 0.22 ng/mL; MED = 2.32 ± 0.11 ng/mL; LOW = 2.03 ± 0.13 ng/mL; $P = 0.0001$). IGF-I plasma concentrations during the pre-parturition period differed between the groups ($P = 0.0002$), days ($P = 0.0001$) and group-collection interaction ($P < 0.0001$). A correlation between NEFA × bPL variables (r = −0.23; $P = 0.03$) was observed; however, a correlation between bPL and IGF-I variables was not found (r = −0.21; $P = 0.27$). Data referring to NEFA concentrations and BCS assessments did not differ between groups ($P > 0.05$). Therefore, pre-parturition bPL does not act directly on the synthesis and maintenance of IGF-I levels in the blood; nevertheless, it can be one of the mediators of lipolysis during this period.

Key Words: NEFA, bPL, IGF-I

W380 Semen quality of bulls supplemented with protected fat and/or vitamin C and selenium. M. M. Guardieiro, F. L. M. Silva, P. L. J. Monteiro Jr, A. B. Nascimento, G. M. Chinelato, W. Arruda, N. M. B. Ferreira, L. R. D. Agostinho Neto, G. B. Mourão, and R. Sartori*, *University of São Paulo, Piracicaba, SP, Brazil.*

Bovine sperm membranes are rich in polyunsaturated fatty acids (PUFAs) and are susceptible to lipid peroxidation (LP) following exposure to anaerobic conditions after natural mating. Dietary rumen protected fat rich in PUFAs associated with antioxidant supplementation is an alternative to prevent LP and improve sperm viability. This study evaluated seminal quality of bulls supplemented with rumen-protected fat and/or vitamin C and selenium. Forty-eight Nelore bulls were confined (3 bulls per pen) and assigned to 4 treatment groups according to the addition of rumen-protected fat and/or antioxidant to the diet. For the initial 30 d, all bulls received the same adaptation diet. Thereafter, for 75 d, the same diet was offered, differing in the addition of: F) rumen-protected PUFAs (rich in linoleic, Megalac E, QGN-Arm & Hammer; 1.5% of dm; n = 12); A) antioxidant (a source of vitamin C and selenium, EconomasE, Alltech Biotechnology; 3 g/head/d; n = 12); FA) Megalac E and EconomasE (n = 12), or C) nothing (Control group; n = 12). Semen collection was performed 7 times every 14 d. Data were analyzed as repeated measures by GLM procedure of SAS. The treatment diets did not affect ($P > 0.10$) the semen volume (6.8 ± 0.3mL), gross-motility (3.2 ± 0.1), or proportion of morphologically normal spermatozoa (90.1 ± 1.4%). On the other hand, the progressive motility was greater for bulls fed FA compared with F or A diets (70.6 ± 1.6 vs. 67.0 ± 1.6 vs. 66.9 ± 1.6%, respectively; $P = 0.06$); however, it was similar to Control group (69.2 ± 1.6%). Independent of the collection period, total number of spermatozoa was lower for bulls fed PUFAs (F and FA) compared with those with no fat feeding (3106.6 ± 407.7 vs. 4261.6 ± 499.6; $P = 0.07$). Bull fed fat also had a greater percentage of total sperm defects at the last experimental evaluation (11.9±1.4 vs. 5.0±1.0%; $P < 0.01$). Bulls fed diets with antioxidants (A and FA) had more spermatozoa in the ejaculate as compared with those with no antioxidant (4224.1 ± 496.9 vs. 3134 ± 410.2, respectively; $P = 0.09$). In conclusion, diet containing the association of PUFAs and antioxidants did not improve the quality of bovine semen. Supported by CNPq, FAPESP, QGN, Alltech and EMBRAPA.

Key Words: spermatozoa, PUFA, antioxidant

W381 Reproductive performance of *Bos indicus* heifers with reduced serum progesterone concentration at the onset of a 5-d Co-Synch + CIDR program. M. V. Biehl*1,2, A. V. Pires[1], M. V. C. Ferraz Junior[2], D. D. Nepomuceno[1], E. M. Ferreira[1], R. S. Gentil[1], L. H. Cruppe[3], and M. L. Day[3], *[1]University of Sao Paulo, Piracicaba, Sao Paulo, Brazil, [2]University of Sao Paulo, Pirassununga, Sao Paulo, Brazil, [3]The Ohio State University, Columbus.*

The objective of this study was to compare reproductive performance of Nellore heifers (n = 162) submitted to the 5d CO-Synch+CIDR (5-d CS) program. The treatments were: HiP_4 (n = 62; 5-d CS in heifers with a CL present at CIDR insertion [d −5]); LoP_4 (n = 35; 5-d CS in heifers with no CL present at CIDR insertion); PGF-LoP_4 (n = 65; 25 mg of PGF2α [PGF] given 2 d before CIDR insertion [d-7] of the 5-d CS in heifers with a CL present on d-8). Ovarian ultrasonography (US) was performed on d-8 and −5, and on d0 to identify the presence of spontaneously formed and GnRH-induced CL, respectively. Blood samples to assess progesterone concentrations were collected on d-5. Heifers presented similar BW (388.4 ± 2.55, kg) and BCS (3.25 ± 0.21, scale of 1 to 5) among treatments. All heifers received 100 µg GnRH (GnRH-1; Cystorelin) at CIDR insertion (d-5). At CIDR removal (d0), heifers received 25 mg of PGF (Lutalyse) and a second 25 mg dose of PGF 24h later. Estrus detection was performed twice daily from d0 to 5 and for rebreeding, from d15 to d24 (AI – AM/PM rule). On d3 all heifers received a second GnRH (GnRH-2) in conjunction with timed AI. Pregnancy diagnosis was performed by US on d32 and 57. Data were analyzed using GLIMMIX procedures of SAS. Ovulation to GnRH-1 was greater ($P < 0.01$) for LoP_4 (85.7%) and PGF-LoP_4 (95.4%) compared with the HiP_4 (25.8%). Estrus detection rate differed ($P < 0.01$) among treatments (14.3; 38.7 and 67.7% for LoP_4, HiP_4 and PGF-LoP_4 treatments, respectively). Timed-AI pregnancy rate tended to be greater ($P = 0.07$) for the PGF-LoP_4 (36.9%) than the LoP_4 (14.3%) treatment with the HiP_4 treatment (29.0%) intermediate and not different from other treatments. Neither rebreeding pregnancy rate (HiP_4, 29.0%; LoP_4, 31.4% and PGF-LoP_4, 18.5%) nor final AI pregnancy rate after the 25d of breeding season (HiP_4, 58.1%; LoP_4, 45.7% and PGF-LoP_4, 55.4%) differed between treatments. In conclusion, reduced serum progesterone concentration at the beginning of a 5d CO-Synch+CIDR program increased the ovulatory response to the first GnRH, but did not improved pregnancy rate to timed-AI.

Key Words: heifer, 5-d CO-Synch + CIDR, progesterone

W382 Estradiol benzoate-based protocol versus GnRH-based protocol for timed AI in dairy cattle. P. L. J. Monteiro Jr.*[1], R. S. Surjus[1], A. B. Nascimento[1], A. P. Lemes[1], A. B. Prata[1], M. C. Wiltbank[2], and R. Sartori[1], *[1]University of São Paulo, Piracicaba, SP, Brazil, [2]University of Wisconsin-Madison, Madison.*

Objective were to compare ovarian dynamics and fertility of dairy cows subjected to a timed AI protocol initiating with either GnRH or estradiol benzoate (EB) and ending with estradiol cypionate (EC) or EB, in a 2 × 2 factorial arrangement. On Day 0 of the protocol, Holstein cows (n = 418 cows; 35.5 ± 1.1 kg of milk/d [Mean ± SE]; DIM: 165.6 ± 12.7; BCS: 2.8 ± 0.03) were treated with GnRH (10 µg buserelin, i.m., Sincrofort, Ourofino; n = 221) or EB (2 mg, i.m., Sincrodiol, Ourofino; n = 197), both associated with intravaginal progesterone (P4; 1.9 g, CIDR, Pfizer). All cows were treated with 2 doses of cloprostenol sodium (0.526 mg, i.m., Sincrocio, Ourofino) on D7 and D8. The CIDR was withdrawn on D8 and AI was performed on D10. Ovulation was synchronized by treatment with EC (1 mg, i.m., ECP, Pfizer; n = 202) on D8 or EB (1 mg; n = 223) on D9. Blood samples were collected on D0 and D7 for serum P4 concentration using RIA. Ovarian ultrasound evaluations were performed on D0, D7 and D10 and pregnancy diagnosis was done at 28 and 56 d after AI. Statistical analyses were performed with the Glimmix procedure of SAS ($P < 0.05$). There was no difference between EC (D8) and EB (D9) on all evaluated traits as well as no interaction among treatments. When comparing EB to GnRH, circulating P4 on D7 was lower in cows receiving EB on D0 (1.8 ± 0.3 vs. 3.2 ± 0.2 ng/mL). Furthermore, more cows treated with EB on D0 had luteolysis between D0 and D7 (49.5 vs. 25.8%). Ovulation after D0 was 10.7 vs. 29.0% for EB and GnRH, respectively. These outcomes resulted in more cows with CL on D7 in GnRH (71.4%) than EB (43.0%). Cows treated with EB on D0 had a smaller ovulatory follicle on D10 (13.9 ± 0.35 vs. 15.0 ± 0.34 mm). There was no effect of treatment on CR at Day 28 (31.2 vs. 34.9%), or Day 56 (27.0 vs. 32.4%), or pregnancy loss (11.7 vs. 5.6%) for EB vs. GnRH, respectively. Thus, initiation of a timed AI protocol with GnRH rather than EB resulted in increased circulating P4 and number of CL on D7, and increased ovulatory follicle size, but no detectable differences in fertility in lactating dairy cows. Acknowledgment: São Jorge Farm, CAPES, CNPq, FAPESP, and Pfizer.

Key Words: TAI, estradiol, progesterone

W383 Effects of fenceline contact at weaning and length of preconditioning period on preconditioning performance and morbidity during the feedlot receiving period. J. E. Anderson*, K. W. Harborth, M. D. Garcia, R. S. Walker, C. C. Williams, and T. G. Page, *Louisiana State University AgCenter, Baton Rouge.*

Fenceline contact at weaning has shown to be a management practice that can reduce the stress during the time following maternal separation. A 45 d preconditioning period is required by many value added programs. Combining these 2 management practices could reduce the length of time calves need to be held in a preconditioning program. Thus a study was conducted over a 2 year period to evaluate if fenceline weaning systems will allow for a 21-d preconditioning (PRECON) period rather than the preferred 45-d PRECON period. Three-hundred cross-bred steer calves from 2 locations (Central Research Station, Baton Rouge, LA and Hill Farm Research Station, Homer, LA) were used over a 2 year period. Both locations were managed independently following the same protocol. Each year, calves were randomly stratified by BW into 4 treatments at each location. Treatments were 1) fence line separation from dam for 7 d period followed by a preconditioning period of 21 d (FL21), 2) fence line separation from dam for 7 d period followed by a preconditioning period of 42 d (FL42), 3) no separation from dam for 7 d period followed by total dam separation and preconditioning of 21 d (S21), 4) no separation from dam for 7 d period followed by total dam separation and preconditioning of 42 d (S42). Calf was the experimental unit. After the initial 7 d weaning period, all calves were placed on pasture for the assigned PRECON treatment. Calves were fed an 18% CP commercial preconditioning ration at 1% of BW during the entire PRECON treatment period. There were no significant differences ($P > 0.05$) between BW at weaning. As expected, a significant difference ($P = 0.03$) was found in shipping weights based on preconditioning time length (21-d PRECON = 266.83kg, 42-d PRECON = 280.43kg). Steers were transported to and managed by a commercial feedlot in Guymon, OK, until harvest. The current results from this study showed no effect of pre- and post-weaning treatment on weaning performance through 60 d in the feedlot.

Key Words: weaning, preconditioning, beef cattle

W384 The effect of breed group and production system on performance of steer in the Colombian Caribbean Coast. R. Patiño[1], L. Salazar[1], C. Villalba[1], K. González[1], F. Porras[1], E. van Cleef[2], and O. Vergara[3], *[1]University of Sucre, Sincelejo, Sucre, Colombia, [2]Kansas State University, Manhattan, [3]University of Cordoba, Montéria, Colombia.*

The objective of this research was to evaluate the effect of breed group and production system (grazing or feedlot) on performance traits of growing steers in the Colombian Caribbean Coast. Steers (n = 90, BW = 260 ± 10 kg) of 3 breed groups [Crossbred (CB), Colombian Zebu (CZ) and 1/2 Angus × 1/2 Brahman (AB)] were randomly distributed to one of the treatments in a 3 × 2 factorial design. Thirty animals from each group were divided into 2 groups of 15 animals, which one was fed in feedlot (FLOT) and the other was pasture-fed (PAST), for a total of 6 treatments. Weight gain, heart girth and body condition were evaluated for 5 mo. Feedlot animals received a total mixed ration consisted of corn silage (42%), grass hay (40%), cottonseed (10%), corn syrup (3%) and cassava flour (5%). Grazing animals rotated in a module of 36 paddocks with *Dichanthium aristatum*, predominantly, with 2-d of occupation, to provide 2200 kg/ha of DM, and free access to water and mineral supplement. The data were analyzed using the GLM procedure of SAS. Weight gain was higher ($P < 0.05$) in feedlot steers (884.1 g/d), compared with grazing animals (819.4 g/d), and there was variation ($P < 0.05$) between groups, with values of 910.2, 846.4, and 799.6 g/day for CB, AB and CZ, respectively. Furthermore, was observed interaction ($P < 0.05$) among management factor and breed group, mainly due to the lower performance of CZ animals. It was also observed an increase ($P < 0.05$) in girth and body condition, which were higher for crossbred steers from the dual-purpose system in the region. Weight gains of the 6 groups were: 980.4 (CB-FLOT), 871.1 (AB-FLOT), 840 (CB-PAST), 820 (AB-PAST), 800.9 (CZ-FLOT), and 798.2 (CZ-PAST) g/day. The results of this study show that animal performance, in terms of weight gain and body size, is a function of breed group, and that performance under grazing or feedlot systems depends on this group, highlighting the animals Zebu for low performance in both production systems.

Key Words: Colombia, livestock, performance

W385 Effects of implant management during the stocker phase on grazing performance, subsequent feedlot performance, and carcass characteristics of beef steers. J. D. Rivera*[1], H. B. Jones[2], M. L. Galyean[3], and G. K. Blue[4], *[1]South MS Branch Experiment Station, Mississippi Agriculture and Forestry Experiment Station, Poplarville, [2]Coastal Research and Extension Center, Biloxi, MS, [3]Department of Animal and Food Sci., Texas Tech University, Lubbock, [4]Elanco, Lawrenceburg, TN.*

Crossbred beef steers (n = 36; BW = 254 kg) were used to evaluate the effects of no implant, 36 mg zeranol given at d 0 and again at d 56, or 25.7 mg of estradiol given at d 0 on grazing performance, subsequent finishing performance, and carcass characteristics. Cattle grazed twelve 1.2-ha annual ryegrass pastures for 99 d, after which they were maintained on common bermudagrass pastures for 12 d until shipment to the feedlot in New Deal, TX. The statistical model included the fixed effect of treatment and random effect of block, with pasture as the experimental unit. During the grazing period, body weight was not affected ($P > 0.10$) by treatment at d 0 or 28; however implant increased ($P < 0.08$) BW and ADG at d 56, 99, and 111. On d 84, cattle receiving estradiol had greater BW and ADG than cattle that received zeranol ($P < 0.08$) and cattle receiving zeranol had greater BW and ADG than cattle not receiving an implant ($P < 0.04$). On arrival at the feedlot and again on d 84, all steers were implanted with 80 mg of trenbolone acetate and 16 mg of estradiol. Due to space limitations, pasture groups were combined, resulting in a total of 6 pens for feedlot data analyses. Pasture implant type did not affect ($P > 0.10$) BW or ADG during the finishing period. Grazing implant affected ($P < 0.01$) dressing percent, with cattle that received estradiol at grazing having a lesser dressing percent than control or zeranol-implanted cattle. Carcass weight, longissimus muscle area, and yield grade were not affected ($P > 0.10$) by implant type. A difference was detected ($P < 0.09$) among grazing treatments for 12th rib fat, with cattle receiving estradiol at grazing having the least amount of 12th rib fat, followed by control cattle, with cattle that received zeranol at grazing having the greatest 12th rib fat. Grazing implant decreased ($P < 0.06$) marbling score. Results suggest that implanting during the grazing period improved pasture performance, had no effect on feedlot performance, and had limited carcass effects.

Key Words: beef cattle, grazing, growth-promoting implant

W386 Fatty acid profiles, meat quality, and sensory attributes of organic versus conventional dairy-beef. E. A. Bjorklund* and B. J. Heins, *University of Minnesota, West Central Research and Outreach Center, Morris.*

Holstein and crossbred dairy steers (n = 49) were evaluated for fatty acid profiles, meat quality, and sensory attributes of organic dairy-beef compared with conventional dairy-beef. Calves were randomly assigned to 1 of 3 replicated groups: conventional (CONV, n = 16), organic (ORG, n = 16), and grass-fed organic (GRASS, n = 17) and were born at the University of Minnesota West Central Research and Outreach Center, Morris from March to May 2011. The CONV steers were fed a diet that contained 80% concentrate and 20% roughage, and ORG steers were fed a diet of organic corn, organic corn silage, and organic protein supplement. Furthermore, ORG steers consumed at least 30% of diet dry matter in pasture during the grazing season. The GRASS steers consumed 100% forage from pasture during the grazing season and hay or hay silage during the non-grazing season. Independent variables for analysis of fatty acid profiles and meat quality were fixed effects of breed and treatment group. For sensory analysis, independent variables were fixed effects of treatment group, replicate, and the interaction of treatment group and replicate, and consumer and the interaction of consumer and treatment group were included as random effects. The GRASS steers (22.9%, 1.3%) were significantly ($P < 0.05$) lower for monounsaturated and polyunsaturated fat than the ORG (42.9%, 2.4%) and CONV (39.4%, 3.1%) steers, respectively. Furthermore, the GRASS steers were higher ($P < 0.05$) for n-3 fat and lower ($P < 0.05$) for n-6 fat than the ORG and CONV steers. For sensory attributes, there were no significant differences for ORG (71.3) and CONV (69.2) steers for overall liking; however, the GRASS (56.3) steers had the lowest ($P < 0.05$) overall liking among beef consumers. The ORG (73.3) steers had higher ($P < 0.05$) flavor liking than the GRASS (56.8) and CONV (69.2) steers. Furthermore, the GRASS (6.3) steers had the highest ($P < 0.05$) scores for off-flavor compared with the ORG (3.9) and CONV (4.1) steers. These data indicate that fatty acid composition can be altered by inclusion of grass and more forage in the diet.

Key Words: organic, grass fed, n-3 fat

W387 Growth measurements, carcass characteristics, and profitability of organic versus conventional dairy-beef steers. E. A. Bjorklund* and B. J. Heins, *University of Minnesota, West Central Research and Outreach Center, Morris.*

The objective of this study was to compare the growth, carcass characteristics, and profitability of organic dairy steers and conventional dairy steers. Holstein and crossbred dairy bull calves (n = 49) were randomly assigned to one of 3 replicated groups at birth; conventional (CONV, n = 16), organic (pasture and concentrate, ORG, n = 16), and organic-grass only (100% pasture, GRASS, n = 17). Calves were born at the University of Minnesota West Central Research and Outreach Center, Morris from March to May 2011. The CONV steers were fed a diet of 80% concentrate and 20%. The ORG steers were fed a diet of organic corn, organic corn silage, and at least 30% of their diet consisted of organic pasture during the grazing season. The GRASS steers grazed organic pasture during the grazing season and were fed organic hay or hay silage during the non-grazing season. Feed intakes were recorded daily with herd management software. A profit function was defined to include revenues and expenses for beef value, feed intake, pasture intake, and yardage. For analysis of body and carcass measurements, independent variables were fixed effects of steer group and breed group. For analysis of profit per steer, independent variables were fixed effects of steer group. The GRASS (358.6 kg) steers had lower ($P < 0.05$) gain from birth to slaughter than ORG (429.6 kg) and CONV (534.5 kg) steers. Furthermore, the GRASS (0.61 kg/d) steers had lower ($P < 0.05$) average daily gain compared with ORG (0.81 kg/d) and CONV (1.1 kg/d) steers. Both organic steer groups had smaller ($P < 0.05$) ribeye area (49.5 cm^2 for GRASS, 65.8 cm^2 for ORG, respectively) compared with CONV (75.4 cm^2) steers. For profitability, GRASS steers had 25% greater ($P < 0.05$) profit per steer (+$151), than CONV steers. Conversely, ORG steers had 169% less ($P < 0.05$) profit per steer (−$1,086) than CONV steers. The higher cost for production of the ORG steers is because of the extreme high value of organic corn. The results suggest there may be a potential market for the male offspring of organic dairy cattle in the Midwest.

Key Words: organic, pasture, profitability

W388 Effect of seasonality on subclinical mastitis and milk composition of a ¾ Holstein × Zebu herd of Minas Gerais State, Brazil. C. V. G. Ladeira[1,4], S. V. Teixeira[1], N. Silva[2], G. M. Costa[3], D. S. Rodrigues[1], L. G. A. Ladeira[1], P. Oliveira[1], T. C. Gouveia[1], R. Rodrigues[2], L. M. Fonseca[2], M. O. Leite[2], and M. M. O. P. Cerqueira*[2], *[1]Empresa de Pesquisa Agropecuaria de Minas Gerais, EPAMIG, Belo Horizonte, Minas Gerais, Brazil, [2]Escola de Veterinaria, Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil, [3]Departamento de Medicina Veterinaria, Universidade Federal de Lavras, Lavras, Minas Gerais, Brazil, [4]FAPEMIG CVZ APQ03680/10, Belo Horizonte, Minas Gerais, Brazil.*

The aim of this study was to evaluate the occurrence of subclinical mastitis in 3/4 Holstein × Zebu cows and the effect of season on somatic cell counts, mastitis pathogens, milk production and composition. The study was conducted at the Santa Rita Experimental Farm belonging to EPAMIG, Brazil. A total of 727 composite milk samples were collected from August, 2011 to December, 2012. Effect of season was considered. The somatic cell count (SCC) and its correlation with milk production, fat, lactose, protein, nonfat and total solids content, and mastitis pathogens were determined. Statistical analyzes were performed using SAS/STAT. Average values for rainy and dry seasons, respectively, were: SCC (5.9 log cells/mL; 5.6 log cells/mL), fat (4.00 g/100 g; 3.73 g/100 g), protein (3.36 g/100 g; 3.41 g/100 g), lactose (4.36 g/100 g; 4.26 g/100 g), total solids (12.64 g/100 g; 12.41 g/100 g), nonfat solids (8.63 g/100 g; 8.68 g/100 g) and milk production (12.47 kg/d; 10.46 kg/d). Higher SCC ($P \leq 0.0001$), fat ($P = 0.001$), lactose ($P = 0.007$), total solids ($P = 0.05$) and milk production ($P \leq 0.001$) were observed during the rainy season (November to February). Seasonal differences did not occur for protein ($P = 0.34$) and nonfat solids ($P = 0.42$). The log SCC presented a positive correlation with parturition order (r = 0.30 and $P < 0.0001$), protein (r = 0.14 and $P = 0.0001$), fat (r = 0.11 and $P = 0.004$) and negative with lactose (r = −0.32 and $P < 0.0001$), milk production (r = −0.08 and $P = 0.03$) and nonfat solids (r = 0.08 and $P = 0.02$). The mastitis pathogens isolated did not affect milk production, fat, protein, nonfat solids, total solids and lactose content ($P > 0.05$). *Staphylococcus aureus* was the main pathogen and it was found in 37.1% of the samples. Other pathogens isolated included *Streptococcus uberis* (14.4%), *E. coli* (3.0%), *Corynebacterium* sp. (3.8%), and *Bacillus* sp. (2.3%). It can be concluded that SCC was greater during the rainy season and affected milk production and almost all milk components. The presence of mastitis pathogens did not result in changes in milk composition.

Key Words: seasonality, milk, quality

W389 Identification of phenotypic predictors of milk yield losses in response to once-daily milking: Preliminary results.

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Extended milking intervals can reduce milk yield but this response is highly variable among cows. Identifying cows with the low milk yield loss associated with milking interval is difficult, restricting the development of milking practices such as once-daily milking. A trial was carried out to identify phenotypic predictors linked to a physical regulation of milk yield due to milk accumulation in the udder. Thirty-two primi- and multiparous Holstein cows producing 34.1 ± 5.4 kg/d of milk at 184 ± 29 d in milk were milked twice a day at 0700 and 1600 h during the 7-d control period (C) and then morning milking was omitted one day (MO, milking omission). Indeed milk loss was shown to occur very rapidly, from the 1st day of implementation. Milk yield and flow were recorded at each milking. Milk fat, protein, lactose, and cell contents were analyzed at each milking for 3 consecutive days of the control period, and on the MO day. Lactose was analyzed in tail blood samples collected 1 h before milking 2 d before MO and on MO day; distances between the 4 teats tips were also measured 1h before milking. Data were analyzed to determine Pearson correlations using SAS. Milk yield decreased by 6.8 kg/d (20%) in response to MO ($P = 0.0001$). The absolute and relative milk losses showed high variability between cows (−0.1 to 13.4 kg/d and −0.5 to 42%, resp.). Milk loss (absolute or relative) was not correlated to C milk yield. Absolute milk loss was negatively but poorly correlated with C milk fat and protein content (r = −0.34 and −0.40; $P = 0.05$) and positively but poorly also with C milk lactose content (r = 0.33; $P = 0.06$). Milk loss was not correlated with C plasma lactose levels and the C total distance between tips. Absolute milk loss was positively correlated to C milk average flow (r = 0.59 and 0.46, resp.; $P < 0.01$) and negatively to C milking time (r = −0.58; $P < 0.001$). In conclusion, milk flow could be a promising key phenotypic predictor of individual milk yield losses in response to once-daily milking and in relation to physical regulation of milk secretion.

Key Words: once-daily milking, milk yield loss, predictor

W390 The effect of body condition score change 15 days prior to calving on lactation curve and production parameters in grazing dairy cows in Ireland. M. R. Sheehy*[1,2], F. J. Mulligan[1], M. M. Schutz[3], M. A. Crowe[1], S. P. M. Aungier[1], and A. G. Fahey[4], *[1]School of Veterinary Medicine, University College Dublin, Dublin, Ireland, [2]Devenish Nutrition Ltd., Belfast, United Kingdom, [3]Dept. of Animal Sciences, Purdue University, West Lafayette, IN, [4]School of Agriculture and Food Science, University College Dublin, Dublin, Ireland.*

Body condition score (BCS) is an indirect measure of energy balance. Energy balance before calving may affect production and health in the following lactation. The objective of this study was to determine if loss of BCS 15 d before calving had an effect on lactation curve characteristics and production. Milk production data were collected at 15 d intervals from calving (d 0) to d 315 of lactation from 93 Holstein-Friesian cows. Body condition scores were assessed on d −15 to d 0 relative to calving (1 = emaciated, 5 = obese). Cows were divided into 2 groups; those that did not lose BCS between d −15 and d 0 (MAINT, n = 50) and those that lost BCS from d −15 to d 0 (LOSS, n = 43). The Woods incomplete gamma function was used to fit individual cow lactation curves using PROC NLIN of SAS. The Woods' function estimated initial daily yield (a, kg/d), rate of increase to peak yield (b, kg/d)and rate of decrease from peak yield (C, kg/d), persistency, time to peak yield (Tm), and peak milk yield (Ym, kg/d). 305-d milk (kg), fat (kg), protein (kg), protein %, fat %, and SCC were recorded for each cow. The effect of BCS group (MAINT and LOSS), parity (primi- and multiparous), and month of calving (1 to 4) and interactions were analyzed using PROC MIXED of SAS. MAINT cows had higher initial daily yield compared with LOSS ($P < 0.05$). Primiparous MAINT cows had a tendency to have a lower C than LOSS cows ($P < 0.10$) and higher Tm ($P < 0.10$). Primiparous MAINT had a tendency for a greater persistency for fat than primiparous LOSS ($P < 0.10$). Multiparous MAINT had a greater Tm for fat than multiparous LOSS ($P < 0.05$). Somatic cell count was lower in multiparous MAINT than multiparous LOSS ($P < 0.05$). In conclusion, MAINT cows had a higher initial yield and delayed Tm and reduced SCC. This may suggest that cows that maintain BCS 15 d before calving undergo less stress during lactation.

Key Words: body condition score, lactation, somatic cell count

W391 Comparison of different types of roofings in individual houses for calves through thermal comfort indexes. R. S. Marçola, P. A. Bustos Mac-Lean*, G. T. Santos, and O. R. Barbosa, *State University of Maringa, Maringa, Parana, Brazil.*

Countries located in the tropics such as Brazil have higher average temperatures throughout the year, thus resulting in thermal stress for animals. Shelters are commonly used to enhance the welfare of suckling calves and protect them against weather odds, which may increase production. This study aimed to evaluate different roofing materials for housing calves in Maringa - Paraná, using black globe temperature and humidity index (BGHI) and radiant heat load (RHL), calculated based on temperature of air, black globe and dew point, wind speed and relative humidity. Sixteen individual shelters were installed and covered by one of 4 types of tiles: ecological tiles, galvanized iron, sheet material Tetra Pak, fiber cement (composite material made of sand, cement and cellulose fibers) tile painted white outside and black inside. There were 4 shelters allotted randomly to each material. Data recordings were made at 8, 10, 14 and 16 h, always in the presence of sunlight, and the results were submitted to ANOVA using the GLM procedure of SAS (2007). Mean separation was conducted using the Tukey test and significance was declared at $P \leq 0.05$. Regardless of the season, values of weather measurements were always higher at 14 and 16 h than at 8 and 10 h, and parameters measured during summer were always the highest. The lowest values of BGHI and RHL were found for the in fiber cement tiles during the hottest hours of the day (BGHI: 79.5 and 79.2 ± 3.5; RHL: 500.4 and 504.4 ± 36.0), but there were no differences during day time for the other materials. These data suggest that recyclable materials such as sheet material Tetra Pak can be used to build shelter roofs, which may contribute to a better environment.

Key Words: individual shelter, thermal comfort index, roof type

W392 Effects of parity and pregnancy status on body weight changes of dairy cows in early lactation. M. L. S. Canha[1], S. L. Viechnieski[2], and R. Almeida*[1], *[1]Universidade Federal do Paraná, Curitiba, PR, Brazil, [2]StarMilk Farm, Céu Azul, PR, Brazil.*

The objectives of this study were to describe parity and pregnancy status differences on daily body weight (BW) changes during the first 100 d of lactation. Data included 26,344 daily BW measurements from 372 Holstein cows that calved from June 2, 2011, to June 1, 2012, in southern Brazil. Cows were automatically weighed on their way back from the milking parlor 3 times daily and were assigned, according to parity, to 3 groups: 152 first-parity (P1), 100 second-parity (P2), and 120 third parity and greater (P3+). For generating variables representing BW changes in early lactation, individual measurements were first

smoothed using cubic splines (TPSPLINE procedure of SAS). This approach used days in milk (DIM) as a single smoothing variable. Parity effects on BW characteristics were estimated using GLM procedure of SAS. Milk production was assessed by the cumulative yield until 100 DIM and reproductive performance by pregnancy status at 180 DIM. Body weight at calving differed ($P < 0.01$) across parities; 570.5, 653.5, and 699.9 kg for P1, P2 and P3+, respectively. Liveweight at nadir also differed ($P < 0.01$) across parities; 521.5, 608.8, and 647.3 kg for P1, P2 and P3+, respectively. Mean days from calving to nadir and mean loss of BW from calving to nadir BW did not differ ($P > 0.05$) across parity; 35.7, 32.9, and 37.8 d, and 48.9, 44.7, and 52.6 kg, respectively for P1, P2 and P3+ cows. There was no difference ($P > 0.05$) on milk yield between cows with good and poor reproductive performance. Cows with desirable reproduction calved lighter ($P < 0.05$) than cows with poor reproductive performance; 632.8 vs. 649.8 kg. Further, cows with shorter days open lost less ($P < 0.01$) weight than cows with undesirable reproductive performance; 42.8 vs. 54.7 kg and −6.5 and 8.3%, respectively. These results support the statement that improvements in fertility of dairy cows should be achieved minimizing BW loss early in lactation.

Key Words: automatic walkover weighing, daily liveweight

W393 Ovarian activity and oocyte quality associated to serum and follicular fluid biochemical profile of crossbreed dairy cows during postpartum in summer and winter. B. G. Alves[2], K. A. Alves[2], R. M. Santos*[1], M. C. Martins[1], L. S. Braga[1], T. H. Silva[1], B. G. Alves[1], A. C. Lucio[1], T. V. Silva[1], M. E. Beletti[1], J. O. Jacomini[1], and M. L. Gambarini[2], *[1]Universidade Federal de Uberlândia, Uberlândia, Minas Gerais, Brazil, [2]Universidade Federal de Goiás, Goiânia, Goiás, Brasil.*

This work was delineated to evaluate the influence of heat stress (HS) and negative energy balance (NEB) on serum metabolic and dominant follicular fluid profile, follicular development and oocyte quality of crossbred dairy cows. The oocytes, blood and follicular fluid samples (follicles ≥9 mm) were obtained on 30, 45, 60, 75 and 90 d of postpartum in summer (n = 30) and winter (n = 30). In the moment of transvaginal follicular aspiration, there were recorded data from follicles number, quality and amount of oocytes, rectal temperatures (RT) and body condition scores (BCS). The ambient air temperature (AT), relative humidity (RH) was collected in each season to calculate the temperature humidity index (THI). The glucose, total cholesterol (TC), triglycerides (TG), urea, sodium (Na), potassium (K) and calcium (Ca) concentrations were determined on serum and follicular fluid (FF) samples. The RT, RH and THI were superior ($P < 0.01$) on summer as well as BCS loss. The TC, TG, urea, K and Ca concentrations on FF were higher in summer ($P < 0.05$). The serum concentrations of glucose, urea, Na and K were superior in winter ($P < 0.05$). The total of aspirated follicles was higher ($P < 0.01$) in winter and the mean of viable oocytes did not differ among seasons. Degenerate oocytes showed positive association ($P < 0.05$) with THI (r = 0.14) and AT (r = 0.13), as well as negative correlation with glucose (r = −0.12) and K (r = −0.11) serum concentrations. The heat stress and NEB induce metabolic changes which compromise the folliculogenesis, follicular dominance and follicular environment resulting in development of oocytes morphologically impaired. Supported by CAPES/PROPP-UFU.

Key Words: oocyte quality, heat stress, dairy cattle

W394 Interference of the production system on milk quality. A. L. Silva, M. I. Marcondes, D. C. Jácome, M. B. Boto, I. M. Batalha, T. R. Pereira, and J. P. P. Rodrigues*, *Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil.*

Criteria for defining the quality of raw milk have changed to meet official regulation demands of industry and consumers in an effort to improve food safety and industrial yield. Our objective was to evaluate raw milk quality in different production systems and its variation throughout the year. The data used in this study were collected from 943 dairy farms in South, Midwest and Central Minas regions of the state of Minas Gerais and in Vale do Paraíba in the state of São Paulo, Brazil. Data were provided by the company Danone with a total of 18,206 samples from the period of January 2009 to September 2011. Data were sorted between confinement, semi-confinement and extensive production systems. The quality factors evaluated were somatic cell count (SCC), total bacterial count (TBC) and protein and fat contents. Data were analyzed in repeated measures over time using the MIXED procedure of SAS (2008). There was no effect of production system on milk protein, fat and SCC. Total bacterial count, however, was affected by production system, and it was related to the type of structure used for feeding. The results were possibly a consequence of the program of payment for quality implemented by the dairy sector since 2002. Seasonal variations were found for milk SCC, TBC, protein and fat: the highest protein values were identified from March to June; the highest fat contents were found from May to August, and TBC and SCC from December to March. In conclusion, the production system did not have an effect on milk fat, protein and SCC; however, confinement systems had a better TBC. We also conclude that both month and year affect milk TBC, SCC, protein and fat with the best milk quality found during the coldest periods of the year. Supported by CNPq, CAPES, FAPEMIG, INCT-CA.

Key Words: fat, protein, SCC

W395 Methane emission from dairy calves, heifers and dry cows. D. P. Bu[1], X. L. Wang[2], L. H. Baumgard[1], J. Q. Wang*[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]Department of Animal Science, Iowa State University, Ames.*

Study objectives were to compare ruminal methane production in calves (n = 4, BW = 130 ± 3 kg), heifers (n = 4, BW = 400 ± 20 kg), and dry cows (n = 4, BW = 550 ± 50 kg). Animals were housed in 3 environmentally controlled chambers (size, 4 × 3 × 2.5 m; one animal/chamber) with indirect calorimetry capabilities for 9 d. Calves and heifers were fed the same TMR diet consisting primarily of corn silage 26.8%, Chinese wildrye 3.7%, alfalfa hay 28.5% and concentrate 41% and the dry cows were fed a TMR diet consisting primarily of corn silage 30.1%, Chinese wildrye 23.3%, alfalfa hay 17.5% and concentrate 29.1%. The temperature of each environmental chamber was maintained at 25 ± 1°C, and humidity was 40 ± 2% (THI = 70.7). Feed offered and orts were recorded and sampled once daily. Feed samples were analyzed for EE, CP and ash and GE was calculated. O_2 consumption, CO_2 and CH_4 production within each chamber was automatically recorded every 30 s by Oxymas instrument (Columbus Instruments, US). Gas consumption and production data around feeding time was excluded due to chamber imbalance. Data was analyzed by SAS (9.0) using MIXED model. Daily CH_4 production was 130.64^a, 261.65^b, and 340.52^c L/d for calves, heifers and dry cows, respectively. However, daily CH_4 production per unit of dry matter intake and total energy intake were 27.02^c, 41.80^a, and 30.38^b, and 6.14^c, 9.40^a, 6.97^b, respectively. Overall, heifers produced more methane per unit of dry matter intake compared with dry cows and calves.

Key Words: cattle, methane emission

W396 Ruminant methane emission during heat stress. D. P. Bu[1], X. L. Wang[1], L. H. Baumgard[2], J. Q. Wang*[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]Department of Animal Science, Iowa State University, Ames.*

The study objective was to evaluate the effect of heat stress (HS) on methane production. Eight female dairy calves (130 ± 3 kg of BW) were used in this trail and fed a TMR designed for lactating cows. Calves were acclimated to environmentally controlled chambers for 7 d. After acclimation, the experiment was conducted for 20 d and was separated into 2 periods (P). The first 10 d was classified as P1 and the second 10 d as P2. During P1, all calves were allowed to eat ad libitum while being maintained in thermal neutral (TN) conditions (20°C). During P2, 4 calves remained in TN conditions (exactly the same as P1) while 4 calves were exposed to cyclical heat-stress (HS) conditions. Between 2100 to 0900 h, the temperature was maintained at 33°C, and between 1000 to 2200 h, the temperature was maintained at 37°C. Reductions in feed intake by HS calves during P2 was determined daily as a percentage of their mean daily ad libitum intake in P1. The TN control calves were pair-fed (PFTN) to the HS calves during P2 to eliminate the dissimilar effect of nutrient intake. Daily dry matter intake for all calves was recorded throughout the experimental. Body temperature indices (respiration rate and rectal temperatures) were obtained 4 times daily (0600, 1000, 1400 and 1800 h). Methane, oxygen and carbon dioxide production was obtained (every 30 s) from the auto recording system during both periods. Compared with PFTN, HS increased ($P < 0.01$) rectal temperature and respiratory rate and tended ($P = 0.09$) to decrease (17.6%) CH_4 emissions. The daily average RQ (CO_2/O2: 0.91) did not differ ($P > 0.05$) between HS and PFTN calves. In conclusion, HS reduced methane production and our data suggests that HS alters rumen fermentation patterns.

Key Words: heat stress, methane emission

W397 Effect of feed delivery frequency on the behavior and productivity of lactating dairy cows. K. D. Hart*[1], B. W. McBride[2], T. F. Duffield[3], and T. J. DeVries[1], *[1]Dept. of Animal and Poultry Science, University of Guelph, Kemptville Campus, Kemptville, ON, Canada, [2]Dept. of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada, [3]Dept. of Population Medicine, University of Guelph, Guelph, ON, Canada.*

The objective of this study was to determine the effect of feed delivery frequency on the behavior and productivity of lactating dairy cows. Twelve free-stall housed, lactating Holstein dairy cows, milked 3×/d, were exposed to each of 3 treatments (over 21-d periods) in a replicated Latin square design. Treatments were feed delivery frequency of (1) 1×/d (at 1400 h), (2) 2×/d (at 1400 and 2200 h), and (3) 3×/d (at 1400, 2200, and 0600 h). Milk production, feeding, lying, and rumination behavior were electronically monitored for each animal for the last 7 d of each treatment period. Milk samples were collected for the last 3 d of each period for milk component analysis. Data were analyzed in a general linear mixed model. Dry matter intake varied with feed delivery frequency ($P_{quadratic} = 0.03$; SE = 0.87), with greatest DMI observed in cows fed 3×/d (27.8 kg/d) compared with when fed 2×/d (27.0 kg/d) or 1×/d (27.4 kg/d). There was no effect of treatment on milk yield (41.3 kg/d), which translated into greater production efficiency ($P_{quadratic} = 0.04$; SE = 0.08) for cows fed 2×/d (1.57 kg milk/kg DMI) compared with 1×/d (1.55 kg milk/kg DMI) and 3×/d (1.53 kg milk/kg DMI. Milk protein % increased with greater frequency of feed delivery (3.15 vs. 3.16 vs. 3.21%; SE = 0.01; $P_{linear} = 0.02$), with multiparous (MP) cows showing the greatest increase with 3×/d feed delivery frequency (3.30%; $P = 0.01$). Cows that did not receive fresh feed at milking had lower DMI during the first hour after milking than those that received fresh feed at all milkings. Meal frequency (9.5 meals/d), size (3.0 kg/meal) and duration (25.2 min/meal) did not vary by treatment. Although lying time (9.3 h/d) did not vary by treatment, PP cows spent more time lying (10.3 vs. 8.3 h/d; SE = 71.0; $P = 0.02$) than MP cows. There was a tendency ($P_{quadratic} = 0.06$; SE = 41.3) for cows to spend more time standing following the first milking when fed 2×/d (144.8 min) compared with 1×/d (118.8 min) and 3×/d (110.8 min). In summary, feed delivery frequency had little effect on the behavior and productivity of dairy cows milked 3×/d, with the exception of DMI and milk protein % being greatest with 3×/d feed delivery.

Key Words: feeding frequency, behavior, parity

W398 Associations between herd-level feeding and housing management practices, feed sorting, and productivity of freestall-housed dairy cows. A. D. Sova[1], B. W. McBride[2], S. L. LeBlanc[3], and T. J. DeVries*[1], *[1]Dept. of Animal and Poultry Science, University of Guelph, Kemptville Campus, Kemptville, ON, Canada, [2]Dept. of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada, [3]Dept. of Population Medicine, University of Guelph, Guelph, ON, Canada.*

The objective was to examine associations between herd-level feeding and housing management factors, feed sorting, and milk production. Twenty-two freestall herds with average lactating herd size of 162 ± 121 cows, feeding TMR, were studied for 7 consecutive days in both summer and winter. In cases of multiple feeding groups, the highest producing group of cows with an even distribution of DIM and parity was studied. The average group size studied was 83 ± 31 cows, consisted of cows 187 ± 47 DIM, with a parity of 2.3 ± 0.6, consuming 24.3 ± 2.6 kg DM, with group-average yield of 34.3 ± 6 kg of milk/d, 3.7 ± 0.3% milk fat, 3.2 ± 0.18% milk protein, and 225,000 ± 129,000 cells/mL SCC. Milk production parameters, including yield, fat, and protein, were recorded through DHI milk testing. A survey of feeding management practices and barn characteristics was administered on each farm. The amount of feed offered and refused was recorded and sampled daily to assess DMI and particle size distribution. Data were summarized across each 7-d period for each farm and analyzed in multivariable mixed-effect regression models. Increased frequency of feed delivery (2× vs. 1×/d) was associated with an increase of 1.4 kg/d DMI ($P = 0.008$), 2.0 kg/d milk yield ($P = 0.047$), and a tendency for 1 point less sorting against long ration particles ($P = 0.1$). Increased 4% FCM was associated with reduced long particle sorting, with every 2% group-level reduction in sorting being associated with an increase of 0.9 kg/d of 4% FCM ($P = 0.036$). Increased feed bunk space was associated with greater group-average milk fat % ($P = 0.006$) and lower SCC ($P = 0.001$), with every 10cm/cow more space associated with an increase of 0.06% milk fat and a 13% reduction in SCC. Overall, our results indicate that factors that improve access to the feed bunk, such as feeding frequency and bunk space, improve group-level DMI, consistency in nutrient intake, and milk production.

Key Words: sorting, production, feeding management

W399 Associations between daily variability in ration characteristics and measures of productivity in freestall-housed cows. A. D. Sova[1], B. W. McBride[2], S. L. LeBlanc[3], and T. J. DeVries*[1], *[1]Dept. of Animal and Poultry Science, University of Guelph, Kemptville Campus, Kemptville, ON, Canada, [2]Dept. of Animal and Poultry*

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The ration supplied day-to-day by the dairy producer may not reflect the TMR formulated, potentially affecting production. The objectives of this study were to determine (1) how TMR fed differs or agrees with TMR formulation, (2) the daily variability in nutrient and physical characteristics of TMR fed on commercial farms, and (3) associations between daily variability in TMR characteristics and group-average productivity measures (milk yield, milk components, DMI, efficiency and feed sorting). Samples of fresh and refused TMR were collected for 7 d in both summer and winter on 22 commercial freestall farms to assess particle size (% long, medium, short and fine using a Penn State Particle Separator), DM, and chemical content. Milk production, including yield, fat, and protein, were recorded through DHI. Multivariable mixed-effect regression models were used to analyze associations between herd-level productivity and coefficients of variation (CV) in TMR characteristics over 7 d. The average TMR delivered exceeded TMR formulation for NeL (+0.05mcal/kg), NFC (+1.2%), ADF (+0.7%), Ca (+0.08%), P (+0.02%), Mg (+0.02%) and K (+0.04%) and underfed CP (−0.4%), NDF (−0.6%) and Na (−0.1%). Greater than 5% CV over the 7 d of the fed ration was observed for refusal rate (CV = 74%), % long particles (CV = 16%), % medium particles (CV = 7.7%), % short particles (CV = 6.1%), % fine particles (CV = 13%), Ca (CV = 7.7%), Mg (CV = 5.2%), and Na (CV = 10%). Every 0.5% increase in NeL variability (NeL = 1.7 ± 0.03 mcal/kg) was associated with 3.2 kg/d lower milk yield ($P < 0.001$; milk yield = 34.3 ± 5.9 kg/d), 1.0 kg/d lower DMI ($P = 0.005$; DMI = 24.3 ± 2.1 kg/d), and 4.3% lower efficiency of production ($P = 0.03$; efficiency = 1.41 ± 0.16 kg/kg). Every 5% increase in variability in % long particles (% long = 19.8 ± 6.5) in the TMR was associated with 1.2 kg/d lower milk yield ($P = 0.02$), 2.6% decrease in efficiency of milk production ($P = 0.02$), and 18.5% increase ($P < 0.001$) in group-average SCC (SCC = 225,000 ± 129,000 cells/mL). These results demonstrate the importance of ensuring TMR consistency to maximize DMI, production, and efficiency.

Key Words: total mixed ration, variability, milk yield

W400 Effect of vaccination against foot-and-mouth disease on growth performance of Korean native goat (*Capra hircus coreanae*). N. Jo[1], J. Jung*[1], J. Lee[1], S. Jeong[1], J. Jeong[1], L. Sun[1], H. Sung[2], K. Son[1], and S. Seo[1], *[1]Division of Animal Biosystem Sciences, Chungnam National University, Daejeon, Republic of Korea, [2]Adbiotech, Seoul, Republic of Korea.*

The objectives of this study were (1) to evaluate the effect of vaccination against foot-and-mouth disease (FMD) on growth performance, nutrient digestibility, hematological response and goat behavior, and (2) to investigate a possible strategy for reducing its adverse effect. A total of 12 Korean native goats (19.8 ± 2.9 kg) were divided into 3 groups and randomly allocated to one of the following treatments: 1) control, 2) co-injection of a commercial vaccine stress reliever (VSR; Anti VS-2, Samyang Anipharm, Korea) and 3) supplementation of 1% gamma-amino butyric acid (GABA, Adbiotech, Korea). The goats were individually housed in a metabolic cage and fed ad libitum with a diet consisting of 60% bermudagrass and 40% commercial concentrate mix. A replicated 3 × 3 Latin square design was used, and each period lasted 4 weeks. The vaccination against FMD was carried out at 2 weeks after the start of each period. Intake, growth performance, nutrient digestibility, hematological response and behavior of the goats were measured before and after vaccination. Although no significant reduction in DMI was observed after the vaccination ($P > 0.05$), the vaccination decreased ADG of the animals ($P < 0.01$). A significant interaction between treatment and vaccination was also observed ($P < 0.05$). Compared with the other treatments, VSR reduced the adverse effect of vaccination for ADG. After vaccination, nutrient digestibility was significantly decreased ($P < 0.01$). The vaccination shortened standing time and extended lying time of the goats. The vaccination also increased the time spent drinking water of the goat ($P < 0.05$). After vaccination, the total number of leukocytes was increased while that of erythrocyte and thrombocyte was decreased ($P < 0.01$). No interaction between treatment and vaccination was observed in nutrient digestibility, goat behavior, and blood cell counts. We concluded that vaccination stress decreased ADG of the goats without depression of diet intake. A reduction in growth performance was primarily due to a decrease in nutrient digestibility. VSR attenuated the adverse effect of vaccination.

Key Words: Korean native goat, vaccination, digestibility

W401 Metabolism of broiler chickens as a function of the rearing period and environmental conditions. S. T. Nascimento*, A. S. C. Maia, M. D. Carvalho, and L. G. Leite, *São Paulo State University (UNESP), Jaboticabal, São Paulo, Brazil.*

The aim of this trial was to settle the metabolism and respiration flow of broiler chickens during the rearing period through indirect calorimetry. Six Cobb broilers allocated in a 6 × 6 Latin square were evaluated for a period of 2 h each during 6 weeks (one evaluation per week). Animals were raised in a climatic chamber, with an average temperature of 23.8°C and 55% of relative humidity. A respiratory mask was developed to measure the tidal volume of broilers coupled to a Spirometer, connected to a flow head with 1 L of capacity, being possible the measurement of respiratory rate and of respiration flow, characterized by the volume of air expired per second. The percentages of oxygen in the inspired air and of carbon dioxide in the expired air from birds were measured, by a connection of the mask to a gas analyzer. The temperature of expired air from birds was measured by a temperature sensor inserted inside the mask. Metabolism (M, W/m^2) of broilers per unit of surface area was obtained through eq.: $M = RF. \{(\Delta O_2.QO_2.0.7633)+(\Delta CO_2.QCO_2.0.2358)\}.A^{-1}$, where RF is the respiration flow, L/s; ΔO_2 is the proportion of oxygen in inspired air, %; QO_2 is the caloric coefficient of oxygen, kJ/L; ΔCO_2 is the proportion of carbon dioxide in expired air, %; Q CO_2 is the caloric coefficient of carbon dioxide, kJ/L; A is the surface area of broilers, m^2. QO_2 and QCO_2 are determined in accordance to respiratory coefficient of birds. Data were tested by analysis of variance and multiple comparison of means by Tukey's test ($P < 0.05$). The statistical model included the effects of schedule of the day, age of broilers, live weight and week of the rearing period. Respiratory flow of broilers was increasing through the rearing period ($P < 0.05$), with an initial respiratory flow of 0.006 L/s in the first week and increasing up to 0.018 L/s in the sixth week of life and it was not influenced by the schedule of the day ($P = 0.2469$). The same was observed for metabolism, which also varied in relation to the body weight and with the age of broilers ($P < 0.05$), air temperature and respiration flow ($P < 0.05$), but not with the schedule of the day ($P = 0.0958$).

Key Words: calorimetry, heat flow, poultry

W402 Methane emission associated to meteorological variables in lambs. A. S. C. Maia*, S. T. Nascimento, R. B. Silva, C. C. M. Costa, and M. D. Carvalho, *São Paulo State University (UNESP), Jaboticabal, São Paulo, Brazil.*

The aim of this trial was to study the influence of environment in methane emissions of lambs in tropical environment. Corriedale lambs (n = 10; 5

males and 5 females) were allocated in a 10 × 10 Latin square (10 animals in 10 different schedules), and each animal was evaluated through one hour per day. The animals were housed during the experimental period, receiving no direct solar radiation. The measurements were done from 8:00 to 18:00. Air and black globe temperatures and air humidity were continuously monitored. Solar radiation was observed through a pyranometer. Heat metabolic production (M, W m^{-2}) was measured through indirect calorimetry. These systems were connected to a facial mask adapted for lambs. The enteric emission of CH_4 (E_{CH4}, L h^{-1}) was monitored by a methane analyzer. Data was submitted to ANOVA (least square method), and the adjusted means were compared by Tukey's test ($P < 0.05$). Statistical analysis considered the effects of sex, animal, day of measurement, schedules of evaluation and its interaction. Respiratory rate and body temperature were higher at 13:00 ($P < 0.05$), respectively of 170 resp.min^{-1} and 40.05°C, which was the schedule of the day with the higher value of solar radiation (800 W.m^{-2}) and air (32°C) and black globe temperatures (35°C). Methane emission in lambs occurs as peaks through the day, and the peaks are more frequent in the first hours of evaluation (morning period, $P < 0.05$), with an average of 8.54 L.h^{-1}, and a reduction in the emission was observed from 11:00 to 15:00 and an increase is observed with a higher intensity after 17:00 ($P < 0.05$), and an average mean of 2.61 L.h^{-1} of methane was observed. The higher values of metabolism were observed between 8:00 and 10:00 ($P < 0.05$). The emission was not continuous through the day, occurring in peaks which are more frequent with the consumption of O_2 and release of CO_2 in each respiration. However, with high air and mean radiant temperatures respiration rate is higher, followed by an increase in tidal volume. This greater volume increased heat loss by respiratory evaporation and a smaller number of methane peaks emission.

Key Words: environment, greenhouse gas, sheep

W403 Influence of trenbolone-estradiol implant level on feedlot performance of hair-sheep. R. Barajas*[1], B. Ortiz[1], and J. J. Alvarez[2], *[1]Facultad de Medicina Veterinaria y Zootecnia, Universidad Autonoma de Sinaloa, Culiacan, Sinaloa, Mexico, [2]Productores de Ovinos de Guanajuato, S.P.R. de R.L., Silao, Guanajuato, Mexico.*

Seven hundred twenty hair sheep (480 ram lambs and 240 ewe lambs) weighing 20.96 ± 0.92 kg, were utilized to evaluate the influence of trenbolone acetate and estradiol ear-implant level on feedlot-performance of hair lambs. Sheep were weighed, grouped by initial weight and sex in 6 blocks of 120 animals, and were placed in 24 elevated pens (4 × 5 m) fitted with plastic-slot floor (30 sheep by pen). Each block was integrated by 4 pens, and the pen constituted the experimental unit. In a complete randomized block design experiment, within a block, pens were randomly assigned to receive one of 4 treatments: (1) No ear implant (CTRL); (2) Ear-implanted with 20 mg of trenbolone and 4 mg of estradiol (T20); (3) implanted with 40 mg of trenbolone and 8 mg of estradiol (T40); and (4) implanted with 60 mg of trenbolone and 12 mg of estradiol (T60). Trenbolone /estradiol levels were obtained with the application of 1, 2 or 3 pellets, from the 6 pellets contained in a regular implant-cartridge of Component TES (Elanco). Sheep were weighed d 1 and 60. Results were analyzed by ANOVA for a randomized complete block design, implanted vs. no implanted sheep were compared using orthogonal contrasts, and the quadratic trend was tested by polynomial contrasts. At the end of the experiment, implanted sheep were 4.3% heavier (34.44 vs. 33.00 kg), and gain 11.5% faster (222 vs. 199 g/d) than CTRL ($P = 0.02$). DMI was not influenced by treatments ($P = 0.73$). Gain:feed ratio was improved 9.4% ($P < 0.01$) in implanted sheep compared with CTRL (212 vs. 195 g/kg). A quadratic response to trenbolone-estradiol implant level on gain:feed ratio was observed ($P = 0.04$), with mean values of 195, 214, 213, and 210 g of gain/kg of DMI for CTRL, T20, T40, and T60 treatments, respectively. It is concluded that trenbolone-estradiol implants improves feedlot-performance of sheep, and that a dose of 20 mg of trenbolone combined with 4 mg of estradiol is enough to produce the maxima feedlot response in hair-sheep

Key Words: feedlot performance, hair sheep, trenbolone

W404 Effects of nursery floor space allowance on body weight and organ characteristics in replacement gilts. S. R. Callahan*[1], M. J. Estienne[1], and A. E. DeDecker[2], *[1]Virginia Tech, Blacksburg, [2]Murphy-Brown LLC, Rose Hill, NC.*

Current research at Virginia Tech focuses on effects of nursery floor space allowance on growth, physiology, and immunology of replacement gilts, with the overall goal of determining if lifetime reproductive performance and sow longevity are affected by conditions to which gilts are exposed early in life. A previous report (Callahan et al., 2013) described a study in which gilts (n = 2,537; BW = 5.6 ± 0.6 kg) were classified by size at weaning and placed in nursery pens of 14, 11 or 8 pigs, resulting in floor spaces of 0.15, 0.19, or 0.27 m^2/pig, respectively; ADG was affected by treatment ($P < 0.01$) and was greatest for gilts allowed 0.27 m^2 floor space each and least for gilts allowed 0.15 m^2. Described here are BW and organ characteristics for a subset of 30 gilts from that experiment. There were 3 to 4 pigs for each combination of size (large, medium, or small) and floor space allowance and data were obtained after 6 wk in the nursery. At harvest, there was a linear effect of floor space ($P < 0.05$) for BW (33.7, 31.8, and 30.4 kg [SE = 1.1 kg] for gilts allowed 0.27, 0.19, or 0.15 m^2/pig, respectively). There was an interaction of size and floor space ($P < 0.01$) for liver weight; Liver weights decreased for large pigs as space allowance was decreased (1330.1, 1093.6, and 1016.7 g [SE = 59.8 g] for gilts allowed 0.27, 0.19, or 0.15 m^2/pig, respectively). There was a linear effect of floor space ($P < 0.01$) for spleen weight, and weights were 79.8, 68.9, and 64.7 g (SE = 4.0 kg) for gilts allowed 0.27, 0.19, or 0.15 m^2/pig, respectively. Kidney and heart weights were not affected by floor space or the interaction of size and floor space ($P > 0.1$). For reproductive organs, weights of the uterus and ovaries, and length and area of the vulva were not affected by floor space, or the interaction of size and floor space ($P > 0.1$), however, the width of the vulva tended ($P < 0.07$) to decrease linearly with decreasing floor space. Further study will determine if these effects influence future reproduction and sow longevity.

Key Words: nursery, floor space, pig

W405 Effect of oxytocin addition to reduced seminal doses using intra uterine AI technique on reproductive performance of sows serviced during summer and autumn in northwest Mexico. J. M. Romo*[1,2], J. A. Romo[1], H. R. Guemez[1,2], and R. Barajas[1], *[1]Facultad de Medicina Veterinaria y Zootecnia, Universidad Autonoma de Sinaloa, Culiacan, Sinaloa, Mexico, [2]Granja Porcina La Huerta, Culiacan, Sinaloa, Mexico.*

Two hundred and 20 3 multi parturient sows were utilized to evaluate the effect of oxytocin addition to reduced seminal doses using intra uterine AI technique on reproductive performance of sows serviced during summer and autumn in the North-West of Mexico. Sows were blocked by parity (3–5) and assigned randomly to be serviced twice with the semen from same boar(s) in one of 2 treatments: (1) Served with a reduced semen dosage equivalent to 1.5×10^9 viable spermatozoa cell diluted in 40 mL of semen dose (CTRL, n = 111); or (2) Control plus addition of 4 IU oxytocin to semen at service time (OX, n = 112). Sows were serviced from June to October 2012, using an intrauterine semen delivery device. The total number born (including mummified fetuses) and total number born alive were counted

at farrowing. As parity have not effect ($P > 0.10$) was removed from the model, and results were compared by ANOVA for a completely randomized design, farrowing date was compared using χ^2 analyses. Treatments had no effect ($P > 0.05$) on litter size (11.0 vs. 10.8) or number born alive piglets (9.8 vs. 9.6). OX increased ($P = 0.03$) 9.6% the farrowing rate, with mean values of 84.68 vs. 93.75% for CTRL and OX, respectively. Results suggest that the addition of 4 IU oxytocin to semen at service time using reduced semen dosage (1.5×10^9 viable spermatozoa cell), improves farrowing rate of multi parturient sows serviced during summer and autumn in the North-West of Mexico, without effect on other reproductive performance variables.

Key Words: artificial insemination, oxytocin, sow

W406 Effect of different gestation housing types on reproductive performance of sows. M. Song[1], S. K. Baidoo[2], J. Kim*[1], H. C. Park[1], and S. W. Seo[1], *[1]Chungnam National University, Daejon, South Korea, [2]Southern Research and Outreach Center, University of Minnesota, Waseca.*

A study was conducted to evaluate effect of housing type on sow performance. A total of 60 sows with mixed parity (218 ± 24 kg BW) were used. During gestation, 28 sows were housed in-group house with electronic sow feeder (space allowance = 1.26 m^2 /sow) and 32 sows were housed in individual stalls (space allowance = 1.8 m^2/sow). Sows from both housing types were moved to farrowing crates on d 109 of gestation and stayed until weaning (18 d post-farrowing). Typical corn-soybean meal diets that met or exceeded nutrient requirements of sows during gestation and lactation were provided to sows. Measurements were reproductive responses of sows after farrowing as well as sow and litter performance during lactation. Sows had similar number of total piglet born regardless of housing type during gestation, but sows in group housing during gestation had more mummies (0.321 vs. 0.064; $P < 0.05$) and stillbirths (0.893 vs. 0.469; $P = 0.073$) than sows in individual stalls during gestation, resulting in difference in the percentage of piglet born alive (90.4 vs. 95.5%; $P < 0.05$). On the other hand, sow and litter performance during lactation was not different between housing types during gestation. In conclusion, group housing for sows during gestation decreased the percentage of piglet born alive by increasing the number of mummies and stillbirths compared with sows housed in individual stalls during gestation.

Table 1. Reproductive performance of sows in different housing (group or individual) types during gestation

Item	Group	Individual	SEM	*P*-value
Sows, no.	28	32		
Total piglet/litter, no.	11.86	11.94	0.59	0.921
Mummies/litter, no.	0.32	0.06	0.08	<0.05
Stillbirth/litter, no.	0.89	0.47	0.15	0.073
Piglet born alive/litter, no.	10.64	11.38	0.54	0.325
Piglet born alive/litter, %	90.42	95.54	1.52	<0.05

Key Words: housing type, reproductive performance, sow

W407 Rectal temperature and infrared thermography of the eye in Nellore beef cattle. A. M. Mobiglia, F. R. Camilo, T. S. Almeida, M. D. Freitas Neto, V. R.M. Couto*, J. C. Pimenta, B. J. M. Lemos, and J. J. R. Fernandes, *Universidade Federal de Goias, Goiania, Goias, Brazil.*

The use of infrared thermography to non-invasively measure animal temperature could minimize the stress caused by aversive procedures used routinely on feedlot. The objective of this study was to correlate the rectal temperature and infrared thermography of the eye in Nellore beef cattle. Therefore, 120 Nellore bulls (393.04 ± 47.30 kg of BW), with average of 20 mo of age, were placed in individual pens. The infrared thermography of the eye was performed using an infrared portable camera (FLIR I7 of Flir Systems Inc.) calibrated with an emissivity value (ε) of 0.95 and spectrum between 7.5 and 13μm. All infrared thermography of the eye was taken approximately 0.5m from the location studied. The infrared thermography of the eye was interpreted using Flir Tools Software (Program version 2.0), on option "iron," and temperature ranging from 0°C to 50°C, with thermal sensibility of ± 1°C. In all photographs, a specific shape (circle) was considered to keep a constant sub-area (eye surface), and the average (°C) was computed. The rectal temperature was measured with a digital thermometer, simultaneously with the infrared thermography of the eye. The data of infrared thermography of the eye and rectal temperature were analyzed by Pearson correlation using statistical software R (R Development Core Team, 2010). The data regarding infrared thermography of the eye and rectal temperature were 35.63 ± 1.60°C and 38.39 ± 0.61°C, respectively. The infrared thermography of the eye ranged between 39.30°C and 31.50°C, whereas, the rectal temperature ranged between 40.30°C and 37.20°C (maximum and minimum). There was significant correlation ($P < 0.05$) between infrared thermography of eye and rectal temperature (0.53). Therefore, the infrared thermography of the eye could estimate the body temperature of Nellore beef cattle.

Key Words: beef cattle, infrared thermography, physiology parameter

W408 Evaluation of a 3-dimensional camera system to measure feed intake. A. N. Shelley[1], D. N. Lau[1], A. E. Sterrett*[2], and J. M. Bewley[2], *[1]University of Kentucky, Department of Electrical and Computer Engineering, Lexington, [2]University of Kentucky, Department of Animal and Food Sciences, Lexington.*

Individual dairy cow feed intake measurements are difficult to obtain. Three-dimensional (3D) imaging using cameras over the feed bunk could be connected to individual animal identification tags to provide automated daily feed intake. The objective of this study was to evaluate the potential utility of a 3-D camera system to measure feed intake. Daily feed weights were obtained from an analog scale and a novel 3D scanning system from January 7 to 26, 2013, at the University of Kentucky Coldstream Dairy. Individual feed bins filled with a lactating cow TMR were provided for each tie-stall housed lactating cow. Data from 272 feed bins were collected from the same 7 cows over the study period. Scale weights (SW) were recorded for each bin of fresh feed each day and for orts the day after. Image weights (IW) were obtained from a 3D image of the bin, using a 3D scanning system with structured light illumination. A computer, connected to a projector enclosed in black plastic to prevent ambient light entrance, created white and black striped frequency patterns on the surface of the feed. Based upon the shifts and distortions in the light and dark boundaries of the frequency patterns on the surface of the feed, QT software GmbH (Berlin, Germany) created a 3D textural surface image of the feed. The collected data points were then triangulated and averaged using MATLAB (The MathWorks Inc., Natick, MA) to create an output image value which was then placed in a linearly correlated equation to create an IW value in Excel 2010 (Microsoft, Redmond, WA). All IW and SW were recorded in Excel 2010. The CORR procedure of SAS 9.3 (SAS Institute, Inc., Cary, NC) was used to calculate the Spearman rank correlation between the SW and IW. Image weights were highly correlated with SW with R = 0.97 ($P < 0.01$; n = 272). Mean (±SD) weights were 16.73 ± 9.53 and 17.03 ± 9.10 kg for the IW and SW, respectively. Development of this imag-

ing technique represents a breakthrough toward using image analysis to measure feed intake.

Key Words: image analysis, feed intake, 3D imaging

W409 Factors affecting rectal and vaginal temperature in Holstein × Zebu crossbred cows in northeastern Brazil. A. N. Costa[2], A. A. Araujo[2], J. V. Feitosa[2], P. A. Montezuma Jr.[2], and K. N. Galvão*[1], *[1]University of Florida, Gainesville, [2]Universidade Federal do Ceará, Fortaleza, CE, Brazil.*

Objectives were to evaluate factors affecting rectal (RT) and vaginal temperature (VT) in the Northeastern region of Brazil. Measurements (n = 2016) of RT and VT were taken at the time of AI from 798 3/4 Holstein × 1/4 Gir and 197 1/2 Holstein × 1/2 Zebu (Gir/Gyr) cows from one dairy from March to December 2011. Apart from information on breed composition, season (dry = Jul-Dec or rainy = Mar-Jun) and the time of day temperatures were measured (morning = 6:00–12:00 h; afternoon = 12:00–18:00 h; night = 18:00–6:00 h) were collected. Data were analyzed using the MIXED procedure of SAS. Cow was included as a random variable. Results are presented as means ± SE. There was high correlation between RT and VT (VT = 1.46 + 0.969 × RT; R-Sq = 92%; $P < 0.001$); however, VT was higher than RT (38.8 ± 0.01 vs. 38.5 ± 0.01°C; $P < 0.001$). Breed composition, season, and time of day affected ($P < 0.001$) RT. Cows with 3/4 Holstein had higher RT than 1/2 Holstein cows (38.6 ± 0.01 vs. 38.4 ± 0.03°C; $P < 0.001$). RT was higher ($P < 0.001$) in the afternoon (38.8 ± 0.01°C) than in the morning (38.3 ± 0.03°C) or night (38.3 ± 0.01°C), but only tended ($P = 0.1$) to be higher in the morning than at night. RT was higher in the rainy season than in the dry season (38.5 ± 0.02 vs. 38.4 ± 0.02°C; $P < 0.0001$). Breed composition and time of day affected ($P < 0.001$) VT. Similar to RT, cows with 3/4 Holstein had higher VT than 1/2 Holstein cows (38.8 ± 0.01 vs. 38.6 ± 0.03°C; $P < 0.001$), and VT was higher ($P < 0.001$) in the afternoon (39.0 ± 0.01°C) than in the morning (38.6 ± 0.03°C) or night (38.5 ± 0.02°C), but only tended ($P = 0.07$) to be higher in the morning than at night. In conclusion, 3/4 Holstein crossbred cows are less capable of thermoregulating than 1/2 Holstein cows.

Key Words: thermoregulation, crossbred, dairy cow

W410 Effects of seasonality on rectal temperature and conception rate in crossbred dairy cows. F. R. Souza[1], T. H. Silva[1], B. G. Alves[1], J. O. Jacomini[1], L. Z. Oliveira[2], and R. M. Santos*[1], *[1]Universidade Federal de Uberlândia, Uberlândia, Minas Gerais, Brazil, [2]UNIRP - Centro Universitário de Rio Preto, São José do Rio Preto, São Paulo, Brazil.*

Heat stress reduces reproductive efficiency in dairy cows due to negative effects on heat detection, oocytes and embryo development. Holstein/Gir crossbred dairy cows are better adapted to hot environments, and thus have less negative effects of heat stress on reproductive performance. The objective of this study was to evaluate effects of seasonality on rectal temperature (RT) and conception rate (CR) in crossbred dairy cows. We analyzed 1219 inseminations of dairy cows from a commercial farm with 480 crossbred Holstein/Gir lactating cows located in the hot climate of Minas Gerais State, Brazil. Cows were maintained on pasture during the rainy season and in loose housing in the dry season and produced 18.75 kg of milk/day. The herd was routinely subjected to a fixed-time AI protocol (TAI) and early pregnancy diagnosis by ultrasound. The rectal temperature was measured at AI by a digital thermometer. The effects of season (autumn/winter vs. spring/summer) and timing of AI (morning vs. afternoon) on RT were analyzed by ANOVA using the SAS program. The effects of season, time of AI and adjusted RT (RT below vs. above average) on CR were analyzed by logistic regression using the SAS program. The average RT was 39.4°C. The RT and CR were affected ($P < 0.01$) by season, i.e., in the hot season crossbred dairy cows had higher RT (39.4 ± 0.56 vs.39.3 ± 0.59°C) and lower CR (25.5 vs. 31.8%). Cows with RT >39.4°C had lower ($P = 0.001$) conception rate (25.8 vs. 32.5%) than cows with RT <39.4°C. The time of AI affected ($P < 0.01$) RT and CR; cows inseminated in morning had lower RT (38.9 ± 0.49 vs. 39.6 ± 0.50°C) and higher CR (32.9 vs. 26.1%) than cows inseminated in afternoon. In conclusion, crossbred dairy cows also had higher rectal temperature and lower conception rate during the hot season, and insemination should be performed in the morning in TAI programs. Supported by CAPES/CnPQ/PROPP-UFU.

Key Words: heat stress, reproduction efficiency, dairy cow

W411 An evaluation of electrical conductivity as a practical tool in mastitis detection. C. Meisar, J. Thayer, and K. Koudele*, *Andrews University, Berrien Springs, MI.*

The electrical conductivity (EC) of cow milk usually increases before or during a bout of clinical mastitis (CM). Technology to detect the changes in EC has been incorporated into commercial milking equipment to facilitate the early detection of mastitis during the milking process. The objective of this study was to determine if this technology was of practical use to the employees of the 750-head dairy farm at Andrews University. EC data was collected from cows with at least one episode of CM during d 3–305 of their lactation (n = 89). To establish a physiological baseline for each cow, a 10-d rolling EC average of each cow was determined. Any increase in EC >20% (percentage recommended by the Afimilk system) above the baseline was marked as a "spike." If a spike was followed within 10 d by an episode of CM then it was a "true alarm." If not, then it was a "false alarm." A "false negative" was CM occurring without a preceding spike. A "true negative" was anytime a cow did not have a spike or CM. Bayes' theorem was applied to the probability of spikes and incidence of CM: P(M|S) = P(S|M) P(M) / P(S|M)P(M) + P(S|NM)P(NM) where P(M|S) is the probability of CM given that there was a spike, P(S|M) is the probability of a spike given that there was CM (true alarms), P(S|NM) is the probability of a spike but no CM (false alarms), P(M) is the probability of a cow having CM as determined by averaging the daily percentage of cows in the herd with CM, and P(NM) is the probability of a cow not having mastitis [1- P(M)]. A spike correctly predicted CM in 29.615% of cases but was a false alarm for 70.385%. Episodes of CM were correctly predicted by spikes 52.294% of the time while 47.706% of the episodes were unpredicted. Therefore, P(M|S) = 0.1059%. Lowering the sensitivity to changes in EC from 20% to 15% resulted in a 60% increase in true alarms but also a 75% increase in false alarms. It is therefore concluded that the EC change detection technology was not a good enough predictor of CM to be used by the milking parlor employees to catch CM in its early stages.

Key Words: electrical conductivity, mastitis, Bayes' theorem

W412 Use of infrared thermography in determining the surface temperature of quail eggshell during incubation. T. C. Santos, P. A. Bustos MacLean*, A. E. Murakami, J. F. Mello, and C. Souza, *State University of Maringa, Maringa, Parana, Brazil.*

This study aimed to evaluate the behavior of the eggshell temperature surface of the of European quail (24 weeks) along the incubation by

infrared thermography. The eggshell temperature was assessed in fertile (n = 60) and infertile (n = 25, 13.26 ± 0.11g) eggs. Fertile eggs were sorted by weight into 3 groups: small (12.68 ± 0.14g), medium (13.49 ± 0.14g) and large (14.31 ± 0.16g). The eggs were incubated in an automatic incubator with fixed relative humidity (60%) and temperature (37.6°C). The temperature of the eggshell was recorded every 24 h for 15 consecutive days with a thermographic camera Fluke Model Ti110. The images were taken 20cm from the lateral surface of the eggs and they were analyzed by the program SmartView 3.2. The temperature was measured at the midpoint of the outer surface of the eggshell. The eggshell temperature of infertile eggs had a quadratic behavior ($y = 35.075+0.0128day-0.00003day^2$, $R^2 = 0.39$). This was probably due to weight loss by dehydration of infertile eggs that lost temperature by evaporation for the incubator environment. These eggs had an average temperature of 36.11 ± 0.79°C. In fertile eggs, the temperature of the eggshell differed among weight classes, with increasing linear behavior for small eggs ($y = 36.567+0.00132day$, $R^2 = 0.39$) and medium ($y = 36.576+0.0018day$, $R^2 = 0.32$) and quadratic ($y = 35.679+0.0093day-0.000015day^2$, $R^2 = 0.39$) for large eggs. The eggshell's temperature remained below air temperature and, in the last days of incubation there was metabolic caloric heat elevation, which caused a higher eggshell temperature. It is concluded that the temperature of the eggshell in European quails can be measured by infrared thermography and this methodology useful in incubation researches.

Key Words: European quail, infrared thermography, incubation

W417 Effect of chromium supplementation on performance of feedlot lambs. T. M. C. Leme*, E. A. L. Titto, C. G. Titto, C. A. S. Bonato, D. L. Jimenez Filho, and S. L. Silva, *Faculdade de Zootecnia e Engenharia de Alimentos, Universidade de São Paulo, Pirassununga, São Paulo, Brazil.*

Recent experiments have demonstrated that chromium supplementation improves weight gain and immune function and reduces morbidity of animals. The aim of this study was to evaluate effect of chromium supplementation on weight gain, DMI, and feed efficiency of feedlot lambs. Sixty-four crossbred White Dorper × Santa Ines lambs (initial BW 18.4 ± 4.7 kg, 60 d old) were allotted to individual pens and confined for 60 d, preceded by 7 d of adaptation. During confinement, all animals received the same diet containing 30% corn silage and 70% concentrate composed primarily of corn, soybean meal and mineral mix, delivered daily at 08:00. The animals were divided into 2 groups, one group in which each animal received 2 mg daily of supplemental organic chromium in the mixed diet with 30 g extra fine corn meal (SC), and a control group (CO) that received only 30 g extra fine corn meal (without supplementation with organic chromium). Feed offered and orts were recorded daily, and weight gain, DMI, and feed efficiency were determined. Animals were weighed at the beginning of the trial and every 14 d. Animal performance was analyzed by ANOVA, considering treatment as fixed effect and sex as random effect. There was no significant effect ($P > 0.05$) of daily supplementation of chromium on BW gain, DMI and feed efficiency. Average weight gain (ADG) in this study was 0.225 kg/d for CO and 0.235 kg/d for SC ($P = 0.373$). The DMI was 1.15 kg/d for the CO and 1.25 kg/d for SC group ($P = 0.288$). Feed efficiency values were 0.198 kg weight gained per kg feed for CO and 0.199 kg weight gained per kg feed for SC ($P = 0.288$). The supplementation of 2 mg per d of chromium did not affect weight gain, DMI and feed efficiency of lambs.

Key Words: dry matter intake, feed efficiency, weight gain

W418 Effects of levels of Boer goats and Dorper sheep on feed intake, digestibility, growth, and slaughter characteristics in the central highlands of Ethiopia. T. Mekonnen[1], K. Kefelegn[2], G. Abebe[3], and A. L. Goetsch*[4], *[1]Sirinka Agricultural Research Center, Sirinka, Ethiopia, [2]School of Animal and Range Sciences, Haramaya University, Haramaya, Ethiopia, [3]Ethiopia Sheep and Goat Productivity Improvement Program, Addis Ababa, Ethiopia, [4]American Institute for Goat Research, Langston University, Langston, OK.*

Twenty-seven male goats (6–9 mo) and 27 male sheep (3–5 mo) were used in 90-d experiments. Animals were indigenous or local goat and sheep genotypes of the central highlands of Ethiopia (LG and LS, respectively) and crossbreds of local with 25 and 50% Boer (B) goats or Dorper (D) sheep. Grass hay (9% ash, 6% CP, and 64–67% NDF) was consumed ad libitum supplemented with 2% BW (DM basis) of concentrate (46% noug seed cake, 28% wheat bran, 24% sorghum grain, and 2% salt; 8% ash, 24% CP, and 24% NDF). Initial BW was 18.1, 20.8, and 24.9 kg for Local, 25%B, and 50%B, respectively (SE = 0.77) and 14.8, 20.3, and 17.9 kg for Local, 25%D, and 50%D, respectively (SE = 0.74). Total DMI ranked ($P < 0.05$) LG <25%B <50%B (675, 763, and 891 g/d) and LS <50%D <25%D (810, 1120, and 980 g/d for LS, 25%D, and 50%D, respectively). Goat ADG was greatest ($P < 0.05$) for 50%B (32, 32, and 53 g for LG, 25%B, and 50%B, respectively) and of sheep was least ($P < 0.05$) for LS (89, 132, and 126 g for LS, 25%D, and 50%D, respectively). Empty BW of goats at slaughter (17.6, 20.7, and 24.3 kg) and hot (9.0, 10.9, and 12.8 kg) and cold carcass weights (8.7, 10.4, and 12.3 kg for LG, 25%B, and 50%B, respectively) ranked ($P < 0.07$) LG <25%B <50%B. Slaughter BW of sheep was 22.8, 32.7, and 31.8 kg for LS, 25%D, and 50%D, respectively (SE = 1.04). Likewise, hot (10.3, 16.6, and 15.3 kg) and cold carcass weights (9.9, 16.2, and 14.9 kg for LS, 25%D, and 50%D, respectively) were lowest for LS ($P < 0.05$). In addition to the difference between 25%B and LG, these results show potential for greater meat yield with 50 vs. 25%B, which would be due to both the greater level of heterosis and higher level of B breeding. The findings also depict considerable opportunity for increased meat production by crossbreeding with D. However, greater benefit was not realized with 50 than 25%D as expected. Nonetheless, the results provide an example of marked improvement in performance possible with 25%D and, presumably, there would be little or no difference in adaptation to harsh production conditions between LS and 25%D.

Key Words: goat, sheep, breed

W421 Effects of level and length of supplementation on carcass amounts and percentages of ash, N, water, total fat, and energy. R. C. Merkel*, T. A. Gipson, Z. Wang, and A. L. Goetsch, *E (Kika) de la Garza American Institute for Goat Research, Langston University, Langston, OK.*

Spanish (S; 28 to 40 wk of age) and Boer (B; 33 to 46 wk) wethers were used to determine effects of level and length of supplementation on carcass amounts and concentrations of ash, N, water, fat and energy. The completely randomized experiment had 110 and 108 d periods (PR). Wethers resided on pastures with free-choice alfalfa hay and supplemented with 0.5 or 1.5% BW (SL; DM basis; L and H, respectively) of a pelleted diet (16% CP, 60% TDN). Five S and 6 B were harvested initially, and 12 per breed (BR) and SL after PR 1 and 2. There were BR differences ($P < 0.05$) in initial BW (33.3 and 23.7 kg), carcass weight (15.4 and 10.9 kg) and amounts of ash (0.71 and 0.45 kg), protein (3.49 and 2.24 kg), fat (3.31 and 2.16 kg), and energy (211 and 137 MJ) for B and S goats, respectively. On a carcass basis B goats had a lower ($P < 0.05$) level of water (51.3 and 55.2%) but more energy than S goats (13.6 and 12.2 MJ/kg). H goats had greater ($P \leq 0.05$) ash (0.97 and 0.87 kg), protein (4.1 and 3.5 kg), and water (12.7 and 11.5 kg) than L goats. H goats in PR2 had greatest ($P < 0.05$) amounts of fat (4.04, 3.65, 6.31, and 4.19 kg; SEM = 0.321) and energy (255, 227, 340, and 243 MJ for PR1H, PR1L, PR2H, and PR2L, respectively; SEM = 15.3), with corresponding differences in % carcass fat and energy/kg carcass. B goats had greater ($P < 0.05$) ash (1.03 and 0.80 kg), water (13.7 and 10.5 kg), fat (5.79 and 3.32 kg), and energy (327 and 206 MJ) than S goats. Carcass protein was greater in B goats in PR1 than PR2 and greater than amounts in S goats (4.58, 4.01, 3.37, and 3.17 kg for PR1B, PR2B, PR2S, and PR1S, respectively; SEM = 0.177; $P < 0.05$). Carcass protein percentage was lowest ($P < 0.05$) for H goats in PR2 (20.1, 18.8, 16.0, and 16.9%, for PR1B, PR1S, PR2B, and PR2S, respectively). The differences in component amounts are in accord with those seen in carcass weight (23.6 and 20.4 kg for H and L; 25.5 and 18.5 kg for B and S; 20.3 and 23.8 kg for PR 1 and 2, respectively). Supplementation and period led to increased weights of carcass components and B goats accumulated fat in the carcass to a greater extent than S goats.

Key Words: meat goat, breed, supplement

W422 Effect of *Jatropha curcas* meal (nontoxic) substituted for soybean meal on apparent digestibility and energy concentration of feed in growing Pelibuey sheep. A. Estrada-Angulo*[1], M. A. Angulo-Escalante[2], J. J. Portillo[1], R. Gutierrez-Dorado[3], A. Rubio-Angulo[1], C. Castro-Martinez[4], F. G. Rios[1], and A. Plascencia[5], *[1]FMVZ-UAS, Culiacan, Sinaloa, Mexico, [2]CIAD-Culiacan, Culiacan, Sinaloa, Mexico, [3]FCQB-UAS, Culiacan, Sinaloa, Mexico, [4]CIIDIR-IPN, Guasave, Sinaloa, Mexico, [5]IICV-UABC, Mexicali, Baja California, Mexico.*

The objective of this study was to determine the effect of nontoxic *Jatropha curcas* meal (JCMNT) as a substitute for soybean meal on apparent digestibility and energy concentration of feed in growing sheep. Twenty male Pelibuey sheep (26.5 ± 0.5 kg) individually housed for 20 d were used in a randomized complete block experiment (blocking by live weight). Dietary treatments were 1) control (without JCMNT), 18.02% CP and 3.60 Mcal DE/kg, and contained 30.0% Sudan hay, 40.5% cracked corn, 15.0% soybean meal, 2.0% zeolite, 10.0% sugarcane molasses, and 2.5% mineral premix; 2) control plus JCMNT, 17.80% CP and 3.58 Mcal of DE/kg, and contained 2.5% JCMNT and 12.5% soybean meal; 3) control plus JCMNT, 17.60% CP and 3.56 Mcal of DE/kg, and contained 5.0% JCMNT and 10.0% soybean meal; 4) control plus JCMNT, 17.40% CP and 3.54 Mcal of DE/kg, and contained 7.5% JCMNT and 7.5% soybean meal; and 5) control plus JCMNT, 17.20% CP and 3.52 Mcal of DE/kg, and contained 10.0% JCMNT and 5.0% soybean meal. The DMI was adjusted to 614 g/d/head (307 g am and 307 g pm). The DM excreted in feces was similar ($P > 0.05$) in control group compared with JCMNT treatments (151.5 vs. 160.8 g/day/head). The apparent digestibility of DM for control and JCMNT treatment groups was similar ($P > 0.05$), with 75.35 and 73.77%, respectively. The DE concentrations were not significantly different ($P > 0.05$) between control and JCMNT treatment groups (3.22 vs. 3.15 Mcal/kg of DM, respectively). The observed/expected DE ratio was similar for JCMNT treatment groups (0.95), but the control treatment group had a ratio of 1.01. These results indicate that the calculated energy of JCMNT was overestimated in this experiment. It is concluded that JCMNT can be substituted for soybean meal for up to 10% of the diet without affecting apparent digestibility of DM and energy concentration in diets for growing Pelibuey sheep. Further, JCMNT had similar energy value as soybean meal when included in diets for growing hair sheep.

Key Words: apparent digestibility, *Jatropha curcas* meal, Pelibuey sheep

W423 Mineral requirements for growth of female Saanen goat kids. F. O. M. Figueiredo*, T. T. Berchielli, K. T. Resende, A. M. Mobliglia, and I. A. M. A. Teixeira, *Univ Estadual Paulista, Jaboticabal, Sao Paulo, Brazil.*

Mineral retention depends on the composition of weight gain (bones, muscles and fat). In general, greater fat deposition reduces mineral deposition and, consequently, mineral requirements of animals. Factors such as sex, breed, age and diet can affect mineral composition and net mineral requirement for weight gain. Recently, few studies have focused on the mineral requirements of goats; however, studies with female goats are scarce. The objective of this study was to estimate the macromineral (Ca, P, Mg, K and Na) net requirements for growth of female Saanen goat kids using the comparative slaughter technique. A total of 18 female Saanen goat kids with BW ranging from 30 to 45 kg were used. At the beginning of the experiment 6 animals at 30.1 ± 0.22 kg BW were slaughtered. Another 6 kids were slaughtered at 38.3 ± 0.38 kg BW and the remaining 6 kids were slaughtered at 45.5 ± 0.13 kg BW. Animals were fed ad libitum. Logarithmized allometric equations were used to calculate macromineral body composition through the relationship between macromineral content and EBW based on the following equations: Log Ca, g = 1.27 + 0.78 × Log EBW; Log P, g = 1.30 + 0.74 × Log EBW; Log Mg, g = −0.13 + 0.81 × Log EBW; Log Na = −0.30 + 0.71 × Log EBW; Log K = 0.57 + 0.782 × Log EBW. Body Ca decreased from 9.21 to 8.27 g/kg EBW; P decreased from 8.68 to 7.65 g/kg EBW; Mg decreased from 0.40 to 0.37 g/ kg EBW; Na decreased from 0.20 to 0.17 g/kg EBW; K decreased 1.52 to 1.32 g/kg EBW, as body weights increased from 30 to 45 kg. Net macromineral requirements for growth decreased from 7.18 to 6.45 g Ca; 6.42 to 5.66 g P; 0.33 to 0.30 g Mg; 0.14 to 0.12 g Na and 1.11 to 0.97 g K/kg of EBW as BW of for the females kids increased from 30 to 45 kg.

Key Words: body composition, gain, macromineral

W424 Effect of *Jatropha curcas* kernel (nontoxic) substituted for soybean meal on productivity and carcass characteristics in finishing Pelibuey sheep. A. Estrada-Angulo*[1], M. A. Angulo-Escalante[2], J. C. Robles[1], I. Contreras[3], H. Davila[1], L. E. Sanchez-Ramirez[1], H. Landeros-Lopez[1], B. I. Castro[1], F. G. Rios[1], and A. Plascencia[4], *[1]FMVZ-UAS, Culiacan, Sinaloa, Mexico, [2]CIAD-Culiacan, Culiacan, Sinaloa, Mexico, [3]FCQB-UAS, Culiacan, Sinaloa, Mexico, [4]IICV-UABC, Mexicali, BC, Mexico.*

To determine the effect of substituting ground nontoxic *Jatropha curcas* kernel (JCKNT) for soybean meal on productivity and carcass characteristics in finishing sheep, 15 male Pelibuey sheep (28.4 ± 1.5 kg) were used in a completely radomized design with the following dietary treatments: (1) control (without JCKNT), 18.02% CP and 3.60 Mcal DE/kg, and contained 30.0% Sudan hay, 40.5% cracked corn, 15.0% soybean meal, 2.0% zeolite, 10.0% sugarcane molasses, and 2.5% mineral premix; (2) control plus JCKNT, 17.02% CP and 3.64 Mcal of DE/kg, and contained 5.0% JCKNT and 10.0% soybean meal; and (3) control plus JCKNT, 16.02% CP and 3.68 Mcal of DE/kg, and contained 10.0% JCKNT and 5.0% soybean meal. Final live weight (FLW), ADG, slaughter weight (SW), hot carcass weight (HCW), Longissimus muscle (LM) area, fat thickness (FT), kidney-pelvic fat (KPF), carcass total fat (CTF), and carcass tissue were determined. FLW was similar ($P > 0.05$) among treatment groups (33.93, 33.55 and 33.61 kg for treatments 1, 2, and 3, respectively). ADG was also similar ($P > 0.05$) for the 3 treatments (177, 169 and 171 g/d). HCW (19.58, 19.31 and 18.68 kg) and KPF (1.35, 1.11 and 1.34%) values were not different ($P > 0.05$) among treatment groups. Total muscle in carcass (67.21, 64.86, and 63.87%), FT (3.37, 2.73, and 2.45 mm), and LM area (14.80, 13.22 and 12.29 cm^2) decreased ($P < 0.05$) with increasing levels of JCKNT in the diet. CTF (11.89, 12.81, and 13.36%) and total bone (20.64, 21.80, and 22.10%) increased with increasing levels of JCKNT in the diet. It is concluded that ground JCKNT can be a substitute for soybean meal at up to 10% of the diet without affecting FLW, ADG, HCW, and KPF. However, JCKNT inclusion modified some other carcass characteristics in finishing hair sheep.

Key Words: carcass characteristic, *Jatropha curcas* kernel, Pelibuey sheep

W425 Effects of short-term oligofructose-enriched inulin supplementation on growth performance and selected fecal characteristics of weanling Saanen kids. C. Kara*[1], Y. Meral[1], H. Biricik[1], A. Orman[2], H. Gencoglu[1], I. Cetin[1], D. Yesilbag[1], G. Deniz[1], and I. Turkmen[1], *[1]Uludag University, Faculty of Veterinary Medicine, Department of Animal Nutrition and Nutritional Diseases, Bursa,*

Turkey, [2]Uludag University, Faculty of Veterinary Medicine, Department of Zootechnics, Bursa, Turkey.

Twenty-four Saanen kids (44 ± 1 d of age) were used to study the effects of oligofructose-enriched inulin supplementation on growth performance, fecal score, fecal pH, and fecal SCFA concentrations. Kids were sorted by parity of their dams and their BW at the beginning of the study and assigned to 1 of 2 groups (control; CG and experimental; EG) at 44 ± 1 d of age. Each group consisted of 12 kids (6 males and 6 females). Kids were weaned early, at 48 ± 1 d of age. Each kid in EG was supplemented with 0.8 g/d and 1.6 g/d of chicory inulin powder enriched by a specific fraction of oligofructose (Orafti Synergy1, BENEO-Orafti S.A., Belgium) from d 1–5 and from d 6–15, respectively, while kids in CG did not receive oligofructose-enriched inulin. Data were analyzed using Statistical Package for the Social Sciences software (SPSS, 2004). There were no differences ($P > 0.05$) in BW, average daily feed intake, and feed efficiency for the whole period between groups. Average daily weight gain (ADG) during d 1–5 was higher for EG ($P < 0.01$), while no differences were observed during d 6–15 and d 1–15 ($P > 0.05$). Fecal score and fecal pH were not different ($P > 0.05$) between groups. Oligofructose-enriched inulin supplementation did not adversely affect fecal score. The amounts of acetate, propionate, and total SCFA (acetate + propionate + butyrate) in feces did not differ ($P > 0.05$) between groups, whereas fecal butyrate concentration tended to be higher ($P = 0.05$) in EG. Because of a tendency to increase fecal butyrate concentration in EG, oligofructose-enriched inulin supplementation may be useful during the intestinal infections with epithelial damage and colonic inflammation.

Key Words: fecal characteristic, growth performance, oligofructose-enriched inulin

W426 Apparent digestibility of dry matter and nutrients from lambs fed diets with or without glycerin. E. M. de Oliveira*, J. M. B. Ezequiel, V. C. Santos, A. P. D'aurea, M. T. CA. Costa, A. C. Homem Junior, V. B. Carvalho, J. R. Paschoaloto, E. H. Fernandes, and C. S. Costa, *Universidade Paulista Júlio de Mesquita - Unesp.*

The aim of this study was to evaluate the apparent digestibility of DM and nutrients in feedlot finished lambs fed diets with or without glycerin. A total of 40 Santa Inês × Dorper intact male lambs (average BW = 21 kg) were kept in confinement stalls and fed Tifton 85 bermudagrass hay as forage, and corn grain, soybean meal, calcarium and mineral premix as concentrate in the ratio 20:80. Experimental diets were G0 - control without glycerin and G10 - 10% glycerin as part of the concentrate. Internal indicator indigestible neutral detergent fiber (iNDF) was used to estimate the values of dry matter digestibility and nutrients. Diet, orts, and fecal samples were collected in first 5 d of the fourth week of the performance test. The samples were composited by animal, oven-dried at 55°C for 72 h for determination of DM, and ground in a Wiley mill to 1 mm for subsequent incubation. The iNDF levels were measured after 264 h of incubation in situ using nylon bags (14 × 7 cm) containing 5 g of the sample. After that, the bags were washed and treated with neutral detergent. The residue was assumed as iNDF. The experimental design was randomized block with 2 treatments and 20 replications, and means were compared by Tukey test at 5% probability. There was a significant reduction ($P < 0.05$) in digestibility of neutral detergent fiber (NDF) in the G10 group. The glycerin, by not having cell wall, has a higher rate of degradation than other energy sources from grains, but in less time. There was no effect ($P < 0.05$) on the digestibility of DM, OM, CP, EE and ADF. Inclusion of 10% glycerin in diet resulted in decreased NDF digestibility, without impairing the digestibility of other nutrients, including DM and OM.

Key Words: biodiesel, co-product, sheep

W427 Blood metabolite and rumen VFA concentrations of lambs fed a diet containing artichoke (*Cynara scolymus*). M. Dehghani-Sanij*, A. Afzalzadeh, K. Rezayazdi, and M. A. Norouzian, *University of Tehran, Tehran, Iran.*

The objective of this experiment was to evaluate the effects of replacing alfalfa hay by artichoke (*Cynara scolymus*) hay on certain blood metabolites, rumen pH, and VFA concentrations in Lori-Bakhtiary lambs. Fourteen Lori-Bakhtiary lambs (30 ± 3.2 kg of initial BW; mean ± SD) were penned individually and used in a completely randomized design with 2 treatments and 7 lambs in each. One group received alfalfa hay as roughage (control; alfalfa 30%, wheat straws 15% and concentrate 55%) and the other group received artichoke (*Cynara scolymus*; test group) hay, which was used in full replacement of alfalfa hay during 78 d. Significant effects ($P < 0.05$) for blood cholesterol (57.4 ± 7 (control) and 46.9 ± 8 (test group) mg/dL) and triglycerides (70.9 ± 10 (control) and 60.7 ± 6 (test group) mg/dL) were observed due to artichoke hay inclusion in the diet. Blood total protein and glucose concentration did not differ between the experimental groups. Treatment did not affect minimum pH, mean pH, maximum pH, standard deviation of mean pH, and duration or area under pH 5.8, indicating that inclusion of artichoke hay did not appear to affect rumen pH. Inclusion of artichoke hay in the diet did not affect total VFA (92.4 ± 2 8.2 and 82.1 ± 14.2 mmol/L in control and test groups, respectively) and individual VFA concentrations in rumen liquor. The acetate, propionate, butyrate, valerate, and iso-valerate in control were 53.4 ± 13.4, 23.15 ± 12.3, 12.46 ± 4.76, 2.03 ± 0.91, and 1.33 ± 0.78 mmol/L, respectively, and in the test group, the concentrations were 51.6 ± 10.2, 18.18 ± 7.1, 9.42 ± 2.4, 1.9 ± 0.55, and 1.02 ± 0.47 mmol/L, respectively. In conclusion, alfalfa hay can be replaced by artichoke hay in the diet of growing Lori-Bakhtiary lambs with no adverse effects on blood metabolites, rumen pH, and VFA concentrations.

Key Words: alfalfa hay, artichoke hay, rumen pH

W428 Mineral metabolism in Saanen and Oberhasli goats during pregnancy. C. J. Härter*[1], A. R. Rivera[1], D. S. Castagnino[1], L. D. Lima[1], H. G. O. Silva[1], A. M. Nunes[1], S. Sgavioli[1], S. M. B. Artoni[1], A. Liesegang[2], N. St-Pierre[3], K. T. Resende[1], and I. A. M. A. Teixeira[1], *[1]Department of Animal Sciences, Universidade Estadual Paulista, Jaboticabal, SP, Brazil, [2]Institute of Animal Nutrition, University of Zurich, Zurich, Switzerland, [3]Department of Animal Sciences, The Ohio State University, Columbus.*

During pregnancy, the maternal body undergoes significant physiological changes. Thus the objective of this study was to evaluate the effect of number of fetuses on physiological changes of calcium (Ca), phosphorus (P), magnesium (Mg), sodium (Na) and potassium (K) during the gestation period for Saanen and Oberhasli goats. The 42 goats used (49.5 kg ± 7.6 BW) were fed ad libitum and distributed in a completely randomized design in a 2 × 2 x 3 factorial as follows: 2 breeds (Oberhasli and Saanen), 2 types of pregnancy (single and twin) and slaughtered at 3 gestation periods (80, 110 and 140 d). Digestibility assays were performed at 50, 80, 110 and 140 d of gestation. Mineral retention during pregnancy was determined in the maternal body, femur, uterus, mammary gland, fetus and fetal fluid. Blood samples were taken during pregnancy to determine the mineral concentration and alkaline phosphatase activity. Bone mineral density was determined in the right femur. Statistical analyses were performed using the SAS MIXED procedure. The availability of Ca and P increased until the end of pregnancy

($P < 0.05$), but the balance of these minerals increased only until 80 d of gestation and then declined ($P < 0.01$). Maternal body weight gain and Ca, P and Mg retention (g/kg) decreased during gestation ($P < 0.01$). Macro mineral retention in maternal body (g/kg) was higher in Oberhasli goats ($P < 0.01$), and their fetuses had higher Ca, P and Mg deposition (mg/g; $P < 0.01$). Mineral retention (mg/g) increased in fetuses according to pregnancy development ($P < 0.01$). In the fetal fluid, P, Mg, Na and K retention (mg/g) increased throughout pregnancy ($P < 0.05$). In the mammary gland, the retention of all minerals (g) increased until the end of pregnancy ($P < 0.05$). Ca, P and Mg metabolism is related to maternal body preparation for future demands until 80 d of gestation, and after this period for the transfer of maternal body reserves for fetal development and colostrum formation. Na and K supply is provided by physiological adjustments. The mineral metabolism is specific to each breed and is not affected by the number of fetuses.

Key Words: fetus, genotype, maternal body reserves

W429 Mineral metabolism of dairy goats under feed restriction during pregnancy. C. J. Härter*[1], A. R. Rivera[1], D. S. Castagnino[1], L. D. Lima[1], H. G. O. Silva[1], A. M. Nunes[1], A. Liesegang[2], N. St-Pierre[3], K. T. Resende[1], and I. A. M. A. Teixeira[1], *[1]Department of Animal Sciences, Universidade Estadual Paulista, Jaboticabal, SP, Brazil, [2]Institute of Animal Nutrition, University of Zurich, Zurich, Switzerland, [3]Department of Animal Sciences, The Ohio State University, Columbus.*

The present study examined the effects of feed restriction on calcium (Ca), phosphorus (P), magnesium (Mg), sodium (Na) and potassium (K) metabolism in goats during gestation. A total of 31 Oberhasli and 32 Saanen (49.0 kg ± 8.9 BW) goats were used in this study. Six of these (3 Oberhasli and 3 Saanen) were slaughtered at the beginning of the experiment to estimate the baseline body composition of non-pregnant goats. The remaining goats were distributed into groups that were subjected to 3 levels of feed restriction (0, 20 and 40% restriction) and slaughtered at different pregnancy stages (80, 110 and 140 d of gestation), in a randomized complete block design with 2 × 3 × 3 factorial arrangement. Mineral balance was determined around 50, 80, 110 and 140 d of gestation. Serum levels of Ca, P, Mg, Na, K, Ca ions and alkaline phosphatase activity were determined during pregnancy. Bone mineral density was determined in the right femur. Mineral retention in maternal body, femur, uterus, mammary gland, fetus and fetal fluid was also determined during gestation. Mixed models with d of gestation, levels of feed restriction, breed and their interactions as fixed effects and blocks as random effect were used for data analysis. Feed restriction caused DM loss in the maternal body ($P < 0.01$). At 40% feed restriction, the retention of all minerals in the body (g/kg BW) decreased ($P < 0.06$), and fetuses were smaller than those of goats without feed restriction ($P < 0.05$). Fetal deposition of P, Na and K (mg/g) was also lower at 40% restriction ($P < 0.06$). In response to the reduction in mineral intake, the maternal body uses its mineral reserves to maintain gestation, while fetal growth is also maintained under mild feed restriction conditions. Severe feed restriction, however, can compromise fetal development because the maternal body gains priority for the use of some nutrients such as P, Na and K.

Key Words: fetal mineral deposition, maternal body, mineral retention

W430 Influence of reducing starch and increasing digestible fiber on hormonal and metabolic profile of lactating ewes. R. S. Gentil*[1], A. Cannas[2], A. V. Pires[1], E. M. Ferreira[1], D. M. Polizel[1], D. Eysink[1], M. V. Biehl[1], and I. Susin[1], *[1]Escola Superior de Agricultura Luiz de Queiroz/Universidade de São Paulo, Piracicaba, SP, Brazil, [2]University of Sassari, Sassari, Sardegna, Italy.*

The variations in hormonal status during lactation reflect nutrient partitioning between milk production and body reserves. Thirty-three lactating Santa Ines ewes (68 ± 3 Initial BW and 13.2 ± 3 DIM; mean ± SD) were used in a randomized complete block design to define an optimal combination between carbohydrate sources (starch and high digestible fiber) that can favor energy partitioning toward milk production at different lactation stages. Ewes were housed individually for 10 wk from the second week of lactation. Animals were fed a 60:40 (concentrate:roughage ratio) TMR with 15 ± 0.4% crude protein. Soybean hulls (SH, source of high digestible fiber) replaced corn (source of starch) by 0, 20 or 40% (DM basis), corresponding to the experimental treatments 0SH, 20SH and 40SH, respectively. Blood samples were collected in the first week of experiment (14 DIM) and every 14 d, 2 h after feeding. The metabolites evaluated were insulin, growth hormone (GH), IGF1, glucose and nonesterified fatty acids (NEFA). A colorimetric assay was used to determine blood glucose and NEFA concentrations. Blood insulin and GH concentrations were determined using RIA. The analysis of blood IGF1 concentrations was made in a chemiluminescent immunoassay analyzer. Data were analyzed using the PROC MIXED procedure (SAS 9.2, 2002). All the variables were unaffected ($P > 0.05$) by replacing corn with SH. There were no effects ($P > 0.05$) of lactation stage on blood glucose and IGF1 concentrations. However, insulin (5.61; 9.89; 9.82; 9.94; 12.87; 10.01 µIU/mL) concentrations increased, while GH (4.31; 4.22; 3.87; 2.72; 2.61; 2.24 ng/mL) and NEFA (0.60; 0.42; 0.31; 0.30; 0.22; 0.20 mEq/L) concentrations decreased ($P < 0.05$) throughout lactation. There was no interaction ($P > 0.05$) between diet and time. Soybean hulls can partially replace corn without effect on hormonal and metabolic profile of lactating ewes.

Key Words: corn, lactation, soybean hulls

W431 Growth and carcass characteristics of ewe lambs fed high-concentrate diets containing increasing levels of calcium nitrate. A. P. A. Freire[1], R. A. Souza[1], D. M. Polizel[1], R. S. Gentil[1], A. V. Pires[1], R. C. Araujo[2], and I. Susin*[1], *[1]Escola Superior de Agricultura Luiz de Queiroz (ESALQ)/USP, Piracicaba, SP, Brazil, [2]GRASP Ind. e Com. LTDA, Curitiba, PR, Brazil.*

Nitrate is a source of nonprotein nitrogen that can be fed to ruminants having the capability of reducing methane production in the rumen. However, nitrate is not currently used due to the risk of methemoglobinemia. Fifty Dorper × Santa Inês ewe lambs (initial BW 37.4 ± 3.1 kg and 185 ± 4 d old) were used in a randomized complete block design, according to initial BW and age, to determine the effects of calcium nitrate on growth and carcass characteristics. Ewe lambs were penned individually during 69 d and fed an isonitrogenous (14% CP, DM basis) total mixed ration composed of 80% concentrate and 20% coastcross bermudagrass hay. The experimental diets contained increasing levels of calcium nitrate replacing soybean meal as follows: 0 (control-N0), 1% (N1), 2% (N2), 3% (N3) or 4% (N4) in the dietary DM. An adaption period of 4 d was used before moving to a higher nitrate level to avoid toxic effects. There was a quadratic response ($P < 0.05$) in DMI (1.42, 1.44, 1.37, 1.32 and 1.19 kg/d for N0, N1, N2, N3 and N4, respectively), ADG (208, 209, 199, 173 and 130 g for N0, N1, N2, N3 and N4, respectively) and feed efficiency (gain:feed = 147, 148, 146, 131 and 102 for N0, N1, N2, N3 and N4, respectively). Dressing percentage, longissimus muscle area and nitrate/nitrite content in meat were unaffected ($P > 0.10$) by experimental diets. However, back fat thickness (11.2, 8.6, 6.3, 6.9, and 8.5 mm for N0, N1, N2, N3 and N4, respectively) had a quadratic response ($P < 0.05$), showing a decrease up to 2% of nitrate. Calcium

nitrate replacing soybean meal up to 2% of dietary DM maintained feed efficiency with no detrimental effect on animal health.

Key Words: nonprotein nitrogen, sheep

W432 Rumen metabolism in lambs fed high-concentrate diets containing increasing levels of crude glycerin. D. M. Polizel, R. S. Gentil, E. M. Ferreira, R. A. Souza, A. P. A. Freire, J. A. Faleiro Neto, A. V. Pires, and I. Susin*, *Escola Superior de Agricultura Luiz de Queiroz (ESALQ)/USP, Piracicaba, SP, Brazil.*

The objectives in this trial were to determine the effects of partial replacement of corn by crude glycerin (CG) on rumen metabolism of ram lambs fed high-concentrate diets. Five Dorper × Santa Inês ram lambs (BW 56.9 ± 6.4 kg), cannulated in the rumen, were used in 5 × 5 Latin square design. Animals were fed an isonitrogenous (15% CP, DM basis) TMR composed of 90% concentrate and 10% coastcross hay. Crude glycerin (83.6% glycerol, DM basis) was included in the ration at 0%, 5%, 10%, 15% or 20% (DM basis), corresponding to the experimental diets G0, G5, G10, G15 and G20, respectively. Every period of the experiment lasted 19 d. The first 15 d were used to adapt the ram lambs with the diets and the remaining 4 d were used for data collection. In the last day of the period, rumen fluid was collected every 2 h, starting prior feeding, 2, 4, 6, 8, 10 and 12 h after feeding. Short-chain fatty acids (SCFA) profile, pH and ammonia nitrogen concentration were determined. Ruminal measures were analyzed as repeated measures over time by using the MIXED procedure (SAS Inst. Inc.) The LSMEANS option was used to generate individual diet means. Orthogonal polynomials for diet responses were determined by linear, quadratic, and cubic effects. Propionate, butyrate, isovalerate, total SCFA, ammonia nitrogen and pH were unaffected ($P > 0.05$) by the experimental diets. There was an interaction ($P < 0.05$) between diet × hour for acetate, ammonia and pH. There was a quadratic response ($P < 0.05$) for acetate (49.28, 43.19, 37.67, 35.38, 37.83 m*M*) and acetate-to-propionate ratio (1.01, 0.88, 0.71, 0.71, 0.76). Isobutyrate concentration (0.44, 0.37, 0.36, 0.26, 0.35 m*M*) decreased ($P < 0.05$) with inclusion of CG. Crude glycerin fed up to 15% of the diet DM decreased acetate and acetate:propionate ratio.

Key Words: co-product, glycerol, short-chain fatty acid

W433 Effect of supplementation with different protein levels on the performance of lambs grazing napiergrass (*Pennisetum purpureum*) pasture. I. F. F. Garcia*[1], F. A. P. Alvarenga[1], D. R. Casagrande[1], J. R. O. Perez[1], P. C. G. Dias Junior[1], V. C. Ferreira[2], and I. G. Pereira[2], *[1]Universidade Federal de Lavras, Lavras, Minas Gerais, Brazil, [2]Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil.*

The aim of the present study was to evaluate the effect of supplements with different crude protein (CP) levels on the development of lambs grazing napiergrass (*Pennisetum purpureum*) pasture. The average initial live weight of 50 crossbred lambs used in this study was 20.2 ± 2.94 kg and the average age was 170 ± 14.4 d. The treatments tested were: control group receiving a mineral mixture; and 4 groups receiving supplements (corn, soybean meal and mineral mixture) with different levels of CP (8, 16, 24 and 32%). A completely randomized experimental design with 5 treatments was used. The averages between groups were compared by Tukey test (5%) and regressions were performed. Lambs were slaughtered after 75 d. Feed consumption was evaluated using chromic oxide and titanium dioxide markers. Fecal egg counts (FEC) were performed to monitor level of worm infection. The control group had higher FEC (808/g of feces) compared with the average of the groups that received CP supplementation (359/g of feces). The weight at slaughter and the EBW were similar between the supplemented groups (average 30.6 and 22.9 kg, respectively) but superior to the control group (24.1 and 17.9 kg, respectively). Although weight gain per day (GPD) increased linearly with increased CP in the diet, the group given an 8% CP supplement had GPD similar to control animals (93.0 g/d). The other groups had an average GPD of 137.6 g/d. The daily DM consumption was 602.1 g/d or 2.36% of BW and was not affected by CP level of the diet. The consumption of CP and OM increased with increasing dietary CP. The area of the rumen papilla was larger for treatment groups given diets with 24 and 32% CP (average 0.23 cm^2) compared with the control, 8% CP, and 15% CP treatment groups (0.15 cm^2). The mitotic index in the rumen was higher for supplemented animals (0.97) than controls. Protein supplementation of lambs grazing napiergrass pasture increases performance, with the best results found at levels of 16% CP or more.

Key Words: nutrients consumption, ruminal tissue, sheep

W434 Effect of a cellulase enzyme additive on hay intake and fiber digestion in goats. S. Hart*, *Langston University, Langston, OK.*

Thirty-six Spanish, Boer, and Boer × Spanish wethers (6 mo of age, 25.0 ± 5.5 kg BW) were used to test the effect of a cellulose/hemicellulase enzyme additive on intake and fiber digestion. Wethers were blocked by BW and breed and randomized to 4 pens with Calan headgates to measure individual intake. Wethers were fed a chopped low quality grass hay (4.8% CP, 48.4 ADF, and 75.3 NDF) at 115% of average intake over the previous 3 d. Two pens of goats were offered a test supplement containing the enzymes and 2 were offered the control supplement. The supplement was composed of 5% of a mineral mix containing trace minerals, 8% liquid molasses, 43% soybean meal, and 44% ground corn. The enzyme preparation (69% distillers dried grains, 30% urea, and 1% enzymes) was incorporated into the supplement at the 2% level. The supplement was fed at 5.5 g/kg BW, resulting in 8.8 g of enzyme preparation/100 kg BW. Blood and ruminal fluid samples were collected before the morning feeding in wk 4 of the study for blood urea nitrogen and rumen ammonia determination. Following the 12-wk intake study, intake was reduced in half the pens to 80% of intake in wk 12, fecal bags were fitted on animals, and fecal and ort samples were collected 5 d for determining digestibility. Data were analyzed with Proc MIXED of SAS. Rumen ammonia and blood urea nitrogen were similar for control and enzyme treatments (6.8 vs. 7.1 mg/dL, SE = 0.38, $P > 0.20$; 13.8 vs. 15.2 mg/dL, SE = 2.3, $P > 0.20$). Hay intake was similar for control and enzyme treatments (2.63% vs. 2.83% of BW, $P > 0.20$; 58.8 vs. 63.0 g/kg $BW^{0.75}$, $P > 0.20$). Dry matter digestibility and protein digestibility were similar (52.8 vs. 53.5%, SE = 1.1, $P > 0.20$; 79.4 vs. 78.4%, SE = 0.8, $P > 0.20$). Neutral detergent fiber digestibility and acid detergent digestibility also were similar (49.8 vs. 50.6%, SE = 1.5, $P > 0.20$; 26.9 vs.25.5%, SE = 3.3, $P > 0.20$). The cellulose and hemicellulase additive did not improve intake of low quality grass hay or increase fiber digestibility in goats.

Key Words: cellulase, fiber digestion, feed intake

W435 Effects of stocking rate and physiological state of meat goats grazing grass/forb pastures on forage intake, selection, and digestion, grazing behavior, and performance. A. R. Askar[1,2], R. Puchala*[1], T. A. Gipson[1], K. Tesfai[1], G. D. Detweiler[1], A. Asmare[1], A. Keli[3], T. Sahlu[1], and A. L. Goetsch[1], *[1]American Institute for Goat Research, Langston University, Langston, OK, [2]Animal and Poultry Nutrition Department, Desert Research Center, Cairo,*

Egypt, [3]Department of Animal Production and Pastoralism, National School of Agriculture, Meknes, Morocco.

Effects of forage conditions with different stocking rates (SR) on performance and grazing behavior of goats could vary with animal physiological state, as influencing nutrient demand and usage. Boer goat does with 2 kids (D; 1 mo after kidding), growing wethers (G; 4 mo initial age), and yearling wethers (Y; 14 mo initial age) grazed 0.4-ha grass/forb pastures, with 1 animal per type in each pasture for a low SR and 2 for a high SR. The experiment started in late spring and was 114 d with 4 periods (P1–4). Forage mass was 2,517, 2,433, 2,506, and 2,452 kg/ha for the low SR and 2,680, 1,932, 1,595, and 1,393 kg/ha for the high SR in P1, P2, P3, and P4, respectively (SE = 335). Botanical composition of the diet based on n-alkanes was similar among animal types ($P > 0.10$). Likewise, chemical composition of forage samples did not differ between animal types ($P > 0.10$), with averages of 11% CP and 53% NDF. Digestibility of OM based on C31 (hentriacontane) was greater ($P < 0.05$) for the low than high SR (66.1 vs. 62.3%). Intake of ME was 1,015, 855, and 692 kJ/kg $BW^{0.75}$ for D, G, and Y, respectively (SE = 57.4) and greater for the low than high SR in P1 (1,204, 789, 682, and 445 for high SR and 1,732, 767, 683, and 531 kJ/kg $BW^{0.75}$ for low SR in P1, P2, P3, and P4, respectively; SE = 93.5). There was an interaction ($P < 0.05$) between animal type and period in ADG (13, −12, −44, −8, 83, 25, −28, 73, 127, 51, −43, and −7 g; SE = 21.5) and time spent grazing (7.5, 5.3, 7.4, 8.6, 78.6, 5.6, 10.0, 9.1, 4.8, 5.9, 8.4, and 9.5 h/d for D-P1, D-P2, D-P3, D-P4, G-P1, G-P2, G-P3, G-P4, Y-P1, Y-P2, Y-P3, and Y-P4, respectively; SE = 0.88). Rate of ME intake was greater ($P < 0.05$) for D vs. G and Y (49.5, 21.9, and 33.9 kJ/min for D, G, and Y, respectively; SE = 5.68) and differed ($P < 0.05$) among periods (57.5, 45.3, 24.8, and 12.9 kJ/min in P1, P2, P3, and P4, respectively; SE = 5.17). In conclusion, with this forage of moderate nutritive value, there were no findings suggesting that levels of forage mass above 1,400 kg/ha would improve performance of meat goats of different physiological states.

Key Words: grazing, meat goat, stocking rate

W436 Performance and consumption patterns of vegetation for commercial crossbred meat goats and hair sheep used to clear woodlands. J. A. Pennington*[1], J. L. Wilkins[2], N. T. Witt[3], and J. D. Caldwell[4], *[1]Lincoln University, Neosho, MO, [2]Crowder College, Neosho, MO, [3]NRCS, Neosho, MO, [4]Lincoln University, Jefferson City, MO.*

Commercial crossbred meat goats (MG; final n = 63 with 33 adults, 2 yearlings, and 28 kids) and crossbred hair sheep (HS; final n = 60 with 33 adults, 1 yearling, and 26 lambs) were used for 8 wk in Jun-Jul, 2012, to clear woodlands that included a mix of available vegetation for consumption. Vegetation was divided into 9 categories (% of total feed available, % eaten by animals): sericea lespedeza (18, 83), buck brush (22, 94), multi-flora rose (5, 97), blackberry/other briers (6, 88), fescue/cool season grasses (4, 93), bermuda/cheat/summer grasses (7, 94), broadleaf/clover/ragweed (9, 92), vines/ivy (3, 100), and trees/hackberry/bushes (26, 89). MG ate a greater percentage ($P < 0.05$) of sericea, rose, blackberry, broadleaf, and trees/bushes than HS; there was no difference ($P > 0.10$) in % eaten for cool season grasses, summer grasses, or vines; buck brush consumption was intermediate ($P = 0.08$). Consumption by MG and HS of individual plants of multi-flora rose ($P < 0.05$) and buck brush ($P = 0.12$) showed similar trends. MG had a higher ($P < 0.01$) browse line (1.41 m) than HS (1.24 m). Estimates of consumption were made weekly after animals were moved from lots of about 0.6 ha. MG ate 96–98% of vegetation and HS ate 93–98% of vegetation until consumption decreased when vegetation matured and extremely hot weather occurred in late July. Performance of 31 does and 31 ewes (1 died of each) showed that does had greater ($P < 0.01$) weight gain and improved ($P < 0.01$) body condition changes and FAMACHA scores compared with ewes. Weight change was +3.9 kg for does and +0.0 kg for ewes during 8 wk trial. Lactation (nursing) status affected or tended to affect gain, change in body condition, final body condition, and FAMACHA scores. Nursing ewes lost 2.2 kg and nonlactating ewes gained 2.3 kg ($P < 0.10$). Nursing and nonlactating does gained weight. Final body condition score was affected ($P < 0.05$) by species and lactation status plus initial body condition score ($P < 0.01$). Overall, both MG and HS cleared the woodlands, but MG ate slightly more vegetation than HS and does performed better than ewes in the woodlands, especially nursing ewes.

Key Words: meat goat, hair sheep, woodland

W437 Effects of continuous or rotational grazing schemes by yearling Katahdin ewes grazing toxic tall fescue in late spring through summer on available forage and forage quality. E. A. Backes*[1,2], J. D. Caldwell[1], B. C. Shanks[1], K. R. Ness[1], A. N. V. Stewart[1], C. A. Clifford-Rathert[1], A. K. Wurst[1], D. L. Kreider[2], and M. L. Looper[2], *[1]Lincoln University, Jefferson City, MO, [2]University of Arkansas, Fayetteville.*

Rotational grazing has increased in popularity in recent years. However, research of grazing management of Katahdin hair sheep on toxic tall fescue [*Lolium arundinaceum* (Schreb.) Darbysh; E+] has not been well reported. Our objective was to evaluate available forage and forage quality measurements by yearling Katahdin ewes grazing E+ using either continuous or rotational grazing schemes in late spring through summer. Over 2 consecutive years, yearling Katahdin ewes (n = 50; 53 ± 1.41 kg initial BW; 3.3 ± 0.09 initial BCS) were stratified by BW and allocated randomly to one of 5 0.4 ha pastures consisting of 2 treatments: (1) Continuous (C; 5 replications); or (2) 4-cell rotation (4R; 5 replications). Available forage measurements were taken monthly for the duration of the study. Twelve disk meter readings were taken per pasture and calibrated on each sampling day. Six alternating forage quality samples per pasture were collected at time of disk meter readings. Available forage did not differ ($P = 0.45$) across treatments, however, available forage ($P \leq 0.05$) was greater for August compared with May, June, and July, but did not differ ($P > 0.68$) for June compared with May and July. In vitro dry matter digestibility (IVDMD) and crude protein (CP) did not differ ($P > 0.53$) across treatments. In vitro dry matter digestibility was greater ($P \leq 0.05$) for May compared with June, July, and August, but did not differ ($P \geq 0.89$) between June, July, and August. Crude protein ($P \leq 0.05$) was greater for May compared with all other months, but did not differ ($P = 0.35$) for June compared with August, but was greater ($P \leq 0.04$) for June and August compared with July. Grazing days did not differ ($P = 0.24$) from C compared with 4R. Therefore, rotational grazing yearling Katahdin ewes on E+ pastures in late spring through summer may not increase available forage, IVDMD, or CP when compared with continuous grazing.

Key Words: grazing, forage quality, Katahdin

W438 Ractopamine hydrochloride on performance of heavy weight pigs. G. Borbolla-Sosa, I. E. Avila-Arres*, A. Pineda-Mejía, R. Martinez-Gamba, P. Arriaga-Montero, and A. Rodriguez, *National University of Mexico (UNAM), School of Veterinary Medicine, Department of Swine Medicine and Zootechnics, Mexico City, Mexico.*

Ractopamine hydrochloride (RAC) has been used to increase lean growth in finishing pigs. In South American countries, RAC is supplied between 70 – 100 kg BW due to the smaller slaughter weights used in these countries. However, small profits and higher feed costs have pushed producers into heavier market weights, and therefore more pressure from buyers regarding the fat content of the carcass. The aim of this study was to evaluate the use of RAC in heavy market pigs. A total of 54 barrows and gilts with an average weight of 96 ± 4 kg were randomly assigned to diets with (RAC), or without (C) ractopamine hydrochloride at a dose of 10 ppm per 1000 kg of feed. ADFI, ADG, G:F, backfat depth (BF), longissimus dorsi muscle depth (LMD) and Lean Meat percentage (LMP) were evaluated in this study. BF and LMD were evaluated with a Real Time Ultrasound device; and LMP by means of a mathematical equation. Experimental period lasted 28 d, and data was analyzed by a Student's *t*-test. ADFI decreased ($P < 0.001$) 7% in RAC barrows. ADG was increased ($P > 0.05$) by 4.4% in barrows and 5.5% in gilts compared with controls (950 vs. 910 g/d in RAC and C barrows, and 960 vs. 910 g/d in RAC and C gilts, respectively). RAC barrows and gilts had a 13 and 7% reduction ($P > 0.05$) in G:F compared with controls. Control barrows had a BF 19% larger ($P < 0.02$) than their RAC counterparts (17.33 vs. 14.56 mm, respectively). In gilts BF was only 3% different ($P > 0.05$), between treatment groups (12.63 vs. 12.27 mm; in C and RAC groups). LMD was increased ($P > 0.05$) 2.5% in RAC barrows (48.8 vs. 49.3 mm), and 4.7% in RAC gilts (49.6 vs. 52.1 mm) compared with C. LMP was 1.6% larger ($P > 0.05$) in RAC gilts compared with C gilts, and 5.8% larger ($P < 0.03$) in RAC barrows than C barrows. RAC in heavy barrows and gilts showed an improvement in the major productive parameters of market pigs.

Key Words: ractopamine, lean deposition, fat deposition

W439 The effect of body weight at feed change timing on carcass, meat and fat quality of heavy gilts. J. Suárez-Belloch[1], M. A. Sanz[2], M. Bellés[1], and M. A. Latorre*[1], *[1]IUCA. Facultad de Veterinaria, Universidad de Zaragoza, Spain, [2]Centro de Investigación y Tecnología Agroalimentaria de Aragón, Zaragoza, Spain.*

A total of 60 Duroc × (Large White × Landrace) gilts of 54.1 ± 0.14 kg BW and 82 ± 3 d of age, were used to study the effect of BW at feed change timing from growing to finishing period (100 vs. 90 vs. 80 kg) on carcass and meat quality and fatty acid (FA) profile of subcutaneous fat. Each treatment was replicated 4 times and the experimental unit was the pen constituted by 5 pigs allocated together. Commercial diets based on maize, barley and vegetable meals and containing 3,200 kcal NE/kg, were provided ad libitum through the trial (17% CP and 0.9% Lys for growing phase and 15.7% CP and 0.7% Lys for finishing phase). Pigs were slaughtered at 120 kg BW because were intended for dry-cured ham industry. Therefore, minimum fat depth at gluteus medius muscle (m. GM) and fresh ham weight are required to pass the hams for being dry-cured. Data were analyzed by GLM of SAS. Bringing forward the feeding change did not modify carcass yield or ham size ($P > 0.10$). However, the change of diet at lighter BWs tended to increase linearly the fat depth at m. GM ($P = 0.06$) which suggests a lower lean yield; in fact, a reduction of the loin weight ($R^2 = 0.76$; $P = 0.03$) was observed although no decrease in the weight of other main cuts such as hams or shoulders was detected. In addition, treatment did not affect water holding capacity, color, tenderness or chemical composition of meat ($P < 0.10$). However, bringing forward the feeding change reduced the total monounsaturated FAs ($P < 0.05$), due to C18:1 ($P < 0.05$), and increased the total polyunsaturated FAs ($P < 0.05$) due to C18:3 ($P < 0.001$). It is concluded that, under our experimental conditions, the change of the diet from growing to finishing period at 80 kg BW had no effect on meat quality but could be interesting, taking into account the improvements in carcass and fat variables, in the case of pigs intended for dry-cured ham industry.

Key Words: feeding change, carcass and fat quality, heavy gilt

W440 Nitrogen balance of immunocastrated pigs receiving diets with or without ractopamine. L. R. Silva, E. Lanferdini, L. G. M. Amaral, C. A. P. Garbossa, H. Silveira, and V. S. Cantarelli*, *Federal University of Lavras, Lavras, Minas Gerais, Brazil.*

The trial was conducted in the Experimental Swine Center at UFLA. A metabolic assay was conducted to evaluate the effect of ractopamine (RAC) on the nitrogen balance of immunocastrated male pigs (IMP) in 2 periods of the finishing phase. Twelve IMP with initial BW of 88.38 ± 7.27 kg were housed in metabolic cages for total collection of feces and urine. The experimental design was a 2 × 2 factorial, with 2 levels of RAC (0 and 10 ppm), and 2 periods of the use of RAC (14 and 28), with 6 replicates of one animal per experimental unit. Diets with RAC had a higher amino acid concentrations (0.65% and 0.75% digestible lysine, in diets with and without RAC) and crude protein (14.61% and 15.31%, in diets with or without RAC), due to higher demand for protein synthesis. The experiment lasted 28 d, separated into 2 14 d periods, with 10 d of adaptation and 4 collection days per period. Nitrogen intake (NI), excreted in feces (NF), and eliminated by urine (NU) were determined and the percent of dietary nitrogen absorbed (NA%), and retained (NR%); and the percent of absorbed nitrogen that was retained (NR/A%) at 14 and 28 d were calculated. All variables were subjected to Tukey test (5%).There were no interactions ($P < 0.05$) between any variables. Due to the fact that RAC diets had a higher amount of nitrogen (amino acids), addition of RAC increased ($P < 0.05$) NI by 3%, but also increased ($P < 0.05$) NR% by 7.5% and NR/A% by 6.6%. These results indicate that RAC alters metabolism, by increasing the efficiency of utilization of amino acids, even in IMP. When we compared the use of RAC between periods, due to the downregulation process that occurs during prolonged use of RAC in the last 14 d, RAC supplementation resulted in increased amount of NU and consequently decreased ($P < 0.05$) by 6.5% the amount of NR% and 6% NR/A% compared with the first 14 d. In conclusion, the use of RAC in the diets of IMP results in better utilization of nitrogen and consequently lower N excretion, but it is more pronounced in the first 14 d of supplementation.

Key Words: immunocastration, ractopamine, nitrogen balance

W441 Effects of lysine and ractopamine on performance, carcass characteristics and economic viability of male pigs immunocastrated during the growing and finishing phases. L. R. Silva, P. B. Faria, L. G. M. Amaral, M. L. T. Abreu, E. Lanferdini, and V. S. Cantarelli*, *Federal University of Lavras, Lavras, Minas Gerais, Brazil.*

An experiment was conducted in the Experimental Swine Center, in the Animal Science Department, of Federal University of Lavras, with the objective of evaluating the effect of lysine concentrations and ractopamine (RAC) in the diets of immunocastrated male pigs (IMP), in growing and finishing phases on performance, carcass characteristics and economic viability. A 56-d experiment was conducted with 48 IMP with an initial BW of 59.22 ± 3.39 kg. The experiment was designed as a 2 × 2 factorial, with 2 concentrations of digestible lysine (DL: 0.9 and 1.0%) in the growing (d0–18) phase followed by the addition or not of RAC in the finishing (d 29–56) phase (0 ppm of RAC and 0.65% of DL, and 10 ppm of RAC and 0.75% DL). Pigs were separated for performance evaluation into 6 replicates and 2 animals per pen. For carcass evaluation and economic feasibility, there were 12 replicates and plot of one animal. Pigs were weighed at the beginning, 14, 28, 42 and 56 d of experiment. At the end of the trial pigs were slaughtered to evaluate carcass characteristics and economic feasibility. All variables were subjected to Tukey test (5%). Changes in performance were observed only in the final 14 d of the study, in which pigs supplemented with RAC had lower ($P < 0.05$) feed intake (4%) and better ($P < 0.05$) feed efficiency (5%). There were positive interactions ($P < 0.05$) only on carcass meat yield between concentrations of DL and RAC, in which the best result was obtained with 1.0% DL followed by the addition of 10 ppm of RAC. Carcass length decreased ($P < 0.05$) 3% while the compactness of carcass increased ($P < 0.05$) 5% when given diets supplemented with RAC. Regarding the economic feasibility study, the results indicated that concentrations of 0.9% DL during the growing phase and 10 ppm of RAC in the finishing phase resulted in higher ($P < 0.05$) rate of bonus (2%). In conclusion nutrition programs meet the nutritional needs of IMP, being economically feasible only if there is a bonus at the slaughter.

Key Words: immunocastration, ractopamine, pig

W442 Influence of ractopamine on the diets of swine stressed by heat. R. Philomeno[2], C. A. P. Garbossa[1], M. R. Junqueira[1], L. G. M. Amaral[1], R. A. Ferreira[1], and V. S. Cantarelli*[1], *[1]Federal University of Lavras, Lavras, Minas Gerais, Brazil, [2]Agroceres Multimix, Rio Claro, São Paulo, Brazil.*

An experiment was conducted in the House's Climate Room Metabolism at the Experimental Swine Center (ESC) at the Animal Science Department, Federal University of Lavras (UFLA). We used 144 barrows (high potential for lean gain) with an average initial BW of 65 kg, with the objective of evaluating the effect of heat stress on the use of ractopamine (RAC) in the finishing phase. The design was a 4× 2 factorial with 4 levels of RAC (0, 5, 10 and 15 ppm), and 2 rearing conditions (thermal comfort at 20°C, and heat stress at 32°C) in 6 replicates with experimental unit represented by 3 animals. Experimental diets were formulated based on corn and soybean meal, meeting the nutritional requirements of the phase and genetic line. The diets with and without ractopamine had the levels of 0.76% and 0.9% of lysine respectively. The experimental period was 28 d and the variables analyzed were: ADG, ADFI, feed conversion (FC), respiratory rate (RR), rectal temperature (RT), hormonal parameters (serum concentration of triiodothyronine - T3), loin eye area, loin depth, backfat thickness and organ weights (heart, kidney and lung). All the variables were subjected to the F test (5%). The use of RAC improved ($P < 0.05$) performance variables, with no significant interaction ($P < 0.05$) with ambient temperature. Similar results were observed for serum concentrations of T3 ($P < 0.05$). Temperature influenced ($P < 0.05$) RR and RT without and interaction with RAC levels. Heart and lung were not influenced by trt ($P > 0.05$). However, kidney weights decreased ($P < 0.05$) with increasing RAC and an interaction of RAC and temperature was observed for liver weight ($P < 0.05$). There were no effects ($P > 0.05$) on carcass variables. We can conclude that RAC improves performance variables, besides interfering concentrations of T3, but does not alter the respiration rate and rectal temperature of pigs, the latter being altered by environmental conditions. The use of ractopamine reduces the weight of the kidney and does not alter carcass characteristics.

Key Words: performance, heat stress, carcass modifier

W443 Lysine levels in diets with different corn starch digestion kinetics for growing pig. N. O. Amaral[2], L. G. M. Amaral[1], F. M. Carvalho Jr.[1], H. Silveira[1], and V. S. Cantarelli*[1], *[1]Federal University of Lavras, Lavras, Minas Gerais, Brazil, [2]Federal Institute of Education, Science and Technology, Machado, Minas Gerais, Brazil.*

This study was conducted to verify the influence of the kinetics of starch digestion on digestible lysine requirement of growing pigs. A total of 120 gilts and barrows, Landrace/Large White genetic line (initial weight of 34.2 kg), were used for performance evaluation and 60 barrows (initial weight of 40.3 kg) were used to determine total tract digestibility and nitrogen balance. The experiment was designed as a 3 × 4 with 3 different maize geometric mean diameters (GMDs: 550, 700 and 850 mm) and 4 concentrations of lysine (0.85, 0.95, 1.05 and 1.15%) totaling 12 treatments and 5 replications. Data were subjected to statistical analysis by SNK test (5%). There was a significant interaction between GMD and lysine concentration for ADFI and feed conversion (FC). Pigs fed 0.85 and 0.95% lysine had lower ADFI of pigs fed the source of slow digested starch (SDS, GMD 850 mm). At 1.05% level, however, this situation was reversed, the ADFI was higher. Moreover, there was a quadratic effect on ADFI of animals receiving SDS in the diet, as the concentration of Lys increased. For FC, pigs fed diets with SDS and 0.85% lysine had a FC 14% lower than those fed diets containing rapidly digested starch (RDS – GMD 550 mm) and intermediate digested starch (IDS, GMD 750 mm). Moreover, there was a quadratic effect RDS and a linear effect to the source SDS as Lys concentration increased. Thus, we conclude that the variation of the kinetics of starch digestion provided by different degrees of grinding of maize influences the lysine requirement of growing pigs (30–60 kg). The particle size of slow starch digestion (850 μm) enhances the efficiency of lysine utilization by pigs.

Key Words: nutrition, particle size, starch digestion

W444 The effect of immunocastration on growth performance and meat quality of heavy gilts . M. A. Latorre*[1], A. Daza[2], A. Olivares[3], and C. J. López-Bote[3], *[1]Universidad de Zaragoza, Zaragoza, Spain, [2]Universidad Politécnica de Madrid, Madrid, Spain, [3]Universidad Complutense de Madrid, Madrid, Spain.*

A total of 48 Duroc × (Large White × Landrace) gilts of 33.2 ± 0.63 kg BW were used to study the effect of immunization against G_nRH on growth performance and on the content and fatty acid (FA) profile of intramuscular fat (IMF) of meat. Each experimental treatment (control vs. immunocastration) was replicated 8 times and the replicate was a pen with 3 gilts. Inmunization was carried out with 2 injections of Improvac (Pfizer) with at least 4 weeks between both injections (1st: 35.0 kg BW, 2nd: 57.6 kg BW). A commercial diet, based on barley, wheat, and vegetable meal and containing 13.74 MJ DE/kg, 13.9% CP, and 0.89% Lys, was provided ad libitum through the trial. Pigs were slaughtered at 125 kg BW because were intended for dry-cured ham industry. Data were analyzed by ANOVA and the statistical model included the gilt

sex as main effect. The castrates ate more feed (2.83 vs. 2.67 kg/d; $P = 0.04$) and grew faster (989 vs. 937 g/d; $P = 0.03$) than entire gilts but the feed conversion ratio was similar (2.86 vs. 2.84 kg/kg; $P > 0.05$). The highest IMF content was found in meat from castrates (5.0 vs. 4.3%; $P = 0.09$). The proportion of total saturated FAs was higher in IMF from immunocastrated than in that from entire gilts (40.8 vs. 38.4%; $P < 0.0001$) due to the higher content in C16:0 ($P < 0.0001$), C18:0 ($P < 0.0001$) and C20:0 ($P = 0.02$). However, the percentage of total monounsaturated FAs was lower in immunocastrates (50.8 vs. 52.3%; $P = 0.004$) because of the lower content in C18:1n-9 ($P = 0.002$). The castrates had lower proportion of C18:2n-6 ($P < 0.10$) and C20:4n-6 ($P = 0.01$) than entire gilts which carried out a lower total polyunsaturated FA percentage (8.34 vs. 9.25%; $P = 0.06$) and polyunsaturated FA/saturated FA ratio (0.20 vs. 0.23; $P = 0.01$) in immunocastrated animals. It is concluded that the immunization against GnRF in gilts improved growth performance and increased the IMF content of meat but impaired its quality related to fatty acid profile.

Key Words: gilt immunocastration, growth performance, fat composition

W445 Performance of growing-finishing pigs fed brewers rice and dried distillers brewers yeast. T. Dokes and O. Gekara*, *University of Arkansas Pine Bluff, Pine Bluff.*

The objective of this study was to determine whether brewers rice and dried distillers brewers yeast can replace all corn and soybean meal, and, significantly increase performance of growing-finishing pigs. Sixty-four Yorkshire × Duroc × Hampshire crosses (BW = 72 ± 13 kg) were randomly assigned to 4 diets: (1) corn/soybean meal (CSM; control); (2) brewers rice/soybean meal (RSM); (3) corn/dried distillers brewers yeast (CBY); (4) brewers rice/dried distillers brewers yeast (RBY). The 4 diets were formulated to be isonitrogenous. The experiment lasted 28 d; BW of finished pigs = 95 ± 14 kg. Variables determined included ADG, apparent total tract digestibility (ATTD) of nutrients (mainly N and P), fecal DM output, G:F, and back fat thickness. All data were analyzed using ANOVA of SAS. Compared with pigs fed on CSM and CBY diets, pigs on RSM and RBY diets gained faster (0.868 vs. 0.730 kg/d; $P < 0.01$), had reduced fecal DM output (0.299 vs. 0.607 kg/d; $P < 0.001$), and fecal loss of N (0.012 vs. 0.020 kg/d; $P < 0.01$) and P (0.012 vs. 0.017 kg/d; $P < 0.01$), had greater ATTD (89.7 vs. 78.9%; $P < 0.001$) and G:F (0.30 vs. 0.25 kg/kg; $P < 0.01$). Pigs fed on RSM and RBY tended ($P < 0.10$) to deposit more back fat compared with CSM and CBY pigs. Brewers rice and dried distillers brewers yeast can complement each other and greatly reduce fecal loss of N and P; thus, can effectively replace corn and soybean meal in diets for growing-finishing pigs.

Key Words: brewers rice, dried distillers brewers yeast, pig

W446 Effects of vegetable oils and residue of winemaking on performance, carcass traits, and pork quality. T. M. Bertol*[1], R. M. L. de Campos[2], E. A. P. de Figueiredo[1], and V. L. Kawski[1], *[1]Embrapa Suínos e Aves, Concórdia, SC, Brazil, [2]Fundação Universidade Federal do Vale do São Francisco, Petrolina, PE, Brazil.*

A 38 d study was carried out to evaluate the effect of dietary oil and grape bagasse on performance, carcass traits and pork quality. Forty barrows with a genetic composition of 50% Landrace, 25% Moura, and 25% Large White, averaging 80.12 ± 4.95 kg, were utilized. Treatments (TREAT) compared were (1) Control: corn-soybean meal based diet; (2) Diet with 1.5% of canola oil (CAN) + 1.5% of flax oil (FLAX); (3) Diet with 1.5% of CAN + 1.5% of FLAX, and 3 and 5% of grape bagasse (GB), for 21 and 17 d, respectively; (4) Diet with 1.5% of CAN + 1.5% of FLAX, and 6 and 10% of GB, for 21 and 17 d, respectively. The diets of TREATs 2, 3 and 4 were maintained isocaloric by replacing wheat bran by GB. The ANOVA model included block (initial weight), and TREAT. Means were compared by protected *t*-test and by orthogonal contrasts: TREAT 1 vs. TREATs 2, 3 and 4; TREAT 2 vs. TREATs 3 and 4; and TREAT 3 vs. TREAT 4 ($P < 0.10$). Average daily gain (ADG) and final weight (FW) increased with dietary oil supplementation (FW = 112.8 ± 1.69^{b}, 120.1 ± 2.00^{a}, 118.6 ± 2.47^{a}, 115.9 ± 2.68^{ab} kg; ADG = 0.862 ± 0.041^{b}, 1.044 ± 0.035^{a}, 1.016 ± 0.037^{a}, 0.944 ± 0.051^{ab} kg, for TREATs 1, 2, 3, and 4, respectively; $P < 0.01$). FW reduced with the inclusion of GB in the diet (contrast TREAT 2 vs. TREATs 3 and 4; $P < 0.05$). Backfat thickness, loin eye area and meat/fat ratio were not affected ($P > 0.05$) by TREATs. The values of pH 24 h after slaughter were higher on TREAT 2 than in the other TREATs (pH 24 h = 5.59 ± 0.03^{b}, 5.71 ± 0.04^{a}, 5.61 ± 0.01^{b}, 5.62 ± 0.04^{b}; $P < 0.06$). Ether extract (EE) of loin was lower and shear force (SF) was higher in the TREATs 2, 3 and 4 (EE = 2.36 ± 0.23, 1.84 ± 0.06, 1.92 ± 0.22, 2.00 ± 0.22%; SF = 1.86 ± 0.15, 2.25 ± 0.25, 2.18 ± 0.17, 2.39 ± 0.21 kg; contrast TREAT 1 vs. TREATs 2, 3 and 4; $P < 0.05$). In conclusion, dietary supplementation with CAN and FLAX, associated to wheat bran and GB, improved growth performance and decreased the intramuscular fat and tenderness, but it did not affect carcass traits. The inclusion of GB in the diet did not affect carcass traits, but the highest level of inclusion decreased growth performance.

Key Words: canola oil, flax oil, grape bagasse

W447 Effect of proportion of nonproductive sow days on lifetime production traits in swine under Thai tropical conditions. U. Noppibool[1], S. Koonawootrittriron[1], M. A. Elzo*[2], and T. Suwanasopee[1], *[1]Kasetsart University, Bangkok, Thailand, [2]University of Florida, Gainesville.*

The proportion of nonproductive days (PNPD, %) over the lifetime of a sow is an indicator for her production efficiency. Sows with lower PNPD would have higher production efficiency. The objective of this study was to investigate the effect of PNPD on lifetime number of piglets born alive (LBA), lifetime number of piglets weaned (LPW), lifetime piglets' birth weight (LBW), lifetime piglets' weaning weight (LBW), lifetime nonproductive sow days (LNPD), and length of productive life (LPL). The data set included 1,222 lifetime production records from 882 Landrace (L) and 340 Yorkshire (Y) sows that had their first farrowing from 2001 to 2008. Sows received similar management and health care under an open-house system in Thailand. The fixed linear model considered the fixed effects of first-farrowing year-season, breed of sow (L and Y), age at first farrowing and PNPD, and the random effect of residual. First-farrowing year-season had a significant effect ($P < 0.0001$) on LBW and LWW. Age at first farrowing had no effect on any trait. Breed of sow only affected LPW ($P = 0.0109$) and LPL ($P = 0.0358$). Yorkshire sows had larger LPW (52.50 ± 1.31 piglets vs. 48.67 ± 0.86 piglets) and longer LPL (772.55 ± 19.82 d vs. 727.68 ± 12.44 d) than L sows. Sows with higher PNPD had significantly ($P < 0.0001$) smaller LBA (−3.79 ± 0.42 piglets/%), LPW (−3.27 ± 0.37 piglets/%), LBW (−6.05 ± 0.70 kg/%), LWW (−25.63 ± 3.06 kg/%) and LPL (−48.99 ± 5.39 d/%), but larger LNPD (3.77 ± 0.26 d/%). These results indicated that reducing PNPD would increase the lifetime production efficiency of sows in this population.

Key Words: lifetime performance, nonproductive sow day, tropics

W448 Characteristics of lifetime preweaning production traits in Landrace and Yorkshire sows under tropical conditions. T. Jaichansukkit[1], T. Suwanasopee[1], M. A. Elzo*[2], and S. Koonawootrittriron[1], *[1]Kasetsart University, Bangkok, Thailand, [2]University of Florida, Gainesville.*

Sow lifetime preweaning production is economically important for commercial swine operations. Knowledge of the characteristics of preweaning production (PWP) traits from the first to the last parity of sows would help improve production efficiency. Thus, the aim of this study was to investigate the characteristics of lifetime PWP traits in Landrace (L) and Yorkshire (Y) sows raised in an open-house system in Thailand. The PWP traits were number piglets born alive (NBA), number of piglets weaned (NPW), average weight of piglets at birth (ABW), and average weight of piglets at weaning (AWW). The data set contained 11,081 records of NBA, NPW, ABW, and AWW from 1,377 sows (1,059 L and 318 Y) farrowed from 2001 to 2012 in a commercial swine population. The characteristics of each PWP trait were first-parity production (FPP), peak-parity production (PPP), number of parities from first to peak production (NFP), and persistency of production (regression coefficient) from third to last parity (P3L). The FPP, PPP, NFP, and P3L for NBA, NPW, ABW, and AWW were analyzed using a linear model that had year-season at first farrowing, genetic group (L and Y), and age at first farrowing as fixed effects and residual as a random effect. Year-season at first farrowing affected ($P < 0.05$) the 4 PWP characteristics for all traits, except for FPP for AWW, PPP for NPW, and P3L for NBA and AWW. Sows that farrowed at older ages in the first parity had higher PWP values for all traits ($P < 0.05$), but had lower peak-parity production values for AWW ($P = 0.047$) and lower number of parities from first to peak production for NBA ($P = 0.009$) and NPW ($P = 0.01$) than sows that farrowed at younger ages in their first parity. Genetic group only influenced ($P < 0.01$) FPP and PPP for NBA and P3L for AWW. Landrace sows had higher numbers of piglets at birth in their first and peak parities, and higher persistency of production from third to last parity than Y sows.

Key Words: pig, preweaning trait, tropics

Graduate Student Competition:
ADSA Southern Section Graduate Student Competition

274 Supplementing a pasteurized milk balancer product to two feeding levels of pasteurized whole milk fed to Holstein calves. K. Glosson*[1], B. Hopkins[1], S. Davidson[1], G. Smith[1], T. Earleywine[2], and C. Ma[1], *[1]North Carolina State University, Raleigh, [2]Land O'Lakes Animal Milk Products, St. Paul, MN.*

Using 80 Holstein heifer calves, this study investigated the effects of supplementing 2 levels of pasteurized whole milk with or without a pasteurized all-milk balancer product (Land O'Lakes Pasteurized Milk Balancer), on the growth of dairy calves. Two locations were used in this trial, NCSU Lake Wheeler Dairy (Raleigh, NC) and NCDA Piedmont Research Station (Salisbury, NC), with 40 calves fed according to the protocol at each site. All calves were removed from their dams after birth (d 0), fed 3.8L pasteurized colostrum, and received their respective treatment from d 1 until weaning at d 56. All calves were fed pasteurized whole milk from d 1 through d 56. There were 4 dietary treatments (n = 20 calves per treatment). Calves on treatment 1 and 2 were fed 3.8 L milk divided into 2 equal feedings from d 1 through d 56. Calves on treatment 3 and 4 were fed 3.8 L milk divided into 2 equal feedings from d 1 through d 14, 5.7L milk divided into 2 equal feedings from d 15 through d 42, and 2.85L milk fed once daily from d 43 through d 56. Treatments 2 and 4 included pasteurized all-milk balancer fed at a rate of 0.23kg per 3.8L of pasteurized whole milk. Calves were weighed and measured for wither height (WH), hip height (HH), and hip width (HW) every 7 d from birth until weaning at d 56. Average daily gain (ADG) and feed efficiency (FE) were calculated from d 0 through d 56. Feed efficiency is the ratio of ADG to dry matter intake (DMI), which included the total of milk dry matter (DM), milk balancer DM, and calf starter DM consumed. Calves fed treatment 4 had greater body weight (BW) and ADG through 56 d of age.

Table 1. BW, HH, HW, WH, ADG and FE as affected by treatment for 80 Holstein heifer calves from birth through weaning at 56 d

	Treatment					
Item[1]	1	2	3	4	SEM	$P \leq$
BW, kg	51.5[a]	54.0[ab]	52.9[ab]	58.8[c]	1.1	0.05
HH, cm	84.1	84.2	84.1	85.1	1.3	0.6
HW, cm	18.4	18.4	18.4	19.0	0.6	0.3
WH, cm	79.8	80.0	80.0	81.0	1.2	0.4
ADG, kg	0.64[a]	0.69[ab]	0.72[b]	0.84[c]	0.02	0.01
FE, kg/kg	0.62[a]	0.63[a]	0.70[b]	0.68[b]	0.02	0.03

[a-c]Means differ ($P < 0.05$).
[1]Average weight and frame measurements were calculated from birth until weaning.

Key Words: calf, growth, pasteurization

275 Methane production in ruminal continuous cultures fed bermudagrass harvested at varying stages of maturity. K. M. Young*[1], N. S. Hill[2], A. Thompson[2], D. W. Hancock[2], J. G. Andrae[1], W. C. Stringer[1], and T. C. Jenkins[1], *[1]Clemson University, Clemson, SC, [2]University of Georgia, Athens.*

Management intensive grazing systems on dairy farms in the Southeast are evaluated for efficient milk production as well as environmental impact. The objective of this study was to examine the relationship between forage maturity and rumen methane production. Tifton 85 bermudagrass was harvested at 5 maturity dates (14 d, 21 d, 28 d, 35 d and 42 d) from plots at the University of Georgia in the fall 2011, freeze-dried and ground (2-mm sieve). Thirty grams of harvested forage was fed daily to separate dual-flow continuous fermenters equipped with a gas sensor system to measure methane concentrations in headspace for 3 7 d periods. Average forage NDF and CP (%DM) ranged from 52.0 to 63.1, and 15.3 to 21.2 respectively. Methane readings were taken at each feeding (0800 and 1600 h) on d 3 and 4, and every hour between feedings on d 5 to 7. Methane data were analyzed by the Fit Model procedure in JMP (SAS Institute) with period and treatment × period interaction as random effects and treatment contrasts comparing 28 d vs. 42 d, and 42 d vs. all other maturities. VFA were determined by GC and the resulting data were analyzed by the glimmix procedure in SAS for variation due to maturity date, time after feeding, and their interaction. Feeding bermudagrass at 42 d decreased ($P < 0.05$) overall average methane production (13.5 mmol/d), compared with the average (19.8 mmol/d) of all other treatments. Average maximum (19.6 mmol/d) and minimum (6.4 mmol/d) methane production for 42 d tended to be lower ($P < 0.10$) than average maximum and minimum production (26.9 mmol/d, 10.9 mmol/d, respectively) of all other treatments. Feeding bermudagrass at 42 d also decreased ($P < 0.05$) overall average methane production compared with 28 d (21.7 mmol/d) and tended to decrease ($P < 0.10$) average maximum methane production compared with 28 d (30.0 mmol/d). Methane per g of DM or g of NDF fed had similar differences between maturities. Acetate/propionate was not affected by maturity (ranged from 4.4 to 4.9). The data suggest that forage maturity has no effect on rumen methane production unless cattle are grazed on bermudagrass of 42 d relative to forages aged 14 d-35 d.

Key Words: continuous culture, methane

276 Effects of feeding calcareous marine algae to Holstein cows beginning prepartum on postpartum performance and serum metabolites. Z. Wu* and J. K. Bernard, *University of Georgia, Tifton.*

Thirty-six multiparous Holstein cows and 12 springing heifers were used in a 9-wk randomized design trial to determine the effect of feeding calcareous marine algae (Acid Buf, Celtic Sea, Ireland) from 3 wk prepartum through 6 wk postpartum on DMI, milk yield and composition, blood and urine metabolites. Within parity, animals were assigned randomly to 4 treatments with a 2 × 2 factorial arrangement beginning 3 wk prepartum through 6 wk postpartum. Prepartum diets were balanced for a −10 DCAD with calcareous marine algae (CMA) or without (CON). Postpartum diets were formulated with either supplemental sodium bicarbonate (NBC) or CMA with a DCAD of 35 and 17, respectively. All diets were formulated to meet NRC requirements for late gestation and early lactation, respectively. No differences ($P > 0.10$) were observed in prepartum DMI which averaged 11.9 and 12.3 kg/d for CON and CMA, respectively. Postpartum DMI, milk yield, percentage of milk fat, protein, lactose, and SNF were not different ($P > 0.10$) among treatments and averaged 18.0, 37.7, 4.03, 2.71, 4.75, and 8.37; 19.8, 38.4, 4.06, 2.84, 4.74, and 8.38; 19.4, 37.5, 4.01, 2.70, 4.75, and 8.41; and 20.0 kg/d, 38.1 kg/d, 4.21%, 2.80%, 4.72%, and 8.37% for CON-NBC, CMA-NBC, CON-CMA, and CMA-CMA, respectively. No differences were observed among

treatments in serum metabolite concentrations prepartum, but serum Na concentrations were greater ($P < 0.05$) for cows fed NBC postpartum compared with CMA. Urinary concentrations of Na exhibited an interaction among treatments postpartum ($P = 0.0201$) and were highest for CON-NBC, intermediate for CMA-NBC, and lowest for CON-CMA and CMA-CMA; 128.62, 100.97, 56.88 and 37.97 mmol/L, respectively. Urinary K concentrations were higher ($P < 0.05$) for cows fed CMA postpartum compared with NBC; 157.78 and 116.76 mmol/L, respectively. Results of this trial indicate that cows feeding CMA prepartum did not affect prepartum DMI or serum metabolites. Performance and serum metabolite concentrations of cows fed CMA postpartum were comparable with that of cows fed NBC.

Key Words: DCAD, milk yield, milk composition

277 Changes in choline esters in blood and milk during early to mid lactation in dairy cows. V. M. Artegoitia*[1], J. M. Middleton[2], F. Harte[1], S. R. Campagna[2], and M. J. de Veth[3,4], *[1]Food Science and Technology, University of Tennessee, Knoxville, [2]Chemistry Department, University of Tennessee, Knoxville, [3]Animal Science, University of Tennessee, Knoxville, [4]Balchem Corporation, New Hampton, NY.*

Choline is an essential nutrient for humans and production animals. The ruminant is a unique animal model as almost all dietary choline is degraded in the rumen and the requirement for choline is not established for dairy cows. Therefore, understanding what choline forms are secreted by the mammary gland may provide an understanding of the lactation requirement for choline in the dairy cow. The objective of this study was to characterize the changes in choline and choline esters in blood and milk occurring in early and mid-lactation. Twelve Holstein cows were selected at calving and managed under the same diet, without choline supplementation. Throughout the study milk and blood samples were collected 3 times during early (wk 1, 2 and 3) and mid lactation (wk 7, 10 and 13). Free choline (Cho) and choline esters, glycerophosphocholine (GPC), lysophosphocholine (LPC), phosphatidylcholine (PtC), phosphocholine (PC) and sphingomyelin (SM), were analyzed using liquid chromatography-tandem mass spectrometry and quantified by using stable isotope-labeled internal standards. Differences reported are all $P \leq 0.01$. Total choline (Cho and all esters) concentration in plasma increased by 5-fold from wk 1 to wk 13 of lactation. The major choline forms in plasma were PtC (79%) and SM (14%) and both remained relatively constant through lactation. The concentration of all esters decreased in milk, except PtC (unchanged) and free choline (increased). The main choline forms in milk were PC (46%), PtC (27%) and Cho (11%). Total choline content in milk was negatively correlated with plasma total choline concentration ($r = -0.62$), whereas the free choline content in milk was positively correlated with total choline concentration in plasma ($r = 0.78$). The total daily milk output of choline (accounting only for choline moiety in esters) was highest in early lactation (averaged 2.7 g/d) and decreased during mid-lactation (wk 13 = 1.5 g/d; SE = 0.2). In summary, the 2-fold higher level of choline output by the mammary gland, combined with lower plasma levels, during early lactation suggest that there is a greater requirement for choline during this period.

Key Words: choline, requirement, LC-MS/MS

278 Characterization of lying time, milk yield, and rumination time with different freestall bases. B. A. Wadsworth*, A. E. Sterrett, C. L. Wood, K. J. McQuerry, J. D. Clark, D. L. Ray, and J. M. Bewley, *University of Kentucky, Lexington.*

Freestall bases may affect dairy cow productivity, longevity, and well-being. The objective of this study, conducted from January 18, 2012, to January 18, 2013, at the University of Kentucky Coldstream Dairy, was to compare daily lying time (LT), milk yield (MY), and rumination time (RUMT), for cows housed in 2 freestall barns. Barn "W" includes 50 Dual Chamber Cow Waterbeds (Advanced Comfort Technology, Reedsburg, WI) (DCCW) and barn "R" includes 50 rubber-filled mattresses (MAT). Both barns were renovated in November 2011 to the correct industry standard stall size for the largest Holsteins in the herd. Stall lengths were 1.8 m. Neck rail heights were 1.2 m, and mean stall widths were 1.2 m. All variables were classified for 96 cows (Holsteins (n = 70), Jerseys (n = 10), and crossbreds (n = 16)). IceRobotics (Edinburgh, Scotland) IceQube sensors, which contain a 3-axis accelerometer, recorded daily LT. MilkLine milking systems (Italy) recorded daily MY. The HR Tag (SCR Engineers, Ltd., Israel) recorded daily RUMT. The GLM procedure in SAS (Cary, NC) was used to evaluate factors influencing LT, MY, and RUMT. All main effects were kept in each model regardless of significance level. Stepwise backward elimination was used to remove non-significant interactions ($P \geq 0.05$). Daily LT was significantly ($P < 0.01$) higher for DCCW (10.79 h/d ± 0.20) than for MAT (10.06 h/d ± 0.22). MY was not significantly ($P = 0.78$) different between DCCW from MAT. Daily RUMT was significantly ($P < 0.01$) higher for MAT (382.10 min/d ± 7.18) than for DCCW (365.54 min/d ± 6.49). In this study, LT was higher for cows housed in freestalls with DCCW as a freestall base. Lying time can be an indicator of a comfortable and desirable resting area. Comfortable lying areas may improve cow leg and hock conditions. Dual Chamber Cow Waterbeds may provide a more resilient resting surface for dairy cows than rubber-filled mattresses. A resilient surface may benefit cow LT, overall productivity, and animal well-being.

Key Words: lying time, waterbeds, freestalls

279 Direct fed-microbial supplementation and milk replacer effects on performance of Holstein calves. A. J. Geiger*[1], S. H. Ward[1], C. C. Williams[2], B. J. Rude[1], C. J. Cabrera[1], K. N. Kaletsch[1], and B. E. Voelz[1], *[1]Mississippi State University, Mississippi State, [2]Louisiana State University, Baton Rouge.*

Forty-four Holstein calves were fed a direct-fed microbial (DFM) and increased CP in the milk replacer (MR) to evaluate performance and mitigation of heat stress. Treatments were: 1) control (CON; 22% CP, 20% fat), 2) MR+ (27% CP, 10% fat), 3) DFM (CON + DFM), and 4) DFMMR+ (MR+ with DFM). DMI, rectal temperatures, respiration scores, rates, and fecal scores were collected daily. Body weight (BW), hip and wither height, heart girth, blood and rumen fluid samples were collected weekly. Effects of treatment, sex, week, THI, and their interactions were analyzed using the MIXED procedure of SAS (Cary, NC). Contrast statements tested effects of milk replacer (CON and DFM vs. MR+ and DFMMR+); of DFM (CON and MR+ vs. DFM and DFMMR+), and CON vs. all other treatments. Birth weight was used as a covariate for BW. Significance was declared at $P < 0.05$. Calves only experienced heat stress (THI >72) on 8 d of the trial. CON calves tended to consume grain earlier compared with all other treatments (6.38 vs. 7.92 d, respectively; $P < 0.07$). Calves fed the MR+ had greater weaning BW (60.1 vs. 49.8 kg, respectively), hip height (87.7 vs. 84.2 cm, respectively), wither height (84.2 vs. 81.1 cm, respectively), and heart girth (91.2 vs. 85.7 cm, respectively; $P < 0.01$) compared with calves fed CON. Calves fed DFM, compared with the other treatments, had the greatest feed efficiency (4.13 vs. 2.07, respectively; $P < 0.01$). Fecal scores were greatest in calves fed

DFM, but rectal temperatures were lower ($P < 0.01$). Blood mineral concentrations, glucose, and hematocrit were not different. Serum protein was greater in calves fed CON compared with others (6.48 vs. 6.13 g/100 mL, respectively; $P < 0.01$). HCO3 and pCO2 were lower in calves fed CON and both were greater in calves fed MR+ compared with MR. DFM supplementation did not affect blood metabolites. Butyrate was lower in calves fed MR+ compared with MR (2.41 vs. 3.77, respectively; $P < 0.01$), but DFM did not have an effect. Isovalerate was greater in calves fed MR+ compared with MR and lower in calves fed DFM ($P < 0.01$). Rumen pH and other VFA were not different.

Key Words: milk replacer, calf, direct-fed microbial

280 Determining effects of castration timing with or without analgesia on growth performance and behavior in beef cattle. A. C. Brown*[1], J. G. Powell[1], E. B. Kegley[1], J. T. Richeson[2], and M. S. Gadberry[1], *[1]University of Arkansas, Fayetteville, [2]West Texas A&M University, Canyon.*

The study objective was to determine the effects of surgical castration at 2 stages of maturity (birth or weaning) with or without pain control (meloxicam) on growth performance and behavior. Bull calves (n = 60) were assigned randomly to treatments at birth. Treatments were (1) surgical castration near birth (BTH), (2) oral administration of meloxicam followed by surgical castration near birth (1 mg/kg BW; BMX), (3) surgical castration at weaning (WNG), or (4) surgical castration at weaning with oral administration of meloxicam (1 mg/kg BW; WMX). For statistical analysis, bulls left intact at birth (BUL) were considered a positive control for observations that occurred before their treatment application at weaning; subsequently, bulls castrated at birth (STR) were considered a negative control during postweaning observations. Data were recorded to determine behavior and growth performance. Calf standing and lying activity was monitored for a 7-d period at both stages (birth or weaning) by recording the x- and y-axes of an accelerometer attached to the metatarsus of the right leg. Body weight was recorded at birth and d 4, 33, 66, 116, 162, 199, 214 (weaning), 228, 246, and 270. Data interpreted from accelerometer recordings revealed 3 distinct behaviors being characterized as lying flat on side, standing, and lying on sternum. Following castration at birth, no treatment differences were observed for any of the behavior positions. Postweaning behavior indicated that STR calves spent the least amount of time standing ($P = 0.007$) when compared with WNG and WMX. Furthermore, WMX calves exhibited a greater proportion of time spent standing ($P = 0.05$) compared with WNG. Average daily gain did not differ between treatments ($P \geq 0.88$) throughout the preweaning period. However, 56 d post-weaning ADG was greatest ($P = 0.02$) in STR, intermediate in WMX, and least in WNG. Early castration near birth did not affect weaning weight or behavior, whereas delaying castration until weaning reduced postweaning ADG, but this reduction was mitigated by the use of meloxicam at the time of castration.

Key Words: castration, meloxicam

281 Effects of pre- and postoperative carprofen on convalescence of calves following umbilical surgery. I. Schulze[1], J. Offinger[1], A. K. List[1], S. Kaestner[2], H. Meyer[1], and J. Rehage*[1], *[1]Clinic for Cattle, University of Veterinary Medicine Hannover, Hannover, Germany, [2]Clinic for Small Animals, University of Veterinary Medicine Hannover, Hannover, Germany.*

Pain management protocols for surgeries in calves should include the application of efficient analgesics. Aim was to evaluate the effects of perioperative treatment with the non-steroidal anti-inflammatory drug carprofen on convalescence of calves following umbilical surgery. In a randomized and blinded study, 23 healthy calves aged 4–7 weeks were treated either with carprofen (n = 12; 1.4 mg/kg, i.v.) or an equivalent volume of physiological saline solution (n = 11), 1 h before and 72 h after surgery. Umbilical surgery took place under isoflurane inhalation anesthesia [induction with xylazine (0.1 mg/kg, i.m.) and ketamine (2 mg/kg, i.v.)] combined with an infiltration of the incision line (15 mL 2% procaine). Before surgery and in the following 10 d, feed intake and weight gain were measured; behavior was assessed using a multiple pain and discomfort scale by direct observation and from video recordings. Sensitivity of the traumatized tissue to palpation was evaluated by means of a visual analog scale. Serum cortisol and pepsinogen levels, red blood cell counts and occult blood in feces were monitored. Continuous data were evaluated by means of the GLM procedure for repeated measurements, scores by Wilcoxon non-parametric tests and frequencies by Fisher Exact Test of the SAS statistical package. Calves in the carprofen-treated group had significantly ($P < 0.05$) higher mean feed intake [0.31 ± 0.03 MJ ME/(kg BW d)] and weight gain (669 ± 197 g/d) than control calves [0.28 ± 0.03 MJ ME/(kg BW d)] and 459 ± 197 g/d). Increased well-being in the carprofen-treated calves was reflected by significantly ($P < 0.05$) lower scores in the multiple pain and discomfort scale (5 ± 0.5 vs. 9 ± 0.6) and visual analog scale (25 ± 4.7 vs. 38 ± 5.0). No group differences were found for red blood cell counts, serum pepsinogen and cortisol and fecal occult blood tests. Perioperative carprofen promotes postoperative well-being resulting in increased feed intake and weight gain. Repeated carprofen treatment appears to have no considerable effects on the integrity of the abomasal mucosa in calves undergoing umbilical surgery.

Key Words: calf, carprofen, pain management

282 Effect of surgical castration of bull calves at different stages of maturity with or without analgesia on the acute phase response (APR) and complete blood count (CBC). H. D. Hughes*[1], J. G. Powell[2], E. B. Kegley[2], A. C. Brown[2], N. C. Burdick Sanchez[3], J. A. Carroll[3], and J. T. Richeson[1], *[1]Department of Agricultural Sciences, West Texas A&M University, Canyon, [2]Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville, [3]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX.*

The study objective was to determine if surgical castration at birth or weaning affects the APR or CBC and whether concurrent administration of an oral analgesic (meloxicam) ameliorates inflammation. Bull calves (n = 29) from the University of Arkansas research herd were assigned to treatment at birth, moved with their dam into pens for 7-d, and returned to pasture until weaning on d 214. Treatments included: 1) castration near birth (BTH), 2) castration near birth with oral administration of meloxicam (1 mg/kg BW; BMX), 3) castration at weaning (WNG), or 4) castration at weaning with oral administration of meloxicam (1 mg/kg BW; WMX). For statistical analyses, bulls left intact at birth were considered a positive control for observations that occurred before their treatment application at weaning; likewise, bulls castrated at birth were considered a negative control (STR) during post-weaning observations. Blood samples were collected from the jugular vein on d 0 (birth), 1, 3, 7, 214 (weaning), 214+6 h, 215, 217, 221, and 228. Whole blood was analyzed for CBC using an automated hemocytometer; serum was analyzed for concentrations of interleukin-6 (IL6), interferon-γ, tumor necrosis factor-α, and haptoglobin (Hp) using an enzyme-linked immunosorbent assay. The APR was not affected by treatment near birth; however, an overall decrease (day effect; $P < 0.001$) in IL6 was observed between birth and d 7. At weaning, Hp was greater ($P \leq 0.005$) for castrates compared with STR on d 214+6 h, 215, and 217 and was greater ($P = 0.05$) in WNG vs. WMX on d 217. Neutrophils (NEU) increased ($P < 0.001$) and red blood cells decreased ($P \leq 0.03$) for castrates on d 214+6 h and 217, respectively; whereas, WMX tended ($P = 0.10$) to have lower NEU than WNG on d 215. Castration at weaning, but not near birth, altered immune parameters. Oral meloxicam reduced serum Hp when administered to calves castrated at weaning, but not in calves

castrated near birth. Therefore, oral administration of meloxicam may be efficacious when surgically castrating older bull calves at or beyond the typical weaning age.

Key Words: castration, haptoglobin, meloxicam

283 Effect of a cooling gel on pain sensitivity and healing of hot-iron cattle brands. C. B. Tucker*[1], E. M. Mintline[1], J. Banuelos[1], K. A. Walker[2], B. Hoar[1], D. Drake[1], and D. M. Weary[2], *[1]University of California, Davis, [2]University of British Columbia, Vancouver, BC, Canada.*

Hot-iron branding is painful for cattle, but little is known about the duration of or effective methods to control this pain. Previous work with pigs indicated that cooling burns with a gel (active ingredient, tea tree oil) improved healing compared with untreated wounds. Steers (210 ± 5 kg) were hot-iron branded and allocated to 1 of 3 treatments: control (n = 24), 1 gel application immediately after branding (1×; n = 12) or 2 gel applications, once immediately after branding and 24 h later (2×; n = 12). Wound sensitivity was assessed by applying, in 5 locations (in the center, at the top of, 5 and 10 cm above the brand and on the non-branded side), a known and increasing force with a von Frey anesthesiometer until the animal showed a behavioral response. Healing was measured with a 6-point scale (1 = fresh brand, 6 = no scabbing and fully re-pigmented). Both measures, along with weight gain and temperature of the wound were recorded before, 24, 48, 72 h and 1, 2, 3, 4, 5, 8 and 10 wk after branding and analyzed with a mixed model. The gel immediately cooled the brand (38.7 ± 0.7 vs. 34.9 ± 0.6°C for the control vs. 1×/2× treatments), but there were no treatment differences in wound temperature at any other time ($P > 0.26$). All wounds were at least partially re-pigmented by 10 wk, but only 46% of brands were fully healed this time. The healing process was slowed in the 2× group (e.g., at 21 d 2.6 ± 0.1 vs. 2.0 ± 0.2, for control/1× vs. 2×, respectively, $P < 0.01$). Brands remained sensitive throughout the 10 wk (before vs. all other time points, in center of brand, $P = 0.01$). Overall, wound sensitivity tended to be lower for the 1× treatment in the center, 5 and 10 cm from the brand (177 ± 31, 318 ± 68, 412 ± 60 vs. 205 ± 29, 355 ± 67, 460 ± 59 g force for the 1× vs. control treatments, $P \leq 0.07$). Weight gain was reduced in the week of branding, but was not affected by gel application. In conclusion, applying gel 1× tended to reduce wound sensitivity. However, 10 wk after the procedure, hot-iron brands remained more sensitive than non-branded tissue and 54% were not fully healed. These results contribute to animal welfare concerns about hot-iron branding.

Key Words: branding, beef, welfare

284 Relationships of various feeding behavior indicia with divergent residual feed intake measurements in Japanese Black cattle. M. McGee*[1], J. A. Ramirez[2], G. E. Carstens[2], J. B. Hall[2], and R. A. Hill[1], *[1]University of Idaho, Moscow, [2]Texas A&M University, College Station, [3]University of Idaho Nancy M. Cummings Research, Education, and Extension Center, Carmen.*

Objectives of this study were to examine relationships among residual feed intake (RFI) and feeding behavior indicia of Japanese Black cattle (Wagyu). Ninety-two yearling Wagyu bulls were examined for RFI and behavioral patterns using a monitoring system (GrowSafe Systems) over a standard 70 d period. Post-test, individual animal RFI was calculated; with top and bottom quartiles (with respect to RFI) used to analyze feeding behavior parameters. A population of 46 animals (n = 23 high RFI; BW initial 420.0 ± 46.1 kg, final 485.8 ± 51.3 kg; n = 23 low RFI BW initial 416.6 ± 63.9 kg, final 485.0 ± 71.3 kg) were examined for feeding behavior. Analyses were performed using Proc GLM procedures of SAS by quartile. Of the behavior variables examined, RFI was positively correlated with feed bout duration (feeding event exceeded 300 s between initial and final transponder reading mean: efficient 4090.4 ± 151.9 s, inefficient: 4546.4 ± 151.9 s; r = 0.40; $P = 0.01$), bunk visit (time at bunk with or without feed intake) duration (mean: efficient 4223.8 ± 158.6, inefficient 4677.0 ± 158.6s; r = 0.38; $P = 0.01$), average meal intake (mean: efficient 1408.4 ± 63.3 s, inefficient 1565.9 ± 63.3; r = 0.31; $P = 0.03$) and meal duration (mean: efficient 7157.2 ± 278.3, inefficient 7813.1 ± 278.3; r = 0.33; $P = 0.03$); defined as one or more feed bouts exceeding 300 s between transponder readings. Residual feed intake was not correlated with feed bout frequency (mean: efficient 31.62 ± 1.65 events, inefficient 35.25 ± 1.65 events; r = 0.22; $P = 0.13$), bunk visit frequency (mean: efficient 36.10 ± 1.89, inefficient 39.92 ± 1.89 events; r = 0.21; $P = 0.17$) or meal frequency (mean: efficient 7.75 ± 0.47 events, inefficient 8.90 ± 0.47; r = 0.23; $P = 0.12$). Results provide insight of the unique characteristics of Wagyu cattle feeding behavior, not reported the literature. A strong positive correlation was found between consumption time and intake. Frequency parameters were not found to be associated with RFI. With this known, research in feeding behavior traits of Wagyu cattle may aid in selection for feed efficiency in this breed.

Key Words: Wagyu, RFI, feeding behavior

285 Effects of supplementing endophyte-infected tall fescue with sainfoin and polyethylene glycol on the physiology and ingestive behavior of lambs. F. Catanese[1,2], R. A. Distel[1,2], and J. J. Villalba*[3], *[1]Centro de Recursos Naturales Renovables de la Zona Semiárida (CERZOS), Bahia Blanca, Argentina, [2]Departamento de Agronomía, Universidad Nacional del Sur, Bahia Blanca, Argentina, [3]Utah State University, Logan.*

Tannins in sainfoin might bind to alkaloids in endophyte-infected tall fescue (E+) and attenuate fescue toxicosis. If so, supplementing E+ with sainfoin will increase use of E+ by sheep and polyethylene glycol (PEG) -a polymer that binds to tannins- will attenuate such response. Thirty-six 2-mo-old lambs were randomly assigned to 3 treatments (12 lambs/treatment). Lambs were individually penned and fed E+ (CTRL), E+ and 200 g DM of fresh-cut sainfoin (SAIN) or the same amount of sainfoin + 33 g of PEG (SAIN+PEG) during 23 d. Daily food intake and rectal temperatures were estimated and jugular blood was extracted at the beginning and end of the period. While in pens, all lambs had choices between the novel forages endophyte-free fescue (E−) and orchardgrass for 4 d. Then, all lambs were allowed to graze a choice of E+ and sainfoin, or a monoculture of E+ for 14 d and grazing behavior was recorded. Response variables were analyzed using a mixed effects model which included treatment and day as fixed effects and lamb as random factor. Lambs in SAIN ingested more E+ than lambs in CTRL ($P = 0.05$), but no differences were detected between lambs in SAIN+PEG and CTRL ($P = 0.12$). Only SAIN lambs had lower rectal temperatures ($P = 0.02$), greater numbers of leukocytes ($P < 0.001$) and lymphocytes ($P = 0.03$), and greater plasmatic concentrations of globulin ($P = 0.01$) and prolactin ($P = 0.02$) than CTRL lambs. Lambs in SAIN showed the greatest intake of E− ($P < 0.001$). When lambs had a choice of E+ and sainfoin, all treatments grazed E+ to the same extent ($P > 0.05$). However, when they grazed on a monoculture of E+, lambs in SAIN+PEG showed the greatest use of E+ ($P < 0.05$). In summary, sainfoin supplementation increased intake of E+, preference for E− and improved some physiological parameters indicative of fescue toxicosis. Tannins in sainfoin partially accounted for such benefits since feeding

PEG along with sainfoin attenuated those responses. However, early exposure to E+ supplemented with sainfoin did not lead to an increased acceptance of or preference for E+ during grazing.

Key Words: alkaloid, ingestive behavior, tannin

286 Behavior of beef cattle as affected by horn fly numbers. A. R. Mays*[1], M. A. Brown[2], and C. F. Rosenkrans, Jr.[1], *[1]University of Arkansas, Fayetteville, [2]USDA-ARS, Grazinglands Research Laboratory, El Reno, OK.*

Beef cattle profitability traits may be influenced by the effect of horn flies on cattle behavior. The objective of this study was to determine if horn flies affected beef cattle behavior. Crossbred cows (n = 53) from Brangus dams were sired by either Bonsmara, Brangus Charolais, Gelbvieh, Hereford, or Romosinuano bulls; and their Angus-sired calves were used in the study. Pasture behavior of individual cows was recorded twice a day (AM and PM) along with total horn fly counts (AM only) from May through October. Cattle were observed and recorded as grazing, lying or standing. Exit velocity (EV) was obtained monthly for cows and calves. Pasture behavior and horn fly numbers were analyzed by mixed model least squares using a linear model that included breed group, behavior (either AM or PM) and month. The linear model for EV included breed type, month and breed × month. Horn fly numbers varied over month ($P < 0.0001$), with the lowest numbers in May (94 ± 42 flies) and highest numbers in August (503 ± 41 flies). Pasture behavior in the AM was not associated ($P > 0.25$) with horn fly numbers; however PM behavior was ($P < 0.05$). Cows observed grazing and lying had greater horn fly numbers than cows observed standing in the afternoon (468 ± 52 and 419 ± 38 vs. 319 ± 27 flies; respectively). Numerically pasture AM behavior showed grazing cows having more horn flies than standing or lying cows. Exit velocity of both cows ($P < 0.0001$) and calves ($P < 0.05$) differed by month. Cow EV was greatest in October (1.42 ± 0.2 m/s) compared with May, June, July and September (2.69 ± 0.2, 2.41 ± 0.2, 2.34 ± 0.2 and 1.98 ± 0.2 m/s; respectively), with August being similar to September and October (1.64 ± 0.2 m/s). Calf EV was greatest in September, July, August and October (0.90 ± 0.2, 0.84 ± 0.2, 0.75 ± 0.2 and 0.74 ± 0.2 m/sec; respectively) compared with June (1.56 ± 0.2 m/s), with May being intermediate (1.06 ± 0.2 m/sec). Horn fly numbers appear to be associated with behavior of beef cattle in this study. The genetic and physiological mechanisms linking horn fly numbers with cattle behavior and profitability traits should continue to be the subject of future investigation.

Key Words: behavior, exit velocity, horn flies

287 The behavior of cattle unloaded for feed, water and rest during long-distance transportation in Canada. H. E. Flint*[1], K. S. Schwartzkopf-Genswein[2], K. G. Bateman[1], and D. B. Haley[1], *[1]University of Guelph, Population Medicine, Guelph, Ontario, Canada, [2]Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada.*

Roughly half of the beef cattle finished in Ontario come into the province from western Canada. Transport regulations indicate that cattle only need to be rested en route (5 h minimum) if their journey is expected to exceed 52 h. There is public concern that this limit is outdated and may compromise cattle welfare. As a first step to evaluating how well cattle are coping with the stress of transit, the objective of our study was to examine the behavior of cattle being rested during long-distance transport. A total of 87 pens of cattle, from 53 different trucks, were observed at a commercial rest stop facility. Truck drivers were surveyed about their loads. During unloading and loading the number of times animals slipped or fell was recorded. Behavior was recorded every 5 min for the first 5 h after unloading, using instantaneous sampling to document the number of cattle eating, drinking and lying. A mixed linear regression model was used for analysis with load as a random effect. The probability of an animal being observed performing a given behavior was the outcome. When feeding behavior was modeled there was increasing odds of feeding as time in transit increased ($P < 0.01$). There was a sex by distance traveled interaction; heifers had a decreased probability of feeding as distance traveled increased, while steers remained constant ($P = 0.02$). When drinking behavior was modeled, odds of drinking increased as outside temperature at unloading increased ($P = 0.02$). Cattle from loads with 4 slips during unloading had greater odds of drinking than those with less ($P = 0.03$). There was a quadratic relationship between distance traveled and drinking behavior where cattle had increasing odds of being observed drinking as distance increased up to a maximum of 1633km traveled then odds of drinking decreased ($P < 0.01$). When lying was modeled, heifers had higher odds of lying than steers ($P < 0.01$) and odds of lying decreased with increasing time in transit ($P < 0.01$). Overall, these results suggest heifers may be more affected by the stress of transit, and that as journey duration increases cattle are more likely to eat and less likely to lie down.

Key Words: beef cattle, transport, behavior

288 Characterizing loads of cattle that stop for feed, water and rest during long-distance transportation in Canada. H. Flint[1], K. S. Schwartzkopf-Genswein[2], K. G. Bateman[1], and D. B. Haley*[1], *[1]University of Guelph, Guelph, ON, Canada, [2]Agriculture & Agri-Food Canada, Lethbridge, AB, Canada.*

Roughly 200,000 beef cattle are transported into Ontario from western Canada each year. By law, if the trip will exceed 52 h, the cattle must be unloaded for feed, water, and rest, for ≥5 h. Some argue handling stress may outweigh the perceived benefits. The objective of our descriptive study was to characterize the loads of cattle stopping at one of 2 rest stations near Thunder Bay, ON and observe unloading/reloading. Drivers voluntarily completed a survey about their load and journey. We observed unloading and reloading for 104 truckloads, recording the time required to do these tasks and counting slips and falls by the cattle. A slip involved the animal losing its balance but remaining upright, while a fall was defined as any part of the animal's body, other than its legs, coming into contact with the ground. We also noted whether the driver carried an electric prod, although we could not quantify prod use. On average the loads we observed were in transit for (mean ± SD) 29.20 ± 4.70 h before reaching the rest station and they stopped for 11.23 ± 2.75 h. The mean number of cattle per load was 100.7 ± 10.0 for weaned calves (<300 kg), 63.9 ± 11.7 for backgrounded (300–550 kg), and 42.9 ± 2.7 for market-weight cattle (>550 kg). The mean time taken to unload was 16.48 ± 5.77 min (n = 89) and was similar to the time required to reload: 15.70 ± 5.43 min (n = 99). The average number of slips and falls per load were low, but fewer occurred during unloading (slips = 0.67 ± 1.10; falls = 0.14 ± 0.38/load) than reloading (slips = 1.51 ± 2.21; falls = 0.33 ± 0.69/load). The drivers of 95/102 loads carried an electric prod while handling their animals. Twenty-three percent of drivers surveyed had taken Certified Livestock Transport training, which is a voluntary animal handling and transportation training program in Canada. In our study drivers stopped for feed, water and rest well before the maximum legal time limit of 48 h. Our results also show that animals are rested for substantially longer than the legal minimum requirement of 5 h. Last, in this study, the unloading and reloading of animals happened relatively quickly with few slips or falls.

Key Words: transportation, beef cattle, welfare

289 Evaluation of temperament scoring methods for beef cattle. R. C. Vann*[1], D. G. Riley[2], D. A. Neuendorff[3], N. C. Burdick Sanchez[4], J. A. Carroll[4], T. H. Welsh Jr.[5,2], and R. D. Randel[3], *[1]MAFES-Brown Loam Exp. Station, Raymond, MS, [2]Department of Animal Science, Texas A&M University, College Station, [3]Texas A&M AgriLife Research, Overton, [4]Livestock Issues Research Unit, USDA-ARS, Lubbock, TX, [5]Texas A&M AgriLife Research, College Station.*

The objective of this study was to evaluate methods of temperament scoring in beef cattle. Crossbred (n = 228) calves were evaluated for temperament by an individual evaluator at weaning by 2 methods of scoring: (1) pen score (1 to 5 scale, with higher scores indicating increasing degree of nervousness, aggressiveness, etc.; groups of 3 animals) and (2) exit velocity (m/s; as the rate the animal traverses 1.83 m upon exiting a squeeze chute). Temperament score was the average of pen score and exit velocity. In addition, these same calves were re-evaluated for temperament with 2 methods of pen score 1 wk later: (1) individual pen score (1 to 5 scale) and (2) group pen score (1 to 5 scale; groups of 3 animals, same format as weaning measure); however every animal was given a pen score regardless of scoring method. Data were analyzed using mixed linear models with sire as a random effect. Age and sire breed of calf did not ($P \geq 0.05$) affect temperament measurements; however, sex of calf did influence group and individual pen score measurements ($P \leq 0.05$) and tended ($P = 0.08$) to influence weaning pen score measurement. Heifers had greater pen score measurements compared with bulls and steers when scored as a group (3.87 ± 0.12 vs. 3.08 ± 0.21 and 3.36 ± 0.14, respectively), and greater than bulls when scored as individuals (3.69 ± 0.13 vs. 3.19 ± 0.21 and 3.37 ± 0.14, respectively) and at weaning. Pen scores in groups were highly correlated ($P \leq 0.0001$) with individual pen score (0.81); weaning pen score (0.62), weaning exit velocity (0.54) and weaning temperament score (0.67). For residual correlation coefficients, pen scores in groups were highly correlated ($P \leq 0.0001$) with individual pen score (0.79); weaning pen score (0.61), weaning exit velocity (0.55), and weaning temperament score (0.66). In summary, (1) female calves have greater pen scores compared with male calves; (2) temperament score did not differ between group or individual pen scoring methods; and (3) results from these methods were highly correlated with each other and with results derived from other established methods of temperament scoring.

Key Words: beef cattle, temperament, pen scoring

290 Effects of weaning, repeated handling and transport on immune- and inflammatory genes and stress hormones. W. R. Binion*, T. H. Friend, J. E. Sawyer, P. K. Riggs, K.J. Kochan, and J. T. Jaques, *Dept. of Animal Science, Texas A&M University, College Station.*

The objective of this study was to determine if changes in expression of certain stress related genes could be useful indicators of stress. Angus sired steers (n = 20) between 5 and 6 mo of age and 166 ± 32 kg were weaned and then transported in 4 groups of 5 steers at a stocking density of 0.9 m^2 per head for 12 h. Jugular blood samples were taken before loading (0 h), and steers were briefly unloaded after 4, 8 and 12 h of transport for resampling. Steers were allowed ad libitum access to feed and water after transport and were then resampled 12 h post transport (24 h). RNA was extracted from leukocytes and transcript levels were quantified by real-time PCR for 15 genes using ribosomal RNA 18S as the reference gene and quantified by the delta delta CT method. Eleven genes (LSP1, IL4R, HSP90AA1, IL10RB, SERP1, HSF2, CCRL1, TNFRSF1A, CXCR2, IL1RN, and IL12B) showed significant increases, or decreases, across the 3 sampling intervals ($P < 0.05$). CCRL1 showed the greatest increase in expression of all genes between the 8 h and 12 h sample ($P < 0.001$) Four genes (CCRL1, CXCR2, IL12B, and TNFRSF1A) decreased in expression during the 12 h recovery period ($P < 0.05$); no genes increased in expression during recovery. Four genes (CCR5, CXCR5, IFIT5, and IK) showed no response to transport or recovery ($P > 0.10$). Serum cortisol, triiodothyronine (T_3), and thyroxine (T_4) increased ($P < 0.05$) in concentration from 0 h to 12 h. Cortisol and T_3 decreased ($P < 0.05$) from 12 h to 24 h, with T_4 unchanged from 12 h to 24 h ($P < 0.30$). Mean weight loss of calves was significant (11.43 kg, $P < 0.05$) from 0 h to 12 h, and did not recover BW ($P = 0.59$) at 24 h. Cortisol, T_3, and T_4 responded to transport stress and recovery. Significant changes in expression for 11 genes indicate that these genes may be useful indicators of detrimental stress.

Key Words: gene expression, transport, stress

291 Genetic parameters of three methods of temperament evaluation of beef calves. S. E. Schmidt*[1,2], D. A. Neuendorff[1], D. G. Riley[2], R. C. Vann[3], S. T. Willard[4], T. H. Welsh Jr.[2], and R. D. Randel[1], *[1]Texas A&M AgriLife Research, Overton, [2]Texas A&M University, College Station, [3]MAFES-Brown Loam, Mississippi State University, Raymond, [4]Mississippi State University-Starkville, Starkville.*

The objective of this study was to estimate the heritability of 3 measures of temperament in Brahman and Brahman-influenced calves (n = 1,209). Individual animal pen scores (PS) were determined by a trained observer who evaluated groups of 4 calves at a time for willingness to approach a human. Exit velocity (EV) was the rate (m/s) at which each calf exited a squeeze chute. Temperament score (TS) was calculated individually (PS+EV/2). Temperament was evaluated at 5 different ages (28 d preweaning, weaning, 28 d postweaning, 56 d postweaning, yearling). Contemporary groups (n = 34) were comprised of calves of the same sex born in the same season of the same year. There were an average of 86 calves per contemporary group which ranged from 60 to 224. Average weaning age (186 d) ranged from 105 to 304 d. Calves were born from 2002 through 2012. Random effects included additive genetic and the permanent environmental variance. The fixed effects analyzed were age of dam, sex of calf, contemporary group, fraction of Brahman (2 levels: 1 and 0.5), age of calf at record, and weaning age. At weaning, the mean PS was 2.68 ± 0.1, the mean EV was 2.41 ± 0.1, and the mean TS was 2.48 ± 0.1. PS was affected by fraction of Brahman ($P = 0.034$) and tended to be affected by age of dam ($P = 0.06$). EV was affected by contemporary group ($P < 0.001$) and tended to be affected by weaning age ($P = 0.074$). TS was affected by contemporary group ($P < 0.001$). All 3 methods of temperament evaluation were affected by age of calf at record ($P < 0.001$). The regression coefficients for PS, EV, and TS were 0.0023 ± 0.0014, 0.0022 ± 0.0012, and 0.0015 ± 0.0012, respectively. Estimates of maternal genetic effects were always 0 and omitted from final models. Estimates of heritability were 0.27 ± 0.1, 0.49 ± 0.1, and 0.43 ± 0.1 for EV, PS, and TS, respectively. Estimates of permanent environmental variances as proportions of phenotypic variance were 0.33 ± 0.1, 0.23 ± 0.1, and 0.33 ± 0.1 for EV, PS, and TS, respectively. There appears to be sufficient additive genetic variance for selective improvement of temperament characteristics in Brahman cattle.

Key Words: temperament, heritability, Brahman

292 Effect of intrauterine dextrose or iodine infusions on clinical cure and reproductive performance of lactating dairy cows with clinical metritis under certified organic management. M. G. Maquivar*[1,2], A. Barragan[2], J. Velez[2], H. Bothe[2], and G. M. Schuenemann[1], *[1]Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, [2]Aurora Organic Dairy, Platteville, CO.*

The objective was to assess the effect of intrauterine infusion of 50% dextrose in water (DEX) or 0.18% povidone-iodine in water (IOD) on clinical cure and pregnancy per AI (P/AI) of lactating dairy cows diagnosed with clinical metritis (MET). Cows (n = 303) from 1 organic dairy herd were screened for MET at 7 ± 3 DIM. Cows with MET (foul-smelling brown-red watery vaginal discharge) were stratified by parity and randomly allocated into 1 of 2 treatments: (1) 1 L of DEX (n = 71) or (2) 1 L of IOD (n = 74). At 26 ± 3 DIM post-therapy, treated cows were re-examined for clinical endometritis (CE; scale 0–3) to assess treatment responses (cured = vaginoscopy score 0 or 1). All cows were subjected to the same reproductive program (estrous detection with tail chalking) and cows displaying signs of standing estrus any time after the voluntary waiting period (45 d) were AI. Body condition score (BCS) was recorded at 7 ± 3 and 26 ± 3 DIM. Pregnancy diagnosis was performed via ultrasonography at 39 ± 3 d post-AI. The proportions of cows that were cured and P/AI to first services were assessed using GLIMMIX. Non-MET cows (n = 158) were included in the analysis. DIM at first service, cervix diameter, BCS at treatment, and rectal temperature at treatment were not different between IOD and DEX groups. The proportion of cured cows tended to be greater for IOD (48.5%) than DEX cows (31.3%; $P = 0.1$). The DIM to first AI was shorter ($P < 0.05$) for non-MET cows (70.3 d) compared with DEX (76 d) or IOD cows (82 d). The DIM to conception was shorter ($P < 0.05$) for non-MET cows (90 d) compared with DEX (105 d) or IOD cows (109 d). IOD treatment tended to improve clinical cure of MET cows. Although non-MET cows had greater P/AI (37.6%; $P < 0.05$), the proportion of P/AI was similar between DEX (16%) and IOD cows (15%; $P > 0.05$). Further investigation is needed to determine the efficacy of intrauterine DEX and IOD therapies for the treatment of MET in organic dairy herds.

Key Words: metritis, dairy cow, organic management

293 Identification of biomarkers in milk for degree of physiological imbalance for lactating dairy cows. K. M. Moyes*[1], J. S. Osorio[2], V. Bjerre-Harpøth[1], B. M. Damgaard[1], V. M. Thorup[1], T. Larsen[1], J. J. Loor[2], and K. L. Ingvartsen[1], *[1]Aarhus University, Tjele, Denmark, [2]University of Illinois, Urbana.*

Identification of biomarkers in milk for degree of physiological imbalance (PI), a situation in which physiological parameters deviate from the normal, is needed for early detection of cows at risk for disease thereby improving animal welfare and performance and economic outcome for farmers. A meta-analysis was conducted using 3 separate studies consisting of 265 cows of 2 breeds (Holstein and Jersey) ranging from parities 1 to 5 extending over an entire lactation period (i.e., 0–69 weeks in milk). An index for PI was generated based on weekly plasma glucose, NEFA and BHBA where PI index = [ln(NEFA)] + [ln(BHBA)] – [glucose]. Composite milk samples were collected and analyzed for fat (%), protein (%), lactose (%), somatic cells (cells/mL), isocitrate (m*M*), free glucose (m*M*), BHBA (m*M*), and glucose-6-phosphate (m*M*). Pearson correlations were generated among the PI index and milk components using SAS. Regression analysis using maximum R-squared was used to identify milk components that best explain variations in degree of PI. PROC MIXED was used to determine the effect of stage of lactation, parity and breed on variations in milk components. Free glucose in milk explained most of the variation in PI for cows in early lactation whereas isocitrate in milk explained most of the variation in PI for cows in later lactation (i.e., >13 wk in milk). We identified free glucose and isocitrate in milk as potential biomarkers for degree of PI for cows throughout lactation. Cows with a greater degree of PI experienced higher isocitrate and lower free glucose in milk when compared with cows with lower degree of PI. Breed and stage of lactation altered concentrations of free glucose and isocitrate; and free glucose in milk was affected by parity. Further investigations of in-line and real-time measurement of these indicators of degree of PI and the use in individual cow and herd management is warranted.

Key Words: physiological imbalance, biomarker, milk

294 Use of digital infrared thermography and oxidative stress biomarkers as a diagnostic tool to diagnose interdigital dermatitis in sheep. S. Talukder*[1] and P. Celi[1,2], *[1]The University of Sydney, Narellan, NSW, Australia, [2]The University of Melbourne, Parkville, VIC, Australia.*

This study reports preliminary data on the use of digital infrared thermography (IRT) and biomarkers of oxidative stress (OS) to diagnose the degree of interdigital dermatitis (ID) lesions in sheep. Interdigital space skin temperatures were obtained from healthy (n = 6) and ID affected (n = 11) crossbred rams with a FLIR T620 series infrared camera and images were analyzed using ThermaCAM Researcher Professional 2.9 software. Interdigital space lesions were scored using a 5 point scoring system (0–4). Blood were sampled from 17 rams and plasma was analyzed for reactive oxygen metabolites (d-ROMs), biological antioxidant potential (BAP), and advanced oxidation protein products (AOPP). The degree of OS was estimated by the ratio of ROMs/BAP (U.Carr./µmol/L) multiplied by 100 to give an OS index (OSI). Footrot scores were used to stratify the rams in 3 groups: Group A (0 > 0.5), B (0.5 > 1.5) and C (≥1.5). Changes in OS biomarkers and skin temperature were analyzed by a linear mixed model using Genstat version 14. We observed that skin temperature was significantly higher in rams with ID lesions ($P < 0.05$; Table 1). It was noted that ROMs and OSI biomarkers did not differ significantly between feet with ID lesions; a trend for higher BAP and AOPP concentrations in rams with footrot score > 1.5 was noted. In conclusion, IRT was reliable in detecting elevated temperature associated with ID in sheep.

Table 1. Oxidative stress biomarkers and interdigital space skin temperature in sheep

	Group				
	A	B	C	SE	*P*-value
ROMs (U.Carr.)	119.7	148.1	118.9	25.5	0.60
BAP (µmol/L)	4012.0	4523.0	3688.0	315.0	0.09
OSI (arbitrary units)	3.0	3.3	3.5	0.1	0.59
AOPP (µmol/L)	17.3	11.9	19.2	2.6	0.08
Max Temp (°C)	35.7[b]	36.6[b]	37.0[a]	0.7	0.04
Min Temp (°C)	30.2[b]	31.5[a]	31.2[a]	0.5	0.02
Average Temp (°C)	33.7[b]	34.9[a]	35.1[a]	0.7	0.05
Footrot score	0.06[c]	1.3[b]	2.2[a]	0.3	0.01

[a–c]Within rows, means followed by different letters are different at $P = 0.05$.

Key Words: infrared thermography, oxidative stress, footrot

295 A clinical diagnostic scoring system for bovine respiratory disease in dairy calves. W. J. Love*[1], S. S. Aly[1,2], P. H. Kass[1], C. M. Drake[3], T. B. Farver[1], H. E. Crockford[2], J. H. Davis[2], A. L. Van Eenennaam[4], and T. W. Lehenbauer[1,2], *[1]Department of Population Health and Reproduction, School of Veterinary Medicine, University of California, Davis, [2]Veterinary Medicine Teaching and Research Center, School of Veterinary Medicine, University of California, Davis, Tulare, [3]Department of Statistics, University of California, Davis, [4]Department of Animal Science, University of California, Davis.*

Bovine respiratory disease (BRD) is an important source of economic loss in dairy and beef calf-raising operations, but reliable clinical diagnosis in calves remains challenging. The objective of this study was to develop a standardized clinical scoring system to identify BRD cases preweaning. A matched case-control study was performed on a large calf ranch in the San Joaquin Valley. Clinical signs were recorded and pharyngeal and nasal swabs were collected from 1774 Holstein calves between July 2011 and January 2012. Clinically ill calves were pair-matched to healthy calves based on age, source farm, and date. Calves ranged from 23 to 69 d of age. Observed clinical signs included ocular and nasal discharge, cough, head tilt, ear droop, fever, increased respiratory rate and effort, decreased appetite, and diarrhea. Viral PCR tests were performed to detect infectious bovine rhinotracheitis virus, bovine viral diarrhea virus, bovine respiratory syncytial virus (BRSV), and bovine coronavirus. Aerobic bacteria and mycoplasma cultures were also performed. Cases were clinically ill and culture- or PCR-positive for one of the following pathogens: BRSV, unpigmented *Mycoplasma* spp., *B. trehalosi*, *H. somnus*, *M. haemolytica*, or *P. multocida*. Controls were clinically healthy and negative for pathogens. Conditional logistic regression (CLR) models were used to determine the importance of each clinical sign for classifying calves as diseased or healthy while accounting for the matched study design. Ocular and nasal discharge, head tilt, ear droop, cough, and fever were forced in the model. Scores were weighted by their CLR coefficients and summed. Nasal discharge, eye discharge, and fever above 39.2°C were each assigned 2 points, and cough, ear droop, and head tilt were each assigned 4 points. A score of 4 or higher was identified as the optimal cut-off for a BRD case. The scoring system correctly classified 89.0% of the cases and controls with 91.7% sensitivity and 86.9% specificity. While neither clinical signs or culture are reference tests for BRD, this system offers a standardized tool to rapidly identify calves at high risk for BRD.

Key Words: bovine respiratory disease, clinical scoring system

296 Assessment of work shift transition of calving personnel on stillbirth in Holstein dairy cows. A. Hunter*, M. G. Maquivar, S. Bas, J. D. Workman, and G. M. Schuenemann, *Department of Veterinary Preventive Medicine, The Ohio State University, Columbus.*

Risk factors affecting stillbirth varies from farm-to-farm and blanket recommendations often fail when applied to a variety of different herds. The objective was to assess the time of birth around the work shift transition (1 h before and 1 h after) of calving personnel (n = 3) on stillbirth in Holstein cows. Prepartum dairy cows (PRIM, n = 1403; MULT, n = 2467) from one commercial dairy herd were monitored (close-up pen) for imminent signs of birth [appearance of amniotic sac (AS) outside the vulva] and moved to a contiguous maternity pen until birth. Calving ease (scale 1–4), time of birth, single or multiple calves, calf sex, calf presentations (forward or backward), time spent in labor, and stillbirth (born dead or died within 24 h after birth) were recorded. According to farm protocol, assistance was provided to cows without calving progress 80 min after AS appearance or earlier (e.g., to correct malposture). The effect of time of birth around the work shift transition of calving personnel on stillbirth was estimated using GLIMMIX. Births were characterized for forward (96%) or backward (4%) presentations, breech (1%), and multiple calves (5.1%). The overall proportion of stillbirth was 8%. PRIM cows had greater proportion of stillbirth (11%) compared with MULT cows (6%; $P < 0.05$). PRIM cows had greater proportion of stillbirth (11.4%) around the shift change compared with MULT cows (5%; $P < 0.05$). Cows experiencing difficult birth, calves born in backward presentations, and the time around the shift change of personnel increased the proportion of stillbirth ($P < 0.05$). Dairymen, consultants, and veterinarians often trouble-shoot high prevalence of stillbirth in dairy herds and this process requires constant monitoring and comprehensive assessment of several events. Proactive communication practices among calving personnel, especially around the work shift transition should be considered to reduce the risk of stillbirth under field conditions.

Key Words: stillbirth, calving management, dairy personnel

297 Validation of two diagnostic methods for endometritis in postpartum dairy cows. J. Denis-Robichaud* and J. Dubuc, *Faculté de Médecine Vétérinaire, Université de Montréal, Saint-Hyacinthe, Québec, Canada.*

The objectives of this observational study were to determine diagnostic criteria for 2 endometritis diagnostic methods and to quantify their effect on subsequent reproductive performance in postpartum dairy cows. Data from 558 Holstein cows (25 herds) enrolled in a randomized clinical trial were used. Cows were examined 34 (±7) days after parturition for endometritis using a standard cytobrush technique. After collection of the endometrial sample, the cytobrush was rolled on a microscope slide for subsequent cytological evaluation using a microscope and was dipped into 1 mL of sterile water for leukocyte esterase (LE) colorimetric testing (Multistix, Bayer Corporation, Elkhart, IN). Cytology results were recorded as the proportion of polymorphonuclear cells and endometrial cells while LE results were recorded in 5 categories: negative, trace, + (small), ++ (moderate), and +++ (large). The voluntary waiting period for breeding was 50 d. Subsequent reproductive events were recorded up to 250 d after parturition. Diagnostic criteria for endometritis were determined based on the maximal sum of sensitivity and specificity for predicting the risk of pregnancy at 120 d after parturition. The effect of these diagnostic criteria on reproductive performance were quantified using logistic regression and Cox proportional hazard models adjusted for herd clustering effect. Cytological endometritis (CYTO) was defined as ≥6% polymorphonuclear cells in endometrial cytology. Endometritis determined by LE testing was defined as colorimetric categories ≥ ++ (moderate). Prevalence of endometritis based on CYTO and LE disease definitions were 41 and 32%, respectively. Both diagnostic methods were associated with a detrimental impact on first service conception risk (CYTO: Yes = 19.3%, No = 35.4%, $P < 0.01$; LE: Yes = 24.5%, No = 35.9%, $P < 0.01$) and on median time to pregnancy (CYTO: Yes = 158 d, No = 113 d, hazard ratio = 1.27, $P < 0.01$; LE: Yes = 136 d, No = 105 d, hazard ratio = 1.28, $P < 0.01$). These findings suggest that CYTO and LE results can be used to diagnose endometritis in postpartum dairy cows.

Key Words: cytology, endometritis, leukocyte esterase

298 The effects of calving assistance on health, reproduction, and survival of Holstein dairy cows. M. Villettaz Robichaud*[1], D. L. Pearl[1], J. Rushen[2], A. M. de Passillé[2], S. M. Godden[3], S. J. LeBlanc[1], and D. B. Haley[1], *[1]University of Guelph, Guelph, ON, Canada, [2]Agriculture and Agri-Food Canada, Agassiz, BC, Canada, [3]University of Minnesota, St-Paul.*

Difficult calvings are known to have negative effects on dairy cows' uterine health, subsequent reproductive performance, and survival. To avoid calving difficulties, some farms, as a matter of practice, assist all cows at calving. We investigated the effects of giving early obstetrical assistance to cows on their health, behavior and survival. On one large commercial dairy farm, out of 257 Holstein dairy cows (primiparous n = 84; multiparous n = 173) enrolled in this study, 134 were randomly assigned to receive early assistance and 123 did not receive any assistance for 1 h. All cows had a normally positioned single fetus and pulling using human force alone given 15 min after the first sight of both hooves was provided for cows that received early assistance. Cows that were not assigned for early assistance that had not delivered within 1 h after the first sight of both hooves were assisted. Of the cows intended to not receive assistance, 26% were assisted after 1 h and 23% of the intended early assisted cows, calved before the 15 min waiting time, e.g., without assistance. The incidence of metritis (n = 53 cases) and the odds of pregnancy (n = 134) or death or culling before 120 DIM (n = 37) and odds of calf stillbirth (n = 7) did not differ significantly between treatment groups (Multivariable logistic regression: $P > 0.05$). However, when looking the time spent standing measured with pedometers, cows in the early assisted group spent 1 h (±26 min) more time standing per day during the 10 d following calving compared with unassisted cows (Mixed model: $P = 0.016$). In uncomplicated calvings, there was no difference in health or pregnancy outcomes between cows with systematically given prompt obstetrical assistance and cows given 1 h to calve undisturbed after initial assessment.

Key Words: calving assistance, calving difficulties, metritis

299 Feeding behavior, milk yield, activity, and insulin sensitivity in lame dairy cows. S. Janssen[1], M. Heppelmann[1], U. Meyer[2], S. Daenicke[2], and J. Rehage*[1], *[1]Clinic for Cattle, University of Veterinary Medicine Hannover, Hannover, Germany, [2]Dept. Animal Nutrition, Friedrich-Loeffler-Institute, Braunschweig, Germany.*

Lame dairy cows often show increased plasma levels of nonesterified fatty acids (NEFA) which may be caused by reduced insulin sensitivity. Thus, aim of the study was to investigate feeding behavior, activity and insulin sensitivity in lame cows. Twenty-one pluriparous lame dairy cows with sole ulcers or white line disease of one hind limb were detected by biweekly lameness scoring (score 2 or 3; scale 0–5) and matched with healthy herd mates (controls) according to parity and days in milk. All cows received functional claw trimming and lame cows claw treatment. Feeding behavior (dry matter intake (DMI), number of trough visits, feeding rate), body weight and milk yield were recorded daily and milk constituents twice weekly from d −7 to d 7 related to the day of lameness detection (d 0). From d0 to d7 pedometers recorded activity and blood samples were collected for analysis of glucose, NEFA, insulin (from which RQUICKI was calculated as a surrogate insulin sensitivity index) and cortisol. Data were analyzed using the GLM procedure for repeated measurements (factors group (G), time and their interaction) of the SAS package. Compared with controls lame cows showed in average longer lying periods (11 vs. 13 h/d, resp., G: $P < 0.01$), spent less time feeding (188 vs. 155 min/d, resp., G: $P < 0.01$), had less trough visits (48 vs. 31 /d; G: $P < 0.05$), and increased feeding rates (116 vs. 143 g/min, resp., G: $P < 0.05$). Daily mean DMI, milk yield and calculated energy balance as wells as mean plasma concentrations of glucose, insulin, and cortisol did not differ between control and lame cows. In control compared with lame cows mean plasma levels of NEFA (175 vs. 340 µmol/L, resp., G: $P < 0.05$) were lower and RQUICKI significantly higher (0.58 vs. 0.44, resp., G: $P < 0.05$). Increased plasma NEFA levels in cows with early detected mild lameness appear not to be caused by reduced DMI. They may be an expression of increased fat mobilization induced by reduced insulin sensitivity or of reduced activity and muscular NEFA utilization. It may be also possible that cows with reduced insulin sensitivity are disposed for claw defects.

Key Words: dairy, insulin, lameness

300 Evaluation of milk leucocyte differential diagnosis for selective dry cow therapy . M. Hockett*[1] and R. Rodriguez[1,2], *[1]Advanced Animal Diagnostics, Morrisville, NC, [2]North Carolina State University, Raleigh.*

This study compared selective dry cow therapy after diagnosis of subclinical mastitis by milk leucocyte differential (MLD; Advanced Animal Diagnostics) to blanket treatment. First and second lactation, Holstein cows (n = 300) at dryoff (223 ± 3 d in gestation) were assigned to CON (n = 151) or SELECT (n = 149) by random number and groups were balanced for lactation number. Quarter milk was aseptically collected < 24 h from dryoff (DRY) and analyzed by MLD. All cows in CON group and cows in SELECT group with subclinical infection by MLD in any quarter (TRT) had all quarters treated with cephapirin benzathine. Uninfected cows received no antibiotics (NOTRT). Teats were sealed by Orbeseal and barrier postdip. Quarter milk was aseptically collected from cows 3 (D3) and 10 (D10) days postpartum. At each sampling, SCC was determined and 0.01 mL was plated for culture analysis. Samples were interpreted as infected if: ≥1 cfu of major pathogen, ≥2 cfu of CNS, or ≥5 cfu of *Bacillus* were observed. Statistical analysis was performed using GLIMMIX procedure of SAS to determine differences in quarter-level infection rates and differences in SCC at DRY, D3, D10. SCC did not differ between CON or Select groups at any time or between TRT and NOTRT groups postpartum. Culture positive rates were similar for CON and SELECT at DRY and D10 and infection rates were higher at DRY and D3, but not D10 for TRT compared with NOTRT (Figure 1). This study indicates the use of MLD to diagnose infected quarters and selective treatment of only infected cows reduced the use of antibiotics and resulted in similar infection rates and SCC 10 d post-calving compared with blanket antibiotic therapy.

Table 1. SCC and culture infection rates of CON, SELECT, TRT and NOTRT quarters at DRY, D3, and D10

	SCC (cells/mL)			Culture infection rate (%)		
Group	DRY	D3	D10	DRY	D3	D10
CON	204,396[a] ± 20,712	307,230 ± 31,265	118,394 ± 17,759	18.5[d]	13.7[g]	14.6
SELECT	238,383[a] ± 23,373	324,927 ± 31,183	79,161 ± 17,930	20.4[d]	17.0[h]	11.9
TRT	411,388[b] ± 28,634	327,462 ± 42,608	81,858 ± 24,157	12.9[e]	13.3[g]	10.9
NOTRT	43,214[c] ± 30,404	322,747 ± 45,929	77,238 ± 25,732	27.1[f]	20.3[h]	12.9

Values with different superscripts differ: [a,b,c]$P < 0.0001$; [d,e,f]$P = 0.01$; [g,h]$P = 0.01$.

Key Words: leucocyte, dryoff, selective

301 Development of a statistical model to predict metritis. G. U. Maier*[1], J. H. Bittar[1], C. A. Risco[1], N. Martinez[2], F. S. Lima[2], L. F. Greco[2], E. S. Ribeiro[2], J. E. Santos[2], M. M. Vercouteren[3], and K. N. Galvão[1], *[1]Department of Clinical Sciences, University of Florida, Gainesville, [2]Department of Animal Sciences, University of Florida, Gainesville, [3]Department of Animal Health, Utrecht University, Utrecht, the Netherlands.*

Metritis is an important disease of the transition period in dairy cows with an estimated incidence of 10–30%. Cows that develop metritis have

decreased milk yields and fertility, and increased odds of being culled from the herd. An accurate model that can predict incidence of metritis may allow for targeted monitoring and/or implementation of preventive strategies to diminish the negative effects of metritis on performance. The objective of this study was to identify risk factors for metritis and to develop a statistical model to predict metritis in dairy cows from data that can be collected within the first week postpartum. Variables housing type (pasture vs. freestall), breed (Holstein, Jersey or Holstein Jersey Cross), dystocia, retained placenta, twins, stillbirth, and blood serum concentrations of calcium, NEFA, and BHBA at 4 ± 3 DIM were collected from 928 dairy cows from 3 dairies. Probabilities for each animal to develop metritis based on 2 logistic regression models [with = Model1 or without blood metabolites = Model2] were calculated and receiver operating characteristics (ROC) curves constructed. Metritis incidence was 13.1%. Variables retained ($P \leq 0.1$) in both models that increased the odds of metritis were freestall housing, twin calvings, retained placenta, dystocia, primiparity, Jersey breed and low body condition score as well as increasing blood levels of NEFA for Model 1. The ROC-derived cut-off probabilities to predict metritis were 0.11 (area under the curve (AUC) = 0.87; $P < 0.001$) and 0.12 (AUC = 0.86; $P < 0.001$) for Model 1 and Model 2, respectively. Model 1 and Model 2 had similar ($P = 0.08$) AUC. Model 1 resulted in Sensitivity (Se) and Specificity (Sp) of metritis diagnosis of 82 and 78% (78% accuracy), and Model2 resulted in Se and Sp of 80 and 75% (75% accuracy). Applying Model 2 to a second data set with 309 cows from another dairy resulted in overall accuracy of 71% (Se = 63% Sp = 71%). We concluded that using a probability cut-off derived from a logistic regression model could accurately predict metritis in our data set; however, accuracy was only moderate using a different data set.

Key Words: dairy cow, metritis, statistical prediction model

ARPAS Symposium: Applied Nutrition of Ruminants—Current Status and Future Directions

302 Nutrient requirements: Derivation, validation, and application. M. L. Galyean*, *Texas Tech University, Lubbock.*

Systems for describing nutrient requirements of animals are intrinsically composed of 2 parts: (1) estimates of animal requirements for nutrients; and (2) estimates of the ability of feedstuffs to meet requirements. Ultimately, these systems contribute to animal health and well-being, but for application, they also should provide a means to reliably predict animal performance and adjust feeding and management practices to achieve economic goals. Changes in feed intake and nutrient requirements associated with sex, breed, physiological state, and the environment add to the complexity of modeling animal requirements. Moreover, the wide variety of feedstuffs used in practical diets and inherent variability in nutrient content within a given ingredient complicate description of feedstuffs. In the US, nutrient requirements for livestock species have been developed by volunteer committees working under the auspices of the Board on Agriculture and Natural Resources of the National Research Council (NRC). Animal nutrient requirements have typically been determined by empirical approaches based on reviews of the literature and analysis of derived and experimental data sets. In recent years, validation of nutrient requirement equations has become an increasingly important part of the NRC process, although the lack of independent data to validate equations continues to be a problem. In the last 2 decades, NRC committees also have emphasized the development of computer models to facilitate practical application of nutrient requirement systems. Although user-friendliness and functionality of these models has improved over time, more effort is needed to ensure that models allow for efficient, practical application of the systems. In addition to issues with validation and model development, describing the concentration and availability of nutrients in feedstuffs is a significant challenge for NRC committees. The recently formed National Animal Nutrition Program, funded through USDA-NIFA, should play an important role in interacting with NRC committees, particularly in providing support for feed composition databases and development and evaluation of computer models.

Key Words: livestock, nutrient requirements

303 Applied nutrition of ruminants: Fermentation and digestive physiology. C. R. Krehbiel*, *Oklahoma State University, Stillwater.*

Since the first observation of the 4 chambers and subsequent identification of its microbial population, the rumen has been investigated for its role in nutrient digestion and to manipulate its microbial ecosystem to increase animal performance and efficiency. Ruminants have the ability to digest plant polysaccharides through substrate-specific enzyme activities of the highly specific population of ruminal bacteria, protozoa, and fungi. A synergistic relationship provides these microorganisms with nutrients, ambient temperature, and a buffered environment to enhance microbial growth, while the microbes provide the host animal with B vitamins, VFA, and microbial cell protein. Microbial populations are not stable and fluctuate with changes in the ruminal environment and diet, resulting in changes in VFA composition and concentration. Recent research using T-RFLP analysis, 16S rDNA libraries, and metagenomic approaches has increased our understanding of the importance of microbial communities within the rumen and the microbial diversity under different dietary environments. Increased understanding of these changes in microbial communities could result in increased microbial growth rates and enzyme secretions in the rumen, resulting in increased digestibility, nutrients delivered to the small intestine, and animal production and efficiency. In addition, increased understanding of molecular-level adaptation of ruminal epithelia and gastrointestinal mucosa may provide the physiological basis for their role in regulation of ruminal pH and nutrient transport. Recent advances and continued study in the area of ruminal fermentation and digestive physiology have the potential to positively affect animal production, health and the environment.

Key Words: digestive physiology, ruminal fermentation, ruminant nutrition

304 Carbohydrates and fat: Considerations as energy and more. M. B. Hall*[1] and M. L. Eastridge[2], *[1]US Dairy Forage Research Center, USDA-ARS, Madison, WI, [2]Department of Animal Science, The Ohio State University, Columbus.*

Historically, carbohydrates and fats were valued on their caloric contributions to diets. Feeding recommendations for these feed fractions now address inclusion levels as well as consideration of the positive and negative effects of specific types of these nutrients. Feed carbohydrate characterization has expanded beyond fiber and nonfiber carbohydrates (NFC). Fiber now encompasses ADF, NDF, physically effective fiber, and fiber digestibility to describe the effect on diet composition, rumination, rumen fill, potential fermentability, and nutrient contribution. The NFC is now parsed into sugars and fructans (both in water-soluble carbohydrates), starch, pectins, and others, all of which may differ in their effects on rumen pH or support of microbial growth. Dietary fat has the advantage of providing energy without increasing the risk of ruminal acidosis. However, there are specific considerations for amounts and types fed in high vs. low forage diets. Fats can affect ruminal fermentation, having the potential to depress fiber digestion or affect ruminal methane production. Considerable research in recent years has focused on providing specific dietary fatty acids (FA) to alter the metabolic function of specific tissues or to alter the FA content of milk for nutraceutical purposes. Rising grain prices and diversion of fats for biofuel are driving livestock industries to seek alternative nutrient sources. Most of the nutritional research on which current recommendations are based involved the use of traditional diets which tended to be rich in grains. Fat and carbohydrate feeding recommendations may need to change with diets high in low starch byproducts. We need to learn how diets with substantially more byproduct feedstuffs ferment, and pass from the rumen, and how they affect nutrient supply and feed efficiency. We can then better predict digestion and the effects on metabolism and thus target supplementation to have the greatest positive effect on food animal production.

Key Words: carbohydrate, fat, ruminant

305 Applied protein nutrition of ruminants—Current status and future directions. F. N. Owens*[1], S. Qi[1], and D. A. Sapienza[2], *[1]DuPont Pioneer, Johnston, IA, [2]Sapienza Analytica, Slater, IA.*

Protein nutrition of ruminants is at a low level of sophistication. Cost and availability of various N sources dictate which will be fed whereas the quantitative supply is selected largely without empirical data. Lack of sophistication is due to imprecision in measuring responses, inadequate

methods to quantify degradation and biosynthesis of protein within the rumen, insufficient knowledge about post-ruminal availability and amino acid needs for various metabolic functions, inconvenience of preparing or delivering diets customized for animal groups with different needs, and unrestrained expectations. Much of the dietary N need for ruminants is met by proteins inherent in energy sources fed (grains, forages, and byproducts). No response to improved protein status should be expected if a diet already yields optimum performance! Experimental designs testing applicable concepts often lack appropriate controls. Commercial successes in protein nutrition have been limited to 3 areas – physical or chemical modification of feeds to alter degradation of dietary protein, NPN products with attenuated ammonia release, and ruminally protected amino acids. Future improvements in protein nutrition likely will come from targeted, small-package supplements or boluses that alter the native microbial population within the rumen or rumen function, not from feedstuffs customized for ruminants or inoculation with novel microbes. New DNA sequencing methods are improving our comprehension of changes in the rumen microbiome. Ruminally protected amino acids could be supplemented more precisely if needs for absorbed amino acids were defined quantitatively, but metabolic requirements should parallel those of non-ruminants for maintenance and production. More practical and economical advancements would be expected from enlightened research about and manipulation of numerous factors to increase the post-ruminal protein supply through a decrease in ruminal proteolysis or an increase in microbial protein synthesis within or flow from the rumen.

Key Words: protein, microbiome, rumen-undegraded protein

306 Mineral and vitamin nutrition in ruminants. J. W. Spears*, *North Carolina State University, Raleigh.*

Requirements and factors that affect dietary requirements for several trace minerals and vitamins in ruminants are still poorly defined. Most B-vitamins and vitamin K are believed to be synthesized by bacteria in the rumen in adequate amounts to meet the animal's requirement. However, several studies indicate that supplementing high producing dairy cows with approximately 20 mg biotin/d can reduce hoof lesions and lameness, and in some instances increase milk yield. The vitamin E requirement for optimal immunity and health in receiving cattle and transition dairy cows continues to be an area of interest, with responses to supplementation varying greatly. Macromineral research in recent years has focused primarily on P and S. Studies clearly indicate that P requirements of cattle are lower than those recommended 20 years ago. Because of increased use of ethanol by-product feeds that are high in S, considerable research has been conducted to determine the effects of high dietary S (in feedstuffs and water) on performance and incidence of polioencephalomalacia. Requirements for certain microminerals are affected by antagonists. Sulfur and Mo are important Cu antagonists that can greatly affect dietary Cu bioavailability, and therefore, requirements. High dietary Fe, when present in a bioavailable form, is a potent Cu and Mn antagonist. Recent research suggests that NRC recommendations for Co and Mn may underestimate requirements. In the past 3 years Cr (in the form of Cr propionate) has been permitted to be supplemented at a maximum concentration of 0.50 mg Cr/kg DM to cattle diets. Chromium enhances insulin sensitivity and responses to supplemental Cr appear to be greatest under conditions of stress (i.e., transition dairy cows, receiving cattle), where insulin resistance commonly occurs. Research continues to increase the understanding of mineral and vitamin requirements of cattle in different production systems.

Key Words: mineral, vitamin, ruminant

Breeding and Genetics: Applications and Methods in Animal Breeding—Dairy II

307 Genetic correlations between feed intake and type traits in dairy cattle. G. Bilal*[1,2], R. I. Cue[2], and J. F. Hayes[2], *[1]Department of Livestock Production and Management, Faculty of Veterinary and Animal Sciences, Arid Agriculture University, Rawalpindi, Punjab, Pakistan, [2]Department of Animal Science, McGill University, Ste-Anne-de-Bellevue, Quebec, Canada.*

The objective of the present study was to estimate genetic correlations between feed intake and type traits with a view to considering the potential of indirect genetic selection for feed intake using type traits in dairy cattle. Feed intake data on 119,388 first lactation Holstein cows were obtained from Dairy Production Centre of Expertise, Valacta. Type trait records on 93,619 cows were obtained from Holstein Canada and were recorded during 1 to 365 d of first lactation. Feed traits included 305-d dry matter intake (DMI), 305-d net energy of lactation intake (NELI) and 305-d crude protein intake (CPI). Type traits included dairy strength, angularity, body depth, stature and final score. The statistical model of analysis for feed intake traits included age at first calving and herd-year-season of calving as fixed effects and random effects of animal and residual. The statistical model for type traits included fixed effects of age at first calving, days in milk and herd-round-classifier and random effects of animal and residual. Additionally, 13 (8 male and 5 female) phantom parent groups were fitted as covariates for all traits. Pedigree of animals with data was traced back 5 generations on both the male and female side to account for relationships among animals. Genetic parameters were estimated by fitting 5-trait animal models under restricted maximum likelihood using Wombat program. Estimates of heritabilities for DMI, NELI and CPI were 0.12, 0.13 and 0.13, respectively. Estimates of heritabilities of dairy strength, angularity, body depth, stature and final score were 0.31, 0.24, 0.30, 0.50 and 0.22, respectively. All phenotypic and genetic correlations between feed intake and type traits were positive. Genetic correlations between angularity and feed intake traits were strong and positive (0.60 to 0.65). Dairy strength showed strong positive genetic correlations (0.48 to 0.54) with feed intake traits . Both stature and body depth showed moderate positive genetic correlations (0.29 to 0.36) with feed intake traits. Angularity, dairy strength, stature and body depth may be useful for indirect selection of feed intake traits in dairy cattle.

Key Words: dairy cattle, feed, type

308 Genetic parameters for methane emissions predicted from milk mid-infrared spectra in dairy cows. P. B. Kandel*[1], M. L. Vanrobays[1], A. Vanlierde[2], F. Dehareng[2], E. Froidmont[2], P. Dardenne[2], E. Lewis[3], F. Buckley[3], M. Deighton[3], S. McParland[3], N. Gengler[1], and H. Soyeurt[1], *[1]University of Liege, Gembloux Agro-Bio Tech, Gembloux, Belgium, [2]Walloon Agricultural Research Center, Gembloux, Belgium, [3]Teagasc, Animal & Grassland Research and Innovation Center, Moorepark, Ireland.*

Genetic selection of low methane (CH_4) emitting animals is additive and permanent but the difficulties associated with individual CH_4 measurement result in a paucity of records required to estimate genetic variability of CH_4 traits. Recently, it was shown that direct quantification of CH_4 emissions by mid-infrared spectroscopy (MIR) from milk. The CH_4 prediction equation was developed using 452 SF_6 CH_4 measurements with associated milk spectra and the calibration equation was developed using PLS regression. The obtained SD of predicted CH_4 was 126.39 g/day with standard error of cross validation 68.68 g/day and a cross-validation coefficient of determination equal to 70%. The equation was applied on a total of 338,917 spectra obtained from milk samples collected between January 2007 and August 2012 during the Walloon milk recording for first parity Holstein cows. The prediction of MIR CH_4 was 547 ± 111 g/d and MIR CH_4 g/kg of fat and protein corrected milk (FPCM) was 23.66 ± 8.21.Multi-trait random regression test-day models were used to estimate the genetic variability of MIR predicted CH_4 and milk production traits. The heritability, phenotypic and genetic correlations between MIR predicted CH_4 traits and milk traits are presented in Table 1. Estimated heritability for CH_4 g/day and CH_4 g/kg of FPCM were lower than common production traits but would still be useful in breeding programs. While selection for cows emitting lower amounts of MIR predicted CH_4 (g/d) would have little effect on milk production traits, selection on MIR predicted CH_4 (g/kg of FPCM) would decrease FPCM, fat and protein yields. These genetic parameters of CH_4 indicator traits might be entry point for selection that accounts mitigation of CH_4 from dairy farming.

Table 1. Heritability (diagonal), phenotypic (below the diagonal) and genetic (above the diagonal) correlations between MIR CH_4 and production traits

Trait	MIR CH_4 (g/d)	MIR CH_4 (g/kg of FPCM)	FPCM	Fat yield	Protein yield
MIR CH_4 (g/d)	0.11	0.42	0.03	0.19	0.04
MIR CH_4 (g/kg of FPCM)	0.59	0.18	−0.83	−0.63	−0.78
FPCM	−0.01	−0.74	0.23	0.87	0.93
Fat yield	0.03	−0.68	0.95	0.24	0.70
Protein yield	0.02	−0.70	0.94	0.82	0.22

Key Words: methane emissions, heritability, dairy

309 Genetics of body energy status of Holstein cows predicted by mid-infrared spectrometry. C. Bastin*[1], D. P. Berry[2], N. Gengler[1], and S. McParland[2], *[1]University of Liège, Gembloux Agro-Bio Tech, Animal Science Unit, Gembloux, Belgium, [2]Teagasc Moorepark Dairy Production Research Center, Fermoy, Co. Cork, Ireland.*

Energy balance (EB) status has been demonstrated to affect health and fertility in dairy cows. Recent research proposed mid-infrared (MIR) analysis of milk, potentially routinely available within milk recording schemes, to predict body energy status of dairy cows. Hence MIR prediction of body energy status is easy, quick and inexpensive and could warrant the inclusion of EB in breeding programs. The objective of this study was to estimate genetic parameters of body energy status traits predicted by MIR spectrometry for Walloon Holstein cows and to investigate their relationships with fertility. Three body energy status traits were considered: direct EB (dEB; MJ/d), body energy content (EC; MJ), and effective energy intake per day (EEI; MJ/d). Only dEB, EC, and EEI MIR predictions that encompassed the variability represented in the prediction equations calibration data set were considered. Genetic parameters were estimated using single-trait 3-lactation random regression models. Data included 336,142 dEB records from 36,694 cows in 580 herds and 354,900 EC and EEI records from 38,531 cows in 607 herds. For all traits, heritability estimates were the highest in mid to late lactation and ranged across lactation from 0.15 to 0.55 for dEB, from

0.10 to 0.30 for EC, and from 0.10 to 0.25 for EEI. Genetic correlations within trait across lactation were stronger than 0.85. Genetic correlations between the body energy status traits and fertility (number of days from calving to conception or days open; DO) were estimated in first-parity cows using bivariate models that included a random regression for body energy status traits. Data included 125,921 dEB, EEI and EC records and 24,419 DO records from 24,419 cows in 361 herds. The genetic correlation with DO ranged from −0.22 to −0.17 for dEB, from −0.30 in early lactation to 0.00 in mid-lactation for EEI, and from −0.05 at 5 d in milk to −0.30 at 305 d in milk for EC. Results from this study indicated that body energy status traits predicted by mid-infrared are heritable but lowly to moderately correlated with DO.

Key Words: energy balance, mid infrared, genetic correlation

310 Heterogeneity across research stations in genetic variation and energy sink relationships for feed efficiency in lactating dairy cattle. R. J. Tempelman*[1], D. M. Spurlock[2], M. Coffey[3], R. F. Veerkamp[4], L. E. Armentano[5], K. A. Weigel[5], Y. deHaas[4], C. R. Staples[6], M. D. Hanigan[7], and M. J. Vandehaar[1], *[1]Michigan State University, East Lansing, [2]Iowa State University, Ames, [3]Scottish Agricultural College, Midlothian, UK, [4]Wageningen UR, Lelystad, the Netherlands, [5]University of Wisconsin, Madison, [6]University of Florida, Gainesville, [7]Virginia Tech, Blacksburg.*

The importance of dairy cattle feed efficiency will further intensify with human population and land constraint pressures. It seems imperative then to coordinate extensive collaboration between research stations in different countries to facilitate large enough databases for genetic improvement while recognizing that potential heterogeneities will exist in the way traits are recorded and related with each other across research stations. Milk, fat, protein, and lactose production, converted to net energy units(MilkE), dry matter intakes (DMI), body weights (BW), and body condition scores (BCS) were collected on 6,061 lactations from 4,341 Holstein cows from research stations in Scotland, the Netherlands, and the United States. Weekly DMI was fitted as a function of MilkE, $BW^{.75}$, BCS, and change in BW (ΔBW), parity, and its interaction with parity with a 5th order polynomial on days in milk (DIM) ranging from 50 to 200d. The residuals from this analysis were considered to be a measure of feed efficiency; i.e., residual feed intake (RFI). Partial regression coefficients of DMI on MilkE and on $BW^{.75}$ were always important ($P < 0.0001$). These coefficients were generally consistent (0.40–0.45 kg/Mcal) for MilkE, whereas partial regression coefficients on $BW^{.75}$ uniformly ranged from 0.06 to 0.16kg/$kg^{.75}$. Significant ($P < 0.05$) partial regression coefficients on ΔBW ranged up to 0.120 kg/kg across stations. Heritabilities for country-specific RFI were based on fitting random regression models and ranged from 0.08 to 0.22 depending on DIM; residual variances were particularly heterogeneous across research stations likely due in part to differences in data recording protocols. The overall heritability from 60 to 90 DIM across all research stations was 0.14 ± 0.03. Hence future genomic selection programs on feed efficiency appear to be promising, provided that care is taken to allow for heterogeneous variance components and relationships across environments between DMI and other energy sink traits as used to determine RFI.

Key Words: residual feed intake, heritability

311 Repeatability and genetic correlations of residual feed intake across stages of lactation in dairy cattle. G. Manafiazar*, T. McFadden, E. Okine, L. Goonewardene, and Z. Wang, *University of Alberta, Edmonton, Alberta, Canada,*

Residual feed intake (RFI) is a measure of net feed efficiency. Animals with low RFI eat less feed than expected on the basis of its maintenance and production levels. To the best of our knowledge, there is no published report on repeatability and genetic correlation among RFI prediction across stages of lactation, which is ultimately essential for wide-scale adaptation of RFI by producers. Individual daily actual energy intake (AEI), monthly body weight, and monthly milk yield and composition data of 200 first lactation cows from 5 to 305 d in milk (DIM) were acquired at the University of Alberta. Daily animal solutions for metabolic body weight (MBW), milk production energy requirements (MPER), and empty body weight changes (EBWC) were predicted from 5 to 305 DIM using random regression Legendre polynomial. Individual RFI value was estimated from the regression of total AEI on total estimated MPER, EBWC, and MBW for the same animal in 4 periods: 5 to 305 DIM (RFI_{lact}) 5 to 105 DIM (RFI_{early}), 106 to 205 DIM (RFI_{mid}), and 206 to 305 DIM (RFI_{late}). A bivariate animal model was used to estimate genetic and phenotypic parameters among the RFIs. Daily RFI_{lact}, RFI_{early}, RFI_{mid}, and RFI_{late} averaged zero, with SD 2.29, 3.41, 3.38, and 3.03 NE_L Mcal/d, respectively. Phenotypic and genetic correlations were significant between RFI_{lact} and RFI_{early} (0.64 ± 0.04 and 0.93 ± 0.42, respectively), RFI_{lact} and RFI_{mid} (0.78 ± 0.03 and 0.96 ± 0.4), RFI_{lact} and RFI_{late} (0.59 ± 0.05 and 0.83 ± 0.22), RFI_{early} and RFI_{mid} (0.26 ± 0.07 and 0.85 ± 0.73), RFI_{early} and RFI_{lact} (0.04 ± 0.07 and 0.49 ± 0.72), and RFI_{mid} and RFI_{late} (0.41 ± 0.06 and 0.98 ± 0.65). Estimated repeatability for RFI was 0.42 ± 0.04. The results showed that RFI was moderately repeatable across stages of lactation, and RFI_{lact} and RFI_{mid} had higher genetic and phonotypic correlations. Therefore, results indicate that dairy industry may select animals based on RFI estimation in the mid stage of lactation.

Key Words: dairy cattle, residual feed intake, repeatability

312 Individual and maternal heterosis in performance traits of Holstein and Jersey crosses with Sahiwal cattle. M. S. Khan*[1], F. Hassan[1], and S. A. Bhatti[2], *[1]Department of Animal Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan, [2]Institute of Animal Nutrition and Feed Technology, University of Agriculture, Faisalabad, Pakistan.*

Crossbreeding of indigenous Sahiwal (S) cattle with Holstein (H) and Jersey (J) started in Pakistan in mid 1970s to see if it could be adopted as a general strategy for upgrading local cattle. Farmers generally rear cattle in a low to medium input system under climatic conditions (−2°C to 52°C). Present study reports preliminary estimates for breed group differences, individual and maternal additive and heterotic effects for some economic traits using data on 178 cows (740 lactations) in a university herd. The 305-d milk yield (305MY, liters) (±SD), total lactation milk yield (TMY, liters) and lactation length (LL, days) averaged 2668 ± 952.9, 3217 ± 1480.4 and 384 ± 40.6, respectively. Age at first calving (AFC, months), calving interval (CI, days) and productive life (PL, months) averaged 49 ± 26.2, 491 ± 155.2 and 41 ± 24.8, respectively. The AFC was minimum in F1 J (40 ± 13.7). The H F1 crossbreds performed better than any other genetic group for milk yield traits. Period and seasons of calving, parity and genetic groups were used as fixed effects. Parity groups were excluded for analyzing AFC while model for PL had period of birth and genetic groups as only fixed effects. Least squares means for 305MY was 3167 ± 1210.2 and 2333 ± 1028.3 for F1 H and F1 J, respectively and lowest (1323 ± 1020.8) for >75% S. The CI did not differ among genetic groups while PL was maximum in F1 H (43 ± 30.7) and minimum (6 ± 28.2) for >75% S. The >75% S group had highest AFC (62 ± 14.2), longest CI (512 ± 165.3) and shortest LL (277 ± 166.8). Individual additive breed effect (*Bos taurus – Bos indicus*)

was 904.8, 1296.2, 75.3 and 13.7 for 305MY, TMY, LL and PL, respectively. Maternal additive genetic effects were significant ($P < 0.01$) for 305MY (−250), TMY (−396) against *Bos taurus* inheritance. Individual heterosis was also significant ($P < 0.01$) for AFC, 305MY, TMY and PL. *Bos taurus* inheritance improved performance but going beyond 75% deteriorated traits, especially the PL. Lifetime performance studies are needed to suggest upgradation policy for local cattle of Pakistan.

Key Words: heterosis, Sahiwal, crossbred

313 Effect of timed AI use on reproductive performance and culling rate in Wisconsin dairy herds. A. H. Souza*[1,2], P. A. Carvalho[1], R. D. Shaver[1], M. C. Wiltbank[1], and V. Cabrera[1], *[1]Department of Dairy Science, University of Wisconsin, Madison, [2]Ceva Sante Animale, Libourne, France.*

We examined the use and effect of synchronization programs on reproductive performance and culling rates in dairy herds in WI. Backups (n = 200) from herds using DC305 were collected from 2009 to 2012. Average lactating cows per herd was 660 (51–7,273) and 305ME production was 12,427kg (9,476–16,112). Service rate (SR) and pregnancy rate (PR) calculations used either the actual voluntary waiting period (VWP) in the herd or were set at 50DIM. Culling rate was defined as the number of culled cows (sold plus dead) over 12 mo divided by the average number of mature cows in the herd. Percentage of breedings done with timed AI was assessed by recorded breeding codes in DC305. Overall, 91% of the herds reported more than 10% of their breeding codes associated with a timed AI protocol, and 52% of all breedings happened following a synchronization program. Herds were divided in quartiles in terms of percentage of breedings by timed AI (Q1 = 0–36%; Q2 = 37–55%; Q3 = 56–69%; Q4 = 67–99%). Average VWP was 57.4d and % pregnant to 1st AI (P/1stAI) was 36.6%. As expected, herds using more timed AI delayed 1st postpartum AI (VWP: Q1 = 49.6 d vs. Q4 = 67.5 d; $P < 0.01$) but had improved P/1st AI (Q1 = 34.9% vs. Q4 = 39.9%; $P < 0.01$). In addition, PR increased from 15.8% to 20.0%, for Q1 and Q4 respectively ($P < 0.01$) with a greater proportion of herds having outstanding reproductive performance (PR >20%; Q1 = 12.3% vs. Q4 = 55.7% of herds; $P < 0.01$). Increased milk production was associated with increased use of timed AI (r = 0.39, $P < 0.01$), increased SR (r = 0.36, $P < 0.01$), no change in P/AI (r = −0.04, $P = 0.53$), increased PR (r = 0.24, $P < 0.01$), and lower early cullings (r = −0.24, $P < 0.01$). Regardless of the proportion of breedings performed with timed AI, PR was not associated with overall culling rate (r = 0.008, $P = 0.91$), but was negatively correlated with later (>300 DIM) cullings (r = −0.32, $P < 0.01$). Younger age at first calving in heifers was associated with greater culling rates in the lactating herd ($P < 0.01$). Thus, timed AI appears to be a critical part of reproductive management programs in WI dairies, particularly in high-producing herds.

Key Words: dairy farm, synchronization program, Ovsynch

314 Genomic divergence of indicine and taurine cattle identified through high-density SNP genotyping. L. R. Porto-Neto[2], T. S. Sonstegard*[1], G. Liu[1], D. Bickhart[3], C. Gondro[6], M. V. da Silva[4], Y. T. Utsunomiya[5], J. F. Garcia[5], and C. P. Van Tassell[1], *[1]USDA, ARS, Bovine Functional Genomics Laboratory, Beltsville, MD, [2]University of Queensland, Gatton, Queensland, Australia, [3]USDA, ARS, Animal Improvement Programs Laboratory, Beltsville, MD, [4]Embrapa Gado da Leite, Juiz da Fora, MG, Brazil, [5]UNESP, Aracatuba, SP, Brazil, [6]University of New England, Armidale, NSW, Australia.*

Our hypothesis is that there are genomic regions of difference between cattle breeds, and some are derived from natural selection and adaptation while others are from artificial selection to form breeds . To better detect genomic regions of difference, animals from the International Bovine HapMap were genotyped for over 750,000 SNP and compared using smoothed FST. The taurine sample was represented by 10 breeds and the contrasting zebu cohort by 3 breeds. Each cattle group had similar numbers of informative markers well distributed across the genome. Principal component analyses and unsupervised hierarchical clustering confirmed the well characterized main division between the subspecies of domestic cattle. The top 1% smoothed FST, associated to positive selection contained 48 genomic regions across 17 chromosomes. The strongest signals were on Chr7: ~50Mb and Chr14: ~25Mb; and each had very different patterns of linkage disequilibrium that potentially represent intrinsic differences between cattle types. The latter region encompassed a region of the genome affecting stature, fertility and sub-cutaneous fat. The bottom 1% of the smoothed FST values included 24 regions across 13 chromosomes, which are potentially associated to balancing selection. These regions overlapped with copy number variants, including the highly variable region at BTA23:~24Mb that harbors a large number of MHC genes. Under these regions, 318 unique Ensembl genes are annotated; many of which are linked to immune response resulting in a significant overrepresentation of immune related pathways. These regions are of particular interest to understand selective pressures to which these subspecies were exposed to and how the genetic background of these populations evolved in response to environmental challenges and human manipulation.

Key Words: SNP, cattle, selection

315 Accuracies of genomic predictions in Hereford using actual 50K, a 28K subset, or 28K imputed to 50K genotypes. M. Saatchi* and D. J. Garrick, *Iowa State University, Ames.*

Routine genomic predictions have been implemented in Hereford beef cattle using the Illumina BovineSNP50 BeadChip (50K). GeneSeek recently released a higher density chip known as GeneSeek Genomic Profiler HD (GGP-HD) including 77,000 SNP markers (77K) with 28,375 GGP-HD (28K) in common. The objective of this study was to compare the accuracies of genomic predictions for 10 traits in Hereford cattle using actual 50K, actual 28K, or 28K genotypes imputed to 50K. A total of 1,081 animals were genotyped with the 50K chip. Genotyped individuals were clustered into 4 groups using K-means clustering with the aim of increasing the within-group and decreasing the between-group pedigree relationships. For each clustered group, those genotypes for 28K markers common to both panels were extracted from 50K genotypes. Those genotypes were imputed to 50K genotypes using phased marker information from the other 3 groups, based on the USDA-AIPL linkage map and BEAGLE phasing software. 4-fold cross-validation was performed using 3 groups for training (those with actual 50K or 28K genotypes) and the fourth group for validation (using either actual, actual 28K genotypes, or imputed 50K genotypes). Deregressed estimated breeding values were used as observations in a weighted analysis that estimated marker effects to derive molecular breeding values (MBV). Bivariate animal models were used for each trait to estimate the genetic correlation between trait and MBV as a measurement of the accuracy of genomic prediction. The accuracies of MBV ranged from 0.20 to 0.44 (on average 0.32) for actual 50K, from 0.06 to 0.23 (on average 0.13) for actual 28K, and from 0.20 to 0.41 (on average 0.31) for imputed 50K genotypes. With the relatively small reductions in the accuracies of genomic predictions, it is safe to recommend the GGP-HD chip for imputing genotypes in Hereford cattle. Using the 28K subset (only those markers common to both GGP-HD and 50K) is not recommended for genomic prediction in Hereford cattle.

Key Words: genomic breeding values, Hereford, GGP

316 Factors associated with recombination in beef cattle. Z.-Q. Weng*[1], M. Saatchi[1], R. Schnabel[2], J. Taylor[2], and D. Garrick[1], *[1]Iowa State University, Ames, [2]University of Missouri, Columbia.*

The objective of this study was to locate recombination hotspots on autosomes, map quantitative trait loci (QTL) influencing genome-wide recombination events, and associate number of haplotypes with 1-Mb window-wide recombination rate in beef cattle. A total of 2,778 Angus and 1,485 Limousin parent-verified sire/offspring pairs with BovineSNP50 genotypes were used in this study. SNPs were removed with call rate < 0.95, minor allele frequency < 0.01, or p value for a Hardy Weinberg Equilibrium test < 0.001. BEAGLE (Browning and Browning, 2007) was adopted to impute missing genotypes. Then, phasing was performed using pedigree-based DAGPHASE (Druet and Georges, 2010) with UMD3.1 assembly. Recombination events were identified by pairwise comparison of all combinations of parental and offspring haplotypes. Double crossovers occurring in intervals <2 cM were attributed to phasing errors and ignored. The expected numbers of recombination events were estimated using Karlin's method that assumes recombination events follow a binomial distribution. Recombination hotspots were detected near 23, 24, 31, 73 and 79Mb on *Bos taurus* autosome (BTA) 15 in Angus, and near 23, 31, 73, 75, and 79Mb in Limousin. BayesC approach in GenSel software was used to map QTL influencing genome-wide recombination events. Top 20 1Mb windows which could explain more than 4% (cumulative) genetic variance were considered to be promising QTL. Based on the information from OMIM and Human-Bovine comparative map, 2 candidate genes were identified in such windows. Specifically, RAD51 located at 37 Mb on BTA10, and MRE11A located at 1 Mb on BTA29. The average number of haplotypes within 1-Mb windows was 43.1 on BTA15. Sixty-eight haplotypes were observed in hotspot windows whose recombination rates > 0.02. The average number of haplotypes observed in coldspot windows whose recombination rate < 0.005 was 22.4. Number of haplotypes declined with window-wide recombination rate, because new haplotypes are formed by recombination. 23, 31, and 79Mb on BTA15 are common recombination hotspots across 2 breeds. Genetic variation in RAD51 and MRE11A influence genome-wide recombination number. Further analyses are needed to validate these results.

Key Words: beef cattle, recombination

317 Genetic effects of GDF8 and CAPN1 for carcass and meat traits. G. L. Bennett*[1], R. G. Tait Jr.[1], S. D. Shackelford[1], T. L. Wheeler[1], D. A. King[1], E. Casas[1,2], and T. P. L. Smith[1], *[1]USDA, ARS, Roman L. Hruska U.S. Meat Animal Research Center, Clay Center, NE, [2]USDA, ARS, National Animal Disease Center, Ames, IA.*

The objective was to improve genetic marker effect estimates of SNP previously associated with muscle traits in beef cattle (F94L marker in GDF8 and 316 marker of CAPN1). Multiyear selection in a composite population segregating both SNP increased minor allele frequency (MAF) to intermediate levels that are more optimal for estimating additive and nonadditive genetic effects. Final MAF of the lysine-encoding allele of GDF8 (allele L), and the C allele of CAPN1 316 were 0.43 and 0.44. During 3 consecutive years following selection, 176 steers were evaluated for carcass, meat quality, tenderness, and meat color traits. Analyses adjusted traits for age at harvest. The 9 genotypes (3 CAPN1 316 × 3 F94L) affected marbling score, ribeye area, adjusted fat thickness, Vision Yield grade (all $P < 0.001$) and L* reflectance ($P = 0.02$). Contrasting the estimates for the 9 genotypes for additive, recessive, and epistatic effects associated with the 2 SNP showed significant ($P < 0.001$) additive effects of F94L allele L for decreased marbling score, adjusted fat thickness, and Vision Yield grade and increased ribeye area and L* reflectance. Differences between FF and LL genotypes were 1.9 to 2.4 RSD for these traits except L* reflectance (1.0 RSD difference). These differences did not reflect the small, nonsignificant difference in carcass weight of 4 kg (0.16 RSD). The F94L L allele tended to be recessive to F for marbling score ($P = 0.08$) and ribeye area ($P = 0.05$). Contrasting CAPN1 316 estimates did not detect significant or suggestive additive, recessive, or epistatic effects for any trait, including tenderness measurements. The F94L L allele, prevalent in Limousin but almost absent in other US breeds, had 1/2 to 2/3 of the effects found for GDF8 mutations in Belgian Blue and Piedmontese, and has strong additive effects for fat and muscle traits that may obscure any relationship of CAPN1 with tenderness. Intermediate frequencies following selection contributed to accuracy of genetic effect estimates.

Key Words: calpain, myostatin, selection

318 CAPN1 and GDF8 genetic marker effects on heifer performance, reproduction, and first calf performance traits in beef cattle. R. G. Tait Jr.*, R. A. Cushman, T. P. L. Smith, H. C. Freetly, and G. L. Bennett, *USDA-ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

To increase the accuracy of effect estimation and assess potential unintended correlated effects for 2 marker systems used commercially for muscling and meat tenderness, a composite beef cattle population segregating the markers was selected for multiple years to increase minor allele frequency (MAF) or frequencies of divergent haplotypes (FDH). Substantial increases in FDH and MAF were achieved, with SNP haplotypes in the μ-calpain 1 gene (CAPN1) (haplotypes C-C or G-T at markers 316 and 4751, respectively) with haplotype increases from 0.264 to 0.386 and 0.195 to 0.332, respectively, and a lysine encoding allele (L) of the F94L marker in myostatin (GDF8) increased MAF from 0.282 to 0.450. The objective of this study was to understand if these markers affect female performance and reproductive traits. Heifers born between spring of 2007 and 2009 from this population (n = 149) were evaluated using MIXED and GLIMMIX procedures of SAS for birth weight, weaning weight, weight at 326 d, 368 d, or 411 d, achieving puberty by 326 d, 368 d, or 393 d, first breeding season pregnancy status, success of weaning first calf. Additionally, first calf performance traits of: birth date, birth weight, weaning weight, weight of calf weaned per cow exposed, and 205-d adjusted weight of calf weaned per cow exposed were evaluated. There were suggestive effects ($P < 0.10$) for GDF8 on own birth weight and CAPN1 on own weaning weight. GDF8 had significant effects ($P < 0.05$) on puberty, with LL homozygotes having a lower proportion of heifers pubertal than FL or FF genotypes, at all 3 time points. However, the delayed puberty effect of GDF8 did not lead to an effect on pregnancy rates ($P = 0.53$). CAPN1 haplotype of the cow did significantly affect ($P < 0.05$) first calf birth weight. Other own performance, reproduction, and first calf performance traits were not affected ($P > 0.10$) by CAPN1 or GDF8 genetic markers in this study. These marker effects for unintended traits may be important for incorporation into the breeding objective and for marker-assisted management strategies. USDA is an equal opportunity provider and employer.

Key Words: calpain, myostatin, puberty

319 Genome-wide association study of reproductive efficiency in female cattle. T. G. McDaneld*[1], L. A. Kuehn[1], M. G. Thomas[2], W. M. Snelling[1], E. J. Pollak[1], T. P. L. Smith[1], and J. W. Keele[1], *[1]USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, [2]Colorado State University, Fort Collins.*

Reproductive efficiency is of economic importance in commercial beef cattle production, as failure to achieve pregnancy reduces the number of calves marketed per cow exposed to breeding. Identification of genetic markers with predictive merit for reproductive success would facilitate accurate prediction of daughter pregnancy rate in sires enabling effective selection of bulls producing daughters with improved fertility. To identify regions of the genome harboring variation affecting reproductive success, we applied a genome-wide association approach based on the >700,000 SNP marker assay. To include the largest number of individuals possible under the available budget, cows from several populations were classified according to reproductive efficiency, and DNA was pooled within population and phenotype before genotyping. Populations evaluated included a research population at USMARC, 2 large commercial ranch populations, and several smaller populations (<100 head) across the US. Significant associations for reproductive efficiency ($P < 1.04$ e-07) were detected by this approach on BTA 5, 13, 15, 18, and 29. A genomic segment located on BTA 5, spanning the region of 25–70 Mb, contained 223 SNP having significant association with classification, representing the most robust signal in the genome. The remaining significant SNP lie on BTA 13 (4 SNP), BTA 15 (1 SNP), BTA 18 (1 SNP), and BTA 29 (1 SNP). In addition to our novel findings, we confirmed previously published associations for over 200 SNP encompassing substantial diversity including *Bos indicus* and *Bos taurus* breeds. From these data we have identified regions of the genome associated with reproductive efficiency. These regions are being evaluated further to identify specific DNA variations that are affecting reproduction in beef cattle. USDA is an equal opportunity provider and employer.

Key Words: bovine, GWAS, reproductive efficiency

320 Molecular mechanism of neuropeptide Y affected by progesterone and estradiol on prepubertal Nellore heifers. J. Diniz-Magalhaes*[1], M. Maturana-Filho[1], J. L. M. Vasconcelos[2], and L. F. P. Silva[1], *[1]Universidade de Sao Paulo, Pirassununga, Sao Paulo, Brazil, [2]Universidade Estadual Paulista Julio de Mesquita Filho, Botucatu, Sao Paulo, Brazil.*

The understanding of the molecular mechanisms by which nutrition, genetics and hormonal treatments affect the beginning of puberty is of great importance for developing strategies aiming to reduce the age at

first calving, and therefore increase the slaughter rate in Nellore cattle. The effects of progesterone device and of endogenous estradiol on the molecular mechanisms controlling the attainment of puberty in Nellore heifers have been investigated. Specifically, the molecular pathways of progesterone (P4) and estradiol on NPY signaling were studied in the hypothalamus. Thirty-five non-pubertal heifers, between 13 and 14 mo of age, were divided into 4 treatments (9 or 8 per treatment): P4 device without estradiol (P-E), P4 device with estradiol (P+E), without P4 device and without estradiol (E−), and without P4 device and with estradiol (E+). The heifers were fed after weaning until they reach approximately 280 kg, with water access. At the end of the hormonal treatments all heifers were slaughtered and the preoptic area from hypothalamus were harvested, processed for analysis and then stored at −80°C. Total RNA of hypothalamus were extracted, treated with DNase I and submitted to cDNA synthesis for gene expression quantification of neuropeptide Y (Npy) and their receptor (Npy1r) by real time PCR (qRT-PCR). The exogenous progesterone increases the Npy expression ($P < 0.05$) on heifers treated only with P4. Similar effect was observed on the E+ treatment. These results indicate that the presence of progesterone and estradiol would be become preoptic area of hypothalamus more sensitive to the inhibitory action of Npy. A comprehensive study of the effects of progesterone administration and endogenous estrogen on attainment of puberty will also be conducted through next-generation sequencing (RNA-Seq), to identify possible candidate genes in the hypothalamus.

Key Words: reproduction, hypothalamus, neuropeptide Y

321 Model comparison in genome-wide association study of fertility traits of first service conception and heifer pregnancy in Brangus cattle. S. O. Peters*[1,2], K. Kizilkaya[3,4], D. J. Garrick[3], R. L. Fernando[3], J. M. Reecy[3], I. G. Imumorin[1], G. A. Silver[5], and M. G. Thomas[5,6], *[1]Cornell University, Ithaca, NY, [2]Berry College, Mt Berry, GA, [3]Iowa State University, Ames, [4]Adnan Menderes University, Aydin, Turkey, [5]New Mexico State University, Las Cruces, [6]Colorado State University, Fort Collins.*

First service conception (FSC) and heifer pregnancy (HPG) binary traits from Brangus heifers (i.e., 3/8 Brahman-*Bos indicus* × 5/8 Angus-*Bos taurus*; n ≈800) were used to compare Bayes C Logit, Probit and Robit models for a genome-wide association study (GWAS). Marker genotypes were from 53,692 loci on the BovineSNP50 chip. Yearling heifers were estrous synchronized, bred by AI, and then exposed to natural service breeding. Reproductive ultrasound and DNA-based parentage testing were used to determine if the heifer conceived by AI or natural service and to code for the traits of FSC and HPG. Success rates for FSC and HPG were 53.3 ± 0.01% and 78.0 ± 0.01%, respectively. Analyses fitted Bayes C, Logit, Probit or Robit model that treated SNP effects as random with an assumed fraction pi = 0.9995 having no effect on phenotype. The fixed effects fitted in the model were year (i.e., 2005 to 2007), location of birth, calving season, age of dam and contemporary group. In GWAS, simultaneous association of 1-Mb SNP windows with phenotype was undertaken with Bayes C, Logit, Probit or Robit analyses using GenSel software. The 1-Mb windows contained 21.3 ± 1.1 SNP. Results showed that there was more concordance in 1-Mb SNP windows among the 3 models for FSC trait than with HPG trait. Among the top fifteen 1-Mb SNP windows across the 3 models, nine 1-Mb SNP windows were common among the models for FSC while only five 1-Mb SNP windows were common for HPG. The nine 1-Mb SNP windows common among the 3 models used for FSC were identified on chromosomes 1, 6, 8, 16, 23 and 26, and the five 1-Mb SNP windows common for HPG were found on chromosome 2, 3, 20, 28 and 29. However, there were no overlapping SNP windows among those associated with these fertility traits. The SNP windows on 28 Mb and 17 Mb of chromosomes 8 and 26 were consistently ranked by the 3 models compared as the greatest contributor to the genetic variance for FSC trait while there was no consistent order for the SNP windows associated with HPG.

Key Words: GWAS, fertility, heifer

322 Discovery and validation of single nucleotide polymorphisms with phenotypic associations in beef cattle grazing endophyte-infected tall fescue. B. Bastin*[1], C. Bagley[3], B. Campbell[1,2], A. Houser[3], C. Kojima[1], A. Saxton[1], J. Waller[1], and L. Wojakiewicz[1], *[1]University of Tennessee, Knoxville, [2]Virginia Tech University, Blacksburg, [3]Tennessee Tech University, Cookeville.*

Development of a multi-locus marker panel will allow for genetic selection for improved production in cattle grazing endophyte-infected tall fescue. Tall fescue (*Lolium arundinaceum* Schreb.) is the most prevalent forage in the Mid-south United States due in part to the presence of the endophytic fungus *Neotyphodium coenophialum*. The fungus, while conferring hardiness to tall fescue, contributes to decreased production efficiency in cow-calf operations. A genome-wide association study was performed using the Illumina 50k bovine SNP chip. Twenty-four SNPs were found to be associated ($P < 0.05$) with adjusted birth weight and adjusted 205-d weights of calves from 48 beef cows at Ames Plantation. Taqman genotyping assays (Applied Biosystems) were subsequently designed to genotype each SNP in beef cattle located at Tennessee Tech University (n = 654), to validate associations in a large, independent herd. Genotype-phenotype associations were tested using mixed models (SAS 9.3, Cary, NC) accounting for variability in calving season in calf-related traits, and least squares means compared with Fisher's least significant difference ($P < 0.05$). Eleven of the GWAS SNPs were informative for such phenotypes as hair coat (scored 1–5), body condition (scored 1–9), weight per day of age (kg/d), adjusted 205-d weight (kg), and days to first calf (Table 1). These data indicate that genetic polymorphisms found to be informative in a small herd can be validated in a larger representative population in a cost-effective manner.

Table 1. Significant associations for GWAS-detected SNPs

			Genotype means		
Phenotypic association	SNP	*P*-value	A	H	B
Hair coat score	BTA9B	0.028	1.7^{B}	1.8^{A}	1.8^{AB}
	BTA9C	<0.001	1.9^{A}	1.6^{B}	1.7^{B}
	BTA9F	0.009	1.8^{A}	1.7^{B}	1.8^{AB}
	BTA9I	0.045	1.7^{B}	1.7^{B}	1.9^{A}
	BTA14J	0.001	1.8^{B}	1.6^{C}	2.0^{A}
	BTA19A	0.003	1.6^{B}	1.8^{A}	1.8^{A}
	BTA26	0.001	1.8^{A}	1.7^{B}	1.6^{B}
Body condition score	BTA11	0.037	5.0^{A}	4.8^{B}	5.1^{A}
Weight gained per day of age	BTA11	0.002	0.52^{A}	0.44^{B}	0.52^{A}
Adj. 205-d weight	BTA14B	0.032	128^{A}	116^{B}	
	BTA23	0.033	129^{AB}	119^{B}	134^{A}
Days to first calf	BTA9H	0.002	749^{B}	1185^{A}	725^{B}
	BTA11	0.024	715^{B}	1073^{A}	781^{B}
	BTA19A	0.001	989^{A}	723^{B}	709^{B}

Key Words: fescue toxicosis, cattle, SNP

323 From giant unilamellar vesicles (GUVs) to lipid organization of bovine milk fat globule membrane (MFGM). H. Zheng*[1,2], R. Jiménez-Flores[2], and D. Everett[1], *[1]Riddet Institute and Department of Food Science, University of Otago, Dunedin, New Zealand, [2]Dairy Products Technology Center, California Polytechnic State University, San Luis Obispo.*

The milk fat globule membrane (MFGM) is believed to play an important role in many physiological processes. The bio-functionalities of the MFGM are regulated, not only by functional molecules (e.g., phospholipids and membrane proteins), but also by their structural organization. However, to date, the structure and dynamics of MFGM are not fully understood. Giant unilamellar vesicles (GUVs) were introduced and developed in biological and physiological studies to investigate the morphology of lipid organization. Lipids were selected [phosphatidylethanolamine (PE, 18:1), phosphatidylcholine (PC, 16:0), sphingomyelin (SM, 16:0 and 23:0) and cholesterol] to construct GUV systems under an alternating current (AC) electrical field in a specially designed chamber. The unitary, binary, ternary and quaternary systems from model combinations of PE, PC, SM and cholesterol were applied to form GUVs, and a comparative study was conducted to find out differences in structural morphology and conditions of GUV formation using microscopic techniques. Images obtained from confocal laser scanning microscopy showed both head group-labeled (lissamine rhodamine B, Rd) and fatty acid tail-labeled (NBD) dyes stained well on GUVs and emitted decent fluorescent signals from laser excitation. The PE-labeled dye was also well-stained in unitary PC-GUV systems. The diameter of the generated GUVs (formed in a sucrose buffer medium) were from 20 μm to more than 100 μm. The current fundamental study provides a reproducible procedure for constructing GUVs from bovine milk phospholipids.

Key Words: giant unilamellar vesicles (GUV), milk fat globule membrane (MFGM), phospholipid

324 Centrifugal washing processes reveal lipid organization of bovine milk fat globule membrane (MFGM). H. Zheng*[1,2], R. Jiménez-Flores[2], and D. Everett[1], *[1]Riddet Institute and Department of Food Science, University of Otago, Dunedin, New Zealand, [2]Dairy Products Technology Center, California Polytechnic State University, San Luis Obispo.*

The milk fat globule membrane (MFGM) is constructed from a backbone of phospholipids and proteins that encapsulate native bovine milk fat globules. To date, the organization of the phospholipid structure is not fully understood. In this study, an innovative approach was carried out to reveal the lipid organization in the MFGM by applying washing procedures with different degrees of stringency to MFG surfaces in simulated milk ultra-filtrate buffer. Three washing methods, M1 (mild: 3000 × *g*, 5 min, 3 washes), M2 (reference: 3750 × *g*, 15 min, one wash) and M3 (intensive: 15000 × *g*, 20 min, 3 washes) were selected to isolate and wash MFGs. The results showed that M3 removed more phospholipids (PLs, 1.38 mg/m^2) from raw MFGs than M1 (1.21 mg/m^2, as evaluated by HPLC) but induced an enrichment of cholesterol (0.50 mg/ m^2) on the surface of MFGs ($P < 0.05$), suggesting that the MFGM structure may be significantly damaged by the M3 process. Moreover, once the native MFGM is damaged, cholesterol may be enriched in the MFG fraction during centrifugal washing rather than lost with the MFGM fragments, which suggests that most of the cholesterol is located in the outer leaflet of the native MFGM. HPLC-ELSD results showed that phosphatidylinositol (PI), phosphatidylserine (PS) and sphingomyelin (SM) were more strongly retained on MFG surface than the more loosely bound phosphatidylcholine (PC) and phosphatidylethanolamine (PE). Relative quantities of PL loss from MFGs during washing were estimated, and the micro-structural morphology was assessed by confocal laser scanning microscopy (CLSM) based on changes in intensities of fluorescent stains. CLSM images confirmed damage to the outer leaflet phospholipid double layer after M3 washing. The current results provide fundamental information about how centrifugal washing can alter the native MFGM, thus further developing the published schematic models of the structure of the MFGM.

Key Words: milk fat globule membrane, phospholipid, confocal laser scanning microscopy

325 Production of dairy-based functional peptides and their fractionation by membrane adsorption chromatography. E. Leeb*, S. Cheison, and U. Kulozik, *Technische Universität München, Freising, Germany.*

The production of functional peptides out of milk proteins offers 2 advantages. First, milk proteins are known to be potential precursors for several functional peptides. Second, milk proteins are a natural source offering good consumer acceptance. However, a target production of peptides requires the application of specific enzymes. Therefore, a comprehensive study using the 2 specific enzymes trypsin and Lys-C was carried out to investigate the production of functional peptides. β-Lactoglobulin was used as model substrate and the release of the ACE-inhibitory peptides f(9–14) and f(142–148) was examined. Peptide composition of the hydrolysate was analyzed by mass spectrometry (MS) over the hydrolysis process and the reproducible release of peptides was determined. For both enzymes the heterogeneity of the hydrolysates was decreasing with increasing hydrolysis duration. Using trypsin a reproducible production of the target peptides was only feasible by total-hydrolysis. In contrast, Lys-C enables the release of the peptide f(9–14) at earlier stages of hydrolysis. However, a target use of the functional peptides is only possible after their separation from the hydrolysate. Therefore a food-grade process to fractionate the hydrolysates was developed using ion-exchange membrane adsorption chromatography (MAC). The application of a 2-step purification process, whereby a strong anion and cation MAC module were coupled, enables the fractionation of all peptides. Process conditions for maximum separation efficiency were determined, using 0.03 mol/L phosphate-buffer at pH 7 for the anion exchange process. This gave 7 fractions in the first step. In the second step the flow-through of the anion exchange process was further separated using a cation exchanger and 0.03 mol/L phosphate buffer (pH 3). With a step-wise NaCl-gradient for both fractionation processes the production of 12 fractions in total was achieved. MS analysis of the fractions showed a recovery of the peptide f(9–14) with 97% and of the peptide f(142–148) with 80% in enriched fractions.

Key Words: enzymatic hydrolysis, ACE-inhibitory peptide, membrane adsorption chromatography

326 Correction of mid-IR fat test for sample to sample variation in fatty acid chain length and unsaturation. K. L. Wojciechowski[1], D. M. Barbano*[1], and E. de Jong[2], *[1]Cornell University, Department*

of Food Science, Northeast Dairy Foods Research Center, Ithaca, NY, [2]Delta Instruments, Drachten, the Netherlands.

Our objective was to use predicted mean fatty acid chain length (mCL, carbon number) and mean fatty acid unsaturation (mUnsat, double bonds per fatty acid) of milk fat from mid-FTIR spectra to improve the accuracy of fat estimation using the classical carbon hydrogen stretch (Fat B) and carbonyl stretch (Fat A). Calibration models for both mCL and mUnsat were calculated, using partial least squares, based on spectra for 268 samples collected over a period of 1.5 year. Of which 219 samples (largely herd milks) were selected to cover a wide variation in regional and dietary dependent milk fat composition. The set was complemented with 49 modified milks spanning an orthogonal set in fat, protein and lactose. Twelve sets of USDA Federal milk market individual farm control milks (10 milks per set), collected over a period of 5 mo, were analyzed for fat by ether extraction and fatty acid composition by both mid-IR transmittance and GLC. The fatty mCL and mUnsat measured by mid-IR were used to apply a linear correction factors to the Fat B and Fat A estimates of fat concentration for each sample. The mean (MD) and standard deviation of the difference (SDD) and Euclidean distance (ED) were calculated for each set of 10 samples for 6 different linear methods of fat estimation by IR in comparison to ether extraction results. The mean ED for Fat A, Fat B, 70% Fat B + 30% Fat A, Fat A corrected for mCL, Fat A corrected for mCL and mUnsat, and Fat B corrected for mUnsat were 0.072, 0.034, 0.040, 0.018, 0.016, and 0.028, respectively. The corrections for mCL and mUnsat improved ($P < 0.05$) the accuracy of Fat A predictions of fat content more than the same corrections applied to Fat B, with a MD between ether extraction and IR for the 120 bulk tank milks of −0.005% fat and a SDD of 0.0123 for the Fat A corrected for mCL and mUnsat.. This work has demonstrated the results from PLS based model predictions of mCL and mUnsat can be used in real time to improve the accuracy of fat testing by mid-IR transmittance.

Key Words: mid-infrared, fatty acid, chain-length

327 The role of milk immunoglobulins in gravity separation of somatic cells in raw skim milk. S. R. Geer* and D. M. Barbano, *Cornell University, Ithaca, NY.*

Our objective was to determine if immunoglobulins (Ig) play a role in gravity separation (rising to the top) of somatic cells (SC) in skim milk. Understanding the mechanism of gravity separation might be used to develop a continuous flow technology to remove SC, bacteria, and spores from milk. Other researchers have shown that gravity separation of milk fat globules is enhanced by IgM. Our recent research found that bacteria and SC gravity separate in both raw whole and skim milk and that heating milk to > 74.5°C for 25s stopped gravity separation of milk fat, SC, and bacteria. Bovine colostrum is a good natural source of Ig. A series of 6 gravity separation columns were used: one contained raw skim and the remaining 5 contained pasteurized skim (>74.5°C for 25s) with increasing amounts of added colostrum to achieve about 0, 0.4, 0.8, 2.0, and 4.0 g/L added Ig. The milks were allowed to gravity separate at 4°C for 22 h, and 6 fractions were collected and analyzed for SC: the bottom 90%, and then each successive 2% layer by weight. The experiment was replicated 3 times using different milk and colostrum. Addition of colostrum restored gravity separation with the SC found in the top 2% of column as a function of added Ig from colostrum increasing ($P < 0.05$) in a dose response relationship (linear regression $R^2 = 0.879$). No difference in SC in the top 2% between the raw skim (82% of total SC) and the pasteurized skim with 4.0 g/L added Ig (77% of total SC) was detected ($P > 0.05$), indicating that 4.0 g/L added Ig restored gravity separation of SC. The percent of SC in the top 2% layer for the other 4 treatments of colostrum (0, 0.4, 0.8, and 2.0 g/L) were lower ($P < 0.05$) than the raw skim and pasteurized skim with 4.0 g/L of added Ig. The spore count of the upper 2% and lower 90% of raw skim milk for the 3rd replicate was determined. Gravity separation of spores was apparent in the raw skim milk with about 72% of total spores in the top 2%, but no spore separation was observed in the pasteurized skim. Igs appear to be at least one of several possible factors involved in the gravity separation of SC, spores and bacteria in milk.

Key Words: gravity separation, somatic cell, colostrum

328 Effect of seasonal variation on the heat stability of UHT and in-container sterilized milk. B. Chen*, A. Grandison, and M. Lewis, *University of Reading, Reading, UK.*

The objective of this study was to investigate the effect of seasonal variation on the heat stability of UHT and in-container sterilized milk produced from 25 batches of raw milk over one year. Heat stability was assessed by measuring the amount of sediment in the bovine milk. The milk produced in summer has more sediment than the other seasons after UHT treatment. In contrast, heat stability was not significantly different for the different seasons for in-container sterilization. Sediment formation in both heat treatments was always accompanied by an increase in casein micelle size. The range of for sediment for UHT and in-container sterilized milk was from 0.10 to 0.29% and from 0.02 to 0.56% respectively. Correspondingly, the casein micelle size for UHT and in-container sterilized milk varied from 224 to 337 nm and from 273 to 381 nm, respectively. In addition, the roles of different stabilizing salts (di-sodium hydrogen phosphate and tri-sodium citrate) on both heat treatments were evaluated. Without stabilizing salts bovine milk produced more sediment when subjected to in-container sterilization compared with UHT processing. Addition of up to 10 m*M* stabilizing salts resulted in a significant ($P < 0.05$) increase in sediment for in-container sterilization, but only a slight increase in UHT processing. Adding up to 2 m*M* calcium chloride increased sediment formation significantly ($P < 0.05$) more after UHT treatment than after in-container sterilization. These results for bovine milk are in agreement with trends found for heat stability of caprine milk, which have been published previously. It was concluded that the effect of seasonal variation on heat stability of UHT milk was significant, but not for in-container sterilized milk. There is no single mechanism or set of reactions that cause milk to produce sediment during heating and that the kinetics are different for UHT and in-container sterilization processes.

Key Words: seasonal variation, heat stability, UHT and in-container sterilization

329 Effect of chemical-physical properties of raw milk on the quality of dairy products in the UK. B. Chen*, A. Grandison, and M. Lewis, *University of Reading, Reading, UK.*

The objective of this study was to investigate the effect of raw milk composition on some selected properties of milk products. Raw bulk cow milk was collected and its composition and physical properties were measured every 2 wk. This milk was then converted to a range of products using standardized methodology and selected properties of these products were measured. Products include evaporated milk, soft cheese, skim milk powder and whipping cream. This project has been replicated with a minimum of 25 batches of raw milk. The range of values for fat and protein were 3.62 to 4.77% and 2.89 to 3.56%, respectively. Ranges for lactose (4.52 to 4.69%), total solids (12.31 to 13.37%), pH (6.73 to 6.87), buffering capacity (pH change from 0.78 to 0.88) and ethanol stability (84 to 100%) were narrower. Ca^{2+}concentration ranged

from 1.68 to 2.55 m*M*. Sediment in raw milk was very low, ranging from 0.03% to 0.13% (dry weight basis). Viscosity ranged from 1.52 to 2.36 cp and density from 1026 to 1031 kg/m^3. Casein micelle size ranged from 132 to 202 nm and freezing point depression from −0.530 to −0.514°C. The highest foaming times were 205 and 96 s for raw and skim milk, respectively, and the shortest were 24 and 19 s. The viscosity range for evaporated milk greatly varied from 9.5 to 243.7 cp and was also affected by the level of added stabilizer. For the whipping cream, the range of value for overrun and whipping time were 94 to 202% and 169 to 261 s which were more variable than foam stability (5.00 to 18.75 mL). The heat stability of skim milk powder showed considerable variability. The ranges of the moisture content and hardness in soft cheese were 46.17 to 64.33% and 0.63 to 4.00 N respectively. It was concluded that variations in raw milk composition influence the properties of manufactured milk products.

Key Words: raw milk quality, physico-chemical properties, best use for milk

330 In vitro and in vivo assessment of the antioxidant activity of whey protein hydrolysates prepared using commercial enzymes. B. Mann*, A. Kumari, K. Prajapati, R. Kumar, and R. Sharma, *National Dairy Research Institute, Karnal, Haryana, India.*

Whey proteins are potential source of antioxidant peptides. Hydrolysis by various food-grade enzymes leads to the production of such peptides. In this study, whey protein hydrolysates (WPHs) were prepared from whey protein concentrate (WPC-70) using commercial proteases (flavorzyme and alcalase) and hydrolysis conditions were optimized by applying response surface methodology. The antioxidant activity was evaluated using in vitro and in vivo assays along with molecular and techno-functional characteristics of these WPHs. These WPHs showed very high antioxidant activities; i.e., 1.41 ± 0.08 (alcalase WPH) and 1.25 ± 0.06 (flavorzyme WPH) μmol of trolox/ mg of protein as compared with intact whey proteins (0.19 ± 0.07μmol of trolox/ mg of protein). Further, these WPHs were evaluated for antioxidant activity by carrying out in vivo studies in mice as animal model. The result showed that the antioxidant enzymes viz. catalase, superoxide dismutase, glutathione peroxidase activities in blood as well as catalase and glutathione activities in liver homogenates increased significantly ($P < 0.05$) in the groups fed with WPHs + oxidized oil compared with oxidized oil fed group. The level of thiobarbituric acid reactive substances in blood and liver homogenates of the group fed with WPHs decreased significantly ($P < 0.05$) compared with the groups fed with oxidized oil. The peptides in WPHs have been identified using LC/MS and the results showed that these hydrolysates contained fragments of β-LG and α-LA. Sequence of these peptides were synthesized and assessed for the antioxidant activity. The peptide α-LA (99–108) showed the maximum antioxidant activity (1.720 ± 0.164 μmol of trolox/ mg of protein). The techno-functional properties of WPHs were slightly inferior to the unhydrolyzed whey protein except whipping ability which showed increase in case of WPHs. The incorporation of these hydrolysates showed increase in the antioxidant activity of flavored milks from 14.4 to 43.3% vis-à-vis control. These WPHs with antioxidant activity could lead to the development of novel foods relevant in health promotion and disease prevention.

Key Words: whey protein, whey protein hydrolysate, antioxidant activity

331 Residual feed intake is repeatable when high and low starch diets are fed to lactating Holstein dairy cows. S. E. Burczynski*, J. S. Liesman, R. J. Tempelman, J. C. Ploetz, M. S. Allen, A. L. Lock, and M. J. VandeHaar, *Michigan State University, East Lansing.*

Residual feed intake (RFI) is a tool to quantify feed efficiency in livestock and is commonly used to assess efficiency independent of production level, BW, or BW change. Seventeen primiparous and 40 multiparous lactating Holstein cows, averaging 674 ± 77 kg of BW, 39 ± 9 kg of milk/d, and 125 ± 33 d postpartum at experiment start, were fed diets of high or low starch content in 2 crossover experiments with 4-wk periods. Soyhulls replaced a portion of ground corn and soybean meal (experiment 1) or a portion of ground corn, soybean meal, and wheat straw (experiment 2) to formulate the low starch diets. High starch diets were approximately 27% NDF and 30% starch and low starch diets were either 44% NDF, 12% starch (experiment 1) or 39% NDF, 16% starch (experiment 2). All diets were approximately 17% CP. Individual dry matter intake (DMI) of a cow was modeled as a function of her cohort group, milk energy output, metabolic BW ($BW^{0.75}$), and BW change within each period; RFI for each cow was the residual error term. For the model, each unit increase in milk energy output, metabolic BW, or BW change was associated with 0.38, 0.14, or 0.17 kg increase in DMI, respectively. High starch diets increased milk energy output by 7%, DMI by 3%, and percentage of gross energy captured as milk and body tissue (GEcap) by 9% ($P < 0.01$) across experiments and parity. Primiparous cows had lower milk energy output, DMI, and GEcap than multiparous cows for both experiments ($P < 0.01$). The difference in RFI between treatments across experiments ranged from −2.5 to 2.8 kg, with a mean absolute change of 0.9 kg (SD = 0.7). The correlation between RFI when cows were fed the high starch diets and RFI when cows were fed the low starch diets was 0.79 ($P < 0.01$) and was similar within each parity and experiment. We conclude that RFI is reasonably repeatable for a wide range of dietary starch concentrations so that cows that are most efficient when fed high corn diets are likely also most efficient when fed diets high in non-forage fiber sources.

Key Words: dairy cow, feed efficiency, residual feed intake

332 The effect of offering differing combinations of forages and cereals on feed intake, total diet composition and the growth and development rates of dairy heifers. Z. Ullah*[1], J. K. Margerison[1], D. Simcock[2], and N. Lopez Villolobos[3], *[1]Institue of Agriculture and Environment, Massey University, Palmerston North, New Zealand, [2]Institute of Food Nutrition and Human Health, Massey University, Palmerston North, New Zealand, [3]Institute of Veterinary and Biological Sciences, Massey University, Palmerston North, New Zealand.*

The experimental objective was to assess the effect of offering milk fed calves starter supplement with one of 3 forage options: moist Lucerne haylage (LH), pasture hay (PH) or no forage (NF), on individual animal feed intake, total diet composition, growth and development rate, and feed conversion efficiency. Sixty Holstein-Jersey crossbred calves were collected from their dams (<6 h of age), weighed and placed in individual pens and fed colostrum. Calves were selected at random and allocated simultaneously to one of the 3 diet treatments (20 calves per treatment) according to live weight and age, such that the treatments were similar for these factors. Whole milk was fed twice daily (10.4% birth weight) till weaning at 49 d of age. Individual animal feed intake was monitored daily, whereas live weight and stature (hip width and height, last rib girth) was measured weekly. Starter intake (g/day) was greater for calves offered PH followed by LH and lowest in NF both pre weaning (PH: 741[a], LH: 582[b], NF: 368[c], SEM, 24.5) and 7 d post weaning (PH: 2152[a], LH: 1677[b], NF: 1253[c], SEM, 47.4). Calves offered PH and LH had greater liveweight gains (g/day) compared with calves offered NF, both pre weaning (PH: 560[a], LH: 540[a], NF: 431[b], SEM, 0.6) and 7 d post weaning (PH: 771[a], LH: 710[a], NF: 600[b], SEM, 11.1). Calf stature did not differ between treatments. In conclusion, calves offered forages had greater starter and total feed intakes, and greater growth rates, but no difference in stature compared with calves not offered forage.

Key Words: dairy, heifer, nutrition

333 Determination of the optimum dietary forage concentration when using canola meal as a primary protein source in lactating dairy cow diets. A. M. Schuler*, K. F. Kalscheur, D. P. Casper, and J. L. Anderson, *South Dakota State University, Brookings.*

Canola meal (CM) is a high quality protein supplement that can be fed to lactating dairy cows. Presently there is little research evaluating the optimum dietary forage concentration when CM is included as the primary protein source in lactating dairy cow diets. Twelve multiparous and 4 primiparous Holstein cows (96 ± 54 DIM) were used in a 4 × 4 Latin square design with 3-wk periods to determine the optimum dietary concentration of forage when using CM as the primary protein source. Diets were formulated to include 42% forage (42F), 50% forage (50F), 58% forage (58F), and 66% forage (66F) concentrations on a DM basis. All diets included 11% canola meal (DM basis). The corn silage: alfalfa haylage ratio (70:30) was maintained across treatment regardless of dietary forage concentration. Diets were similar in crude protein and metabolizable protein. Dry matter intake (DMI) linearly decreased with increasing forage concentration ($P = 0.001$). Milk production was similar ($P > 0.10$) among treatments. Milk fat percentage and yield linearly increased with increasing dietary forage concentration ($P < 0.05$). Milk protein percentage tended to decrease with increasing forage concentration ($P = 0.06$). Milk protein yield and energy-corrected milk were not affected by forage concentration. Feed efficiency (FE) increased linearly with increasing forage levels ($P = 0.001$). Mid-lactation Holstein dairy cows fed an increasing forage to concentrate ratio in conjunction with CM as the primary protein source did not alter milk yield while decreasing DMI resulting in improved feed efficiency.

Table 1.

	Treatment					
Item	42F	50F	58F	66F	SEM	*P*-value[1]
DMI, kg/d	28.0	27.0	25.8	24.8	0.69	L
Milk, kg/d	40.1	40.4	40.8	39.1	1.12	NS
Fat, %	3.17	3.22	3.37	3.52	0.17	L
Fat, kg/d	1.26	1.28	1.35	1.37	0.07	L
Protein, %	2.98	3.00	2.96	2.94	0.05	LT
Protein, kg/d	1.19	1.21	1.20	1.14	0.04	NS
ECM, kg/d	38.0	38.4	39.5	38.7	1.23	NS
FE (ECM/DMI)	1.36	1.44	1.54	1.57	0.05	L

[1]L = linear effect ($P < 0.05$); LT = linear trend ($P < 0.10$); NS = $P > 0.10$.

Key Words: canola meal, dairy cow, forage concentration

334 Moment and allocation of corn silage on dry matter intake and milk production of grazing dairy cows. D. A. Mattiauda*[1], M. Carriquiry[1], S. Tamminga[2], F. Elizondo[1], and P. Chilibroste[1], *[1]Departamento de Produccion y Pasturas, Facultad de Agronomia, UdelaR, Paysandu, Uruguay, [2]Department of Animal Science, Wageningen University, Wageningen, the Netherlands.*

Thirty-three multiparous Holstein cows were used in a randomized block design to study the effects of feeding strategies (corn silage allocation during the day) in early lactation (48 ± 17.8 d). All cows (separated by treatment) had access to an ungrazed daily strip of pasture (1535 ± 289 kg DM/ha; forage allowance: 15 kg DM/cow) from 0900 to 1500 h and received 2.7 kg DM of concentrate at each milking (0430 and 1530 h). Corn silage (3.9 kg DM/d) was offered 100% at 1700 h (T1), at 0800 h (T2) or equally distributed at 1700 and 0800 h (T3). Experimental period lasted 7 wk with 1 wk of adaptation and 6 wk of measurements. Milk yield was recorded daily and milk samples were collected weekly (2 consecutive days) for fat, protein, and lactose composition. Cow BCS was recorded every 2 wk. Individual herbage DMI was determined during 4 d at wk 7 in 12 cows (4 complete blocks), using n-alkanes. Data were analyzed with a mixed model including treatment, week of treatment and their interaction (if corresponded) as fixed effects and block as a random effect. Herbage DMI was greater ($P < 0.04$) for T1 and T3 than T2 cows (10.3, 8.5, and 11.0 ± 0.68 kg/d for T1, T2, and T3, respectively) which defined a difference between treatments in total DMI (19.5, 17.7, 20.0 ± 0.68 kg/d for T1, T2, and T3, respectively). There was no difference in milk yield among treatments (25.2 ± 0.62 kg/d) but fat percentage was greater ($P < 0.04$) for T3 than T2, being intermediate in T1 cows (3.85, 3.66 and 3.89 ± 0.072% for T1, T2, and T3, respectively), resulting in a trend ($P = 0.10$) for greater 4% fat-corrected milk yield (24.6, 23.7 and 25.3 ± 0.84 kg/d for T1, T2, and T3, respectively). Protein (2.97 ± 0.048%) and lactose (4.74 ± 0.045) percentages did not differ among treatments. Cow BCS was greater ($P < 0.03$) for T3 than T2, being intermediate in T1 cows (2.42, 2.37, 2.52 ± 0.063 for T1, T2, and T3, respectively). Corn silage allocation related to grazing session had an effect on DMI and productive performance, probably due to the integration of the animal grazing strategy and rumen fermentation.

Key Words: feeding strategy, corn silage, grazing

335 Predicting dry matter intake of Holstein calves. J. C. M. Lima[1], J. P. P. Rodrigues[1], M. I. Marcondes*[1], M. M. Campos[2], T. E. Silva[1], A. S. Treece[1], N. C. S. Gonzaga[1], and A. F. W. Oliveira[1], *[1]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil, [2]Embrapa Gado de Leite, Juiz de Fora, Minas Gerais, Brazil.*

This study aimed to develop a model to predict dry matter intake (DMI) in dairy calves. Thirty-two male Holstein calves, with 3 d of age and average live weight of 35.56 ± 5.86 kg, were used. The animals were distributed into a completely randomized design and allocated in individual houses. The treatments consisted of different amounts of raw milk (12.43% DM; 3.19% fat; 2.68% CP on natural matter basis), which were: 2, 4, 6 and 8 L/day, fed twice a day, in 8 replications. All calves were fed starter (19.75% CP) ad libitum and feed intake was registered daily from 3 to 59 d old. Total dry matter intake (TDMI; kg/day) was obtained summing milk dry matter intake (MDMI) and starter dry matter intake (SDMI; kg/day). TDMI equations were regressed for each treatment by days according to the model: $TDMI = \beta_0 + e^{(\beta 1 \times d)}$. SDMI was regressed by milk intake (MI; liters/day) and day according to the model: $SDMI = \beta_0 \times MI + \beta 1 \times e^{((\beta 2 \times MI + \beta 3) \times d)}$. The TDMI equations obtained for each treatment was: $TDMI = 0.2405(\pm 0.0165) \times e^{0.0279(\pm 0.0010) \times d}$; $TDMI = 0.3156(\pm 0.0135) \times e^{0.0262(\pm 0.0007) \times d}$; $TDMI = 0.4957(\pm 0.0227) \times e^{0.0173(\pm 0.0007) \times d}$ and $TDMI = 0.7068(\pm 0.0215) \times e^{0.0125(\pm 0.0005) \times d}$ for 2, 4, 6 and 8 L/day, respectively. The β_0 values indicate that initial intake was greater with greater milk amounts, while β_1 suggests that the rate of increasing in dry matter intake was more expressive for calves fed lower milk amount. Afterward, β_0 and β_1 of each equation were linear regressed on milk intake to compose a single equation to predict TDMI in calves. The equations to predict TDMI and SDMI according to milk intake and age were, respectively: $TDMI = (0.079 \times MI + 0.0449) \times e^{((-0.0028 \times MI + 0.0348) \times d)}$ and $SDMI = -0.013 \times MI + 0.125 \times e^{((-0.003 \times MI + 0.034) \times d)}$. Negative value obtained for parameters linked to milk intake (β_0; β_2) suggests that initial starter intake was lower for greater milk intake. Considering that when using 2 prediction equations the sum of random errors might be greater, it is suggested to estimate SDMI by the equation: SDMI = DMI – MDMI. It can be concluded that TDMI and SDMI can be explained by calf age and milk intake. Supported by CNPq/Fapemig.

Key Words: calf, milk, starter

336 Abrupt changes in forage dry matter of one to three days affect intake and milk yield in lactating dairy cows. J. Boyd*[1] and D. R. Mertens[2], *[1]US Dairy Forage Center, Madison, WI, [2]Mertens Innovation & Research LLC, Belleville, WI.*

Our objective was to determine the effects of 1, 2, and 3d changes in forage DM on lactating cow performance across stage of lactation or parity. Data was compiled from 2 studies: Study A (fall 2009) early lactation cows averaging 65 DIM and 43.3 kg milk/d and Study B (fall 2012) late lactation cows averaging 192 DIM and 40.7 kg milk/d (total of 44 primiparous and 44 multiparous Holstein cows) housed in a tie stall barn. Within parity, cows were assigned to 1 of 11 blocks based on production and days in lactation. Study design was replicated 2 × 2 Latin Squares for each set of 1-, 2-, or 3-d treatments. Each period consisted of a 3-d pre-treatment, 1- to 3-d treatment, and a 3-d post-treatment phase. Diets were control (Ctrl) with no water added and treatment (Trt) with water added to decrease forage DM by 8%-units, to mimic rainfall events on a bunker silo and feeding an imprecise ration based on as-fed ratios of ingredients. Ctrl rations were adjusted daily to maintain DM ratios of ingredients. Feed offered was adjusted daily for both Ctrl and Trt based on the previous day's refusal. Milk yield was recorded daily and samples were taken 2× daily. Forages, TMR, and refusals were sampled daily and concentrates sampled 2× weekly. Chemical composition (DM, CP, aNDF) of samples were determined by NIR. Data was analyzed using Proc MIXED of SAS with cow within parity-block as a random variable. On d 1, DMI was reduced 2.3 ($P < 0.0001$), 1.5 ($P < 0.0001$), and 0.91 kg ($P < 0.0001$), for the 1-, 2-, and 3-d treatments, respectively, but DMI recovered during the following 1 to 3 d even during Trt phases. Although daily milk decreased slightly on d 1 of each Trt, the decrease was largest on d 2: −1.06 ($P = 0.003$), −1.48 ($P = 0.0003$) and −0.79 kg ($P = 0.03$), for the 1, 2, and 3d treatments, respectively. No parity effect was observed, but late lactation cows were not as susceptible to diet DM change as early lactation animals. We concluded that abrupt changes in forage DM causes economically significant reductions in daily milk yield, but the duration of the change does not worsen the losses if offered ration amounts are adjusted daily.

Key Words: DM changes, silage, feeding

337 Dry matter intake in crossbred dairy calves. A. L. Silva[1], M. I. Marcondes*[1], M. M. Campos[2], T. E. Silva[1], A. S. Trece[1], J. S. A. A. Santos[1], S. G. S. Moraes[1], and J. P. P. Rodrigues[1], *[1]Universidade*

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The liquid-feeding phase is extremely important in animal production systems. Therefore, it becomes necessary to establish measures to maximize animal performance during this phase. Dry matter intake (DMI) affect directly the animal performance, because it's the main determinant of entry of nutrients to meet animal requirements. The objective was to determine the DMI for crossbred Holstein-Zebu calves aged between 0 and 60 d. The experiment was conducted at Department of Animal Science, at Universidade Federal de Viçosa, Brazil. Eighteen male calves, crossbreed Holstein-Zebu, with initial BW of 36 ± 5.5 kg, were used. The animals were allotted to 3 treatments, with 6 replications. Treatments consisted of 3 different levels of milk intake, which were 2, 4 and 8 L/d. The animals had free access to water and concentrate (starter), which was formulated in accordance with the requirements presented in NRC (2001). The animals were fed twice a day, at 6:00 and 15:00, and starter intake was measured every day at 6:00h. Environmental variables were also considered: relative humidity (RH), temperature and humidity index (THI) and black globe temperature and humidity index (BGTHI). Environmental effects, milk intake and age were used in a multiple regression model, considering both linear and quadratic effects, to estimate calves DMI. The test was conducted using the MIXED procedure, at the level of significance of 5%. The DMI was affected by milk intake ($P < 0.001$), THI ($P = 0.0453$) and age of the animals ($P < 0.001$). However, no significant quadratic effects were observed ($P > 0.05$), thus the final regression can be expressed by equation. DMI = 0.4272 + 0.6741 × M – 0.0059 × THI + 0.0122 × D; where: DMI = Dry matter intake (kg/day), M = Milk intake (kg/day of DM), THI = Temperature and humidity index (without dimensional), D = Age of animal (days). The SI can be estimated by the difference between the total DMI and the DMI from milk. It can be concluded that the DMI in calves can be estimated using parameters as milk intake, THI and age of animals.

Key Words: environmental effect, feed, milk

338 The study of ruminal degradation of canola meal in dairy cows. Y. J. Tian[1,2], Y. Zeng[1,2], Z. J. Cao[1,2], and S. L. Li*[1,2], *[1]College of Animal Science and Technology, China Agricultural University, Beijing, China, [2]State Key Laboratory of Animal Nutrition, Beijing, China.*

The objective of this paper was to determine the rumen degradability of Canola. Two types of diets were formulated at a 4:6 (DM basis) concentrate: forage ratio according to 1.3× maintenance or 2.5× maintenance nutrients levels, respectively. Ruminal degradation rates of dry matter (DM) and crude protein (CP) of 2 kinds of canola meals (CM1, CM2) and 2 other kinds of domestic regular rapeseed meals (DRM1, DRM2) were determined using in situ method in the cows fed the above 2 types of diets. The results suggested that ruminal degradation kinetics of DM and CP of the 4 kinds of rapeseed meals had the similar variation trend. The effective degradation of DM and CP were higher for all the rapeseed meals measured in the cows fed the diets with 1.3× maintenance compared with the 2.5× maintenance level. With the same nutrients levels, DM and CP digestion rates of CM was generally higher than that of DRM. The total digestion rates of CP of CM were no differences between 2 maintenance nutrients levels. However, the total digestion rate of CP of DRM on the 1.3× maintenance nutrients level was higher than that on the 2.5× maintenance nutrients level.

Table 1. Rumen effective degradation of DM (top) and CP (bottom) in cows fed diets at 1.3 and 2.5× maintenance level

Sample	1.3×	2.5×	SEM	P-value[1]
CM 1	48.45	45.30	1.09	0.158
CM 2	49.22	47.11	1.28	0.453
DRM 1	45.12	39.18	1.23	0.002
DRM 2	51.05	43.16	1.88	0.019
CM 1	59.86	52.61	1.77	0.024
CM 2	61.58	57.61	1.22	0.104
DRM 1	57.11	49.30	1.54	<0.001
DRM 2	66.93	55.76	2.25	0.001

[1]$P < 0.05$ = significant difference, $P < 0.01$ = very significant difference.

Key Words: canola meal, rumen degradation, dairy cow

339 Meta-analysis: Effect of corn silage hybrid type on intake, digestion, and milk production by dairy cows. L. F. Ferraretto* and R. D. Shaver, *University of Wisconsin–Madison, Madison.*

A meta-analysis was performed to evaluate the effects of corn silage hybrid type on digestion, rumen fermentation and lactation performance by dairy cows using a data set of 139 treatment means from 45 peer-reviewed articles published 1990–2013. Categories for hybrids differing in grain and stalk characteristics, respectively, were: conventional (CONG), nutridense (ND), high oil (OIL), and waxy (WAXY); conventional, dual-purpose, isogenic or low-normal fiber digestibility (CONS), brown midrib (BMR), high fiber digestibility (HFD), and leafy (LFY). Genetically-modified (GM) hybrids were compared with their genetically similar non-biotech counterpart (ISO). Data were analyzed using Proc Mixed in SAS with hybrid as fixed and trial as random effects. Silage nutrient composition was similar ($P > 0.10$), except for lower ($P < 0.01$) CP% and EE% for CONG than ND and OIL. Milk fat content and yield and protein% were lowest ($P < 0.05$) for OIL. Intake, milk production and total tract nutrient digestibilities were unaffected ($P > 0.10$) by grain hybrid type. Except for lower ($P < 0.001$) lignin% for BMR, lower ($P < 0.05$) starch% for HFD than CONS, and a trend ($P < 0.10$) for higher NDF% for HFD, silage nutrient composition was similar ($P > 0.05$) among hybrids of different stalk type. Intake, milk, and protein yield were 1.6, 1.3, and 0.05 kg/cow/d, respectively, greater ($P < 0.01$) for BMR than CONS and LFY on average. Likewise, DMI and milk yield were 0.6 and 0.9 kg/cow/d greater ($P < 0.01$) for HFD than CONS. Total tract NDF digestibility was greater ($P < 0.001$) and starch digestibility reduced ($P < 0.01$) for BMR and HFD than CONS or LFY. Rumen pH tended ($P < 0.10$) to be lower for BMR than CONS. No differences in lactation performance were observed for GM compared with ISO ($P > 0.10$). Except for negative effects of OIL on milk fat and protein percentages, differences were minimal among corn silage hybrids differing in grain type. Except for positive effects of BMR and HFD on intake and milk yield, differences were minimal among corn silage hybrids differing in stalk type. However, reduced total tract starch digestibility for BMR merits further study.

Key Words: corn silage, hybrid, dairy cow

340 Responses of late lactation cows to forage substitutes in diets supplemented with byproducts. M. B. Hall*[1] and L. E. Chase[2], *[1]US Dairy Forage Research Center, USDA-ARS, Madison, WI, [2]Department of Animal Science, Cornell University, Ithaca, NY.*

In a drought year with forage shortages and high grain prices, a study was performed to evaluate cow lactation response to lower forage diets supplemented with forage substitutes and byproduct feeds. No corn grain or soybean meal was used. The design was a randomized complete block with a 2 wk covariate period. Forty-eight lactating cows were offered a high forage TMR in the covariate period and 1 of 4 diets in a 4-wk feeding period. Experimental diets contained wheat straw (WS)/ sugar beet pulp (SBP) at 0%/12%, 3%/9%, 6%/6%, or 9%/3% of diet DM. The rest of the diet DM was comprised of 20% corn silage, 20% alfalfa silage, 25.5% corn gluten feed, 8% distillers grains, 5% whole cottonseed, 7% cane molasses/whey blend, and 2.5% vitamin and mineral mix with monensin. Diet DM averaged 16.5% CP, 35% NDF, and 11% starch. DMI declined linearly ($P = 0.03$) and milk kg tended to decline linearly ($P = 0.08$) as WS increased. As WS increased, actual milk fat kg did not change ($P > 0.57$), but protein kg declined linearly ($P = 0.02$). Experimental diets did not differ in 3.5% fat-and protein-corrected milk kg (FPCM; $P > 0.19$). Average FPCM in the experimental period (34.6 kg) did not differ from the covariate period (34.2 kg; $P = 0.48$), but FPCM/DMI was greater with the covariate diet than with the experimental diets (1.50 vs. 1.28, $P < 0.01$). MUN tended to be greater for 9%WS than for other diets ($P = 0.12$). Time spent ruminating increased linearly from 566 to 703 min/d with increasing WS ($P < 0.01$). There was a tendency for ruminal pH to increase from 0 to 4 h post-feeding (5.91 to 6.16; $P = 0.11$), and pH was lower with 0% WS than the other diets ($P = 0.01$). Use of forage substitutes in low starch/ high byproduct diets can maintain good milk production and components in late lactation cows. Future research should evaluate long-term effects on body condition changes.

Table 1.

	Straw % of DM				
Item	0%	3%	6%	9%	SED
DM intake, kg	26.9	25.9	25.9	25.4	0.64
Milk, kg	32.2	32.7	31.5	30.8	0.88
Fat, kg	1.38	1.38	1.32	1.37	0.06
Protein, kg	1.06	1.07	1.03	0.98	0.03
MUN, mg/dL	10.0	10.9	10.6	12.0	0.46

Key Words: byproduct, dairy cow, forage

341 Performance of dairy cows as affected by dietary starch level and supplementation with monensin during early lactation. M. M. McCarthy*[1], T. Yasui[1], C. M. Ryan[1], G. D. Mechor[2], and T. R. Overton[1], *[1]Cornell University, Ithaca, NY, [2]Elanco Animal Health, Greenfield, IN.*

The objective of this study was to evaluate the effect of dietary starch level and monensin (M) supplementation on performance of dairy cows during early lactation. Primiparous (n = 21) and multiparous (n = 49) Holstein cows were fed high starch (HS) or low starch (LS) diets beginning at parturition with a topdress pellet containing 0 or 450 mg/d of M in completely randomized design with a 2 × 2 factorial arrangement of treatments. Prior to parturition all cows were fed a common controlled energy diet with daily topdress of either 0 or 400 mg/d M consistent with postpartum treatments. From d 1 to 21, cows were fed HS TMR (26.2% starch, 34.3% NDF, 22.7% ADF, 15.5% CP) or LS TMR (21.5% starch, 36.9% NDF, 25.2% ADF, 15.4% CP) with a daily topdress of either 0 or 450 mg/d M. From d 22 through 63 cows were fed HS with their assigned daily topdress. Interactions of starch content × M supplementation were not significant. Cows fed HS from wk 1 to 3 postcalving had greater increases in milk yield during wk 2 and 3 postcalving compared with LS cows ($P = 0.002$), but HS cows also had lower percentages of milk fat ($P = 0.01$), true protein ($P = 0.05$), lactose ($P = 0.05$), and total solids ($P = 0.009$) during the same period. This resulted in similar yields of 3.5% FCM and ECM between starch treatments. Cows fed HS diets had higher DMI in wk 2 and 3 postcalving ($P = 0.04$) and lost less BCS during wk 1 to 3 ($P = 0.04$), contributing to lower ECM/DMI during this period for HS cows ($P = 0.002$). Cows fed M had higher DMI from calving through wk 9 of lactation (20.0 vs. 18.9 kg/d; $P < 0.02$). Cows fed M had higher milk yields during the first 9 wk of lactation (37.3 vs. 35.1 kg/d; $P = 0.05$), but had similar yields of both 3.5% FCM and ECM because of trends for lower milk fat content during early lactation ($P = 0.10$). In part because of similar yields of ECM between these treatments and higher DMI for cows fed M, ECM/DMI during the first 9 wk of lactation was not affected by M treatment. Overall, cows fed HS had faster increases in milk and DMI and lost less BCS postpartum and cows fed M had higher milk and DMI during the first 9 wk of lactation.

Key Words: early lactation, starch, monensin

342 Effects of alfalfa hay particle size in diets supplemented with unsaturated fat: Feeding behavior and performance of dairy cows. A. Kahyani[1], G. R. Ghorbani[1], M. Khorvash[1], S. M. Nasrollahi[1], K. A. Beauchemin[2], and S. Ding*[2], *[1]Isfahan University of Technology, Department of Animal Sciences, Isfahan, Iran, [2]Lethbridge, Agriculture and Agri-Food Canada, Research Centre, Lethbridge, AB, Canada.*

The objective was to evaluate the effects of increasing the physically effective fiber (peNDF) intake of lactating dairy cows fed diets supplemented with unsaturated fat on feeding behavior and performance. The peNDF content of the diets was increased by incorporating 24% (DM basis) alfalfa hay (AH), which varied in particle size (PS). Nine multiparous cows averaging 87.8 ± 14.8 DIM and weighing 653 ± 53 kg were randomly assigned to a triplicate 3 × 3 Latin square. During each of 3 21-d periods, animals were offered one of 3 total mixed rations that were chemically similar but varied in PS of AH: fine, medium, and long, with a geometric mean particle length of 2.1, 3.6, and 5.0 mm, respectively. All diets were supplemented with yellow grease at 2% of dietary dry matter (DM). Data were analyzed using the mixed model procedure of SAS to account for effects of square, cow within square, and treatment. The treatment was considered a fixed effect; square, period and cow within square were considered random effects. Increasing PS quadratically affected DM intake (DMI) (24.68, 25.38, and 23.70 kg/d, for fine, medium, and long, respectively; $P < 0.05$). Increased peNDF intake decreased eating rate ($P < 0.05$), did not affect feed sorting ($P > 0.05$), and increased eating and total chewing per kg DMI ($P < 0.05$). Daily rumination time exhibited a quadratic response ($P < 0.05$), with highest rumination time for the medium diet. There was a quadratic response in actual (41.5, 43.3, and 40.4 kg/d) and 4% fat-corrected milk production as well as milk protein yield ($P < 0.05$). There was a linear increase in milk fat content with increasing PS ($P < 0.05$), but milk fat content and fat to protein ratio were low for all treatments likely due to adding yellow grease to a diet containing a high level of non-forage carbohydrates (42.2% DM). The study indicates that increasing PS of AH in diets containing unsaturated fat can help to elevate peNDF intake results in the improvement of chewing activity, DMI, and milk yield and milk fat production.

Key Words: alfalfa hay particle size, feed sorting, unsaturated fat

Dairy Foods Symposium: Dietary Influence on Milk Synthesis of Health-Promoting Components in Bovine and Human Milk

343 Hot topics in human milk composition. M. K. McGuire*[1], K. Hunt[2], J. Williams[2], and M. A. McGuire[2], *[1]Washington State University, Pullman [2]University of Idaho, Moscow.*

Human milk continues to be the "gold standard" in terms of optimal infant nutrition during the first 4 to 6 mo of life, although its composition is variable and incompletely understood. The purpose of this talk will be to highlight 3 areas of intense current research concerning human milk composition, as well as reviewing what is known about the effects of maternal diet and putative infant health outcomes. The first topic is the potential for human milk to be classified as a "symbiotic" food containing both pre- and probiotic constituents. Indeed, one of the most abundant components of human milk is a large and diverse group of complex carbohydrates (human milk oligosaccharides; HMO), which appear to be largely indigestible by the infant's intestinal enzymes but which may modulate healthy development of the infant's gastrointestinal (GI) microbes. Human milk oligosaccharides are also thought to impart health benefits via modulation of the immune system and direct interactions with pathogenic GI microbes. Some data also suggest that HMO might mediate microbial metabolism. Noteworthy, however, is the fact that the oligosaccharides currently added to some proprietary infant formulas are structurally quite different from those common in human milk; this likely has important functional health outcomes (or lack, thereof) for the recipient infant. Recent studies have also shown that human milk, even when produced by healthy women without signs or symptoms of mastitis, contains a rich and diverse community of bacteria. This finding, along with evidence that the human milk microbiome can be influenced by maternal probiotic consumption, suggests that consumption human milk might be particularly critical for establishing a healthy complement of GI microbiota during early life and that this effect may be modulated, at least in part, by maternal diet. Finally, research continues to support a strong and consistent effect of maternal diet on relative milk n-3 and n-6 fatty acid contents, although results of controlled clinical trials are mixed in terms of relating this variation to short- and long-term effects on infant health and wellbeing.

Key Words: human milk, oligosaccharides, microbiome

344 Increasing n-3 fatty acids in milk through pre- and post-harvest approaches: Challenges and opportunities. A. L. Lock*[1] and D. E. Bauman[2], *[1]Michigan State University, East Lansing, [2]Cornell University, Ithaca, NY.*

Milk fat is a complex mixture of saturated and unsaturated fatty acids (FA) and varies according to breed, season, stage of lactation, and nutrition of dairy cattle. The amount of omega-3 FA in milk, in particular 20:5 n-3 (EPA) and 22:6 n-3 (DHA), are of interest as they are beneficial in the maintenance of human health and prevention of chronic diseases. Enhancing their content in milk requires an understanding of the interrelationship between dietary supply of FA, rumen fermentation, and mammary gland synthesis. Milk fat content of n-3 FA is generally low (<0.5% total FA), and this is mainly 18:3 n-3 (ALA). EPA and DHA are typically present in very low amounts (<0.1% total FA). Efforts to increase n-3 FA have often involved feeding diets that have a high content of ALA (e.g., flaxseed, pasture). While this approach increases milk fat content of ALA, it has little effect on levels of EPA or DHA because of limited Δ^6-desaturase activity in the mammary gland of the cow. Humans also have limited Δ6-desaturase activity, hence there is increasing interest in the use of fish oils, fish byproducts, and marine algae in dairy cattle diets as sources of EPA and DHA, as well as plant sources of stearidonic acid (18:4 n-3), an n-3 FA that bypasses the Δ^6-desaturase reaction. Transfer of dietary EPA and DHA to milk fat, however, is very low (<4%); this is related to their biohydrogenation in the rumen and because they are not transported in plasma lipid fractions that serve as major mammary sources of FA uptake. Despite this, modest changes have been achievable, and in some markets specialty milk and dairy products are currently available that have been enriched with EPA and DHA. Claims of large percentage increases in n-3 FA in dairy products should, however, be considered with caution due to their initial very low levels. Opportunities for greater enrichment of n-3 FA will likely rely on post-harvest fortification of milk, if deemed desirable. Finally, it is import to recognize that all dairy products are an excellent source of nutrients for the human population regardless of n-3 FA content.

Key Words: human health, milk fat, n-3 fatty acid

345 Influence of dietary pro- and prebiotics on the bovine rumen microbiome and milk synthesis. K. Griswold*[1], K. Harvatine[2], and T. R. Callaway[3], *[1]Kemin Industries Inc., Des Moines, IA, [2]The Pennsylvania State University, University Park, [3]USDA-ARS, College Station, TX.*

There is tremendous interest in changing milk composition to improve potential health benefits to both newborn calves and humans. Synthesis of milk within the dairy cow is dependent on the supply of nutrients (e.g., AA, lactose, fatty acids, minerals) at any given point in time. The nutrient supply is heavily influenced by the rumen microbiome as up to 85% of animal's diet is altered or entirely converted by their metabolism. Therefore, altering the rumen microbiome through the use of probiotics, prebiotics, or both (synbiotics) represents a potential opportunity to alter milk synthesis and influence milk composition. Probiotics are, by definition, viable microorganisms or end products of their fermentation that when consumed in adequate amounts confer a health or performance benefit on the host. Prebiotics are host-indigestible ingredients that can be fermented by the gastrointestinal microbiota that result in specific changes in the composition and/or activity of the microbiota, thus conferring benefit(s) upon host health. The effect of pro- and prebiotics on milk synthesis by the dairy cow is complicated by the enormously intricate relationship between ruminal, liver and mammary gland metabolism. Therefore, our objective is to outline the short and long-term opportunities for manipulating milk synthesis with pro- and prebiotics and describe the challenges that must be overcome to both create repeatable, realistic changes in milk composition and develop market opportunities that will convince dairy producers to utilize pro- and prebiotics to this effect.

Key Words: probiotic, prebiotic, milk synthesis

346 Functional components in milk: Effects on processed dairy product quality and human health. S. Duncan*, *Virginia Tech, Blacksburg.*

Subtle changes in milk composition can have a significant effect on milk and dairy product quality and shelf life. As research progresses to better

understand the implications of maternal (bovine, human) nutrition on milk composition and role in infant nutrition, the implications on milk and dairy product quality and human health also must be considered. Changes in fatty acid composition and antioxidant capacity associated with an increase in n-3 fatty acids and polyphenolic compounds, respectively, can contribute to reducing the risk of some chronic diseases. These modifications can change physical properties and oxidative susceptibility of milk, influence milk flavor and texture characteristics, alter ingredient functionality in dairy-based and food products, and affect consumer perception of quality and health value. Polyphenolic components are recognized for antioxidant and antimicrobial functionality, which are valuable functions for protecting milk from oxidation and bacterial spoilage, yet are also commonly recognized for a bitter taste. Dietary sources may increase the concentration of photosensitive molecules, such as chlorophyll, in milk increasing the risk of light-induced oxidation. Modifications in rumen fermentations that increase unsaturated as well as short chain fatty acids, may lead to increased susceptibility to autoxidation and rancidity. Processing and packaging considerations for specialty products are needed to protect the healthful components as well as flavor of milk throughout shelf life.

Key Words: antioxidants, n-3, packaging

347 The Missouri Show-Me-Select Replacement Heifer Program: Tracking reproductive performance of heifers and AI sires. J. M. Thomas*, J. M. Nash, N. T. Martin, B. D. Mayhan, M. F. Smith, S. E. Poock, and D. J. Patterson, *University of Missouri, Columbia.*

The Show-Me-Select Replacement Heifer Program has resulted in improved reproductive efficiency of beef herds in Missouri and offers a unique opportunity to collect reproductive performance data on large numbers of heifers throughout the state. Program objectives include (1) implementation of a total quality management plan to enhance health and management of replacement beef heifers; (2) improvement of marketing opportunities for producers while adding value to Missouri-raised heifers; and (3) creation of reliable sources of quality replacement heifers based on management, reproduction, and genetics. Enrolled heifers must meet minimum management standards and follow approved animal health regimens. Prebreeding exams [reproductive tract scores (RTS)] are performed by licensed veterinarians before the breeding season. Additionally, pregnancy diagnoses must be performed within 90 d of the start of breeding and reconfirmed after the end of the breeding season. In recent years, program participants have increased use of fixed-time AI (FTAI) programs in their herds. Data collected from 2010 to 2012 were used to evaluate relationships between RTS and pregnancy outcome after FTAI. The reproductive tract scoring system ranges from 1 to 5: 1 = infantile; 2 and 3 = noncycling/prepubertal; 4 and 5 = cycling/pubertal. Among 8,308 heifers from approximately 120 herds enrolled in 2010–2012, RTS and FTAI pregnancy rate (PR) were as follows: RTS 5 (n = 3,044; FTAI-PR = 57%); RTS 4 (n = 2,496; FTAI-PR = 52%); RTS 3 (n = 2,448; FTAI-PR = 48%); RTS 2 (n = 298; FTAI-PR = 34%); and RTS 1 (n = 22; FTAI-PR = 5%). These data support the practice of establishing prebreeding criteria for identification of heifers that are good candidates for a FTAI program. Additionally, the Show-Me-Select Replacement Heifer Program tracks the performance of FTAI sires utilized among heifers in the program. Among the 10 most heavily utilized AI sires (each with over 200 services respectively), overall FTAI pregnancy rates range from 44.3% to 67.5%. As data continues to accumulate, this information may become a valuable resource for selecting reliable FTAI sires.

Key Words: heifer development, reproductive management, beef cattle

348 The Missouri Show-Me-Select Replacement Heifer Program: Tracking sales and economic impact. J. M. Thomas*, J. M. Nash, N. T. Martin, B. D. Mayhan, D. S. Brown, M. F. Smith, S. E. Poock, and D. J. Patterson, *University of Missouri, Columbia.*

The Show-Me-Select Replacement Heifer Program has assisted program participants in capturing the additional value associated with elite replacement females. The objectives of the program include (1) implementation of a total quality management plan to enhance health and management of replacement beef heifers; (2) improvement of marketing opportunities for beef producers while adding value to Missouri-raised heifers; and (3) creation of reliable sources of quality commercial and purebred replacement heifers based on management, reproduction, and genetics. Over the past 16 yr, 722 farms enrolled 104,918 heifers in the program. Twenty-seven regional extension livestock specialists coordinate the program and work closely with 222 veterinarians involved with the program statewide. Heifers are required to undergo a prebreeding evaluation and must meet minimum health and management standards. Heifers meeting the minimum requirements for enrollment are classified as Tier 1. Heifers may be further distinguished as Tier 2 if the sire of the heifer meets minimum accuracy requirements for specified traits at the time of sale, including: calving ease direct, calving ease maternal, weaning weight, carcass weight, and marbling. Sales data from fall 2010 through fall 2012 were evaluated. Tier 2 heifers carrying AI sired pregnancies ($1,967) sold on average for $329 more per heifer than Tier 1 heifers carrying natural service sired pregnancies ($1,638). Similarly, Tier 1 heifers carrying AI sired pregnancies ($1,830) sold for $192 more per heifer than Tier 1 heifers carrying natural service sired pregnancies. To date, the Show-Me-Select Replacement Heifer Program facilitated the sale of 25,276 heifers in 119 sales from 1997 through December 2012. The aforementioned sales generated interest from 8,063 registered buyers and resulted in $30 million in gross sales revenue. Heifers have sold into 18 states, including AR, AZ, CO, FL, GA, IA, IL, IN, KY, KS, LA, MO, NE, OK, SC, SD, TN, and TX. The Show-Me-Select Replacement Heifer Program is estimated to have had over a $65 million impact on Missouri's economy since the program's inception.

Key Words: heifer development, reproductive management, beef cattle

349 Investment analysis of automated estrus detection technologies. K. A. Dolecheck*, G. Heersche Jr., and J. M. Bewley, *University of Kentucky, Lexington.*

Assessing the economic implications of investing in automated estrus detection technologies can be overwhelming for dairy producers. The objective of this project was to create a producer-friendly dashboard tool for investment analysis of automated estrus detection technologies. Farm specific (FS) inputs adjustable by the end user included herd size, milk price, milk yield, feed cost, voluntary waiting period, current estrus detection rate, current conception rate, culling rate, days in milk to stop breeding a cow, cull milk yield, replacement cow cost, and cull cow value. Up to 3 different estrus detection technology systems could be evaluated at one time using system cost, cow unit cost, installation cost, percentage of units to replace per year, maintenance cost per year, estrus detection rate, and conception rate as inputs. Investment analysis results included the following for each system: days open (DO), reproductive cull percent (RCP), years to break even (BE), and net present value (NPV). To demonstrate model utility within an average dairy farm comparing 2 systems, inputs were collected from DairyMetrics (Dairy Records Management Systems, Raleigh, NC), FAPRI (Food and Agricultural Research Institute, Columbia, MO), and published literature. Technology investment and maintenance costs were obtained from technology manufacturers for the AfiTag Pedometer Plus (PP) (S.A.E. Afimilk, Kibbutz Afikim, Israel) and Select Detect (SD) (Select Sires, Plain City, Ohio). The modeled DO and RCP before intervention were 150.70 and 9.56%, respectively. The DO, RCP, BE, and NPV after adopting each system were PP: 118.39, 1.99%, 4.99, and $15,928, respectively, and SD: 109.56, 0.96%, 7.40, and $7,023, respectively. Additional breakeven analysis was conducted to determine the estrus detection rate that would result in a NPV of zero for each technology. The resulting estrus detection rates for PP and SD were 59.79% and 65.07%, respectively. Dairy producers considering purchasing an automated estrus detection technology system may use this model as a decision support tool.

Key Words: estrus detection, economic dashboard, precision dairy farming

350 Development of a smartphone application tool to assess and reduce heat stress in livestock. B. Scharf*[1], P. A. Eichen[1], J. S. Travlos[2], and D. E. Spiers[1], *[1]Division of Animal Science, University of Missouri, Columbia, [2]Agricultural Electronic Bulletin Board, University of Missouri, Columbia.*

Climate variability is becoming a fact of life for livestock producers with the 3 hottest summers and 10 warmest years on record all occurring in the past 15 years. This increase in ambient temperature has tremendous impact on the agriculture industry with significant losses to livestock production amounting in excess of 1.5 billion dollars during a typical year. Thermal stress indices to help alleviate these losses have existed for years, but are underutilized because they require elaborate combinations of environmental (e.g., weather) and physiological (e.g., body temperature) data. Therefore, a native smartphone application (Apple) was created that combines weather input (current and projected) with individual animal information to aid the producer in the decision-making process to reduce heat strain and improve animal welfare. Features of this application include the ability to enter animal variables (e.g., breed, health) to identify current and future levels of stress for specific environment and animal groups. The framework of the application is built on a 3-tier design with tier 1 comprised of streaming current ambient conditions. The second tier is composed of the characteristics which define the animal and include known determinants of environmental interaction (i.e., health, production level). The final tier allows the user to collect individual animal responses to the environment (i.e., respiration rate) and combine this data with tier 1 and 2, resulting in herd specific suggestions to alleviate heat strain. This information is stored on the phone and also may be sent to a server for later viewing. Ultimately, the goal of this project is not only to develop a smart phone application for extension, but to create a research tool that provides exchange of data between producers and researchers. It also is the conduit for the generation of more specific models in future versions. This project will hopefully provide a framework for others to develop and implement the "extension through a smartphone" approach for solutions to problems facing animal agriculture around the world.

Key Words: heat stress, smartphone application, livestock

351 Estimation of U.S. dairy disease costs through stochastic simulation. D. Liang*[1], L. M. Arnold[1], M. M. Schutz[2], and J. M. Bewley[1], *[1]University of Kentucky, Lexington, [2]Purdue University, West Lafayette, IN.*

The objective of this research was to estimate common dairy disease costs using the dynamic, stochastic, simulation farm-level model described by Bewley et al. (2010). This model was constructed using Microsoft Excel (Microsoft, Seattle, WA) and the @Risk Monte Carlo simulation add-in (Palisade Corp., Ithaca, NY). A 170 cow US dairy, with default herd parameters established using DairyMetrics (Dairy Records Management Systems; Raleigh, NC) and published literature, was simulated through 5000 iterations. Total disease costs were summarized in 8 categories: veterinary fees, drugs, discarded milk, lost milk, culling, extended days open, death, and labor. An electronic survey was conducted to provide updated estimates for veterinary fees, drugs, and labor costs associated with clinical mastitis (CM), subclinical mastitis (SCM), ketosis (KT), metritis (MT), lameness (LM), milk fever (MF), left displaced abomasum (LDA), and retained placenta (RP). Forty-one surveys were completed. The survey results and total disease costs are shown in Table 1.

Table 1. Mean (± SD) of common dairy disease treatment costs, including drug costs, veterinary fees, and producer labor costs, and total disease costs for different lactations (primiparous and multiparous animals)

Costs ($)	CM	SCM	MT	KT	LDA	RP	LM	MF
Drugs	73.52 ± 40.79	48.70 ± 30.35	90.14 ± 41.37	75.47 ± 48.25	139.51 ± 80.81	67.51 ± 32.97	77.23 ± 47.00	62.24 ± 39.31
Veterinary fees	25.11 ± 19.86	24.01 ± 20.07	20.90 ± 14.49	26.22 ± 20.17	120.85 ± 68.24	24.33 ± 19.36	39.15 ± 28.48	48.60 ± 39.99
Producer labor	11.12 ± 6.42	8.05 ± 4.81	9.89 ± 5.12	12.16 ± 6.60	15.86 ± 8.85	13.25 ± 7.70	15.80 ± 8.69	15.22 ± 8.81

	LDA	CM	MT	RP	KT
Primiparous ($)	470.95 ± 114.12	352.45 ± 58.26	311.03 ± 46.23	294.80 ± 50.67	162.97 ± 52.98
Multiparous ($)	700.98 ± 125.18	298.31 ± 53.76	420.55 ± 61.55	274.27 ± 44.65	212.53 ± 56.00

Key Words: stochastic simulation, diseases cost, animal health economics

352 Quality Beef by the Numbers: Linking economic incentives with technology adoption. D. J. Patterson*, J. M. Thomas, M. F. Smith, and D. S. Brown, *University of Missouri, Columbia.*

The beef industry is a leading segment of our nation's economy and efforts to increase the value of beef cattle have widespread effects. In Missouri, the Show-Me-Select Replacement Heifer Program changed production practices related to management of beef heifers. Effects of these changes are realized by producers, veterinary practices, feed dealers, the pharmaceutical and AI industries, and related local economies. The recent addition of Tier Two to the Show-Me-Select Program encourages expanded use of fixed-time AI with genetically superior high-accuracy sires. Adoption of these technologies is resulting in 2 significant outcomes: Increased numbers of genetically superior females, and a similar increase in numbers of genetically superior steer mates. Increased domestic and global demand for high-quality proteins, coincident with the decline in the US beef cow inventory, offers the potential to increase premiums for high-quality beef products. Stacking reproductive and genetic technologies sets the stage for a new programming effort. Quality Beef by the Numbers (QB) streamlines production and marketing of cattle with a focus on high-quality endpoints. The program involves a partnership including the University of Missouri, Irsik and Doll Feed Yard (Garden City, KS), Pratt Feeders (Pratt, KS), Accelerated Genetics, Genex Cooperative, Select Sires Mid-America, and Certified Angus Beef. The program is intended to (1) support the adoption of reproductive and genetic technologies that will add value to beef cattle produced and marketed in the US; (2) provide access to marketing grids that reward producers of high-quality cattle; and, (3) provide beef producers with access to a comprehensive database that will support improvements in management and marketing of cattle from conception to harvest. The QB mission will improve the profitability of beef cow-calf operations by facilitating the adoption of applied reproductive and genetic technologies that add value to beef cattle produced and marketed in the US and contribute to improvements in beef quality to satisfy increasing domestic and global demand for high-quality beef.

Key Words: high-quality beef, AI, high accuracy sires

353 Determining strategies for youth livestock exhibitors to be effective ambassadors for animal agriculture. K. Lancaster*, C. Brady, and M. Tucker, *Purdue University, West Lafayette, IN.*

Youth participants in livestock agriculture are an invaluable, yet largely untapped, resource in establishing positive relationships with the non-agricultural public, especially at fairs and other livestock events where they interact and converse with event visitors. To determine key strategies to teach youth exhibitors to be effective ambassadors for animal agriculture, 8 livestock industry professionals with ties to youth livestock exhibitors were individually interviewed for this qualitative study. Subjects were identified based on recommendations from an expert panel, their professional qualifications and involvement with youth livestock activities. Interview questions were developed after a review of relevant literature, and sought information about subjects' backgrounds, information youth exhibitors should know, common questions asked by visitors, and recommended communication strategies to be used by exhibitors interacting with visitors. Subjects were from diverse backgrounds and had a range of experience in the livestock industry, with all but one employed in an agriculture-related field at the time of the research. Three overarching themes emerged from the interview data: exhibitors must have knowledge about their animals and be familiar with relevant industry issues; exhibitors must be able to answer questions effectively and positively; and exhibitors must be aware that they represent all of agriculture to visitors at the fair. Subjects agreed that general knowledge about the animal, activities taking place at the event, and an understanding of current events and hot topics surrounding animal agriculture were essential for youth exhibitors. They suggested that youth exhibitors prepare for interactions with visitors before the event, use language and terms appropriate to the visitors' experience, and frame answers positively. Also emerging from the research was the importance of exhibitors understanding that they are serving as ambassadors for agriculture and the accompanying need for them to interact with the public in a positive and engaging manner.

Key Words: youth exhibitor, ambassador, livestock

354 Youth motivation to participate in animal-related career development events. C. Brady*, A. Fisher, and N. Knobloch, *Purdue University, West Lafayette, IN.*

Career development events (CDE) are an integral part of many youth animal science extension programs. The purpose of this study was to assess youth motivation for participating in these events. The instrument used was developed based on the expectancy value theory and social cognitive theory, with a 5-point Likert scale measuring agreement to statements (1 = none to 5 = quite a lot). Five factors were tested: Attainment (personal importance of doing well), Cost (negative aspects of participation), Intrinsic (interest/enjoyment of the activity), Self-Efficacy (belief in ability to do well), and Utility (relationship of activity to future goals). The instrument was reviewed by an expert panel, and tested using confirmatory factor analysis and Pearson's correlation. Internal validity was tested on each subscale using Cronbach's α, with coefficients from 0.70-.91. The instrument was distributed to youth participants at State CDE for Dairy Judging (n = 171), Hippology (n = 159), Livestock Judging (n = 143), Meat Judging (n = 198), Poultry and Egg Judging (n = 158), and Livestock Skillathon (n = 267). Utility had the highest mean score of 4.07 ± 0.81, followed by Cost (3.88 ± 0.97), Intrinsic (3.66 ± 1.00), Self-Efficacy (3.62 ± 0.97), and Attainment (3.43 ± 1.02). Cohen's d test for effect size showed a small effect size between Utility and Cost (0.21), Cost and Intrinsic (0.22), Cost and Self-Efficacy (0.27), and Intrinsic and Attainment (0.22); a small-medium effect size between Utility and Intrinsic (0.45) and Cost and Attainment (0.45); and a medium effect size between Utility and Self-Efficacy (0.50) and Attainment and Utility (0.69). Livestock participants had the highest scores in all categories, with all mean scores over 4. Poultry and Egg had the lowest Utility (3.80 ± 0.78), Self-Efficacy (3.06 ± 0.91), and Intrinsic (2.89 ± 0.89) scores, while Hippology had the lowest Attainment score (3.00 ± 1.09) and Meat Judging had the lowest Cost score (3.64 ± 1.06). This study demonstrates that youth motivation for participation in CDE is multi-faceted, and to some degree event specific. This information can be useful for recruitment and retention of event participants.

Key Words: career development, youth, motivation

Forages and Pastures Symposium: Forage Systems Adaptable to Dry Conditions

355 Between droughts and floods—Climatic effects on forage and livestock production systems. D. Niyogi*, *Purdue University, West Lafayette, IN.*

The record drought of 2012 brought the issue of climatic vulnerability to the agricultural enterprise front and center. The swings in the temperature patterns associated with higher frost and freeze risks, as well as the midseason heat stress and heavy rain/severe weather risks have brought about potentially newer climatic regimens to light. Several associated shifts are apparent in regional growing season length, cropping patterns and irrigation demands. Nonclimatic forcings such as regional landuse/cover patterns due to urbanization and regional policies have also contributed to newer vulnerabilities to the agricultural enterprise. This presentation will review the various climatic / weather processes and trends that have been observed and are expected in the coming decades. The potential effects from the traditional sensitivity approaches will be discussed, followed by a bottom-up vulnerability approach for understanding the climatic (and non-climatic) stresses on production systems. Efforts underway to link the different indices for identifying triggers and regimen shifts, societal issues, and decision making process with several data intensive /computational efforts will also be presented. The largest vulnerability appears to be in the availability of water resources within the regional setup. A clear need for adapting a newer mode of operation leaving the traditional "business as usual" view is starting to emerge.

Key Words: climate, drought, vulnerability assessment

356 Foraging through the dry times: Novel approaches to improving drought tolerance in forage crops. M. J. Oliver*[1], A. Yobi[1], and J. C. Cushman[2], *[1]USDA-ARS-PGRU, Columbia, MO, [2]University of Nevada, Reno.*

Increasing global uncertainty about food security, expanding desires for animal protein, intensifying extremity of weather events, and growing demands on the world's supply of fresh water all drive the need for forage crops that require less water to maintain productivity and that tolerate episodes of drought. The development of low-water-input forages useful for current livestock production enterprises in semi-arid and arid regions can be promoted by understanding cellular processes that are adaptive for drought tolerance in grasses and by evaluating novel forage grasses for use in arid areas. New strategies for improvement of drought tolerance in forage crops have focused on *Sporobolus*, a genus of grasses used historically as forage in stressful arid or saline environments. A sister-group contrast has been used to compare the response of the transcriptomes, proteomes (in progress), and metabolomes of the desiccation-tolerant (DT) species, *Sporobolus stapfianus*, and the desiccation-sensitive (DS) species, *S. pyramidalis*, to various degrees of shoot dehydration. Genes, gene networks, and metabolic processes with adaptive value for the establishment of cellular dehydration tolerance have been identified as strategically important for forage crop improvement. An important link between dehydration tolerance, oxidative metabolism, and nitrogen storage and remobilization has been identified that is the focus of on-going targeted metabolomics studies. Forage potential (under variable irrigation) has been evaluated for 3 *Sporobolus* species that could be suitable for both feed supplementation and rangeland reclamation. Data indicate that these good-quality forage grasses can be produced using considerably less water than currently devoted to arid-land beef cattle production using conventional forage species. The powerful combination of genomic resources, novel gene discovery, and successful field tests validates these *Sporobolus* species as attractive models for further improvement.

Key Words: drought tolerance, forage grass, water use

357 Field experience with drought-tolerant maize. S. Soderlund*, F. N. Owens, and C. Fagan, *DuPont Pioneer, LaSalle, CO.*

Drought-tolerant maize hybrids are being marketed by several seed companies. Such hybrids were developed by phenotypic and marker-assisted selection with various degrees of irrigation water restriction or through genetic modification. Crop productivity and survival are progressively reduced as drought intensifies. Water needs differ due to differences in root structure, evaporative loss, capacity to store water or enter temporary dormancy, and plant genetics. Availability of water differs widely not only with rainfall and irrigation but also with numerous soil and agronomic factors (soil type, slope, seeding rates, and tillage practices). Reduced weed competition, enhanced pollen shed and silk production, and deep, robust root growth reduce the negative effects of drought. Genetically selected drought-tolerant maize hybrids yield more grain even when drought conditions are not apparent due either to reduced water extraction or greater tolerance of intermittent water shortages. In Pioneer trials, whole plant NDF digestibility of maize increased with water restriction, perhaps due to an increased leaf to stem ratio. Efficiency of water use, measured as dry matter or potential milk yield per acre per unit of available water, responded quadratically to water restriction, first increasing and then decreasing as water restriction increased. For grain production, water restriction has its greatest negative effect during silking or post-silking through reducing kernel number or kernel fill. For silage production, water restriction during the vegetative growth stage negatively affects terminal plant height and biomass yield. Earlier relative maturity maize hybrids, through earlier pollination, may help avoid mid-summer heat stress at this most critical growth period and reduce the number of irrigation events needed. Although drought tolerance of maize hybrids has been improved due to genetic selection or biotech approaches, selecting locally adapted hybrids or crops, adjusting seeding rates, and modifying tillage practices are key considerations for optimal water utilization for grain and forage production.

Key Words: water, drought, maize

358 Using mixtures of summer forages for improved forage yields in dry conditions. C. Teutsch*, *Virginia Tech's Southern Piedmont AREC, Blackstone.*

Corn silage is grown on more than 76,000 ha in Virginia and North Carolina and is the primary component of dairy rations throughout the southeastern United States. Although the yield potential of corn grown for silage is high, it is also sensitive to environmental stress. Dry conditions during any stage of corn growth can significantly reduce corn silage yields. In contrast to corn, forage sorghum possesses a much higher level of drought tolerance and increased water use efficiency. Planting mixtures of corn and forage sorghum may reduce the risk of low yields during years with below average rainfall and above average temperatures. A study to evaluate the effect of planting corn alone or in

mixtures with forage sorghum was conducted at Virginia Tech's Southern Piedmont AREC, located near Blackstone, VA. The experimental design was a randomized complete block with 4 replications. Corn and forage sorghum were planted alone or as a mixture consisting of corn (28,000 kernels/ha) and 4 rates of forage sorghum (2.25 to 9 kg/ha) in late May 2010 and 2011, approximately a month after the optimal corn planting date. The yield and nutritive value were evaluated when the forage sorghum reached the soft dough stage. Adding as little as 4.5 kg/ha of forage sorghum to late planted corn doubled (11.0 to 26.0 Mg/ha) and tripled (12.1 to 32.0 Mg/ha) the adjusted silage yield (35% DM) in 2010 and 2011, respectively. These data indicate that forage sorghum grown either in mixtures with corn or alone could help to mitigate the effects of drought and high temperatures in silage production systems in southeastern United States, especially on soils that are marginal for corn silage production.

Key Words: drought, forage, mixture

Meat Science and Muscle Biology Symposium: Implants, Muscle Development and Meat Quality

359 Cattle implants: Past and future. S. K. Duckett* and S. L. Pratt, *Clemson University, Clemson, SC.*

Anabolic implants are routinely used in the finishing phase of beef production to improve animal performance and feed efficiency. Implanting during the feedlot phase on average increases ADG 18%, feed intake 6%, feed efficiency 8%, carcass weight 5% and ribeye area 4% compared with non-implanted controls. Implants reduce the cost of beef production, which is important given current high feed costs and beef prices. In a 1996 review of 37 implant trials, the use of a combination (estrogenic and trenbolone acetate) implant increased returns by $77 per hd compared with non-implanted steers. If calculated in today's prices, a combination implant would increase returns by $163 per hd. However, concerns about potential negative effects of implants on marbling scores, quality grades, and tenderness exist. Changes in Warner-Bratzler shear force values of steaks from implanted steers are small (<0.5 kg) and appear related to an increase in initial tenderness, possibly due to hypertrophy of muscle fiber, instead of alterations in postmortem proteolysis. The increase in ribeye size observed with implanting may also reduce marbling scores through a dilution effect. The effect of anabolic implants on gene expression has shown that implanting downregulates certain lipogenic (SCD-1, FASN, ELOVL6) genes in steers with low quality grades (Select-) but not in implanted steers with high quality grades (Choice-). Examination of the adipocyte's transcriptome has shown that 36 genes were differentially expressed due to implant treatment. More research is needed to further determine how anabolic implants alter lipogenic gene expression to address changes in marbling deposition with implant usage. Given our current high feed costs and cattle prices, anabolic implants are one of the most cost effective technologies that can be utilized in beef production systems.

Key Words: beef, implant

360 Implant and beta agonists affect beef palatability. M. F. Miller* and A. J. Garmyn, *Texas Tech University, Lubbock.*

The use of anabolic implants has a long-standing place in the cattle feeding industry, due their positive effect on growth performance and subsequent profitability. However, implants can have adverse effects on carcass quality, shear force, and eating quality based on the dose and frequency of administration, or what some may refer to as the aggressiveness of the implant regimen. Within the past decade, a new class of growth promotants – known as β-adrenergic agonists (βAA) – has emerged in the beef feeding industry. Currently, 2 have gained FDA approval for use in beef finishing diets to improve performance and yield. Much like anabolic implants, these repartitioning agents can have negative effects on Warner-Bratzler shear force (WBSF), but the differences do not translate directly to consumer responses for palatability and acceptance in some instances, especially when tenderness is managed through postmortem aging. As researchers continued to investigate the mechanisms driving βAA, inevitably this led to consideration of the interaction between βAA and anabolic implants. Early work combining zilpaterol hydrochloride (ZH) with anabolic implants improved performance and carcass yield with additive negative effects on WBSF. Similar results were produced when pairing ZH with anabolic steroids equipped with various release patterns. As with any tool, the key to success is proper management. Certain cattle populations may be better suited to receive growth promotants such as implants and βAA, and postmortem management of subprimals becomes vital when producers take more aggressive approaches to improve performance and yield. The objective of this review is to overview research findings related to the effect of growth promotant technologies on beef palatability, focusing specifically on the role of implants and β adrenergic agonists on beef tenderness and consumer palatability.

Key Words: β-agonist, implant, palatability

361 Mechanisms of growth hormone and IGF-I stimulation of skeletal muscle growth in cattle. H. Jiang* and X. Ge, *Virginia Polytechnic Institute and State University, Blacksburg.*

Both growth hormone (GH) and IGF-I have growth-promoting effects on skeletal muscle. We conducted 2 studies to understand the mechanisms by which GH and IGF-I stimulate skeletal muscle growth in cattle. In the first study, we determined whether GH stimulates skeletal muscle growth in cattle through IGF-I produced in skeletal muscle. We isolated satellite cells from adult cattle and allowed them to proliferate as myoblasts or induced them to differentiate into myotubes. Addition of GH to the culture medium increased protein synthesis but had no effect on protein degradation or myoblast proliferation. Addition of IGF-I to the culture medium stimulated protein synthesis, and this effect was much greater than that of GH. Addition of IGF-I to the culture medium also inhibited protein degradation and stimulated myoblast proliferation. Neither GH nor IGF-I affected myoblast differentiation into myotubes. We also observed that GH had no effect on IGF-I mRNA expression in bovine muscle cells and that GH administration to cattle did not alter IGF-I mRNA expression in skeletal muscle while increasing IGF-I mRNA expression in liver and IGF-I concentration in blood. These data together suggest that GH and IGF-I have largely different effects on bovine skeletal muscle cells and that the growth-promoting effect of GH on skeletal muscle is unlikely mediated through locally produced IGF-I. In the second study, we determined the signaling pathways that mediate the different effects of IGF-I on bovine muscle cells using the PI3K inhibitor LY294002, the ERK inhibitor PD98059, and the mTOR inhibitor rapamycin. Our data suggest that both the MEK/ERK and PI3K/AKT pathways mediate the stimulatory effect of IGF-I on bovine myoblast proliferation. We also identified cyclin D2 as a downstream component of the PI3K/AKT pathway that mediates the stimulatory effect of IGF-I on bovine myoblast proliferation. Our data suggest that both the MEK/ERK and PI3K/AKT pathways mediate the stimulatory effect of IGF-I on protein synthesis in bovine myotubes through p70S6K and that the PI3K/AKT pathway mediates the inhibitory effect of IGF-I on protein degradation through FoxO3a.

Key Words: growth hormone, IGF-I, muscle

362 Role of satellite cells in anabolic steroid-enhanced muscle growth in feedlot steers. W. R. Dayton* and M. E. White, *University of Minnesota, St. Paul.*

Androgenic and estrogenic anabolic steroid implants are widely used to enhance rate and efficiency of muscle growth in feedlot cattle. Although the mechanism of action of these compounds is not known, recent studies indicate that their effects on muscle satellite cells (MSC) play a central role. Treatment of steers with a combined estradiol (E2)/

trenbolone acetate (TBA) implant results in a 2-fold increase ($P < 0.05$) in the number of MSC that can be isolated from the longissimus dorsi muscle. This is significant because satellite cells are the source of nuclei needed to support postnatal muscle fiber hypertrophy and are thus crucial in determining the rate and extent of muscle growth. Implantation with E2 /TBA increases the levels of circulating IGF-1 ($P < 0.05$) and results in a 3-fold increase in muscle IGF-1 mRNA level ($P < 0.05$). Thus, IGF-1 may play a role in the increased satellite cell number observed in implanted steers. To further explore the role of satellite cells in the mechanism of anabolic steroid-enhanced muscle growth, we have examined the effects E2 and TBA on cultured bovine satellite cells (BSC). Both E2 and TBA stimulate IGF-1 mRNA expression in cultured BSC ($P < 0.05$). Interestingly, E2 stimulates IGF-1 expression through binding to the G protein-coupled estrogen receptor (GPER-1) rather than through interaction with the classical estrogen receptors. Even under culture conditions in which IGF-1 expression levels are not increased, treatment with E2 or TBA stimulates proliferation and protein synthesis and inhibits protein degradation in cultured BSC, suggesting that both E2 and TBA can affect satellite cells via mechanisms that do not involve increased IGF-1 expression. Studies utilizing siRNA silencing and specific receptor tyrosine kinase inhibitors suggest that estrogen receptor-α, GPER-1, insulin-like growth factor receptor-1 and the epidermal growth factor receptor may play roles in the effects of E2 on proliferation, protein synthesis and protein degradation in cultured BSC.

Key Words: anabolic steroid, satellite cell

363 Apparent and standardized ileal amino acids digestibility of wheat-distillers dried grains with solubles without or with exogenous protease for broilers and turkeys. A. Adebiyi* and O. Olukosi, *Scottish Rural University College, Edinburgh, United Kingdom.*

A total of 84 Ross 308 male broilers (Exp. 1) or 84 BUT 10 male turkeys (Exp. 2) at 28 d of age were used for determination of the apparent (AIAAD) and standardized ileal amino acid digestibility (SIAAD) of wheat distillers dried grains with solubles (wheat-DDGS). The birds in both experiments were allocated to 4 dietary treatments consisting of 2 nitrogen-free diets (without or with protease) and 2 semi-purified diets (without or with protease) in which wheat-DDGS was the only source of amino acids (AA). In each of the 2 experiments, there were 7 replicate pens and 3 birds per replicate pen. Protease was added to the diets at a rate of 4,000 protease units per kg. For both broilers and turkeys, the AIAAD or SIAAD of Lys and Asp were very low regardless of protease supplementation. In Exp 1, AIAAD ranged from 35% (Ala) to 75% (Pro) without added protease whereas the range was 42% (Thr) to 82% (Pro) with protease supplementation. Supplemental protease improved ($P < 0.05$) the AIAAD of only Arg and Pro and tended ($P < 0.10$) AIAAD of Met. Without protease supplementation, SIAAD ranged from 51% (Ala) to 84% (Pro) whereas the range was from 65% (Ala) to 93% (Pro) with added protease. Protease addition improved ($P < 0.05$) the SIAAD of Arg, Leu, Phe, Met, Val and Pro by 21, 14, 13, 26, 13 and 10 percentage points, respectively. In Exp. 2, AIAAD was lower than 50% for all AA except for Glu (70%) and Pro (81%) without supplemental protease. On the other hand, SIAAD ranged from 41% (Thr) to 89% (Pro) without added protease whereas the range was from 56% (Arg) to 88% (Pro) with added protease. With the exception of Cys and Pro, protease supplementation improved ($P < 0.05$) the AIAAD and SIAAD of all other AA from between 5 to 19 percentage points. It was concluded from the current experiments that the AIAAD and SIAAD of wheat-DDGS are quite variable and exogenous protease can improve the utilization of AA in wheat-DDGS for broilers and turkeys.

Key Words: wheat DDGS, amino acid digestibility, protease supplementation

364 Effect of a β-mannanase and a β-glucanase combined with a native β-mannanase in diets containing corn-soybean meal-dried distillers grains with solubles and soybean hulls on nursery pig performance. M. Meyers[1], D. Kelly[1], B. Richert[1], J. Ferrel*[2], and D. Anderson[2], *[1]Purdue University, West Lafayette, IN, [2]Elanco Animal Health, Greenfield, IN.*

One-hundred thirty-six weanling pigs (initial BW = 5.44 ± 0.019 kg; 17.9 d age) were used to evaluate the effect of a β-mannanase (HTm) and a β-glucanase combined with a native β-mannanase (ZYM) in a corn-soybean meal-dried distillers grains with solubles diet on nursery pig growth performance. Pigs were allocated in a randomized complete block design into mixed-sex pens, stratified by litter and initial BW to 4 dietary treatments, 6 pens per treatment with 5 or 6 pigs per pen. Dietary treatments included: T1, Positive Control (3519, 3455, 3374, 3400 kcal/kg ME; by phase, respectively); T2, Negative Control (3419, 3355, 3274, 3300 kcal/kg ME; by phase, respectively); T3, T2+HTm (0.04 MU/kg mannanase); T4, T2+ZYM (0.08 MU/kg glucanase, 0.10 MU/kg mannanase). Pigs were fed 4 dietary phases over 5 wk: phase 1 (d 0–5), phase 2 (d 5–12), phase 3 (d 12–19), and phase 4 (d 19–33). Diets contained 0, 5, 10, 20% corn DDGS and 1.65, 1.98, 2.59, 2.29% soybean hulls by phase, respectively. Individual BW and pen feed disappearance were recorded on d5, 12, 19, and 33 and data were analyzed using GLM procedure in SAS. Phase 1 ADG and G:F increased ($P < 0.05$) for T1 and T3 versus T2 and T4, while T4 had greater ($P < 0.05$) ADG over T2 and similar G:F. BW on d5 was greater ($P < 0.05$) for T3 versus T2 and T4. Phase 2 ADG and ADFI tended to be greater ($P < 0.10$) for T3 and pigs fed T3 were heavier ($P < 0.05$) at the end of phase 2 than all other treatments. Phase 3 G:F tended to be greater ($P < 0.10$) for T4 versus T3. Phase 4 ADG was increased ($P < 0.05$) for T3 versus all other treatments, while T1 and T4 ADG tended ($P < 0.10$) to be greater than T2 (536, 515, 584, 553 g/d, T1-T4, respectively) and ADFI was greater ($P < 0.05$) for T3 versus T1 and T2 (765, 771, 851, 824, g/d, T1-T4, respectively). Overall ADG was increased ($P < 0.05$) for T3 versus all other treatments (363, 345, 396, 374 g/d, T1-T4, respectively), and T3 ADFI was greater than T1 and T2 ($P < 0.05$). Supplementation of diets with β-mannanase alone and in combination with β-glucanase can improve nursery pig growth.

Key Words: swine, β-mannanase, β-glucanase

365 Effects of dietary fiber and a xylanase and β-glucanase blend on performance and jejunal electrophysiological properties and transport associated gene expression in growing pigs. A. K. Agyekum*[1], J. S. Sands[1], A. Regassa[1], E. Kiarie[3], D. Weihrauch[2], W. K. Kim[1], and C. M. Nyachoti[1], *[1]Department of Animal Science, University of Manitoba, Winnipeg, Manitoba, Canada, [2]Department of Biological Sciences, University of Manitoba, Winnipeg, Manitoba, Canada, [3]DuPont Industrial Biosciences, Marlborough, Wiltshire, UK.*

The effects of supplementing a high fiber diet with exogenous enzymes on intestinal nutrient uptake and transporter activities have not been investigated. Thus, we evaluated the effects of a high fiber diet and xylanase and β-glucanase blend (XB) on performance, jejunal electrophysiological properties (JEP), and gene expressions of Na-dependent glucose transporter 1 (SGLT1), cationic amino acid transporter ($b^{o,+}$), and a mucin gene (MUC1, as an indicator for endogenous AA losses). Twenty-four growing pigs (22.4 ± 0.7 kg BW) were individually housed and randomly assigned to 3 experimental diets to give 8 pigs per diet. The diets were based on corn and soybean meal with either 0% (CTRL) or 30% co-fermented wheat and corn distillers dried grains with solubles (HF); the third diet was HF supplemented with XB (HF+XB). At the end of the 21-d experiment, BW and feed intake, plasma glucose (GLU), and urea nitrogen (PUN) concentrations were determined. Pigs were then euthanized to determine JEP (transepithelial short-circuit current and conductance) and jejunal gene expression using Ussing chambers and quantitative real-time reverse transcription PCR, respectively. Data were analyzed using Proc GLM of SAS with dietary treatment as the main effect in the model. Dietary treatment had no effect ($P > 0.10$) on feed intake and GLU, but pigs fed the CTRL diet had higher ($P < 0.05$) ADG, G:F, and PUN than pigs fed either HF or HF+XB. Additionally, ADG and G:F of pigs fed HF+XB were not different ($P > 0.10$) from pigs fed the HF diet. Furthermore, dietary treatment had no effect ($P > 0.05$) on JEP or jujenal SGTL1, $b^{o,+}$, and MUC1 gene expression. In the present study, the reduced performance of pigs fed HF and HF+XB could not be explained by the jujenal electrophysiological properties or nutrient transporter gene expression.

Key Words: high fiber, xylanase and β-glucanase blend, jujenal electrophysiological properties

366 Effect of xylanase and β-glucanase on performance, nutrients and energy digestibility and retentions and plasma metabolites in nursery pigs fed wheat-barley diets. E. Kiarie*[1], A. Péron[1], A. Owusu-Asiedu[1], P. H. Simmins[1], and C. M. Nyachoti[2], *[1]Dupont Industrial Biosciences-Danisco Animal Nutrition, Marlborough, Wiltshire, UK, [2]University of Manitoba, Winnipeg, MB, Canada.*

Two experiments were conducted to investigate the efficacy of xylanase and β-glucanase blend (XB) in wheat and barley-based diets for piglets. In Exp. 1, 48 piglets (7 kg BW) were used to evaluate growth performance and apparent total tract digestibility (ATTD) in a 2 phase feeding program. The diets were (A) basal (Phase I: 29% wheat, 26% barley; phase II: 37% wheat, 28% barley), (B) basal + 50 g XB/ton, and (C) basal + 100g XB/ton. The DE in basal was 3.2 Mcal/kg as fed. The xylanase and β-glucanase blend (Danisco Animal Nutrition, Marlborough, Wiltshire, UK) had guaranteed activity of 12,200 and 1,520 units/g, respectively and chromic oxide was used as indigestible marker. Based on BW and sex, piglets were assigned to pens (n = 2) to give 8 pens per diet. Feed intake and BW were measured weekly and fecal samples were collected on pen basis at the end of each phase. Supplemental XB linearly increased ($P < 0.05$) ATTD of DM, CP and energy in both phases. Trends were observed for increased ADG ($P = 0.07$, quadratic) in the overall linked to trends for higher ADFI ($P = 0.09$, linear) in phase I. In Exp. 2, phase II diets (Exp. 1) were fed to 18 growing barrows (20 kg BW) individually housed in metabolism crates (n = 9) that allowed separate collection of feces and urine to determine energy and N retentions. Pigs were fed (4% BW) their assigned diet twice daily for 5 d of adjustment followed by a 5-d total collection of feces and urine and at the end of the trial pigs were fasted overnight and bled to obtain plasma. A linear response ($P < 0.05$) to supplemental XB was observed for ATTD of energy and CP, ME, N retention and plasma glucose. Specifically, pigs fed diet C had higher dietary DE content (3.80 vs. 3.68 Mcal/kg DM) and plasma glucose (107 vs. 102 mmol/l) than diet A. In conclusion, xylanase and β-glucanase blend tended to improve growth performance and improved nutrients and energy utilization in wheat barley based diet for piglets.

Key Words: xylanase and β-glucanase, piglet performance, nutrient utilization and retention

367 The effect of a combination phytase and carbohydrolase enzyme on performance and bone mineralization of pigs from 6 weeks to slaughter at 105 kg. P. G. Lawlor[1], P. Cozannet[2], D. P. Preveraud*[2], A. Preynat[2], W. F. Ryan[1], and P. B. Lynch[1], *[1]Pig Production Development Unit, Teagasc, Moorepark, Fermoy, Co Cork, Ireland, [2]Adisseo France S.A.S. CERN, Commentry, France.*

Experiment was conducted to assess effect of a combination of carbohydrolase (from *Penicillium funiculosum*) and 6-phytase (from *Schizosaccharomyces pombe*) enzymes (enz; Rovabio Max, Adisseo, France) on performance and bone mineralization of pigs (n = 192 pairs) fed maize-soybean meal diets. Pigs were selected at 28 d of age, penned in pairs and fed a common diet meeting animal requirements for 14 d. Thereafter, 4 diets were formulated for each of 4 stages to slaughter at 147 d post-weaning: (1) Positive control (PC), formulated to meet the recommendations of the National Research Council (NRC 1998); (2) Negative control 1 (NC1; DE × 0.98, CP × 0.98, −1.0 g Ca/kg and −1.2 g dig P/kg), (3) Negative control 2 (NC2; DE × 0.97, CP × 0.97, −1.0 g Ca/kg and −1.2 g dig P/kg), and (4) Negative control 3 (NC3; DE × 0.97, CP × 0.97, −1.5 g Ca/kg and −1.7 g dig P/kg). NC diets were supplemented with enz (50g/ton of feed) resulting in 7 treatments presented as pellet. Feed disappearance, wastage and individual pig BW were recorded at the beginning and end of each phase. Data were analyzed using GLM procedures of SAS with pen, sex and treatment as fixed effects. Furthermore, the effect of reformulation and enzyme were tested using orthogonal contrasts. Reductions in dietary constituents in control treatments reduced BW, ADFI, ADG throughout the trial ($P < 0.001$). Differences among PC and NC3 were 50 kg, 228 g/d and 127 g/d, respectively. Intermediate values were obtained for NC1 and NC2. Addition of enz to NC diets increased BW, ADFI and ADG up to slaughter and improved Gain:Feed ($P < 0.001$) to d 112 of the trial. Improvement averaged 30 kg, 463 g/d, 393 g/d and 0.03, respectively. There were increases in area bone mineral density (aBMD) of the foot from d 77 onward ($P < 0.01$) and metacarpal aBMD ($P < 0.01$) from d 112 onwards when enz was added. No effect ($P > 0.05$) was found on metacarpal Ca or P content. Enzyme addition to pig diets of low nutrient density can return the performance of the pigs and metacarpal and foot aBMD to levels reached by pigs fed diets meeting NRC recommendations.

Key Words: performance, phosphorus, enzyme

368 The efficacy of graded levels of a new 6-phytase from *Buttiauxella* spp. expressed in *Trichoderma reesei* on ileal amino acid digestibility in pigs fed a corn-soybean meal-wheat midds-corn DDGs-based diet. S. A. Adedokun*[1], A. Owusu-Asiedu[2], P. Plumstead[2], and O. Adeola[1], *[1]Department of Animal Sciences, Purdue University, West Lafayette, IN, [2]DuPont Industrial Biosciences-Danisco Animal Nutrition, Marlborough, UK.*

A total of 16 cannulated pigs were used to evaluate the effect of a new 6-phytase derived from *Buttiauxella* spp. expressed in *Trichoderma reesei* on apparent ileal digestibility (AID) of amino acid (AA), N, Ca, and P. Pigs were fed 4 diets for 2 periods in a crossover design. Within each period, there were 4 blocks of 4 pigs per block with each diet represented within each block. The average initial BW in periods 1 and 2 were 22 and 30 kg, respectively. Each period lasted 9 d with fecal collection on d 5 and 6 and 12-h ileal digesta collection on each of d 7, 8, and 9. Pigs received daily feed allowance of approximately 4.5% BW. The experimental diets were based on corn, soybean meal, wheat middlings, and corn distillers dried grain with soluble. Phytase was added at 0, 500, 1000, or 2000 FTU/kg to the basal diet formulated to contain 189, 9.9, 4.57, and 6.25 g/kg of CP, Lys, P, and Ca, respectively. The addition of phytase improved ($P < 0.05$) AID of DM, N, Ca, and P. Increasing phytase supplementation linearly and quadratically increased ($P < 0.05$) the AID of Ca and P. Phytase supplementation of the basal diet improved ($P < 0.05$) AID of P from 46 to 61%. Contrasts showed that phytase supplementation of the basal diet increased ($P < 0.05$) AID for 5 indispensable AA (Arg, Ile, Leu, Phe, and Val), 5 dispensable AA (Asp, Cys, Glu, Ser, and Tyr) as well as for total AA. Furthermore, phytase supplementation to the basal diet showed a tendency ($P < 0.1$) to increase ileal digestibility of His, Lys, Thr, Ala, Gly, and Pro. Ileal digestibility of Met and Trp was not significantly affected by phytase. Increasing level of phytase supplementation resulted in linear increases ($P < 0.05$) in AID of 5 indispensable AA (Arg, Ile, Leu, Phe, and Val) and 2 dispensable AA (Asp, and Glu). The result from this study showed that in addition to increasing P and Ca utilization, the new *Buttiauxella* phytase expressed in *Trichoderma reesei* enhanced ileal digestibility of N and AA in growing pigs in a dose-dependent manner.

Key Words: amino acid, ileal phosphorus digestibility, phytase

369 Effect of enzyme supplementation on the net energy content of dry extruded-expelled soybean meal fed to growing pigs. D.

E. Velayudhan*, J. M. Heo, and C. M. Nyachoti, *University of Manitoba, Winnipeg, Manitoba, Canada.*

The aim of this study was to determine the effect of a multi-enzyme complex (MC) on the net energy (NE) content of dry extruded-expelled soybean meal (DESBM) fed to growing pigs. Twenty-four barrows (16.9 ± 0.76 kg) were allotted in a completely randomized design to 4 dietary treatments to give 6 replicates per treatment. Dietary treatments were; a corn soybean meal basal diet (Diet A), a diet containing Diet A and DESBM in a 80:20 ratio with a constant corn:soybean meal ratio (Diet B), Diet B + 0.05% MC (Diet C) and Diet B + 0.1% MC (Diet D). The MC used was a mixture of carbohydrases and phytase (Superzyme OM). Pigs were fed in metabolism crates for a period of 16 d at 550 kcal of metabolisable energy (ME)/kg $BW^{0.60}$/d to determine digestible energy (DE) and ME contents using total collection method. Thereafter, pigs were moved into an indirect calorimeter (IC) where heat production was measured over a 36-h period based on O_2 consumption and CO_2 production. The energy content of DESBM was calculated using the difference method. The DE and ME contents obtained were 3,365, 3,361, 3,401 and 3,381 kcal/kg DM and 3,260, 3,245, 3,295 and 3,283 kcal/kg DM for Diet A, B, C, and D, respectively. Corresponding values for NE were 2,897, 2,823, 2,848 and 2,842 kcal/kg DM. The heat production values among treatments (i.e., A, B, C and D) were 1,595, 1,606, 1,602 and 1,595 kcal/kg DM and those for fasting heat production were 1,231, 1,184, 1,173 and 1,154 kcal/kg DM, respectively. Thus, the NE content of DESBM was determined to be 2,527, 2,652 and 2,621 kcal/kg DM in treatment B, C and D, respectively. Respective values obtained with published equations were 2,305, 2,435 and 2,362 kcal/kg DM. Data was analyzed using mixed procedure of SAS 9.2. The results demonstrated that enzyme supplementation improved ($P < 0.0001$) the energy content of both diet and test ingredient. In conclusion, supplementation with MC at 0.05% and 0.1% of the diet improved NE values of DESBM by 4.9% and 3.7%, respectively.

Key Words: dry extruded expelled soybean, net energy, pig.

370 Assessment of oxidative stress biomarkers in exhaled breath condensate and blood of dairy heifer calves from birth to weaning. R. Ranade[1], S. Talukder[1], G. Muscatello[1], and P. Celi*1,2, *[1]Faculty of Veterinary Science, The University of Sydney, Sydney, NSW, Australia, [2]Melbourne School of Land and Environment, The University of Melbourne, Parkville, VIC, Australia.*

This study reports preliminary data on systemic and respiratory biomarkers of oxidative stress (OS) in healthy dairy calves from birth to weaning. Blood and exhaled breath condensate (EBC) were sampled from 19 female calves within 24 h from birth, and then at 6, 12 and 18 weeks of age. Values of reactive oxygen metabolites (d-ROMs), biological antioxidant potential (BAP), and advanced oxidation protein products (AOPPs) were determined in blood, while EBC samples were assayed for hydrogen peroxide (H_2O_2) levels. The degree of OS was estimated by the ratio of ROMs/BAP (U.Carr./µmol/L) multiplied by 100 to give an OS index (OSI). Changes in OS biomarkers were analyzed by a linear mixed model using Genstat version 14. The elevated BAPs observed in healthy calves may be significant in facilitating rapid metabolism associated with growth and development in the young calf. The observed decrease of AOPP is of interest as it is a marker of protein oxidation and is also considered to mediate pro-inflammatory responses, therefore suggesting that the calves recruited in this study did not experience any subclinical inflammatory conditions. This study successfully measured OS biomarkers in blood and EBC in the dairy calves. Our findings suggest that the calves enrolled in this study did not experience OS, and therefore the redox homeostatic control mechanism was adequately developed from birth to weaning. In conclusion, our study reports the physiological concentrations of some novel OS biomarkers in calves which may be considered as a reference standard when comparing further studies.

Table 1. Oxidative stress biomarkers in calves

	Calf age (wk)					
	1	6	12	18	SE	*P*-value
ROMs (U.Carr.)	179	161	154	160	8.5	0.218
BAP (µmol/L)	3814[a]	3313[b]	3250[b]	3832[a]	115	<0.001
OSI (arbitrary units)	4.7	4.9	5.1	4.3	0.3	0.326
H_2O_2 in EBC (µmol/L)	23.8[ab]	23.1[ab]	16.2[c]	45.0[d]	1.5	<0.001
AOPP (µmol/L)	28.9[a]	20.1[b]	15.7[b]	14.6[b]	1.4	<0.001

[a–c]Within rows, means followed by different letters are significantly different at $P = 0.05$.

Key Words: oxidative stress, calves, EBC

371 Prenatal transportation alters the metabolic response of Brahman bull calves exposed to a lipopolysaccharide challenge. J. A. Carroll*[1], N. C. Burdick Sanchez[1], M. C. Roberts[2,4], D. M. Price[2,4], B. P. Littlejohn[2,4], R. C. Vann[3], T. H. Welsh Jr.[4], H. D. Hughes[5], J. T. Richeson[5], and R. D. Randel[2], *[1]Livestock Issues Research Unit, USDA-ARS, Lubbock, TX, [2]Texas A&M AgriLife Research, Texas A&M University System, Overton, [3]MAFES-Brown Loam, Mississippi State University, Raymond, [4]Texas A&M AgriLife Research, Texas A&M University System, College Station, [5]Department of Agricultural Sciences, West Texas A&M University, Canyon*

This study was designed to determine if prenatal transportation influences the metabolic response to a postnatal LPS challenge. Pregnant Brahman cows (n = 96) matched by age and parity were separated into transported (TRANS; n = 48; transported for 2 h on gestational d 60, 80, 100, 120 and 140) and non-transported control groups (CONT; n = 48). From these treatments, bull calves (n = 16 per trt) were identified at weaning (176 ± 2 d of age) to subsequently receive a LPS challenge. We previously reported an effect of TRANS on temperament (TEMP); therefore bulls were also grouped based on TEMP score [Calm (C); Intermediate (I), or Temperamental (T)]. On d −2 bulls were transported by trailer from Overton to Lubbock, TX. On d −1, bulls were fitted with indwelling jugular cannulas and placed in individual stalls. On d 0 blood samples were collected at 0.5-h intervals from −2 to 8 h, and again at 24 h relative to LPS challenge (0.5 µg/kg BW) at Time 0. Serum was analyzed for glucose, insulin, nonesterified fatty acids (NEFA), and blood urea nitrogen (BUN) concentration. All variables increased post-LPS ($P < 0.01$). Glucose was 8 and 13% greater in TRANS than CONT pre- and post-LPS ($P < 0.01$), and was 11 and 8% greater in T than C and I bulls pre-LPS ($P < 0.01$). Post-LPS glucose was affected by TEMP, with this response influenced by prenatal transportation ($P < 0.01$). Insulin tended ($P = 0.09$) to be greater in TRANS than CONT bulls pre- and post-LPS. Post-LPS insulin was greatest in the C TRANS and I CONT bulls ($P < 0.01$). Pre-LPS NEFA was 18% greater in CONT than TRANS bulls ($P = 0.02$), and was greatest in I bulls ($P < 0.01$). Post-LPS, NEFA was also greater in I bulls ($P < 0.01$). The BUN was greater both pre- and post-LPS in the C TRANS bulls ($P < 0.01$). In summary, both prenatal transportation and TEMP had significant effects on the metabolic response before and after LPS, with prenatal transportation altering the observed metabolic responses within temperament groups. The altered metabolic response in the TRANS bulls may help explain differences observed in markers of the acute phase response in these bull calves following the LPS challenge.

Key Words: cattle, immune, transportation

372 Effects of an intramammary lipopolysaccharide challenge on metabolism and mammary immune response in hyperketotic dairy cows. M. Zarrin*[1,2], H.A. van Dorland[1], O. Wellnitz[1], and R.M. Bruckmaier[1], *[1]Veterinary Physiology, Vetsuisse Faculty, University of Bern, Bern, Bern, Switzerland, [2]Department of Animal Science, Yasouj University, Yasouj, Iran, [3]Graduate School for Cellular and Biomedical Sciences, University of Bern, Bern, Bern, Switzerland.*

Energy requirement and inadequate feed intake induces negative energy balance (NEB) in early lactating dairy cows. Elevation of ketone bodies is a frequent metabolic adaptation during NEB. Previous studies showed positive correlation between high plasma BHBA concentration and risk and severity of mastitis. The objective of this experiment was to study the effects of an intramammary lipopolysaccharide (LPS) challenge accompanied by hyperketonemia on metabolism and mammary immune responses in mid-lactation dairy cows. Thirteen dairy cows were randomly assigned to 2 treatment groups including an intravenous Na-DL-β-OH-butyrate infusion (HyperB, n = 5) to achieve elevated plasma BHBA concentrations (1.7 mmol/L), and a 0.9% saline solution infusion (Control, n = 8) for 56 h. After 48 h of infusion, 2 udder quarters were stimulated with 200 µg of *Escherichia coli* LPS. Blood samples were taken hourly during the infusion. Udder biopsies were taken at 48 h after the start of infusions immediately before the LPS challenge, and at the end of infusions. Blood samples were analyzed for blood metabolites,

cortisol, glucagon, and insulin concentrations. The mRNA abundance of candidate genes was determined by RT-qPCR in udder tissues. Difference between before and after LPS challenge in the measured parameters and area under the curve were evaluated by ANOVA with treatment as fixed effect in the model. Intramammary LPS challenge increased somatic cell count (SCC), rectal temperature, plasma glucose, cortisol, glucagon, and insulin concentration in both groups, but SCC, plasma glucose, and glucagon concentration remained lower in HyperB than the control ($P < 0.05$). IL-8, IL-10, citrate synthase, mRNA abundance increased during the LPS challenge in LPS quarters in HyperB ($P < 0.05$). RANTES mRNA abundance decreased ($P < 0.01$), and toll-like receptor 4 mRNA abundance tended to decrease in control group ($P = 0.08$). The results demonstrate that BHBA infusion affects metabolism and immune response of mammary gland to LPS challenge which may reflect the increased susceptibility for mastitis during spontaneous hyperketonemia.

Key Words: cow, ketone body, LPS

373 Effects of supplemental amino acids and chromium propionate on metabolism and neutrophil function in peak lactation dairy cows. K. Yuan*, C. F. Vargas, L. K. Mamedova, E. C. Titgemeyer, and B. J. Bradford, *Kansas State University, Manhattan.*

The study objective was to evaluate effects of chromium propionate (CrPr, KemTRACE Chromium Propionate 0.04%, Kemin Industries Inc.), rumen-protected Lys (LysiPEARL, Kemin Industries Inc.) and Met (MetiPEARL, Kemin Industries Inc.), or both on metabolism and neutrophil function in dairy cows near peak lactation (38 ± 15 DIM, 43.0 ± 7.0 kg/d milk). Forty-eight individually fed Holstein cows (21 primiparous, 27 multiparous) were stratified by calving date in 12 blocks and randomly assigned to 1 of 4 treatments within block. Treatments were control, CrPr (8 mg/d Cr), RPLM (10 g/d Lys and 5 g/d Met, intestinally available), or CrPr plus RPLM. Treatments were premixed with ground corn and top-dressed at 200 g/d for 35 d. On d 21 and 35 of treatment, blood samples were collected for analysis of plasma metabolites and hormones, and blood neutrophils were isolated from cows in 6 blocks for analysis of transcript abundance (TA) of pro-inflammatory cytokines. Tumor necrosis factor α (TNFα) and interleukin 1β (IL-1β) TA in neutrophils in the basal state or after 12 h of lipopolysaccharide (LPS) activation was quantified by qPCR. Data were analyzed as a complete block design with a factorial arrangement of treatments and sample day as a repeated measure using ProcMIXED in SAS. Plasma glucose, NEFA, and glucagon were unaffected ($P > 0.10$) by treatments. Plasma insulin was increased ($P = 0.01$, by 13%) by RPLM. Basal TNFα TA in neutrophils was decreased by CrPr ($P = 0.03$, by 80%) on d 21 but not on d 35. After LPS activation, CrPr tended ($P = 0.09$) to increase neutrophil TNFα TA. These results suggest that CrPr supplementation may decrease basal inflammatory status, but improve innate immune response upon activation. Basal IL-1β TA in neutrophils was decreased ($P = 0.03$) by RPLM, and the decrease in response to RPLM was greater when CrPr was provided (RPLM x CrPr, $P = 0.04$, by 78%). No treatment effect ($P > 0.10$) was observed for IL-1β TA after LPS activation. Collectively, results indicate that supplemental CrPr and RPLM provided for 5 wk had minimal effects on metabolism but may modulate neutrophil function in lactating cows.

Key Words: lysine, methionine, chromium

374 Polymorphonuclear leukocyte transcriptomics in transition Holstein cows fed two levels of dietary energy prepartum. M. J. Khan*, D. E. Graugnard, S. L. Rodriguez-Zas, and J. J. Loor, *University of Illinois, Urbana.*

Efficient activation of polymorphonuclear neutrophils (PMN) is central for an effective immune response. The peripartal period is characterized by marked changes in inflammatory status that are functionally related with impaired immune responses in the cow. Whole-transcriptome adaptations of PMN to prepartal dietary energy level and change of physiological state remain unknown. We used a bovine microarray (Agilent) for transcript profiling of PMN RNA isolated on −14 and 7 d around parturition from cows (8/diet) fed a control (high-straw, CON; NEL = 1.34 Mcal/kg) or moderate-energy (OVE; NEL = 1.62 Mcal/kg) diet during the entire dry period. The ANOVA model included diet, day, and diet × day as fixed effects, and cow within diet as random effect. The raw *P*-values from ANOVA were adjusted using a False discovery rate (FDR) to minimize false-positives. At an FDR $P < 0.01$ there were 318 (downregulated = 151, upregulated = 167) and 1,015 (downregulated = 354, upregulated = 661) differentially expressed genes (DEG) at d −14 and d 7. The KEGG pathways analysis using the Dynamic Impact Approach (DIA) uncovered major changes in metabolism at d 7 due to the effect of OVE vs CON. Amino acid metabolism and Metabolism of Terpenoids and Polyketides were the most impacted and downregulated pathways among metabolism categories. Of the top-5 most-impacted pathways in OVE compared with CON on d −14 and 7, we observed inhibition of "phenyalanine, tyrosine and tryptophan biosynthesis," "Terpenoid backbone biosynthesis," "Fat digestion and absorption," and "Phenylalanine metabolism"; whereas, "Glycosaminoglycan biosynthesis" was activated. "Cell growth and Death" was the most impacted activated pathway in cellular process KEGG category. Results suggest that overfeeding energy prepartum had profound effects on PMN transcriptomics, which may be functionally related to their function.

Key Words: PMN, microarray, bioinformatics

375 Efficacy of ampicillin trihydrate for therapy of metritis in lactating dairy cows. F. S. Lima*, A. Vieira-Neto, G. S. F. M. Vasconcellos, R. S. Bisinotto, N. Martinez, L. F. Greco, L. D. P. Sinedino, R. D. Mingoti, K. N. Galvão, C. A. Risco, W. W. Thatcher, and J. E. P. Santos, *University of Florida, Gainesville.*

Objective was to compare ampicillin trihydrate (AMP) with ceftiofur hydrochloride (CEFT) as treatment for metritis in dairy cows. Holstein cows had rectal temperature (RT) measured daily for the first 12 DIM, and fever was characterized by RT >39.4°C. Vaginal discharge (VD) was scored at 4, 6 and 8 DIM, and on any day a cow had fever. Cows with VD score 5 (reddish/brownish foul smell) were diagnosed with metritis (MET). Within cows with MET (n = 528), they were segregated as those with (n = 216) or without (n = 312) concurrent fever. Cows with metritis were blocked by parity and type of metritis (with or without fever), and assigned randomly to receive 11 mg/kg of AMP (n = 259) or 2.2 mg/kg of CEFT (n = 269) daily for 5 d. A cohort of healthy cows (NOMET, n = 268) was selected randomly as controls. Cows with metritis had RT measured on d 1 to 7, and d 12 after initiation of treatments, and VD scored on d 5, 7, and 12. Cure was characterized by VDDIM, VD was scored for diagnosis of clinical endometritis (CE, VD > 2, mucopurulent discharge). Data were analyzed using PROC GLIMMIX of SAS. Efficacy of treatments is depicted in the Table. Cure on d 5 and 7 increased for AMP compared with CEFT. Cure of metritis was less when cows had concurrent fever (Table). Cows receiving AMP had decreased ($P = 0.03$) prevalence of CE than those treated with CEFT (58.5 vs. 67.8%). Prevalence of CE was greater ($P < 0.01$) for cows previously diagnosed with MET than NOMET (63.2 vs. 27.2%). Treatment did not affect the proportion of cows that left the herd by 60 DIM (AMP = 3.8 vs. CEFT = 7.2%). Ampicillin is an efficacious alternative for therapy of metritis in dairy cows.

Table 1.

	AMP		CEFT		*P*-value		
Parameter	No Fever	Fever	No Fever	Fever	TRT	Fever	TRT × Fever
Cows, no.	152	107	160	109	—	—	—
RT,[1] °C	39.04	39.31	39.02	39.22	0.09	0.01	0.20
Fever,[2] %	12.5	33.2	12.9	28.2	0.47	0.01	0.34
Cure, %							
d 5	48.4	25.6	28.4	18.5	0.01	0.01	0.33
d 7	69.0	49.7	57.3	34.6	0.01	0.01	0.69
d 12	88.0	79.2	90.6	81.1	0.50	0.01	0.82

[1]RT = mean RT from d2 to 12 after enrollment.
[2]Fever = incidence of fever.

Key Words: dairy cow, ampicillin, metritis

376 Use of digital infrared thermography (IRT) and oxidative stress (OS) biomarkers as a diagnostic tool to diagnose interdigital dermatitis in sheep. S. Talukder*[1] and P. Celi[1,2], *[1]Faculty of Veterinary Science, The University of Sydney, Narellan, NSW, Australia, [2]Melbourne School of Land and Environment, The University of Melbourne, Parkville, VIC, Australia.*

This study reports preliminary data on the use of digital infrared thermography (IRT) and biomarkers of oxidative stress (OS) to diagnose the degree of interdigital dermatitis (ID) lesions in sheep. Interdigital space skin temperatures were obtained from healthy (n = 6) and ID affected (n = 11) crossbred rams with a FLIR T620 series infrared camera and images were analyzed using ThermaCAM Researcher Professional 2.9 software. Interdigital space lesions were scored using a 5 point scoring system (0–4). Blood were sampled from 17 rams and plasma was analyzed for reactive oxygen metabolites (d-ROMs), biological antioxidant potential (BAP), and advanced oxidation protein products (AOPP). The degree of OS was estimated by the ratio of ROMs/BAP (U.Carr./µmol/L) multiplied by 100 to give an OS index (OSI). Footrot scores were used to stratify the rams in 3 groups: Group A (0 to 0.5), B (0.6 to 1.5) and C (≥1.5). Changes in OS biomarkers and skin temperature were analyzed by a linear mixed model using Genstat version 14. We observed that skin temperature was significantly higher in rams with ID lesions ($P < 0.05$; Table 1). It was noted that ROMs and OSI biomarkers did not differ significantly between feet with ID lesions; a trend for higher BAP and AOPP concentrations in rams with footrot score > 1.5 was noted. In conclusion, IRT was reliable in detecting elevated temperature associated with ID in sheep.

Table 1. Oxidative stress biomarkers and interdigital space skin temperature in sheep

	Groups				
	A	B	C	SE	*P*-value
ROMs (U.Carr.)	119.7	148.1	118.9	25.5	0.60
BAP (µmol/L)	4012.0	4523.0	3688.0	315.0	0.09
OSI (arbitrary units)	3.0	3.3	3.5	0.1	0.59
AOPP (µmol/L)	17.3	11.9	19.2	2.6	0.08
Max Temp (°C)	35.7[b]	36.6[a]	37.0[a]	0.7	0.04
Min Temp (°C)	30.2[b]	31.5[a]	31.2[a]	0.5	0.02
Average Temp (°C)	33.7[b]	34.9[a]	35.1[a]	0.7	0.05
Footrot score	0.06[c]	1.3[b]	2.2[a]	0.3	0.01

[a–c]Within rows, means followed by different letters are different at $P = 0.05$.

Key Words: infrared thermography, oxidative stress, footrot

377 Effect of cattle temperament as determined by exit velocity on lung respiratory lesions and liver disease. T. B. Schmidt*[1], J. W. Dailey[2], J. W. Waggoner[3], A. H. Voyles[4], C. D. Alexander[4], J. O. Buntyn[1], K. I. Domenech[1], M. Schneider[4], and J. A. Carroll[2], *[1]University of Nebraska-Lincoln, Lincoln, [2]USDA-ARS, Lubbock, TX, [3]Kansas State University, Garden City, [4]Garden City Community College, Garden City, KS.*

The objective of this trial was to use exit velocity as a means of determining temperament of cattle to evaluate the effect of temperament on animal health. At the time of processing, exit velocity and BW were recorded on 20 pens of cattle (2,877 hd) at a commercial feedlot. Infrared sensors affixed to the alleyway at a distance of 2.75 m were used to remotely trigger the start and stop of a timing system. Exit velocity (m/sec) was recorded and cattle were placed into pens for the duration of the feeding period. Cattle were classified as temperamental (TEMP) and non-temperamental (NTEMP) based upon exit velocity. Twenty percent of each pen was classified as TEMP based the fastest exit velocity; the remaining 80% was classified as NTEMP. At the conclusion of the feeding period, cattle were transported to a commercial abattoir and harvested. At the time of harvest, the livers and lungs of each animal were evaluated. Livers were assessed based upon the Elanco Liver System and lung lesions were assessed based up a hedonic scale of 1 – 4; 1 = no lung lesions, 2 = plauritis lesions, 3 = portions/lobes of lung missing, and 4 = collapsed/consolidated lesions. No difference ($P = 0.18$) in liver abscesses was observed; 4.9 and 3.8% of NTEMP and TEMP cattle were positive for liver abscesses, respectively. Overall, 39 and 31% of N-TEMP and TEMP cattle exhibited lungs lesions, respectively. Assessment of lesions revealed that 64, 14, and 22% of the lesions observed in NTEMP cattle were scored as 2, 3, and 4, respectively. For TEMP cattle, 68, 12, and 20% of lesions observed were scored as 2, 3, and 4, respectively. Based upon the scale for lung lesions, lesions were greater ($P = 0.006$) for NTEMP cattle compared with TEMP cattle (1.61 ± 0.02 vs. 1.46 ± 0.05). Results of this trial indicate that based upon temperament, there is no difference in occurrence of liver disease; however, cattle classified as NTEMP had decreased hedonic lung lesion scores, indicating that N-TEMP cattle may be more susceptible to respiratory challenge. These data could be utilized to develop alternative health management strategies for temperamental cattle in feedlots.

Key Words: temperament, lung, lesion

378 Relationship between cattle temperament as determined by exit velocity and carcass merit in beef cattle. T. B. Schmidt*[1], J. W. Dailey[2], J. W. Waggoner[3], A. H. Voyles[4], C. D. Alexander[4], J. O. Buntyn[1], K. I. Domenech[1], M. Schneider[4], and J. A. Carroll[2], *[1]University of Nebraska-Lincoln, Lincoln, [2]USDA-ARS, Lubbock, TX, [3]Kansas State University, Garden City, [4]Garden City Community College, Garden City, KS.*

The objective of this trial was to use cattle temperament, as determined by exit velocity only, as a means to evaluate the effect of temperament on carcass merit and the possible utilization of exit velocity alone as a sorting tool within the feedlot. At the time of processing, exit velocity and BW were recorded on 20 pens of cattle (2,877 hd) at a commercial feedlot. Infrared sensors affixed to the alleyway at a distance of 2.75 m were used to remotely trigger the start and stop of a timing system. Exit velocity (m/sec) was recorded and cattle were placed into pens for the duration of the feeding period. Cattle were classified as temperamental (TEMP) and non-temperamental (NTEMP) based upon exit velocity.

Twenty percent of each pen was classified as TEMP based the fastest exit velocity; the remaining 80% was classified as NTEMP. At the conclusion of the feeding period, cattle were transported to a commercial abattoir and harvested. Data collected included: HCW, REA, back fat, KPH, and marbling scores. At the time of processing, BW was greater ($P < 0.001$) for NTEMP cattle compared with TEMP (326 ± 1.43 kg vs. 319 ± 2.88 kg). At harvest, NTEMP cattle had greater HCW ($P < 0.001$; 370 ± 1.70 kg vs. 365 ± 3.43 kg), back fat ($P < 0.001$; 1.30 ± 0.004 cm vs. 1.22 ± 0.008 cm) and yield grade ($P = < 0.001$; 2.35 ± 0.02 vs. 2.15 ± 0.04) when compared with TEMP cattle. Temperamental cattle had larger ($P = 0.03$) REA compared with NTEMP (101 ± 0.04 cm^2 vs. 99 ± 0.08 cm^2). Overall, 81.5% of TEMP cattle had a yield grade ≤ 2 compared with 77% for NTEMP cattle. Marbling scores were greater ($P = 0.003$) for NTEMP cattle compared with TEMP (417 ± 1.65 vs. 406 ± 3.34). Percent of carcasses grading USDA Standard were 3.79% for TEMP compared with 1.52% for NTEMP cattle and percentage of N-TEMP carcasses receiving a quality grade of Choice was 54.34% compared with 49.1% for TEMP cattle. The results of this trial indicate that temperamental cattle produce lighter weight carcasses with decreased USDA YG and decreased marbling. Based upon these results, the use of exit velocity as an indicator of temperament may be a feasible tool for sorting cattle upon arrival at the feedlot.

Key Words: temperament, carcass, merit

379 Single nucleotide polymorphisms of lactate dehydrogenase B and body condition effects on beef cow productivity. T. L. Devine*, O. T. Alaamri, D. Philipp, M. L. Looper, and C. F. Rosenkrans, Jr., *Division of Agriculture, Department of Animal Science, University of Arkansas, Fayetteville.*

Lactate dehydrogenase (LDH) catalyzes the conversion of pyruvate to lactate (forward; LDHf) or lactate to pyruvate (reverse; LDHr). Objectives were to determine effects of promoter and coding sequence of single nucleotide polymorphisms (SNP) of the LDH B gene on serum concentrations of metabolites and calving rate in beef cows. Primers were designed for PCR amplification of a 457- and 452-base pair fragment of the bovine LDH B promoter and coding sequence, respectively. Four SNP were detected (G-348A, A-261G, N-222D, and C541A). Deletion of 6 nucleotides (GGCCGC) was detected at base N-222D. Brahman-influenced cows (n = 99) were managed to achieve either low (BCS = 4.3 ± 0.1) or moderate (BCS = 6.4 ± 0.1) body condition (BC). Cows grazed stockpiled and spring growth, endophyte-infected tall fescue [*Lolium arundinaceum* (Schreb.) Darbysh] pastures to obtain desired BC. Serum samples were collected 35 d before the breeding period to quantify concentrations of LDH, IGF-I, and NEFA. Concentrations of IGF-I tended ($P < 0.08$) to be influenced by a BC x genotype interaction. Cows in low BC and heterozygous at base position −348 had decreased IGF-I (50 ± 9 ng/mL) compared with all other cows (89 ± 7 ng/mL). Cows heterozygous at SNP A-261G and N-222D had greater ($P < 0.05$) LDHf activity than homozygous cows. Concentrations of NEFA were increased ($P < 0.02$) in heterozygous cows (267 ± 14 μEq/L) than homozygous cows (206 ± 14 μEq/L) at base position C541A. Cows that were heterozygous (GA) at base position −348 had a lower calving rate than homozygous cows with the primary allele (53 vs. 79%, respectively). Polymorphisms of the promoter and coding region of the LDH B gene were associated with blood metabolites that mediate nutritional status of cattle; polymorphisms of the promoter region also were related to calving rate. Identification of cows with specific genotypes within the promoter and coding region of the LDH B gene may assist beef producers in selecting cattle that may have enhanced productivity.

Key Words: beef cows, lactate dehydrogenase B, single nucleotide polymorphism

380 Production traits of spring- and fall-calving Senepol cows in the tropics. R. W. Godfrey* and A. J. Weis, *University of the Virgin Islands, St Croix, Virgin Islands.*

This study was conducted to evaluate production traits of Senepol cows calving in the spring or fall on St. Croix. Cows were bred by natural service for a 60-d period each year starting in June or December and calved in the spring of 2009, 2010, 2011 and 2012 (n = 332 data points) or the fall of 2009, 2010 and 2011 (n = 93 data points). Data collected at breeding, calving and weaning was cow BW, hip height (HHT) and condition score (CS; 1 = thin, 9 = fat). Calf data (n = 190 data points) included birth (BRWT), weaning weight (WWT) and 205-d adjusted weaning weight (AWWT). Data were analyzed using GLM procedures with season and year as main effects and CHISQ for proportional data. At breeding, fall calving cows were heavier ($P < 0.0001$) than spring calving cows (624 ± 9 vs. 562 ± 5 kg, respectively) and had higher ($P < 0.0001$) CS (7.3 ± 0.1 vs. 6.8 ± 0.1, respectively). At calving, fall calving cows were heavier ($P < 0.0002$) than spring calving cows (628 ± 9 vs. 586 ± 6 kg, respectively). Calving rate was similar ($P > 0.10$) between fall and spring (49.5 and 50.8%, respectively). At weaning fall calving cows were heavier ($P < 0.001$) and had greater HHT ($P < 0.0001$) than spring calving cows (616 ± 10 vs. 561 ± 6 kg, 138.1 ± 0.7 vs. 134.5 ± 0.4 cm, respectively) but there was no difference ($P > 0.10$) in CS (6.2 ± 0.1 vs. 6.3 ± 0.1, respectively). There was no difference ($P > 0.10$) in BRWT or AWWT between spring and fall herds (40 ± 0.4 vs. 40 ± 0.6 kg, and 223 ± 3 vs. 230 ± 5 kg, respectively). Cow efficiency, measured as the ratio of WWT to cow BW at weaning, was greater ($P < 0.008$) in spring than in fall calving cows (42.7 ± 0.9 vs. 38.4 ± 1.4%, respectively). The percentage of calves born that survived to weaning was higher ($P < 0.05$) in the spring herd than in the fall herd (89.5 vs. 78.9%, respectively). Calving interval was similar ($P > 0.10$) between fall and spring herds (408 ± 22 vs. 445 ± 13 d, respectively). The larger cows were not as efficient as smaller cows and Senepol cattle managed to calve in the spring had better productivity than fall calving cows under the conditions on St. Croix.

Key Words: cattle, calf, tropics

381 Evaluation of hair coat, tick burden and production traits of Senepol cows in the tropics. R. W. Godfrey* and A. J. Weis, *University of the Virgin Islands, St Croix, Virgin Islands.*

The Slick hair gene found in Senepol cattle has been reported to contribute to their heat tolerance and tropical adaptation. This study was conducted to evaluate the relationship between hair coat, tick burden and production traits of Senepol cows under tropical conditions. Multiparous (n = 141) and primiparous (n = 19) Senepol cows calving in the fall of 2010 and 2011 and the spring of 2011 and 2012 on St. Croix were evaluated for hair coat phenotype, tick burden, BW and condition score (CS; 1 = thin, 9 = fat) at weaning. Hair coat was scored using 1 = slick, 2 = rough and 3 = hairy. Tick burden was scored using 1 = clean, 2 = light, 3 = moderate and 4 = heavy. Data were analyzed using GLM procedures with season and year as the main effects. The proportion of cows scored as hairy, rough or slick was 1.3, 17.1 and 89.6%, respectively. The proportion of cows that had clean, light, moderate or heavy tick burden scores was 32.5, 10.6, 37.5 and 19.4%, respectively. Tick score was correlated with hair score in primiparous but not multiparous cows (r = 0.606, $P < 0.02$ vs. r = −0.063, $P > 0.10$, respectively). Tick or hair score was not different ($P > 0.10$) between primiparous and multiparous cows (1.7 ± 0.2 vs. 2.1 ± 0.1 or 1.3 ± 0.1 vs. 1.2 ± 0.1, respectively). Lactating cows had a higher ($P < 0.0005$) tick score than nonlactating cows (2.4 ± 0.1 vs. 1.8 ± 0.1, respectively) but there was no difference ($P > 0.10$) in hair score (1.2 ± 0.1). There was no difference ($P > 0.10$) in hair score or tick score between pregnant and non-pregnant cows (1.2 ± 0.1 and 2.1 ± 0.1, respectively). Slick cows were heavier ($P < 0.09$; 607 ± 8 vs. 575 ± 17 kg, respectively) and had higher CS ($P < 0.08$; 6.9 ± 0.1 vs. 6.5 ± 0.2, respectively) than non-slick (rough or hairy) cows. There was no difference ($P > 0.10$) in BW or CS between cows with (tick score 2, 3 or 4) or without (tick score 1) ticks (602 ± 9 vs. 599 ± 13 kg or 6.7 ± 0.1 vs. 6.9 ± 0.2, respectively). Tick burden had no influence on BW or CS, but slick cows were heavier and had higher CS than non-slick cows further supporting the hypothesis that slick cattle are more suited to the tropical environment.

Key Words: cattle, hair coat, tick

382 Evaluation of hair coat, tick burden and production traits of Senepol calves in the tropics. R. W. Godfrey* and A. J. Weis, *University of the Virgin Islands, St Croix, Virgin Islands.*

The Slick hair gene found in Senepol cattle has been reported to contribute to their tropical adaptation. This study was conducted to evaluate the relationship between hair coat, tick burden and growth of Senepol calves in the tropics. Senepol calves born in fall 2010 and 2011 and spring 2011 and 2012 on St. Croix were evaluated for BW, hip height (HHT), hair coat phenotype and tick burden at weaning (n = 80) and as yearlings (n = 50). Hair coat was scored using 1 = slick (SL) or 2 = non-slick (NSL). Tick burden was scored using 1 = clean, 2 = light, 3 = moderate and 4 = heavy. Data were analyzed using GLM procedures with season, year and hair coat as the main effects. The proportion of calves scored as SL or NSL was 39 and 61%, respectively. The proportion of calves with clean, light, moderate or heavy tick burden scores was 43.3, 37, 12.6 and 7.1%, respectively. Tick score was lower ($P < 0.03$) at weaning than as yearlings (1.7 ± 0.1 vs. 2.1 ± 0.1, respectively) but there was no difference ($P > 10.0$) in hair score (1.5 ± 0.1 vs. 1.5 ± 0.1, respectively). There was no difference ($P > 0.10$) in tick score at weaning between SL and NSL calves (1.6 ± 0.2 vs. 1.8 ± 0.1, respectively) but NSL calves had higher ($P < 0.05$) tick scores than SL calves as yearlings (1.7 ± 0.2 vs. 2.3 ± 0.2, respectively). At weaning SL calves were heavier ($P < 0.009$) than NSL calves (241 ± 6 vs. 219 ± 5 kg, respectively) but not ($P > 0.10$) as yearlings (308 ± 8 vs. 292 ± 6 kg, respectively). Weaning weight was higher ($P < 0.04$) in clean calves than it was in calves with a high tick burden (233 ± 6 vs. 188 ± 20 kg, respectively). Clean calves had a greater ($P < 0.06$) ADG at weaning than did calves with a high tick burden (0.89 ± 0.03 vs. 0.72 ± 0.09 kg/d, respectively). There was no difference ($P > 0.10$) in yearling BW between calves that were clean or had a high tick burden (308 ± 9 vs. 319 ± 14 kg, respectively). Clean calves had a greater ($P < 0.04$) ADG at yearling than did calves with a high tick burden (0.45 ± 0.03 vs. 0.34 ± 0.09 kg/d, respectively). Tick burden can have a greater influence than hair coat phenotype on Senepol calf weights up through yearling age.

Key Words: cattle, hair coat, tick

383 Effects of conventional and natural production programs on carcass characteristics and retail meat attributes. C. L. Maxwell*[1], B. K. Wilson[1], B. T. Johnson[1], B. C. Bernhard[1], C. F. O'Neill[1], K. J. Winn[1], K. R. McCullough[1], T. A. Harlan[1], M. M. Kinna[1], B. D. Bloomberg[1], D. L. VanOverbeke[1], C. J. Richards[1], D. L. Step[3], E. A. DeVuyst[2], C. R. Krehbiel[1], *[1]Department of Animal Science, Oklahoma State University, Stillwater, [2]Department of Agriculture Economics, Oklahoma State University, Stillwater, [3]Department of Veterinary Clinical Sciences, Oklahoma State University, Stillwater*

The objective of this study was to evaluate conventional and natural production programs through annual pasture and finishing with 2 roughage levels on carcass characteristics and retail meat attributes. Beef steers (n = 180; initial BW = 250 ± 19.1 kg) were randomized to one of 2 treatments in the pasture phase. Steers were implanted with 40 mg of TBA, 8 mg estradiol, and 29 mg tylosin tartrate (Conventional; CONV) or received no implant (Natural; NAT). The 2 treatments grazed winter annual pasture for 109 d. Steers (160 steers; 5 steers/pen; 8 pens/trt) were assigned to a 2 × 2 factorial RCBD during finishing. The first factor was production program (NAT vs. CONV), and the second 7 vs. 12% roughage (DM basis; LOW vs. HIGH.) During finishing, CONV steers were given 120 mg of TBA, 25 mg estradiol and 29 mg tylosin tartrate, fed monensin and tylosin for the entire feeding period, and fed zilpaterol hydrochloride for the last 20 d of the trial. At harvest, 17–18 strip loins/treatment were collected for retail meat attribute analysis. There were no effects of treatment on 12th rib-fat thickness ($P \geq 0.16$). Hot carcass weight was increased by 62 kg (424 vs. 362 kg; $P < 0.01$), dressing percentage increased 1.6% units (64.9 vs. 63.3%; $P < 0.01$), and ribeye area was increased by 16.9 cm^2 (100.9 vs. 84.0 cm^2; $P < 0.01$), decreasing USDA Yield grade (3.09 vs. 3.54; $P < 0.01$) for CONV compared with NAT. Natural steers had a higher percentage grading Premium Choice (48.7 vs. 18.7%; $P < 0.01$), a higher percentage of USDA Yield grade 4 and 5 (25.4 vs. 9.3%; $P < 0.01$), and a higher percentage of abscessed livers (39.6 vs. 10.5%; $P < 0.01$) compared with CONV. Conventional had increased slice shear values (21.27 vs. 18.00 kg; $P < 0.01$) and Warner-Bratzler shear force (3.89 vs. 3.41, kg; $P < 0.01$) compared with NAT, resulting in lower initial tenderness and connective tissue scores in a trained taste panel (6.8 vs. 7.1 and 6.9 vs. 7.1, $P < 0.01$, respectively.) The results of this study indicate conventionally raised cattle produce more total product with a minimal decrease in consumer detectable retail product quality.

Key Words: cattle, feedlot, conventional

384 Effects of conventional and natural production programs on winter annual pasture and feedlot performance. C. L. Maxwell*[1], B. K. Wilson[1], B. T. Johnson[1], B. C. Bernhard[1], C. F. O'Neill[1], D. L. VanOverbeke[1], D. L. Step[3], E. A. DeVuyst[2], C. J. Richards[1], and C. R. Krehbiel[1], *[1]Department of Animal Science, Oklahoma State University, Stillwater, [2]Department of Agriculture Economics, Oklahoma State University, Stillwater, [3]Department of Veterinary Clinical Sciences, Oklahoma State University, Stillwater.*

The objective of this study was to evaluate conventional and natural production programs through annual pasture and finishing with 2 roughage levels. Beef steers (n = 180; initial BW = 250 ± 19.1 kg) from a single ranch in Oklahoma were randomized to one of 2 treatments in the pasture phase. Steers were implanted with 40 mg of TBA, 8 mg estradiol, and 29 mg tylosin tartrate (Conventional; CONV) or received no implant (Natural; NAT). The 2 treatments were comingled and grazed winter annual pasture for 109 d. During pasture grazing, CONV steers had an 18.5% improvement in ADG (1.22 vs. 1.03 kg/d; $P < 0.01$), and a heavier final BW (385 vs. 366 kg, $P < 0.01$), compared with NAT steers. Steers (160 steers; 5 steers/pen; 8 pens/trt) were assigned to a 2 × 2 factorial RCBD in the feedlot phase. The first factor was production program (NAT vs. CONV), and the second factor was 7 vs. 12% roughage (DM basis; LOW vs. HIGH). During finishing, CONV steers were given 120 mg of TBA, 25 mg estradiol and 29 mg tylosin tartrate at processing, were fed monensin and tylosin for the entire feeding period, and fed zilpaterol hydrochloride for the last 20 d of the trial. Both groups were fed 135 d. There were no program × roughage level interactions ($P \geq 0.07$). Conventional steers ate 6.9% more fed (11.8 vs. 11.0 kg/d; $P < 0.01$), gained 28.4% faster (1.90 vs. 1.48 kg/d; $P < 0.01$), and were 24.2% more efficient (0.164 vs. 0.132; $P < 0.01$), compared with NAT. There was a trend for LOW steers to eat less feed (11.3 vs. 11.5 kg/d; $P = 0.13$) and gain faster (1.73 vs. 1.66 kg/d; $P = 0.09$), resulting in an improvement in feed efficiency (0.153 vs. 0.144; $P < 0.01$) compared with HIGH. There was a 26% improvement in estimated daily carcass weight gain (1.55 vs. 1.23 kg/d), 17.8% improvement in carcass efficiency (0.132 vs. 0.112; $P < 0.01$), and 14.0% improvement (1.30 vs. 1.14 Mcal/kg; $P < 0.01$) in calculated NE_g retained for CONV vs. NAT. The results of these data show that the technologies used in CONV production result in significant improvement in efficiency and performance.

Key Words: cattle, conventional, natural

385 Effects of suckling restriction, flushing and body condition score at calving on metabolic and endocrine profiles of primiparous beef cows grazing native pasture . P. Soca*[1], M. Carriquiry[2], M. Claramunt[3], G. Ruprechter[4], and A. Meikle[4], *[1]Departament of Animal Production and Pastures, EEMAC, School of Agronomy, Universidad de la Repblica, Paysand, Uruguay, [2]Department of Animal Production and Pastures, School of Agronomy, Universidad de La Republica, Uruguay, Montevideo, Uruguay, [3]Department of Animal Production, School of Veterinary, Universidad de La Republica, Uruguay, Paysand, Uruguay, [4]Laboratory of Nuclear Techniques, School of Veterinary, Universidad de La Republica, Uruguay, Montevideo, Uruguay,*

The objective was to analyze the effect of type of suckling restriction, flushing and body condition score (BCS) at calving on metabolic-endocrine profiles and reproduction of primiparous beef cows at grazing. Primiparous cows (n = 56) in anestrous were assigned randomly to a 2x2 factorial arrangement of suckling management and flushing and classified by BCS at calving (low ≤ 3.5 = L, moderate ≥ 4 = M; 1–8 visual scale). Suckling-restriction treatments started at 55 ± 10 d postpartum (DPP)(0 = initiation of the treatment) and consisted of applying nose plates to calf for 12 d (i.e., TS treatment) or 5 d of isolation of the cow-calf pair followed by nose plates for 7 d as calves were reunited with their mothers (i.e., IS treatment). Nutritional treatments (flushing = F vs. control = NF) started immediately after suckling restriction with cows receiving or not 2 kg/d of whole-rice middling for 22 d. Repeated variables and probability of early (EP) and total (TP) pregnancies were analyzed using a time repeated measure analysis and lineal model respectively. Cortisol was reduced after the suckling treatments. BCS evolution and ADIP were affected by the interaction among BCS at calving and Days ($P < 0.06$). Moderate BCS cows had greater BCS than L cows. Low BCS cows presented a reduction in ADIP, while M maintained them. Cholesterol, insulin and IGF-I were affected by interaction among Days, BCS at calving and flushing ($P < 0.03$). F increased cholesterol in both BCS at calving ($P < 0.001$), while insulin and IGF-I increased during F only in M BCS at calving ($P < 0.01$). IGF-I increased in all BCS groups during suckling. Moderate BCS reduced postpartum anestrous interval (PPI) (L = 123 vs. M = 98 d $P < 0.0004$). The EP was affected by BCS at calving (L = 0.5 vs. M = 0.8 $P < 0.008$). TP was affected by F (F = 1 vs. NF = 0.6 $P < 0.02$) and BCS at calving (L = 0.6 vs. M = 1 $P < 0.0001$). Results confirmed the value of tactical intervention and BCS at calving relevance as a link between nutrition-metabolic and reproduction processes in primiparous cows.

Key Words: flushing, suckling restriction, primiparous cow

386 Effects of metabolic imprinting on growth performance of early-weaned beef steers. P. Moriel*[1], S. E. Johnson[3], M. Hersom[2], M. McCann[3], D. E. Gerrard[3], P. G. Martins[1], J. M. B. Vendramini[1], and J. D. Arthington[1], *[1]University of Florida, Ona, [2]University of Florida, Gainesville, [3]Virginia Tech University, Blacksburg.*

A 2-yr study evaluated the effects of calf management system after early-weaning (EW) on growth performance of beef steers. On d 0, Brahman × British steers (n = 40 in yr 1 and 38 in yr 2; mean BW = 95 ± 15 kg; age = 74 ± 14 d) were stratified by age and BW, and randomly assigned to a control treatment that was normally weaned (NW) on d 180, or 1 of 3 EW treatments: (1) EW and grazed on ryegrass pastures for 60 d (yr 1) or 90 d (yr 2) then on bahiagrass pastures until NW (EWRYEG), (2) EW and fed a high-concentrate (3.5% of BW) diet in drylot until d 180 (EW180), or (3) EW and metabolically imprinted by feeding a high-concentrate diet (3.5% of BW) for 90 d then grazed on bahiagrass pastures until d 180 (EW90). Steers were assigned to 1 of 2 pens per treatment. Steers on pastures were supplemented with concentrate (69% TDN and 20% CP) at 1.0% BW until d 180. Treatment × year effect was detected ($P = 0.02$) for ADG from d 0 to 90, but not ($P = 0.18$) from 90 to 180. From d 0 to 90 of yr 1, EW90 and EW180 steers had greater ($P < 0.0001$) ADG than NW and EWRYEG, which did not ($P = 0.37$) differ (0.99, 1.00, 0.63 and 0.57 ± 0.043 kg/d, respectively). In yr 2, NW steers tended ($P = 0.09$) to have greater ADG from d 0 to 90 than EWRYEG steers (0.87 vs. 0.75 ± 0.046 kg/d). Thus, EW90 and EW180 steers were heaviest ($P < 0.0001$) on d 90 of yr 1 and 2, whereas NW steers had similar ($P = 0.30$) BW in yr 1, but greater ($P = 0.02$) BW in yr 2 than EWRYEG steers (149 and 174, 187 and 191, 188 and 188, and 153 and 163 ± 3 kg for NW, EW180, EW90 and EWRYEG in yr 1 and 2, respectively). From d 90 to 180, ADG was greatest for EW180 steers, intermediate for NW, and least for EW90 and EWRYEG steers ($P \leq 0.01$; 1.29, 0.90, 0.65 and 0.68 ± 0.039 kg/d, respectively). On 180 of yr 1 and 2, EW180 steers were ($P \leq 0.08$) heaviest and EWRYEG lightest, whereas EW90 and NW steers had ($P = 0.19$) similar BW (295 and 300, 202 and 229, 239 and 247, and 226 and 250 ± 7 kg for EW180, EWRYEG, EW90 and NW steers in yr 1 and 2, respectively). Thus, different nutritional management systems for EW steers result in significant differences on BW at the time of normal-weaning.

Key Words: metabolic imprinting, beef steer, high-concentrate

387 Effects of metabolic imprinting on growth performance of early-weaned beef heifers. P. Moriel*[1], S. E. Johnson[3], M. Hersom[2], P. G. Martins[1], J. M. B. Vendramini[1], and J. D. Arthington[1], *[1]University of Florida, Ona, [2]University of Florida, Gainesville, [3]Virginia Tech University, Blacksburg.*

A 2-yr study evaluated the effects of calf management system after early-weaning (EW) on growth performance of beef heifers. On d 0 (yr 1 and 2), Brahman x British heifers (n = 40 in yr 1 and 38 in yr 2; mean BW = 87 ± 13 kg; age = 72 ± 12 d) were stratified by age and BW, and randomly assigned to a control treatment that was normally-weaned (NW) on d 180, or 1 of 3 EW treatments: (1) EW and grazed on ryegrass pastures for 60 d (yr 1) or 90 d (yr 2) then on bahiagrass pastures until NW (EWRYEG), (2) EW and limit-fed a high-concentrate (3.5% of BW) diet in drylot until d 180 (EW180), or (3) EW and metabolically imprinted by feeding a high-concentrate diet (3.5% of BW) for 90 d then grazed on bahiagrass pastures until d 180 (EW90). Heifers were assigned to 1 of 2 pens per treatment. On d 180, heifers were grouped by treatment and grazed on bahiagrass pastures until the start of breeding season (d 332). Heifers on pastures were supplemented with concentrate (69% TDN and 20% CP) at 1.0% BW until d 180 and 1.5% BW from d 180 to 332. Treatment × time × year effects were detected ($P < 0.0001$) for BW from d 90 to 180, but not ($P \geq 0.12$) from d 0 to 90 and d 180 to 332. On d 90, EW90 and EW180 heifers were heavier ($P \leq 0.09$) than NW and EWRYEG heifers, whereas EWRYEG heifers were lighter than NW heifers (172, 169, 143 and 149 ± 2 kg, respectively). On d 180 of yr 1 and 2, EW180 heifers were heaviest and EWRYEG lightest ($P \leq 0.01$; 267 and 270, and 184 and 208 kg for EW180 and EWRYEG in yr 1 and 2, respectively). In yr 1, NW heifers achieved similar ($P \geq 0.61$) BW compared with EW90 heifers on d 180 (217 vs. 220 ± 4 kg), whereas in yr 2, NW and EW90 heifers had similar BW on d 150 and 180 (206 and 221, and 209 and 220 ± 4 kg for NW and EW90 on d 150 and 180, respectively). On d 332, EW180 heifers were heaviest, whereas NW, EW90 and EWRYEG heifers had similar BW ($P \geq 0.09$; 362, 324, 326 and 313 ± 5 kg, respectively). Thus, heifer management systems following early-weaning result in significant differences on BW at the time of normal weaning and at the start of breeding season.

Key Words: metabolic imprinting, beef heifer, high-concentrate

388 Effect of in utero heat stress on insulin response of calves after weaning. S. Tao*, A. P. A. Monteiro, M. J. Hayen, and G. E. Dahl, *University of Florida, Gainesville.*

Heat stress during the dry period not only negatively affects subsequent lactation in the cow, but may also affect the calf postnatally. Previous studies suggest that calves born to cows heat-stressed during late gestation have lower birth weight but similar overall weight gain during the pre-pubertal period compared with normothermic conditions in utero. However, it is unclear if insulin sensitivity of peripheral tissues, and thus metabolism, of calves is altered in their postnatal life after in utero heat stress. The aim of the present study was to examine the effects of maternal heat stress during the dry period on insulin response at peripheral tissues of calves after weaning. Calves (10/treatment) were born to cows exposed to heat stress (HT) or cooling (CL) when dry. Calves were immediately separated from their dams and fed 3.8 L of high quality colostrum within 1 h after birth and then 1.9 L 12 h later. All calves were fed 1.9 L to 3.8 L pasteurized milk in the morning and afternoon from 2 to 42 d of age and then only in the morning until weaning at 49 d. Calf starter and water were offered ad libitum starting at 2 d of age. All calves were managed in the same manner throughout the study. A glucose tolerance test (GTT) and an insulin challenge (IC) were performed on all calves at 55 d of age. Gestation length was not affected (HT: 277 ± 1.8 d; CL: 279 ± 1.8 d) by heat stress during the dry period, but HT calves were born lighter (40 ± 1.4 vs. 45 ± 1.4 kg, $P = 0.03$) compared with those cooled in utero. Both groups of calves had similar weaning weight (HT: 68 ± 3.2 kg; CL: 71 ± 3.3 kg) and body weight gain from birth to weaning (HT: 28 ± 2.2 kg; CL: 26 ± 2.3 kg). Relative to those cooled in utero, HT calves had similar insulin response to GTT and insulin clearance during IC but faster glucose clearance during GTT and stronger glucose response to IC. In conclusion, in addition to impaired fetal growth, maternal heat stress during the dry period enhances the insulin response at peripheral tissues of calves after weaning, which may suggest a possibility of accelerated lipogenesis and fat deposition in early life.

Key Words: heat stress, insulin response, dairy calf

Teaching/Undergraduate and Graduate Education: New Approaches to Animal Sciences Curriculum

389 Integrated Program for Reducing Bovine Respiratory Disease Complex (BRDC) in Cattle, Coordinated Agricultural Project (CAP): Translation of research into teaching programs in 2013. M. G. Thomas*[1], G. R. Hagevoort[2], T. T. Ross[2], R. M. Enns[1], H. Van Campen[1], A. L. Van Eenennaam[3], H. L. Neibergs[4], C. Chase[6], and J. E. Womack[5], *[1]Colorado State University, Fort Collins, [2]New Mexico State University, Las Cruces, [3]University of California, Davis, Davis, [4]Washington State University, Pullman, [5]Texas A&M University, College Station, [6]South Dakota State University, Brookings.*

Bovine respiratory disease complex is a common cause of morbidity and mortality in cattle, especially young animals exposed to stress. This disease is considered a complex because of numerous pathogens, environmental and management factors. The general research objective of this CAP is to use genomic approaches to identify chromosome regions associated with susceptibility to BRDC. Results will be translated to beef and dairy industries via selective breeding tools and methods for disease prevention and management (http://www.brdcomplex.org/). A translational effort is encompassed in teaching and extension efforts. The educational infrastructure of this CAP is greatly assisted because its' activities are organized within established and collaborating programs, Southern Great Plains Dairy Consortium-Teaching (SGPDC-T; http://sgpdct.tamu.edu/) and Engaging the New Biology Graduate Education Online (http://enbgeo.iddl.vt.edu/). Objectives of the teaching effort include (1) sponsor students to attend SGPDC-T, where research components of the BRDC-CAP are ongoing, and (2) develop 2 nationally accessible distance-learning courses on the integration of animal health management with genomic and animal breeding approaches (i.e., Improvement of BRDC Resistance and Animal Health and Genetic Approaches to Disease). The SGPDC-T module for herd health has been greatly enhanced by involving veterinary expertise. Specifically, laboratory instruction of symptoms and necropsy demonstration was beneficial to help students visualize consequences of BRD on calf health. The research component of this CAP is presenting and publishing genomic. This information is being discussed and is incorporated into content of the on-line courses. This CAP is in the third year of a 5-year effort and welcomes additional student participation, especially students from under-represented minorities. In summary, the education component of the BRDC-CAP (USDA-AFRI 2011-68004-30367) is benefiting from multi-disciplinary learning approaches that coincide with the genomic research of susceptibility to BRDC.

Key Words: cattle, disease, genomics

390 Predicting instructor quality in undergraduate animal science courses using the IDEA survey. M. J. Anderson, K. J. Stutts, M. M. Beverly, and S. F. Kelley*, *Sam Houston State University, Huntsville, TX.*

The Individual Development and Educational Assessment (IDEA) survey uses student feedback to assess and improve teaching, learning, and the higher education process. The IDEA survey contains questions pertaining to course objectives, teaching methods and styles, and a description of the course with the goal of determining the quality of the instructor and overall course. The objective of this study was to determine which of the survey questions were most important when predicting the quality of the instructor in undergraduate animal science courses. A step-wise regression analysis was performed on data from 238 courses spanning a 6-year period. Thirty-five of the 43 questions on the survey were included in the analysis. Eight questions were not included in the analysis because they involved students' preconceptions that could not be affected by the instructor during the course. This analysis indicated that only 9 of the 35 questions entered into the model were significant. These 9 questions had an r^2 of 0.7620, compared with an r^2 of 0.7808 for all 35 questions. The analysis indicated that these 9 questions account for the majority of variation within the model. The top 3 questions with positive relationships toward predicting the quality of instructor were: The instructor (1) displayed a personal interest in students and their learning, (2) explained course material clearly and concisely, and (3) found ways to help students answer their own questions. Conversely, 2 questions describing the progress on developing skills in expressing oneself orally or in writing and the instructor's ability to inspire students to set and achieve goals that challenged them, had negative relationships when predicting the quality of the instructor. This indicated that students believed that these areas were counterproductive toward increasing the overall quality of the instructor. In conclusion, an animal science instructor can improve the quality of their teaching by displaying an interest in the students, being very clear on their explanations of course material, and by helping students establish critical thinking skills.

Key Words: IDEA, undergraduate teaching, animal science

391 Developing an undergraduate animal science beef cattle industry tour course to facilitate experiential learning. J. L. Wahrmund* and A. J. Cooper, *Department of Agricultural Sciences, Texas A&M University-Commerce, Commerce.*

An undergraduate course for animal science students was developed at Texas A&M University-Commerce to provide students unique experiential learning opportunities. The beef industry in Texas and the Southern Plains is greatly diverse. Types of operations and management styles change by region and with the available resources within that area. Students enrolled in the course gain first-hand and hands-on experiences by visiting beef operations and facilities that are unique to their geographical regions. Many students majoring in Animal Science at Texas A&M University-Commerce plan to seek careers in the beef industry. It is important that these students have opportunities, such as those available in this course, to understand and appreciate the many segments of the beef industry and how these segments work together, despite their diversity. Students also gain a better understanding of growing niche markets and products. This 3-credit hour course is taught during a 13-d mini-mester, and begins with traditional classroom instruction. Students are provided an overview of the course, including information regarding each of the facilities and operations to be visited. During the remainder of the first week, day trips are planned to tour facilities and operations within approximately 2-h drive of Commerce, TX, including cow-calf operations, backgrounding operations, a feed mill, and breed association headquarters. During the second week, an overnight trip is planned. Students and instructors leave on Monday and return on Friday. Locations toured during the second week include those facilities and operations that are unique to geographic regions other than Northeast Texas. Stops during the overnight tour trip include feedlots, harvesting facilities, and outdoor cattle management operations specific to the geography of particular regions. After the overnight tour portion completes, students return to the classroom for the final 3 d

of the course for reflection and a final examination. Student learning outcomes are assessed by comparing and pre- and post-examinations and questionnaires.

Key Words: education, experiential learning, undergraduate

392 Using case studies to provide a global perspective on reproductive management decision-making. K. G. Pohler*[1], A. Ball[2], and M. F. Smith[1], *[1]Division of Animal Sciences, University of Missouri, Columbia, [2]Division of Applied Social Sciences, University of Missouri, Columbia.*

The ability to solve problems on an international scale is becoming increasingly important. Within the United States, a large proportion of the agricultural labor force consists of international workers; therefore, the ability to educate and communicate cross-culturally is essential. As part of the curriculum in Reproductive Management, a senior level course, we developed 5 case studies that required solving reproductive management problems in Brazil. Learning objectives of these case studies included (1) Become more knowledgeable of Brazilian beef production, (2) Enhance critical thinking and decision making skills, (3) Solve management problems in another country, and (4) Connect theory to practice in an international work place. During the fall 2012 semester, students were assigned to a case study in groups of 3. Each group prepared a 3–4 page report that included a clear statement of the problem; detailed description of the problem solution; and a list of related research or government articles. Further, students summarized the case in both English and Portuguese. During a lab session of the course, students presented their cases and recommendations in a poster session format. Prior to working on these case studies approximately 30% of the students indicated they had some international experience (e.g., study abroad opportunity or travel with family) with 70% having no prior international experience. Nearly half of the students indicated minimal knowledge of the Brazilian beef industry. Outcomes from these case studies included (1) Increased competency of students' reproductive management skills, (2) Ability to integrate and apply classroom/lab information toward solving a production problem, (3) Increased ability to work as a team and solve problems cooperatively, and (4) An overall 80% change in their perception of international agriculture. Collectively, the case studies accomplished the learning objectives and allowed students to engage in problem solving on an international scale.

Key Words: case studies, problem solving, international agriculture

393 Elements of mastitis unit integrated through blended learning. C. A. Allen* and W. L. Hurley, *University of Illinois, Urbana.*

Traditional teacher-centered classes assign readings to prepare for in-class lecture, homework to demonstrate mastery, and exams to assess knowledge. In contrast, blended learning (BL), also known as hybrid courses, mixed mode teaching, backward classroom, or reverse instruction, uses computer technology to partially or fully deliver course content. The shift of content delivery to an online medium provides the opportunity to use in-class time for engaging students in problem-based hands-on learning activities, and applying their knowledge through practical work, group presentations and solving realistic problems. The instructor's role becomes one of facilitator of learning rather than transmitter of knowledge. An upper-level undergraduate course in lactation biology at the University of Illinois extensively uses BL. The mastitis unit provides an example of how BL is implemented. Students gain access to background information on mastitis via an online module available through a course management system. Included in the online module is information on mastitis, definitions, resources, sample case studies, and a quiz. Students find information about dairy farms and dairy cattle, terminology, mastitis types, pathogens involved, and strategies for solving the mastitis cases. Students are given sample case studies and are expected to explain the cases, solve them, and give recommendations. The 2 sample cases also provide conclusions and recommendations from the attending veterinarian. An online quiz assesses the student's knowledge regarding the background mastitis content. Students also visit the university dairy farm to gain context for the mastitis information provided and the online cases. In class, students work in groups solving additional mastitis cases. The groups then share their case solutions and conclusions with the class through a creative, image-rich presentation mode. Students actively engage in refining their understanding of mastitis and the cases during these class presentations. Adapting this mastitis unit to a BL format allows for an integrated presentation of the topic and a robust learning environment.

Key Words: animal sciences, blended learning, mastitis

394 Alternative class exercise for information retention and retrieving course materials. D. Masser[1], J. Falk[1], and A. Ahmadzadeh*[2], *[1]Dept. Ag Ed. & 4-H Youth Develop, University of Idaho, Moscow, [2]Dept. Animal & Vet. Sci., University of Idaho, Moscow.*

Research has shown that memory retention is improved when course materials make an imprint in students' memory, or the students experience excitement and/or pressure during the learning process. Using a dairy science course, the objective of this particular classroom exercise was to evaluate the effect of using quiz bowls on students' active learning, retention of information, and students' satisfaction, attitudes and achievement. The quiz bowl, as an alternative method of reviewing the course materials, was performed at the end of the semester and before the final exams. Each student was assigned to prepare 5 challenging questions and provide the answers from the course materials. Students were informed that 70% of these questions would be used in the final exam. To conduct the quiz bowl, teams of 4 to 5 students were formed. Two teams competed during each round, and all teams participated, hence all students had the opportunity to become engaged. Students who had completed the course within the past 4 years were asked to complete a questionnaire to assess their satisfaction with the quiz bowl as a course review for the final exam. On a scale from 0 to 100, students rated their degree of agreement on each question in the survey. Responses were collected and summarized (mean ± SD). Fifty-three out 74 students responded. Mean response score across all questions was 88.5 ± 3. The mean score to main questions were as follow: retention of information = 86.7 ± 14; better prepared for the final exam = 91.3 ± 11; increased critical thinking = 85.5 ± 13; satisfaction with the amount of information included in the quiz bowl = 90.1 ± 12; preference of quiz bowls vs. traditional course review = 89.2 ± 18; learning the course content = 86.3 ± 16; satisfaction with the questions prepared by the class = 85.2 ± 12; satisfaction with questions prepared by the class = 85 ± 12. Based on the students' responses, quiz bowl may be used as a viable alternative method for enhancing students' learning and information retention.

Key Words: quiz bowl, course review, information retention

395 The captive wild animal management minor at the University of Missouri—A partnership between Animal Sciences and Fisheries and Wildlife Sciences. T. A. Strauch*, M. R. Ryan, and J. N. Spain, *University of Missouri.*

In 2007, the Division of Animal Sciences and the Department of Fisheries and Wildlife Sciences at the University of Missouri began offering a minor in captive wild animal management. The initiative was based on student interest in exotic animals and exotic animal husbandry. The curriculum was structured around existing courses, taking advantage of academic strengths in the 2 primary disciplines and designed with input from national leaders in the captive wild animal industry. Students complete common core courses, and choose advanced courses that best match their professional goals. Two new courses and a required internship experience were developed. The minor requires a minimum of 38 credit hours, but if a student's major is animal sciences, fisheries and wildlife sciences, or biological sciences, 18–23 of the 38 credit hours are embedded in requirements for the major. New courses include an introductory course, with guest speakers who are professionals in the field, and a senior seminar in captive wild animal management. Student interest has been high. At any given time, roughly 140 students state they are pursuing the minor, representing 17–20% of the total undergraduates in each discipline. Approximately 84% are female. In 2012, 25.6% of incoming animal sciences freshmen expressed their primary species interest as zoo animals, second only to small animals at 30.2%. Students have interned at locations in 11 states and career interests include, but are not limited to, zoo keeping, endangered species conservation, advanced research, veterinary medicine, wildlife rehabilitation, and production agriculture. To date, 65 students have graduated with the minor. Within a year of graduation, the students have been professionally active as follows: wild animal position, n = 18; graduate school, n = 11, domestic animal care, n = 4; research assistant, n = 3; vet school, n = 3; other/unknown, n = 26. The minor furthers student knowledge in whole animal biology, encourages students to integrate information across disciplines, and broadens skills for future employment in animal related careers.

Key Words: interdisciplinary, wild animals, management

396 Developing a curriculum addressing legal issues in animal agriculture. E. Rumley*, *Animal Science, University of Arkansas, Fayetteville.*

Consider laws such as California's Proposition 2, regulations including those governing organic production, and policies such as FDA's guidance for the use of antimicrobials in livestock and poultry. In today's increasingly regulated society, legal issues are affecting agriculture, and specifically animal agriculture, in more varied ways. As a result, students focusing on animal sciences are increasingly confronted by laws and regulations that affect their future lives and careers. To address this need, an issues-oriented course discussing the legal issues involved in the production of poultry, swine and livestock has been developed at the University of Arkansas. The curriculum focuses on the laws, regulations and policy arguments involved in different aspects of animal agriculture. The course begins with an overview of the American legal system and develops into a discussion of animal welfare vs. animal rights, highlighting the legal implications of each viewpoint. From there, course topics range from animal welfare to humane slaughter, from farm animal confinement to the use of antimicrobials, and from food labeling to animal identification. Students completing the course are able to identify areas in need of additional legal study, areas undergoing policy shifts at the local, state, regional and national levels, and areas in which close scrutiny of legal and policy matters can result in effects to poultry, swine and livestock operations.

Key Words: law, legal issues

Graduate Student Competition:
ADSA-ASAS Northeast Graduate Student Competition

397 The evaluation of a flavor enhancer on intake and production of high producing lactating dairy cows. C. Merrill*[1], M. C. Windle[1], W. F. Souza[2], I. R. Ipharraguerre[3], and L. Kung Jr.[1], *[1]University of Delaware, Newark, Delaware, United States, [2]Universidade Federal de Viçosa, Vicosa, Minas Gerais, Brazil, [3]Lucta S.A., Motornes de Valles, Spain.*

The objective of this study was to evaluate the effect of improving forage palatability on DM intake, milk production and composition, and rumen pH of lactating cows. Twenty one multiparous and 7 primiparous Holstein cows averaging 697 kg in body weight (SD ± 81), 54 DIM (SD ± 32), and consuming 23 kg DMI (SD ± 8) were fed a base TMR comprised of 45% corn silage, 10% alfalfa haylage, and 45% concentrate. After a 2-wk adjustment period, cows were blocked by production, parity, and DIM and randomly assigned to one of 2 treatments for 10 wk. Each treatment had 2 cows with previously fitted rumen fistula. In-dwelling probes were placed in the rumens of the fistulated cows, once weekly, and rumen pH was measured every 30 min for 48 h. For one half of the cows, the forage portion of the diet was pretreated with a palatability enhancer (Luctarom SBS-R, Lucta, S.A., Spain) that was premixed in water to achieve a projected dose of 12 mL/cow/d before mixing into a TMR (TRT). The remaining half of the cows were fed a similar TMR but the forage was mixed with water only (CTRL). Production data were analyzed as a completely randomized and covaried with pre-treatment values. Rumen pH was analyzed in a factorial design with repeated measures with treatment, week, and treatment x week as main effects. For all animals, there were no differences ($P > 0.05$) between treatments for DMI and milk production and composition. However, when data from only multiparous animals were analyzed (n = 10 for TRT and 11 for CTRL) there was a tendency for greater DMI (+1.5 kg/d, $P < 0.07$) and milk production (+3.9 kg/d, $P < 0.10$) for cows fed TRT. Compared with CTRL, cows fed TRT had higher ($P < 0.01$) mean rumen pH and spent less time ($P < 0.02$) throughout the day with pH below £ 5.8. There was no difference between treatments in particle size distribution of the TMR throughout the day as evaluated with a PSU Particle Size Separator Box. Improving the palatability of the forage fraction of the TMR fed to multiparous dairy cows may help to stabilize the daily pattern of ruminal pH and increase DMI and milk production.

Key Words: flavor, feed intake, palatability

398 Poor maternal nutrition affects postnatal growth and development of lambs. K. N. Peck*, M. L. Hoffman, M. E. Forella, A. R. Fox, K. E. Govoni, and S. A. Zinn, *Department of Animal Science, University of Connecticut, Storrs.*

Poor maternal nutrition can affect growth and development of offspring, which may lead to obesity and disease later in life. We hypothesized that lambs born to poorly nourished ewes would have reduced growth rate and increased fat, with corresponding changes in the somatotropic axis, leptin, insulin and glucose. Ewes (n = 36; 12/treatment) were assigned 1 of 3 diets; 100% (CON), 60% (RES), or 140% (OVER) of NRC requirements at d 31 of gestation until parturition. One lamb per ewe (n = 35; 11 to 12/treatment) was used, 18 were euthanized at birth and 17 were fed a control diet until 3 mo and then euthanized. Crown rump length (CRL), heart girth (HG), and BW were measured and blood samples were collected at regular intervals until slaughter. A glucose tolerance test (GTT) was performed at 3 mo. Glucose (colorimetric), insulin (ELISA), leptin (RIA), and IGF-I (RIA) were quantified in blood. Body weight and HG were 13 and 6% greater in OVER vs. CON ($P \leq 0.05$), respectively at birth and 3 mo. At birth, CRL was 5% greater in OVER vs. CON ($P = 0.05$). Heart weight was 38% greater in OVER vs. CON at birth and 27% greater at 3 mo ($P = 0.01$). At birth, relative to CON, liver weight was 43% greater in OVER ($P = 0.01$), and loin eye area was 17% smaller in RES ($P = 0.01$). At 3 mo, backfat was reduced by 50% ($P = 0.04$) in RES vs. CON and OVER. At 3 mo, IGF-I concentrations were greater in OVER vs. CON (150 ± 55, 155 ± 47, 335 ± 78 ng/mL; CON, RES, OVER, respectively; $P = 0.05$). During weaning (wk 1 to 4), RES had 33% greater ($P = 0.06$) leptin concentrations than CON. There were 35% greater insulin concentrations in OVER vs. CON ($P = 0.01$) from birth to 3 mo. During the GTT, relative to CON, peak glucose concentrations in OVER were 18% less ($P = 0.1$); fasting insulin concentrations in RES were 67% greater ($P = 0.09$); and insulin:glucose in OVER were 93% greater ($P = 0.01$) and in RES were 50% greater ($P = 0.1$). In conclusion, OVER lambs were larger, exhibited cardiac hypertrophy and were hyperinsulinemic at 3 mo. This could indicate predisposition to metabolic syndrome programmed by maternal overnutrition during gestation.

Key Words: maternal nutrition, sheep, somatotropic axis

399 Poor maternal nutrition affects muscle fiber size in the semitendinosus muscle of lambs. J. S. Raja*, M. L. Hoffman, K. E. Govoni, K. Peck, S. A. Zinn, and S. A. Reed, *University of Connecticut, Storrs.*

Poor maternal nutrition leads to impaired myogenesis and reduced postnatal growth in lambs. Potential mechanisms for these defects include the formation of fewer muscle fibers during development and/or alterations in regulators of muscle growth postnatally. We hypothesized that poor maternal nutrition would increase muscle fiber cross sectional area (CSA) at birth and increase myostatin protein expression in muscles postnatally. Multiparous ewes (25 Dorset, 7 Shropshire and 4 Southdown) were housed individually and fed 100% (CON), 140% (OVER) or 60% (RES) NRC Requirements for ewes pregnant with twin lambs starting on d 31 ± 1.3 of gestation. One-half of the lambs in each group were slaughtered within 24 h of birth. The remaining lambs were fed a control diet and euthanized at 3 mo of age. At necropsy, semitendinosus muscle was collected and either embedded in OCT and frozen for determination of muscle CSA or snap-frozen for protein analysis. Data were analyzed via ANOVA. At birth, the muscle fiber CSA of lambs from OVER and RES ewes was 47% and 57% greater, respectively than lambs from CON ewes (CON: 553.3 ± 62.8 μm^2, OVER: 817.1 ± 26.0 μm^2, RES: 871.5 ± 114.4 μm^2; $P < 0.01$). At 3 mo the muscle fiber CSA of lambs from OVER and RES ewes was 15 and 17% smaller than lambs from CON ewes (CON: 2139.5 ± 40.3 μm^2, OVER: 1775.6 ± 65.1 μm^2, RES: 1809.4 ± 90.1 μm^2; $P < 0.01$). Additionally, at 3 mo there was no difference in the protein expression of the myostatin precursor (CON: 1.0 ± 0.08, OVER: 1.04 ± 0.80, RES: 1.40 ± 0.64; fold change from CON; $P = 0.77$), latency associated peptide (CON: 1.0 ± 0.71, OVER: 1.18 ± 0.69, RES: 1.43 ± 0.23; fold change from CON; $P = 0.87$) or active protein (CON: 1.0 ± 0.09, OVER: 1.35 ± 0.84, RES: 2.40 ± 1.38; fold change from CON; $P = 0.61$) in lambs from any group. In conclusion, poor nutrition during gestation leads to altered prenatal and postnatal muscle development. Future studies will focus on alterations in signaling pathways influencing postnatal muscle growth.

Key Words: muscle, maternal nutrition

400 Poor maternal nutrition during gestation alters satellite cell number and mRNA expression of genes involved in myogenesis and the somatotropic axis in the muscle of lambs. M. L. Hoffman*, R. C. Forbes, S. A. Reed, K. N. Peck, S. A. Zinn, and K. E. Govoni, *University of Connecticut, Storrs.*

Muscle growth and development is negatively affected by poor maternal diet during gestation. We hypothesized that poor maternal nutrition during gestation would alter satellite cell number and gene expression in the muscle of lambs. Thirty-six multiparous ewes were individually housed and fed 100% (C), 60% (R), or 140% (O) of requirements for ewes pregnant with twin lambs (NRC, 1985) starting at d 31 ± 1.3 of gestation. Lambs were euthanized 24 h after birth (n = 18) or at 3 mo of age (n = 17; maintained on a control diet). Semitendinosis muscle was collected immediately following euthanasia for immunohistochemistry and gene expression analysis. Satellite cells were identified as paired box protein (Pax)-7 positive cells adjacent to muscle fibers. Data were analyzed using ANOVA. Body weights were 13% greater in O than C at birth and 3 mo ($P \leq 0.05$) of age. Maternal diet did not affect mRNA expression of myogenic factors [myogenin, Pax7, or myoblast determination protein (MyoD)] at birth or 3 mo ($P \geq 0.48$). However, mRNA expression of myostatin was 2.9 ± 0.5-fold greater in O ($P = 0.07$) at birth but not at 3 mo ($P = 0.36$). Gene expression of follistatin was greater in R ($P = 0.06$) and O lambs at birth ($P = 0.04$) but not at 3 mo ($P = 0.37$). Similar to previous findings, IGF-I expression was 2.3 ± 0.6-fold greater in R ($P = 0.07$) at birth. In O lambs, IGFBP-3 was reduced 2.8 ± 0.1-fold relative to C at birth ($P = 0.01$). At birth, there were a greater number of Pax7(+) cells in R ($P = 0.10$) and O ($P = 0.05$) lambs (9.0 ± 0.6, 14.0 ± 2.2, 16.0 ± 1.1% of total fiber associated nuclei; C, R, and O, respectively), but not at 3 mo ($P > 0.05$). In conclusion, maternal diet may affect muscle development by altering expression of mediators of muscle growth and the somatotropic axis. The changes in satellite cell number may be a mechanism by which poor maternal nutrition affects muscle growth. Future studies will evaluate mRNA expression in these cells to determine how their role in postnatal muscle development may be altered by poor maternal nutrition.

Key Words: maternal nutrition, muscle, satellite cell

401 Pre- and postweaning flavor exposure affects piglet performance after weaning. D. Solà-Oriol[1], L. Mesas[2], A. Ortiz*[2], J. J. Mallo[2], and J. F. Pérez[1], *[1]SNiBA. Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra, Spain, [2]Norel, Madrid, Spain.*

The aim of the present study was to evaluate the importance of flavor exposure during gestation and lactation on piglet performance after weaning. The effect of Fluidarom 1003 inclusion (375 g/Tm; 15% of anise as active ingredient) on piglet performance after weaning was studied following a 2 × 2 factorial arrangement were the main factors were the inclusion of Fluidarom 1003 to the sows diet or the postweaning diets. A total of 80 crossbred sows were offered Fluidarom 1003 flavored (F, n = 40) or control (C, n = 40) feed during last 42 d of gestation and the entire lactation (28 d). Creep-feed (F or C) was offered to each litter according to the sow treatment. After weaning, a total of 480 piglets were offered F or C feed for 35 d, resulting in FF, CF, FC and CC piglets (n = 12). Litters were standardized in number and weight by cross fostering within each treatment. Sow and litter performance was controlled until weaning. After weaning, piglets were distributed into blocks according to initial BW, and feed intake and BW of piglets was weekly monitored to calculate ADFI, ADG and feed to gain ratio (FGR). Performance data was analyzed with ANOVA by using the GLM procedure of SAS taking into account pre- and postweaning exposure to Fluidarom 1003. No differences were observed between treatments on sow and litter performance during the gestation and lactation periods ($P > 0.10$). Preweaning, but not postweaning exposure to Fluidarom 1003 increased postweaning BW from 7 to 35d (+5.8%; $P < 0.01$). Higher ADFI (+17.7%; $P = 0.001$) and ADG (+14.9%; $P = 0.002$) was observed for piglets FF and FC than CC at the end of the prestarter (0 to 14d post-weaning) due to the preweaning exposure. Higher ADFI (+6.7%) was observed for piglets FF, FC and CF than CC for starter period (14 to 35d; FF = 742, FC = 723, CF = 722 and CC = 650; $P < 0.01$). Overall, higher ADFI (+8.8%) was observed for piglets FF, FC and CF than CC for the entire period (0 to 35d; FF = 564, FC = 548, CF = 537 and CC = 485; $P < 0.01$) due to the pre- and postweaning exposure ($P < 0.01$). It is concluded that the pre- and postweaning exposure to Fluidarom 1003 may improve pig performance after weaning.

Key Words: flavor, learning, piglet

402 Effects of a dietary blend of antioxidants on carcass characteristics and meat quality in pigs fed a high oxidants diet. T. Lu*[1], A. F. Harper[1], J. Zhao[2], J. M. Scheffler[1], R. A. Dalloul[1], and M. J. Estienne[1], *[1]Virginia Tech, Blacksburg, [2]Novus International Inc., St. Charles, MO*

The study aimed to determine the effects of dietary supplementation with a blend of antioxidants (AOX) on carcass characteristics and meat quality in finishing pigs fed a high oxidants diet. Eighty crossbred barrows (10.9 ± 1.4 kg BW, 36 ± 2 d) were randomly allotted to 4 treatments with 5 pens of 4 pigs per treatment. Pigs in 3 treatment groups were fed a high oxidants diet containing oxidized soy oil (5%) and a source of PUFA (3.5%). Treatments included: 1) high oxidants diet with vitamin E at 11 IU/kg (VE); 2) high oxidants diet with Agrado Plus (Novus International, St. Charles, MO; a proprietary blend of ethoxyquin and propyl gallate) at 135 mg/kg (AOX); 3) high oxidants diet with AOX and VE (AOX+VE); and 4) standard control with no oxidized soy oil or PUFA (SC). At the end of the 118 d trial, 2 pigs from each pen were harvested for determination of loin quality, belly quality and carcass characteristics. Data were analyzed using GLM of SAS with Tukey's multiple comparison. Pigs fed the VE diet showed symptoms of "yellow fat disease" in most adipose tissues. Compared with SC, VE pigs ($P < 0.05$) had decreased dressing percentage (65.7% vs. 74.2%), lighter carcass weights (61.5 vs. 109.3 kg), less 10th rib back fat (1.41 vs. 2.78 cm), less lean body mass (27.5 vs. 44.6 kg), and smaller loin eye area (25.2 vs. 44.3 cm^2). In addition, higher water content (77.4% vs. 74.7%), and less extractable fat content (0.95% vs. 2.43%) were found in longissimus muscle of VE pigs ($P < 0.05$). However, drip loss with the VE treatment was less than SC (0.46% vs. 3.98%, $P = 0.02$), which was associated with a tendency for a higher muscle pH_{24h} (5.74 vs. 5.54, $P = 0.07$). Diet supplementation with the blend of antioxidants (AOX and VE+AOX) attenuated these effects such that the characteristics were similar to SC ($P > 0.05$). However, the SC pigs had redder loin muscle color (higher a* value) and firmer bellies than the AOX and AOX+VE pigs. Feeding the oxidative stress diet caused a series of detrimental changes in carcass characteristics and meat quality, while AOX addition attenuated many of these independent of VE addition.

Key Words: pig, antioxidant, meat quality

403 Efficacy of a purified enzyme to detoxify fumonisins in swine diets. U. Hofstetter*[1], K. Naehrer[1], and C. A. Mallmann[2], *[1]Biomin Holding GmbH, Herzogenburg, Austria, [2]Universidade Federal de Santa Maria, Santa Maria, Brazil.*

A 42 d feeding trial was conducted at the swine experimental unit of SAMITEC, University Santa Maria, Brazil, to evaluate the efficacy of a fumonisin degrading enzyme (FUMzyme) to diminish the toxic effects of fumonisin B1 (FB1) on the performance of growing piglets. Fumonisin was added (50 µg/kg) to the basal ration and the enzyme was added at 0.0% FUMzyme (control), 0.25% FUMzyme and 0.5% FUMzyme for the 3 treatments. A total of 30 piglets with an initial weight of 11.6 kg were used. There were 10 piglets per treatment with 1 piglet per replication (1 pig per 0.70 $m^{2,}$ pen). Each pen was equipped with semiautomatic feeders and drinkers with feed and water given ad libitum. Parameters measured included ADFI, BW, ADG and G:F, relative weight of organs (liver and lungs) and hematological analysis (total plasmatic protein and sphinganine/sphingosine ratios (Sa/So)).These parameters were analyzed by analyses of variance (ANOVA). Differences between means were compared by Tukey's test ($P \leq 0.05$). ADFI of piglets consuming the control ration (0.0% FUMzyme) was reduced throughout the experimental feeding period. Piglets consuming either ration containing the enzyme had a significant higher ADFI (1.26 kg and 1.21 kg) than piglets fed the control ration (0.83 kg). Piglets fed rations containing either 0.25% or 0.50% of the FB1 degrading enzyme presented superior BW (44.68 kg and 42.82 kg) and ADG (0.79 kg and 0.74 kg) compared with piglets fed the control ration (BW, 28.88 kg and ADG, 0.41 kg). There were no statistical significant differences in lung weight and total plasmatic proteins between treatments. Piglets fed the control ration had statistical significant higher G:F (0.51), relative liver weight (2.93 kg) and Sa/So ratio (8.34) compared with piglets in the other 2 treatments (G:F, 0.63 and 0.61, relative liver weight 1.89 kg and 1.77kg, Sa/So 6.72 and 6.25). Performance of piglets fed a FB1 contaminated ration was improved by the inclusion of either level (0.25% and 0.5%) of FUMzyme. It could be concluded that the negative effects of fumonisin B1 on piglet performance can be alleviated by inclusion of a fumonisin degrading enzyme.

Key Words: fumonisin, piglet

404 Effect of dietary propolis supplementation on growth performance, blood profiles, relative organ weight, and meat quality in broilers. H. L. Li*, H. C. Jang, and I. H. Kim, *Department of Animal Resource & Science, Dankook University, Cheonan, Choognam, South Korea.*

The objective of the current study was to evaluate the effects of dietary propolis on growth performance, blood profiles, relative organ weight and meat quality in broilers. A total of 720, 1-d-old male ROSS 308 broiler chicks (BW = 40.1 ± 0.1 g) were randomly allocated to 1 of 5 dietary treatments (9 pens with 16 broilers per pen). Dietary treatments were (1) NC, negative control diet; (2) PC, NC + 0.01% avilamycin; (3) PRO1, NC + 0.05% propolis; (4) PRO2, NC + 0.10% propolis; (5) PRO3, NC + 0.20% propolis. The broilers were weighed and feed intake was recorded by pen on d 0, 14, and 28 to calculate growth performance. At the end of the experiment, 27 broilers were randomly selected from each treatment (3 birds per pen) and blood samples were collected for measuring white blood cells, red blood cells, lymphocyte and immunoglobulin G concentration. After blood collection, the same broilers were weighed individually and slaughtered for the measurement of relative organ weight and meat quality. Birds fed PRO2 diet had a higher ($P < 0.05$) body weight gain (1 to 2 wk, 392 vs. 372 g; 1 to 4 wk, 1481 vs. 1430 g) and a lower ($P < 0.05$) feed conversion ratio (1 to 2 wk, 1.439 vs. 1.505; 1 to 4 wk, 1.510 vs. 1.582) than those fed NC diet during 1 to 2 wk and 1 to 4 wk. A higher ($P < 0.05$) blood IgG (1.80 vs. 1.45 mg/dL) concentration was observed in PRO2 treatment compared with that in NC treatment. The relative weight of liver (3.69 vs. 3.13%) and abdominal fat (1.72 vs. 1.45%) in PRO2 was higher ($P < 0.05$) than in NC. No differences ($P > 0.05$) were found on meat quality among treatments. In conclusion, results indicated that the use of propolis at the 0.10% level increased growth performance, blood IgG concentration and relative organ weight in broilers.

Key Words: broiler, growth performance, relative organ weight

ADSA Multidisciplinary and International Leadership Keynote (MILK) Symposium: Colostrum Quality, Analytical Methods and Processing Challenges

405 The role of colostrum components on neonatal development and growth with emphasis on the calf. M. E. Van Amburgh*[1], H. M. Hammon[2], and F. Soberon[3], *[1]Cornell University, Ithaca, NY, [2]Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany, [3]Shur-Gain USA, Nutreco Canada Inc., Guelph, ON, Canada.*

Colostrum, in comparison with milk, is known to be rich in immunoglobulins (60× cow), as well as hormones and growth factors such as relaxin (>19× pig), prolactin (18× cow), insulin (65× cow), IGF-1 (155× cow), IGF-2 (7× cow), and leptin (90× humans) (Odle et al., 1996; Blum and Hammon, 2000; Wolinski et al., 2005; Bartol et al., 2008) among many other factors that have biological activity in the neonate. This biological activity has been characterized in cattle, pigs and other mammalian species. In neonatal pigs, there are relaxin receptors present at birth in uterine and cervical tissues, and colostrum-derived relaxin induces estrogen receptor differentiation and proliferation of those tissues. Further, the development of the neonatal calf is influenced by colostrum intake when compared with non-colostrum diets. Maturation and function of the neonatal gastrointestinal tract in calves occurs through some of the hormones contained in colostrum. Nutritive and non-nutritive factors, such as the hormones and growth factors, affect intestinal growth and function, and enhance the absorptive capacity of the gastrointestinal tract. Glucose absorption increases and glycogen concentrations in liver rise significantly when colostrum instead of a milk-based diets are fed in the first meal. Growth, feed intake, feed efficiency and long-term productivity of calves receiving increased levels of colostrum, independent of the immunoglobulin status of the calf have been observed. In a recent study, calves were fed 4 L or 2 L of colostrum at birth and the 4 L group received an additional 2 L within 12 h. Calves fed greater amounts of colostrum consumed 8.5% more milk replacer, had an 18% increase in pre-weaning ADG, a 12% increase in postweaning feed intake, and a 25% increase in post-weaning ADG through 80 d of life indicating that colostrum potentially affects appetite regulation which enhances growth and possibly feed efficiency. Overall, colostrum is an important vehicle of communication between mother and offspring, through lactocrine signals that enhance developmental functions beyond the immune system.

Key Words: colostrum, calf, lactocrine

406 Colostrum: Bioactive components and its role in transmitting maternal signals that regulate neonatal health and development. T. B. McFadden*, *University of Missouri, Columbia.*

All mammals are completely reliant upon mammary secretions (colostrum and milk) for successful reproduction. In other words, mammalian neonates depend on those secretions to provide nutrients and bioactive factors necessary for survival and subsequent growth and development. Although humans have learned how to intervene in this fundamental process, the now universal acceptance that breast milk provides the ideal diet for human infants highlights the complexity and importance of milk components and illustrates that evolution is wiser than man in selecting the optimal match of components to requirements of the young. Milk and colostrum also provide a postpartal route for chemical communication from mother to young. Thus, it is logical that milk components include many bioactive factors that influence both immediate and long-term function and health. Colostrum is a unique mammary secretion and colostrum formation involves massive translocation of bioactive molecules from the mother's blood into mammary secretions and thereby delivery to the neonate. The most noteworthy of these molecules are the maternal immunoglobulins, primarily IgG1, which are transferred to the calf, providing passive transfer of immunity and thereby reducing risk of death or disease. In general, however, colostrum provides an avenue for chemical communication between the dam and the neonate that exists for as long as the young continue to nurse. For example, information as to the dam's nutritional, hormonal, immunological, microbial and even seasonal status can be conveyed via mammary secretions. In addition, recent recognition of the role of the gut microbiome as a key determinant of immunological and digestive system development opens new avenues by which colostral secretions can have long-term effects on future health and vitality of offspring. This paper will review the mechanisms involved in hormonal regulation and mammary secretion of these factors and their subsequent effects on neonatal growth and development of the calf, with emphasis on factors concentrated in colostrum.

Key Words: colostrum, bioactive molecule, mammary secretion

407 Colostrum and human health. D. Haines*[1,2], W. Duff[3], and P. Chilibeck[3], *[1]Department of Veterinary Microbiology, The Western College of Veterinary Medicine, The University of Saskatchewan, Saskatchewan, Canada, [2]The Saskatoon Colostrum Co. Ltd., Saskatoon, Canada, [3]College of Kinesiology, University of Saskatchewan, Saskatchewan, Canada.*

The selection of dairy animals to produce large quantities of milk has resulted in the production of excess volumes of colostrum. There are several companies in North America and elsewhere that collect, heat treat and spray dry manufacture colostrum for supplementation of calves and increasingly for use as natural health products in pets and human beings. In addition to immunoglobulin there is a diverse array of relatively high levels (compared with milk) of factors including non-specific antimicrobial compounds and factors that affect growth, differentiation and metabolism in the newborn and which presumably may be of benefit to adults. Bovine colostrum ingestion by people has been shown to have a variety of benefits including improved immune function, decreased incidence and severity of infectious disease, improved gastrointestinal health and improved athletic conditioning. The latter effect has been speculated to be either through improved health, through anti-inflammatory effects that benefit muscle strength building and/or from the anabolic effects of the high levels of insulin-like growth factor (IGF1) present in colostrum. Most studies have looked at the "athletic conditioning" effects of colostrum in young people. Older individuals have decreased muscle strength compared with younger people and it is postulated that many of these and other adverse effects of aging are linked to the age-associated decline in levels of IGF-1 which logically may improve with supplementation. Older people (n = 40, ≥50 years) were given either 60 g/day whey protein powder or bovine colostrum for 8 weeks and subjected to 3-times weekly resistance training and tested for changes in strength, muscle size, body composition and cognitive function. Both whey and colostrum supplemented groups significantly increased upper body strength, muscle thickness, lean tissue mass, decreased body fat percentage and improved cognitive function. In addition the colostrum-

supplemented group increased leg press strength (baseline 122 ± 40 kg and post 145 ± 53 kg) compared with the whey-supplemented controls (baseline 143 ± 51 kg and post 151 ± 58 kg). These data show there were substantial benefits of 8 weeks of weight training along with either whey protein powder or bovine colostrum in older adult volunteers and that colostrum supplementation had additional benefits to leg muscle strength not demonstrated with whey protein powder.

Key Words: colostrum, human health, whey protein

408 Improving the value of colostrum through application of novel processing technology. H. Patel*[1] and T. Carroll[2], *[1]Dairy Science Department, South Dakota State University, Brookings, [2]Fonterra Research Center, Palmerston North, New Zealand.*

Milk and milk products contains numerous essential nutrients, that may provide health benefits to consumer. Colostrum is the early milk produced by cows during the first several days after the calf's birth. Bovine colostrum contains many beneficial substances including bioactive components such as immunoglobulins (Ig), lactoferrin (LF) and other health promoting components such as oligosaccharides, growth factors (GF) such as IGF1, TGFβ1 and TGFβ2, antimicrobial compounds and immune-regulating constituents. However, many studies in the literature suggested that Ig, LF and GF are very sensitive to heat treatment. We compared the effects of different heat treatments with high pressure processing (HPP) on colostrum and pure Ig in the range of 150 to 800 MPa and in the pH range of 3.0 to 7.0. The results of our study demonstrated that Ig, LF and GF are very sensitive to heat, but they are pressure-resistant. More than 60 to 70% of Ig and GF were retained at all pH in the range of 5.0–7.0, whereas more than 90% of IG and growth factors were retained in the samples pressure-treated in the pH range of 3.0–4.0. The study clearly demonstrated that HPP is an ideal non-thermal technology for processing of formulations containing heat sensitive bioactive components present in milk and colostrum. HPP can be applied to improve the value of colostrum by designing ambient stable long shelf-life colostrum products and beverages containing high level of active Ig, LF and GF.

Key Words: colostrum, high pressure processing (HPP), immunoglobulin and growth factors

409 Bovine colostrum as a source of milk growth factors: technological aspects. Y. Pouliot* and S. F. Gauthier, *STELA Dairy research Center, Institute of Nutrition and Functional Foods (INAF), Université Laval, Québec, QC, Canada.*

Bovine colostrum contains several highly attractive molecules among which milk growth factors have been already been exploited to develop health ingredients. The most abundant growth factors in bovine milk and colostrum are insulin-like growth factor-I (IGF-I), transforming growth factor-β 2 (TGF-β2), epidermal growth factor (EGF), and basic fibroblast growth factor, respectively. However, even in colostrum, their concentration is very low (≤1,000 ng/mL). Designing cost-effective methods to extract growth factors from colostrum and substantiating the extracts with relevant scientific data on their bioactivity represent the 2 main challenges in the development of growth factor-rich protein ingredients. Our work has encompassed the many technological aspects involved in the development of protein-based health ingredients from bovine colostrum, including milking, processing/ fractionation and characterization of the extracts. Identifying the optimal period for collecting colostrum after parturition represents a critical step. It was found that TGF-β2, TGF-β1 and IGF-1 concentrations in liquid colostrum decreased rapidly (<12 h). However when reported on protein content, the values remained interesting within the first 48 h after parturition. Removing caseins from colostrum was found to have a major effect on the growth factor content of the extracts. Approaches using polysaccharides such as λ-carrageenan (λ-CG) or pectin were developed and enabled a partition of major growth factors between casein fractions and serocolostrum. Those studies highlighted potential interactions between some growth factors and casein micelles. Protein-based growth factors extracts were characterized for their protein composition, in vitro digestibility, and also, for several bioactive properties. Altogether, the experimental data evidence that protein-based milk growth factor extracts can modulate inflammatory processes in different models such as neutrophils from healthy humans, intestinal mucosae and skin lesions. However, understanding the mechanisms and ascribing specific activities to individual growth factors or compounds has yet to be achieved.

Key Words: growth factor, colostrum

410 Group size alters postures, and maintenance, oral, locomotor, and social behaviors of veal calves. E. M. Abdelfattah*[2], M. M. Schutz[3], D. C. Lay Jr.[1], J. N. Marchant-Forde[1], and S. D. Eicher[1], *[1]USDA-ARS, W. Lafayette, IN, [2]Banha University, Moshtohor, Qalyubia, Egypt, [3]Purdue University, W. Lafayette, IN.*

The objective of this study was to evaluate the effect of group size on behavior of veal calves. Holstein-Friesian bull calves (n = 168; 44 ± 3 d of age), were randomly assigned to 1 of 3 treatments of group housing with 2, 4, or 8 calves per pen (1.82 m^2 per calf for all groups). Behavior was observed from video data recorded from 0700 to 1700 h using instantaneous scan sampling every 5 min within 30 min observation sessions, one day each month for 5 mo. Continuous focal sampling around feeding time (30 min before feeding, 30 min during feeding, and 30 min after feeding) on d 0, 1, 5, 14, 42, and 70 after grouping focused on all instances of oral and aggressive behaviors. Data were analyzed as a RCB with repeated measures using PROC MIXED (SAS). Calves in groups of 2 spent more time at the feeders ($P = 0.001$) than calves in groups of 4 or 8. Calves housed in groups of 4 or 8 showed more conspecific contact ($P \leq 0.05$), standing ($P < 0.001$), and less self-licking ($P < 0.001$) than calves housed in groups of 2. An interaction ($P = 0.001$) between treatment and month was observed for manipulation of objects. Calves in groups of 2 manipulated objects more than calves in groups of 4 or 8 in mo 3. While in mo 4, calves in groups of 2 and 4 manipulated objects more than calves in groups of 8. An interaction ($P < 0.001$) between treatment and month was reported for lying behavior; in mo 2, calves from groups of 2 lay more than calves from groups of 4 or 8, while in mo 3 and 5 calves in groups of 2 and 4 lay more than calves in groups of 8. An interaction ($P = 0.003$) between treatment and month was observed for walking; in mo 4 and 5, calves from groups of 4 and 8 walked more than calves from groups of 2. During feeding times group size had no effect ($P > 0.05$) on any behavioral patterns except for duration of conspecific contact. Groups of 2 had had more ($P = 0.01$) conspecific contact than groups of 4 or 8. Additionally, occurrence of play and aggression were similar ($P > 0.05$) around feeding for all treatments. In conclusion, larger groups changed how oral needs were manifested and increased use of available space, improving social welfare.

Key Words: group size, behavior, veal calf

411 Efficacy of radiant barrier covers in reducing heat in polyethylene calf hutches. W. R. Binion* and T. H. Friend, *Dept. of Animal Science, Texas A&M University, College Station.*

The objective of this study was to determine the ability of a radiant barrier hutch cover to moderate the effect of ambient temperature and radiant energy in polyethylene hutches. The cover consisted of a single layer of 2-sided reflective aluminized polyester film with polyester scrim reinforcement (reflectivity = 95%, R = 2.7). At each of 2 dairies, 6 hutches were either un-covered (control) or had reflective covers across the top and sides of the hutch, leaving the front, back, and pen exposed. Each hutch had a 1.2 × 1.8-m attached outdoor wire pen. Calves were allowed ad libitum access to feed and water. Loggers mounted 20 cm above the flooring, on the interior side of each hutch, recorded interior temperature at 30-min intervals over 24 d during late August to early September. The mean daily interior peak temperature over the 24-d observation period (40.5 ± 10.0°C) was 4.2 ± 0.2°C less ($P < 0.05$) in the hutches with the reflective cover than in the un-covered hutches, and did not differ ($P = 0.72$) between dairies. During the 10 d of the observation period with the highest peak temperatures (43 ± 7.5°C), reflective covers resulted in an interior hutch temperature 4.7 ± 0.1°C lower ($P < 0.001$) when compared with the control. Interior roof temperatures were recorded on 4 different days using an infrared thermometer during the early afternoon. Interior roof temperature (43.3 ± 16.7°C) was 9.3 ± 1.7°C lower ($P < 0.001$) for the reflective hutches compared with the control. Highest recorded interior hutch temperatures during the overall sampling period were 50.5°C for control, and 43.5°C for the reflective hutches. Reflective barriers moderated hutch microclimate, suggesting reflective covers can be useful for reducing solar heating of hutches.

Key Words: dairy, radiation, hutch

412 Adoption of practices to improve cow comfort on dairy farms. C. Nash*[1], D. Kelton[1], D. Pellerin[2], T. DeVries[3], A. M. de Passillé[4], J. Rushen[4], G. Charlton[4], E. Vasseur[5], and D. Haley[1], *[1]University University of Guelph, Guelph, ON, Canada, [2]Université Laval, Québec, QC, Canada, [3]University of Guelph – Kemptville Campus, Kemptville, ON, Canada, [4]Agriculture and Agri-Food Canada, Agassiz, BC, Canada, [5]University of Guelph – Alfred Campus, Alfred, ON, Canada.*

The Canadian code of practice for the care and handling of dairy cattle include requirements and recommendations that aim to improve cow comfort. However the degree of implementation of these practices at the farm level is unknown. The objective of this project was to encourage the implementation of cow comfort practices on farm and identify barriers that producers face when considering these changes. In this intervention study, we visited 40 farms in Ontario and measured the level of cow comfort on each farm through various animal (body condition, injuries, lying time), management (cleaning and feeding routine) and resource (stall design and pen design) based measures. We then provided each producer with a diagnostic tool to evaluate risk factors for cow comfort on their farm using the code of practice recommendations. We conducted semi-structured interviews with these producers 12 to 18 mo later to determine if they had adopted new practices to improve cow comfort and meet code of practice requirements. Data on producer demographics, types of changes that were made and prevention to further change was also collected. The mean age of producers was 45 years (range: 27–61) with an average herd size of 115 (47–530). The sample included 23 freestall, 15 tiestall and 2 automated herds. Of the producers interviewed, 60% had received post-secondary education. Following our intervention, 73% of producers had made changes. The most commonly adopted cow comfort practices were improved bedding managements (22.7%), improved hoof-trimming management (18.2%) and improved stall base (18.2%). The most commonly identified barriers for the prevention of further change were lack of funds (43.3%), satisfaction "with the comfort of their cows" (30%) and lack of time (23.3%). Only 25% of the non-adopters had identified a successor for their farm, while 64% of the producers that had made changes had identified a successor. These results demonstrate that our intervention study was successful at encouraging change on dairy farms; however, certain barriers still exist to the implementation of cow comfort practices, including farm decisions about successorship.

Key Words: adoption, cow comfort, diagnostic tool

413 Effect of stocking density on lying behavior of dairy cows. K. M. Lobeck*, M. I. Endres, A. R. Dresch, and R. C. Chebel, *University of Minnesota, St. Paul.*

The objective of this study was to investigate the effect of 2 feedbunk stocking densities on prepartum lying behavior of dairy cows. Jersey cows at 4 wk before expected calving date were assigned randomly to 1 of 2 treatments. Treatments were 80% (38 cows/48 headlocks; 80D) or 100% (48 cows/48 headlocks; 100D) feedbunk stocking density. Headlocks were 0.61 m. Four pens with sand bedded freestalls were utilized: 2 multiparous and 2 primiparous pens over 3 repetitions. Cows were balanced for body condition score and no cows with locomotion score > 2 were included in the study. One hundred-2 80D and 123 100D cows were selected as lying behavior focal cows. Lying behavior was measured with HOBO Pendant G data loggers. The mean number of focal cows in each pen was 19 with a range of 14–23 cows. Loggers were attached to the cow's rear leg 1 d after entrance to the pen and were left on for 12 d, removed for 7 d and reattached for 12 d or until the cow calved. Data were analyzed by Proc Mixed in SAS. Overall there were no differences between treatments for lying time (12.8 ± 0.04 h/d). Primiparous cows in the 80D and 100D treatments spent 12.5 and 12.4 h/d lying down, respectively, whereas multiparous cows in the 80D and 100D treatments spent 12.4 and 13.0 h/d lying down, respectively. There was a treatment by lactation interaction ($P = 0.02$). Multiparous cows in 100D treatment pens spent 0.6 h/d more lying down than 100D primiparous cows ($P < 0.01$). There were differences in the number of lying bouts between treatments and lactation number. Multiparous cows in the 100D treatment had 0.91 more bouts/d than 80D cows (14.7 vs. 13.8; $P < 0.01$). Primiparous cows had more lying bouts than multiparous cows (16.1 vs. 12.3; $P < 0.01$). Lying bout duration did not differ between treatments (1.32 ± 0.04 h). Multiparous cows had longer ($P < 0.01$) lying bout duration (1.54 h) than primiparous cows (1.13 h). In conclusion, 100% stocking density only affected the number of lying bouts with no differences between treatments for lying time and lying bout duration. More differences in lying behavior were observed between multiparous and primiparous cows.

Key Words: lying behavior, stocking density, feedbunk space

414 The effect of stall surface compressibility on dairy cow behavior. A. C. Main*[1], C. B. Tucker[2], N. B. Cook[3], T. F. Duffield[1], and D. B. Haley[1], *[1]University of Guelph, Guelph, ON, Canada, [2]University of California, Davis, [3]University of Wisconsin, Madison.*

Optimizing the time dairy cows spend lying is critical for production, rest, and welfare, and one of the most important factors influencing lying behavior is the softness of the stall surface. Our objective was to determine whether aspects of the cow's activity and lying behavior change with the use of 2 stall bases, differing in their compressibility. A foam and gel mattress were compared (gel = more compressible, 5.7 psi, vs. foam = 11.6 psi). Nonlactating Holstein dairy cows (n = 18) were kept individually in a freestall barn where they had been housed previously. Cows experienced 2 stall surfaces, 3 d/surface, in a balanced order. Prior to onset of the study cows had free access to both surfaces for 24 h. Behavior was video recorded and accelerometers were used to record standing and lying. The first 2 d on each surface were acclimatization days so this video data was not analyzed. A logistic regression model with a logit-transformation was run to analyze the odds ratios and the proportion of time cows spent on each stall surface lying, standing and perching (standing with front legs in the stall, back legs in the alley) on the final d on each surface (d 3 and 6). There was a lower odds of lying on the foam stall (OR = 0.88, $P = 0.11$) and an increased odds of perching on the foam compared with the gel stalls (OR = 1.37, $P = 0.11$), however these were non-significant. Cows were at a higher odds of standing in the foam stall compared with the gel (OR = 1.52, $P = 0.014$). Paired *t*-tests calculated from the accelerometer data indicated that the mean lying bout frequency, duration and lying time were similar on both surfaces (mean ± SE; bout frequency gel = 9.0 ± 0.57 vs. foam = 9.5 ± 0.57, $P = 0.1656$; bout duration gel = 1.7 ± 0.05 vs. foam = 1.7 ± 0.05, $P = 0.70$; lying time foam = 15.0 ± 0.37 vs. gel = 15.2 ± 0.27, $P = 0.8769$ h/24 h). These findings are consistent with previous studies that report higher standing times on firmer stall surfaces, even when no differences in lying time exist. As with this previous work, other indicators such as the preference for and long-term health implications of these surfaces are likely important and warrant further investigation.

Key Words: cow comfort, stall flooring, dairy cow

415 Effect of parity on daily activity patterns prior to parturition in Holstein dairy cows. M. Titler*, M. G. Maquivar, S. Bas, E. Gordon, P. J. Rajala-Schultz, K. McCullough, and G. M. Schuenemann, *Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, OH.*

Recognizing the signs of imminent birth for primiparous (PRIM) and multiparous (MULT) cows and utilizing proactive management practices around the time of calving are critical to prevent the negative effects of dystocia on both the dam and calf. The objective of the present study was to assess the effect of parity (PRIM vs MULT) on activity patterns of cows experiencing unassisted births 4 d before parturition. A total of 130 unassisted Holstein cows (PRIM, n = 31 and MULT, n = 99) housed in freestall barns from 3 dairy herds were used. Periparturient animals were moved into a close-up pen 15 d before the expected calving date and were monitored for imminent signs of birth (appearance of amniotic sac outside the vulva) and then moved into a contiguous maternity pen until birth. Electronic data loggers (IceQube, IceRobotics, Edinburgh, UK) were placed on the hind leg of prepartum PRIM and MULT cows 7 ± 3 d before the expected calving date and remained until 14 ± 3 DIM. Calving ease (CE; scale 1–4) of cows, parity, and calving date and time were recorded. The number of steps, standing time (min), number of lying bouts (LB), and mean duration of LB (min) were recorded. Data were analyzed using MIXED (activity patterns) and GLIMMIX (stillbirth) procedures of SAS. The effect of parity on activity patterns of cows were adjusted for the effect of herd. The proportion of stillbirth was not different ($P > 0.05$) between PRIM and MULT cows. Unassisted PRIM cows spent less ($P < 0.05$) time standing (16–19%), had fewer LB (32–45%), and LB of longer duration (22–37%) 2 d, 1 d and 12 h before birth compared with MULT cows. These findings provided evidence that unassisted PRIM and MULT cows had distinct behavioral activity patterns 1–2 d before calving. Recognizing the signs of parturition as well as the cow activity patterns before calving, especially for PRIM cows, should be considered for precision calving management practices. The use of electronic data loggers to monitor cow activity may allow calving personnel to identify those cows at risk for dystocia 24 h around the clock; thus, improving the overall cow-calf survival and welfare.

Key Words: cow activity, stillbirth, calving management

416 Effect of cow genotype and milk production system on cow behavioral activities. A. I. Roca-Fernández*[1], C. P. Ferris[2], E. R. Vance[2], and A. González-Rodríguez[1], *[1]Agrarian Research Centre of Mabegondo, La Coruña, Galicia, Spain, [2]Agri-Food and Biosciences Institute, Hillsborough, United Kingdom.*

This trial studied the behavioral activities of 2 cow genotypes (n = 80), Holstein-Friesian (HF, n = 40) vs. Jersey x Holstein-Friesian (Jx, n = 40), when managed within 2 milk production systems, a low inputs grazing system (G, n = 40) vs. a high inputs confinement system (C, n = 40). A randomized block design with a 2 × 2 factorial arrangement of treatments was performed using primiparous (n = 20) and multiparous (n = 60) spring calving cows (161 DIM) from AFBI Hillsborough cattle. Four treatments were established (n = 20): HF-G, HF-C, Jx-G and Jx-C. Cows were observed in 3 periods (P1, end July; P2, middle August; P3, end August) at 20 min. intervals between 1600 and 2200 h and 0700–1400 h. Individual cow behavioral activities were recorded: feeding, lying, standing and ruminating. Data were analyzed using REML analysis by Genstat. Cows in the C system showed higher ($P < 0.001$) milk yield (MY) (+6.9 kg cow^{-1} day^{-1}) than those in the G system (20.1 kg cow^{-1} day^{-1}). The HF cows (+3.1 kg cow^{-1} day^{-1}) showed higher ($P < 0.01$) MY than the Jx cows (22.0 kg cow^{-1} day^{-1}). The Jx cows showed higher milk protein (g kg^{-1}) ($P < 0.05$, +1.9) and fat content (g kg^{-1}) ($P < 0.01$, +4.2) than the HF cows (35.7 and 44.4 g kg^{-1}, respectively). Cows on the G system spent more time ($P < 0.001$) grazing (522 min.) than those on the C system spent feeding (173 min). Cows on the C system spent more time ($P < 0.001$) lying (C, 411 vs. G, 212 min), standing (C, 236 vs. G, 85 min) and ruminating (C, 244 vs. G, 141 min) than those on the G system. Time spent lying ($P < 0.001$), feeding ($P < 0.01$) and ruminating ($P < 0.001$) differed between periods, while time spent standing did not differ between periods. The G cows spent more time lying (+53 min) and ruminating (+21 min) in P3 than in P1 (289 and 186 min., respectively). None of the behavioral activities were affected by cow genotype. To conclude, cows normally adapt their daily time budget to the selected milk production system for satisfying cows' feeding, lying, standing and ruminating needs.

Key Words: cow breed, milk production system, behavioral activities

417 Thermal comfort and milk production of two dairy genotypes during the summer in central Chile. C. Herrera[1], R. Larrain[1], F. Gonzalez[1], T. L. Mader[2], and R. A. Arias*[3,4], *[1]Pontificia Universidad Catolica de Chile, Santiago, Chile, [2]University of Nebraska-Lincoln, Lincoln, [3]Universidad Catolica de Temuco, Temuco, Chile, [4]Nucleo de Investigacion en Produccion Alimentaria, Temuco, Chile.*

A total of 29 mature cows (15 Holstein and 14 Montbéliarde × Holstein), 67 ± 6 d in milk, were used to assess animal thermal comfort and milk production during the summer time. The study was conducted at 33°40′12″ S, 70°35′06″ W, in 3 periods: January 18–25, February 4–8, and March 19–24 of 2010. All cows were fed with the same diet (corn silage and alfalfa), kept in open pens with shaded areas, and milked 3 times per day. Thermal comfort was estimated based on respiration rates (RR) and the comprehensive climate index (CCI). The CCI combines 4 meteorological variables. Each cow received a device to record tympanic temperatures (TT) at 10 min intervals. Data were analyzed under a CRD arrangement ($\alpha = 0.05$). The MIXED procedure of SAS was used for repeated measurements analysis with genotype, hour, type of day and their interaction as factors in the model. When CCI ≥20°C, type of day was considered as warm day (Wd). Over the 19 d of study 18 were Wd. There was no difference for mean TT between genotypes ($P = 0.19$). The TT was higher during Wd than during normal days (37.78 vs. 37.68 ± 0.068°C, $P < 0.001$). The interaction genotype by hour was significant, with Holsteins having a lower TT at 5:00 ($P = 0.038$) and a trend for lower TT between 2100 and 1100 h. The interaction between type of day and hour was significant, with higher TT during Wd between 2200 and 0400 h, at 1600, 1900 and 2000 h. There was also a trend for higher TT during Wd at 1700 and 1800 h. No differences were observed for milk production between genotypes. There was an inverse correlation (IC) of CCI between 1200 and 1700 h on milk production at midday milking ($P = 0.008$), and a trend for an IC at the afternoon milking ($P = 0.059$). Cows had higher RR ($P < 0.001$) in the afternoon (68.0 ± 13.4) vs. morning (56.7 ± 9.6). Only 1% of cows had moderately high RR during the morning (1100 h) but 6% had it during the afternoon (1600 h). The use of shade plus during daytime plus the decreasing air temperature at night could explain the lack of differences in milk production. Finally, based on our results we conclude that both genotypes showed a slight degree of heat stress.

Key Words: heat stress, tympanic temperature, animal behavior

418 Effect of age and anatomical differences in dairy cattle craniums on placement and success of captive bolt for humane euthanasia of cattle. S. S. Aly*[1,2], T. W. Lehenbauer[1,2], S. Jenkins[2], M. Cuneo[3], J. D. Champagne[2], and J. P. Reynolds[4], *[1]Department of Population Health and Reproduction, School of Veterinary Medicine, University of California, Davis, Davis, [2]Veterinary Medicine Teaching and Research Center, School of Veterinary Medicine, University of California, Davis, Tulare, [3]William R. Pritchard Veterinary Medical Teaching Hospital, School of Veterinary Medicine, University of California, Davis, [4]The College of Veterinary Medicine, Western University, Pomona, CA.*

The AVMA lists penetrating captive bolt as a method for humane euthanasia of cattle conditional on immediate loss of consciousness and subsequent death. At the recommended placement, the intersection between the base of the horns and medial canthi, personnel report cattle may not become immediately unconscious. The objective of this trial was to identify the optimum placement for euthanizing cattle using a captive bolt. A total of 271 calves and 156 adult cows from 17 dairies and 2 calf ranches in California were randomly assigned to one of 4 placements. Candidate placements targeted the brain stem and were identified using post-mortem cross-sections of cattle crania. In calves, placements included 1 and 2 inches above the AVMA recommended placement (control) and the occipital region. In cows, placements included 2 and 3 inches above the control, and the occipital region. The 2 inch and occipital placements were each 2.15 times more likely to result in immediate loss of consciousness compared with the control placement in calves ($P < 0.01$). Similarly, calves euthanized at the 1 inch placement were 2 times more likely to result in immediate loss of consciousness compared with the control ($P < 0.01$); however, only the 2 inch and occipital placements resulted in immediate loss of consciousness in 100% of the calves. In cows, the 3 inch placement was 4.25 times more likely to result in immediate loss of consciousness compared with the control in cows ($P < 0.01$). Similarly, the 2 inch and occipital placements were each 4 times more likely to result in immediate loss of consciousness compared with the control in cows ($P < 0.01$); however, only the 3 inch placement resulted in immediate loss of consciousness in 100% of the cows. In comparison, the control resulted in immediate loss of consciousness in 46.4% of calves and 23.5% of cows. Results of the field trial showed that higher placements of the captive bolt were more likely to result in immediate loss of consciousness in both calves and cows.

Key Words: cattle euthanasia, captive bolt, placement

419 Comparison of milk and blood test strips and Fossomatic milk analysis for measurement of β-hydroxybutyrate in periparturient dairy cattle. D. J. Wilson*[1] and G. M. Goodell[2], *[1]Utah State University, Logan, [2]The Dairy Authority, Greeley, CO.*

β-Hydroxybutyrate (BHB) is a ketone measured in blood or milk of dairy cattle shortly after calving for detection of ketosis, usually associated with negative energy balance. Blood test strips (tested in Precision XTRA meter), milk test strips (Keto-Test), DHIA milk meter collected samples and hand stripped milk samples, both latter milks tested with Fossomatic milk analyzer, were compared for BHB measurement. All samples were collected on the same day from study cows. Preliminary study found almost no cows detected as ketotic after 14 DIM. Therefore, 304 Holstein cows from 1 – 14 DIM in 3 herds were blood and milk sampled for BHB testing described above (one 80 cow test and 28 other cows had no stripped samples). Most test methods had continuous results but one (milk strip) had categorical results (0, 50, 100, 200, 500, 1000 μmol BHB/L); analysis compared whether or not each pair of BHB tests categorized the same cows as ketotic or non-ketotic (concordant, C) or disagreed on their status (discordant, D). Blood strips detected 20 ketotic (K) (≥1200 μmol BHB /L), 284 non-ketotic (N); milk strips detected 21 K (BHB ≥200 μmol/L category on strip), 279 N; milk meter Foss detected 13 K (≥200 μmol/L), 273 N; stripped milk Foss detected 34 K (≥200 μmol/L), 162 N. Test comparisons: blood/milk strips 6 K/K, 266 N/N (91% C), 13 K/N, 15 N/K (9% D); blood/milk meter Foss 3 K/K, 257 N/N (91% C), 16 K/N, 10 N/K (9% D); blood/stripped milk Foss 4 K/K, 158 N/N (83% C), 4 K/N, 30 N/K (17% D); milk strips/milk meter Foss 4 K/K, 256 N/N (91% C), 17 K/N, 9 N/K (9% D); milk strips/stripped milk Foss 11 K/K, 160 N/N (87% C), 2 K/N, 23 N/K (13% D); milk meter Foss/stripped milk Foss 2 K/K, 152 N/N (81% C), 7 K/N, 30 N/K (19% D). Sensitivity (Se) and specificity (Sp) depend upon "gold standard" chosen; e.g., if blood strips are gold standard, Se of milk strips = 32%, Sp = 95%. Results show that the BHB test methods agreed well for most non-ketotic cows, but tests did not agree well on classification of ketotic cows. Calibration improvements are needed for Fossomatic testing of BHB in milk.

Key Words: BHB, ketosis, milk

420 Does every cow need antibiotic treatment at dry-off? P. J. Rajala-Schultz*[1] and A. H. Torres[2], *[1]Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, [2]Dpto Produccion Animal y Tecnologia, DCV- UCLA, Tarabana, Estado Lara, Venezuela.*

Importance of dry cow management in maintaining good udder health has long been recognized and antibiotic dry cow therapy (DCT) is a cornerstone in most mastitis control programs. The objective of this study was to evaluate whether selective DCT can maintain udder health in US dairies. Routine antibiotic treatment of all quarters of all cows at the end of lactation (blanket DCT) has long been recommended and is practiced in majority of US dairies. In recent years, due to global concerns over agricultural use of antimicrobial drugs and development of antimicrobial resistance, selective DCT, which recommends treatment of infected cows only, has received increasing attention. To evaluate the need for treatment of healthy cows, 414 presumably uninfected, low SCC cows in 4 Ohio dairy herds were randomly assigned to receive or not to receive antibiotic DCT. Intramammary infection (IMI) status over the dry period (DP), clinical mastitis (CM) in early lactation and milk yield and SCC during the next lactation were used as outcomes in statistical analyses. The results suggested that dynamics of IMI over the DP varied considerably between groups, herds and across different causal agents of IMI. There was no significant difference in the risk and time to contract CM during the first 30 d between treated and untreated low-SCC cows ($P = 0.550$), based on survival analysis. Similarly, milk production during the following lactation did not significantly differ between the treated and untreated low SCC cows ($P = 0.6672$), using PROC MIXED in SAS (SAS Inst. Inc., Cary, NC). In general, also analyzing data with PROC MIXED in SAS, SCC was lower (by 16%, $P = 0.0261$) among treated than untreated cows, even though the opposite was also observed in some herds. Overall, herd was a significant confounder in all analyses, suggesting that outcome is highly dependent of the herd and some herds may benefit from blanket DCT while others can maintain good udder health with selective treatment. Therefore, advice to dairy producers regarding dry cow management and DCT should be herd-specific, considering individual situation in each herd.

Key Words: milk production, selective dry cow therapy, udder health

421 Effect of intrauterine dextrose therapy on reproductive performance of lactating dairy cows with clinical endometritis under certified organic management. M. G. Maquivar*[1], A. Barragan[2], J. Velez[2], H. Bothe[2], and G. M. Schuenemann[1], *[1]Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, [2]Aurora Organic Dairy, Platteville, CO.*

The objective was to assess the effect an intrauterine infusion of 50% dextrose in water (DEX) on clinical cure and pregnancy per AI (P/AI) of lactating dairy cows diagnosed with clinical endometritis (CE) compared with untreated control cows (CON). Cows (n = 2856) from 1 organic dairy herd were screened using vaginoscopy for CE at 26 ± 3 DIM and scored using a 0–3 scale (0 = clear mucus, 1 = flakes of purulent exudates, 2 = >50% purulent exudates, and 3 = hemorrhagic discharge mixed with purulent exudates). Cows scored as 2 or 3 were stratified by parity and randomly allocated into 1 of 2 treatment groups: (1) untreated control cows (CON, n = 460) or (2) 200 mL of DEX (n = 417). Fourteen days post-therapy (at 40 ± 3 DIM), CON and DEX cows were re-examined to assess the treatment responses (clinical cure = vaginoscopy score 0 and 1). All cows were subjected to the same reproductive program (estrus detection with tail chalking) and cows displaying signs of standing estrus any time after the voluntary waiting period (45 d) were AI. Body condition scores (BCS) were recorded at calving, 26 ± 3 and 40 ± 3 DIM. Pregnancy diagnosis was performed via ultrasonography at 39 ± 3 d post-AI. The proportion of cows that cured and P/AI were assessed using GLMMIX of SAS. DIM at first service, BCS at treatment, uterine health status, cervix diameter, and rectal temperature at treatment were not different between CON and DEX cows. Cows with CE had greater ($P < 0.05$) cervical diameters at the time of treatment compared with cows without CE. The proportion of cows that cured tended to be greater for DEX (56%) compared with CON cows (49.7%; $P = 0.08$). DIM to first service was shorter for cows without CE (74 d) compared with DEX (85 d) or CON cows (86 d). The proportion of P/AI for first services was greater ($P < 0.05$) for DEX (25.6%) compared with CON cows (19.7%). Cows without CE had greater ($P < 0.05$) P/AI for first services (35.6%) compared with DEX or CON cows. These findings provide evidence that the use of intrauterine DEX improved P/AI for lactating cows diagnosed with CE under organic management.

Key Words: dairy cow, clinical endometritis, organic management

422 Effects of supplementation with tropical plants on the performance and parasite burden of goats. M. A. Zarate[1], J. J. Romero*[1], J. A. Sapora[1], N. J. Forman[1], J. A. Grace[1], M. G. Taylor[1], J. M. Kivipelto[1], A. S. Edison[2], C. H. Courtney[3], and A. T. Adesogan[1], *[1]Department of Animal Sciences, IFAS, University of Florida, Gainesville, [2]Department of Biochemistry and Molecular Biology, University of Florida, Gainesville, [3]Department of Pathobiology, College of Veterinary Medicine, University of Florida, Gainesville.*

Experiment 1 determined the effect of supplementing bahiagrass hay (BH, *Paspalum* notatum Flügge) with perennial peanut (PP, *Arachis glabrata* Benth.) or sericea lespedeza (SL, *Lespedeza cuneata* Dum.-Cuors. G. don) hay or mucuna (MP, *Mucuna pruriens* cv. Mucuna ceniza) or papaya (PY, *Carica papaya* L.) seeds on intake, digestibility and N retention of goats. Thirty-eight Boer × Spanish × Kiko male goats with low fecal egg counts (FEC, <50 eggs/g; 27.4 ± 5.7 kg BW) were dewormed, blocked by BW and fed BH alone or supplemented with PP or SL hay (50% of diet DM), or MP (10% of diet DM) or PY seeds (10 g/day). Hays were fed ad libitum for 14 d of adaptation and 7 d of measurement. The experimental design was a randomized complete block and the statistical model included treatment, block and goat. All supplements increased N intake ($P = 0.07$) but only PP and SL increased DM intake ($P = 0.11$). Feeding MP reduced ($P < 0.01$) ruminal pH and in vivo DM digestibility ($P < 0.01$). MP and PP increased ($P < 0.01$) N digestibility, whereas SL reduced NDF digestibility ($P = 0.07$). Experiment 2 determined the effect of the diets on growth and parasite burden. On d 22, goats were randomly allocated to pens (3 pens per treatment, 2–3 goats per pen) and fed Experiment 1 diets with 150 g/head/day of a corn-soybean supplement for 42 d. Goats were naturally infected with gastrointestinal nematode (GIN) L-3 larvae and *Eimeria* (EIM) oocysts by grazing on bahiagrass pasture for 5 h daily. The experimental design was a randomized complete block and the statistical model included treatment, block, time (repeated) and pen. Feeding PY and PP reduced ($P < 0.05$) FEC of EIM. Feeding PY, SL, and PP reduced FEC of GIN by 72 ($P < 0.01$), 52 ($P < 0.01$), and 32% ($P > 0.1$), reduced ($P < 0.01$) abomasal adult GIN counts by 78, 52, and 42%, and decreased ($P < 0.01$) plasma haptoglobin concentrations by 42, 40, and 45% relative to feeding BH. Dry matter intake was increased ($P < 0.05$) by SL, PY and PP but ADG and gain to feed ratio were unaffected. Supplementation with PP, SL, and PY increased DMI of goats and decreased their parasite burdens.

Key Words: goat, *Haemonchus*, deworm

423 Effects of electromagnetic field on testes and semen characteristics in male New Zealand White rabbits. O. Yildiz-Gulay*[1], M. S. Gulay[1], A. Ata[1], and A. Balic[2], *[1]Mehmet Akif Ersoy University, Faculty of Veterinary Medicine, Burdur, Turkey, [2]Sakarya Toyota Hospital, Sakarya, Turkey.*

Electrical magnetic fields (EMF) could be dangerous because it might affect free radical production, tumor formation and fertility. The number of constructions under or near the power lines increased greatly in recent years. Power lines near houses and work places became EMF for people that live and work in those buildings. Thus, the aim of the current study was to understand the effect of EMF on some testes and semen characteristics in male New Zealand White rabbits. After being trained for semen collection for 2 wk, rabbits were assigned randomly to 2 treatment groups of 8 each; treatment groups (T) were housed 6 m under high voltage power lines (380 kV, 32 μT), whereas controls (C) kept 500 m away from the power lines (0.21 μT) for 7 wk (1 spermatogenesis duration). During the experimental period semen samples were collected weekly from all rabbits. At the end of 7 wk, 10 mL of blood was withdrawn from the ear arteries of each rabbits and 4 rabbits per treatment were euthanized. Remaining rabbits were kept at normal laboratory condition for another 7 wk for recovery. During the experimental period, reproductive organs weights, testicular histology, semen quality, plasma testosterone concentrations and libido were evaluated. Semen quality and libido were also evaluated in the remaining animals during the recovery phase. Proc MİXED procedure of SAS was used to estimate weekly least squares means for sperm characteristics. Proc T-Test procedure was used to analyze remaining variables between groups. Decrease in the plasma testosterone concentrations, paired testes weight and the accessory sex glands weight were noted at the end of experimental period for T compared with C ($P < 0.05$). Libido remained normal for both groups. Although no histopathologic lesions were apparent, significant decrease was observed in seminiferous tubule diameters for T compared with C ($P < 0.05$). Moreover, there was a transient teratozoospermia and asthenozoospermia, which returned to normal by wk 7 of recovery period. Thus, data suggest that exposure to ambient EMF causes transient depression on semen quality in rabbits.

Key Words: electromagnetic field, spermatogenesis, testis

424 Weights of abdominal fat depots in dairy cows. C. Raschka[1], L. Locher[1], A. Kinoshita[1], U. Meyer[2], S. Daenicke[2], K. Huber[3], and J. Rehage*[1], *[1]Clinic for Cattle, University of Veterinary Medicine Hannover, Hannover, Germany, [2]Dep. of Animal Nutrition, Friedrich-Loeffler-Institute, Braunschweig, Germany, [3]Dep. of Physiology, University of Veterinary Medicine Hannover, Hannover, Germany.*

Regular control of body condition by scoring (BCS) or sonography (back fat thickness, BFT) is frequently part of herd health management programs in dairy cows although BCS and BFT consider only the subcutaneous (sc) adipose depot. Because fat from abdominal depots appears to be more easily mobilized than fat from the sc depot aim of this study was to measure and to compare weights of different adipose depots in dairy cows. Fourteen German Holstein cows were slaughtered and body weight, withers height and weight of subcutaneous and other fat depots were assessed. Abdominal fat depots were differentiated in retroperitoneal, perirenal, mesenterial, and omental depots. Also fat in the thoracic cavity was weighted. Means, standard deviation and range of weights as well as Pearson correlations between weights of different fat depots were calculated using the SAS statistical package. Body weight of studied cows ranged between 615 and 902 kg, withers height between 138 and 158 cm, and total weight of assessed body fat between 27 and 145 kg (4–17% of body weight). In average from total body fat the percentage of sc fat was 29% ± 6 (mean ± SD; range 21 - 44%), of abdominal fat 65% ± 5 (range 51 - 74%), and of thoracic fat 6% ± 2 (range 5 - 10%). Related to total abdominal fat the proportion of omental fat was 37% ± 5 (range 25 - 45%), of mesenterial 36% ± 6 (range 25 - 53%), of retroperitoneal 18% ± 5 (range 12 - 30%), and of perirenal fat 9% ± 2 (range 5 - 14%). Weight of abdominal and sc fat depots correlated significantly with total fat weight ($r = 0.99$, $P < 0.001$ and $r = 0.93$, $P < 0.001$, resp.). Correlation between sc and abdominal fat weight was $r = 0.86$ ($P < 0.01$). In dairy cows the weight of abdominal fat depots is about 100% higher than of sc fat depots. Omental and mesenterial fat weights account for about 75% of total weight of abdominal fat. Since the correlation between weights of sc and abdominal fat depots was only moderate it may be necessary to reconsider if BCS and BFT reflect sufficiently body condition in dairy cows.

Key Words: adipose, herd health, lipomobilization

425 Effects of hops (*Humulus lupulus* L.) β-acid extract on inulin fermentation and growth of *Streptococcus bovis*. B. E. Harlow*[1], L. M. Lawrence[1], and M. D. Flythe[2,1], *[1]University of Kentucky, Lexington, [2]United States Department of Agriculture, Agricultural Research Service, Forage-Animal Production Research Unit, Lexington, KY.*

The ingestion of large quantities of rapidly fermentable carbohydrates (e.g., fructan or starch) has been associated with the development of equine laminitis. The fermentation of these compounds in the equine hindgut can lead to an overgrowth of gram-positive bacteria (*Streptococcus bovis*), increased lactic acid production and decreased hindgut pH. Antibiotics that inhibit gram-positive bacteria (e.g., virginiamycin) can mitigate microbial disturbances associated with carbohydrate overload. However, natural products, such as plant-derived antimicrobials may also be effective. Hops contains antimicrobial β-acids that inhibit gram-positive bacteria. This study was designed to determine if hops β-acids could inhibit fructan fermentation by *S. bovis*. Growth experiments were conducted in anaerobic media with 0.1 or 0.6% inulin (model fructan). Hops β-acid extract was added (0.45, 4.5, 9.0 ppm final concentration) to triplicate bottles, which were inoculated (1% vol/vol) with stationary phase *S. bovis* and incubated (39°C) for 24 h. Optical density (OD) was determined by spectrophotometry (600nm) every 30 min for 9 h. Growth rates were determined by linear regression (0–3 h). The pH, OD and lactate concentrations (HPLC; ion exchange chromatography, refractive index) were determined at 0 and 24 h. Data were analyzed using the PROC ANOVA procedure of SAS (9.3) with post hoc Fishers LSD test. The maximum specific growth rate of *S. bovis* on 0.1 and 0.6% inulin was inhibited by β-acid extract ($P < 0.0001$). In 0.6% samples, 4.5 ppm β-acid decreased the growth rate from 0.27 to 0.06/h ($P < 0.05$). Compared with inulin-only controls, final OD was lower with treatment indicating a decrease in *S. bovis* growth ($P < 0.0001$). Also, β-acids mitigated pH disturbances ($P < 0.0001$). In 0.6% inulin samples, the 4.5 ppm treatment had a higher pH than the control (5.92 vs. 5.70; $P < 0.05$). Likewise, less lactate was produced with increasing β-acid concentration in 0.6 and 0.1% samples ($P < 0.0001$). These results indicate that, hops β-acid extract could inhibit the growth of *S. bovis* and mitigate disturbances associated with the pathogenesis of laminitis.

Key Words: horse, microflora, streptococci

426 Clinical ketosis and standing behavior in transition cows. A. J. Itle*, J. M. Huzzey, D. M. Weary, and M. A. G. von Keyserlingk, *Animal Welfare Program, Faculty of Land and Food Systems, University of British Columbia, 2357 Main Mall, Vancouver, BC, Canada.*

Changes in behavior can be useful in the early identification of sick animals; changes in standing behavior are now far easier to monitor with the availability of electronic data loggers. Ketosis is an important disease, especially in the days after calving. The objective of this study was to compare the standing behavior of dairy cows with and without clinical ketosis during the days around calving. Serum BHBA was measured in 150 cows twice weekly, from 3 to 21 d after calving. Standing behavior was measured from 1d before calving (d −1) to 21 d after calving using data loggers. Retrospectively, 10 cows with clinical ketosis (BHBA >2.9 μmol/L) were randomly selected and matched by parity with 10 control cows (BHBA <1.2 μmol/L). Data were stratified into periods around calving as behavioral responses were expected to change depending on day relative to calving and stage of illness as it developed over time. Five periods were defined: d −1, d 0, wk +1 (d 1–7 postpartum), wk +2 (d 8–14) and wk +3 (d 15–21). Differences in standing behavior between ketotic and control cows were analyzed by period using the mixed procedure of SAS; cow was considered the experimental unit. The average (±SD) DIM until first signs of clinical ketosis were observed was 11.7 ± 5.6 DIM. Ketotic cows had fewer standing bouts on d −1 (10.3 ± 1.3 vs. 15.8 ± 1.9 bouts/d; $P = 0.03$) and d 0 (13.7 ± 1.0 vs. 20.0 ± 1.3; $P = 0.003$) relative to calving, compared with control cows; the number of standing bouts was not affected by health status after calving. Average standing bout duration was longer for ketotic cows on d 0 (1.3 ± 0.1 vs. 0.7 ± 0.1 h/d; $P = 0.009$) but no different than control cows during the other periods. The total daily standing time of ketotic cows was longer than control cows on d 0 (17.0 ± 0.8 vs. 13.9 ± 1.0 h/d; $P = 0.003$) but not during the other periods. These results suggest that differences in standing behavior before calving may be useful for the early detection of ketosis in dairy cows.

Key Words: BHBA, dairy cattle, health

427 Lactipro improves performance and health of calves after feedlot arrival. K. A. Miller*, C. L. Van Bibber-Krueger, and J. S. Drouillard, *Kansas State University, Manhattan.*

Two experiments were conducted to determine effects of Lactipro, administered as a 100-mL oral drench at initial processing, on health and performance of calves following arrival in the feedlot. Lactipro is a probiotic containing a live culture of *Megasphaera elsdenii* (10^9 cfu/mL) a lactate-utilizing bacteria. In Exp. 1, 1294 crossbred steers (BW = 119 ± 0.59 kg) were received from Mexico over a 13-d period. Calves were placed into feedlot pens and given free access to long-stemmed grass hay, and then processed 24 h later. At processing steers were assigned to Control and Lactipro (100-mL oral dose) groups based on alternating order through the processing chute. Cattle were housed in 38 pens (5 pens/treatment with 15 to 16 steers/pen and 14 pens/treatment with 39 to 42 steers/pen) and fed a 55% concentrate diet ad libitum. Steers were observed daily for signs of undifferentiated bovine respiratory disease (BRD). Steers diagnosed as morbid were taken to the processing area for treatment (1st therapy, tilmicosin; 2nd therapy, enrofloxacin; 3rd therapy, long-acting oxytetracycline). There were no differences in DMI, ADG, and gain efficiency ($P > 0.5$); overall incidence of BRD was 3.25% and not different for Control and Lactipro groups ($P > 0.15$); but Lactipro steers tended to require fewer 2nd-time antibiotic therapies ($P = 0.06$). In Exp. 2, crossbred calves (504 bulls, 141 steers; BW = 201 ± 4.9 kg) from Texas were housed in 24 pens with 25 to 30 calves/pen. Allocation to treatments, feeding, and daily evaluations were as in Exp. 1. Calves dosed with Lactipro had greater DMI, ADG, and gain efficiency ($P \leq 0.05$) compared with Control calves. Incidences of 1st and 2nd therapeutic treatments were 31% and 33% less, respectively, for Lactipro compared with Control calves ($P < 0.05$), but third-time antibiotic therapies and mortalities were not different ($P > 0.10$). Total cost/calf for therapeutic treatment was 13% less ($P < 0.05$) for Lactipro calves compared with Control cattle. Dosing calves with Lactipro at processing was effective as a method for improving performance and decreasing clinical signs of BRD.

Key Words: bovine respiratory disease, Lactipro, *Megasphaera elsdenii*

428 Relationship between post-milking standing time, lameness, milking order, and incidence of intramammary infection in dairy cows. M. E. A. Watters*[1], H. W. Barkema[2], K. E. Leslie[3], M. A. G. von Keyserlingk[4], and T. J. DeVries[1], *[1]Dept. of Animal and Poultry Science, University of Guelph, Kemptville Campus, Kemptville, ON, Canada, [2]Production Animal Health, University of Calgary, Calgary, AB, Canada, [3]Dept. Population Medicine, University of Guelph, Guelph, ON, Canada, [4]Animal Welfare Program, University of British Columbia, Vancouver, BC, Canada.*

The objective of this study was to determine the relationship between post-milking standing time, lameness, milking order, and the risk of intramammary infection (IMI) in dairy cows milked 3×/d. Forty Holstein cows (<200 d DIM with SCC < 100,000 cells/mL) from each of 4 freestall dairy herds, milking 3×/d, were enrolled for a total of 160 cows in a longitudinal study. Cows were 80 ± 43 DIM at the study start and were followed for three 28-d periods. Data loggers were utilized to record lying behavior in cows for 5 d at the start of each period. Quarter-level milk samples were collected for bacteriological culture on d 1 of each period. A new IMI was defined as a positive culture sample following a negative culture. Cows were lameness scored (scale of 1 = sound to 5 = severely lame) at the end of each 5-d recording period. Time of milking, milk production, and feed delivery times were also recorded. A multivariable logistic regression model was used to determine the risk factors for IMI. Across the study, cows spent 9.9 ± 2.2 h/d lying down and had an average post-milking standing duration of 88.3 ± 48.6 min. Over the study, 12.4% of focal cows were identified as being lame (score ≥ 3). Post-milking standing duration was 7.5 min shorter in lame cows (P = 0.05). A total of 240 new IMI were detected from 1214 quarters at risk for an incidence rate of 2.58 IMI/quarter-year at risk. Coagulase-negative staphylococcus (CNS) and *Corynebacterium bovis* were responsible for 47% and 38%, respectively, of detected IMI. The relationship between post-milking standing duration and IMI incidence was non-linear. Cows that stood for >90 but <120 min post-milking tended (P = 0.08) to be at reduced risk for an IMI compared with those cows which stood for < 60 min post-milking (OR = 0.67, 95% CI = 0.37, 1.22). Cows milked in the latter half of the milking order were at an increased (P = 0.009) risk for IMI (OR = 1.88, 95% CI = 1.17, 3.02). These results suggests that reduced IMI incidence in freestall-housed cows milked 3×/d can be achieved by encouraging cows to remain standing for 90–120 min post-milking and minimizing the time cows wait to be milked.

Key Words: behavior, freestall, mastitis

429 Milk components as predictors for ruminal indigestion/acidosis in lactating dairy cows. S. Kirchman[1], P. J. Pinedo*[2], F. P. Maunsell[1], C. A. Risco[1], and G. A. Donovan[1], *[1]Department of Large Animal Clinical Sciences, College of Veterinary Medicine, University of Florida, Gainesville, [2]Texas A&M AgriLife Research & Extension Center-College of Veterinary Medicine & Biomedical Sciences, Texas A&M University System, Amarillo.*

The objective was to investigate biological markers in milk that could be used to detect rumen indigestion before overt clinical signs. Milk component data from 23 Holstein cows (>30 DIM) diagnosed with rumen indigestion were evaluated. Variables were measured using the AfiFarm system and included milk yield, body weight, percentage milk fat, milk protein and lactose, fat:protein and fat:lactose ratios measured in the 16 milkings before and after diagnosis of indigestion. For each case of rumen indigestion, 2 control cows were selected for comparison. Diagnostic criteria for rumen indigestion included deviation of ≤ −20% in milk yield at the AM (morning) milking, reduced rumen motility and no detectable abnormalities in other organ systems. At time of diagnosis, a sample of rumen fluid was collected from all cows using an oro-ruminal probe and the rumen pH was measured. Deviations between values around the time of diagnosis and the mean for the previous 10 d were calculated for all the variables in cases and matched controls. Comparisons between cases and controls were made by ANOVA. Statistical significance was set at $P \leq 0.05$. Average pH was slightly higher in case cows (pH 6.47) than in control cows (pH 6.29). Case average milk deviation was −30%, at 0 milking (at diagnosis). Control cows did not show any significant deviations in variables studied. In case cows, there was a significant deviation in milk fat percentage (+11%, +10%, +8%) and fat:protein ratio (+7%, +10%,+7%) around diagnosis (−1, 0, +1 milking) compared with control cows. Milk protein showed no significant changes while lactose deviations decreased (<−1% deviation) from −2 to +3 milking ($P < 0.10$). The fat:lactose ratio showed the most significant change in deviations (+13%, +13%, +12%) at −2 to +1 milkings. Results suggest that changes in percent milk fat and milk fat:protein ratio, in combination with a decrease in milk yield may serve as possible biochemical markers to detect rumen indigestion. Changes in milk fat:lactose ratio alone occurred 12 to 24 h before milk yield deviation and may be a good screening test for rumen acidosis in lactating dairy cows

Key Words: ruminal indigestion/acidosis, biological markers

430 Effects of cow size on dry matter and residual feed intake of lactating beef cows. R. S. Walker*[1], R. M. Martin[2], L. Gentry[3], G. Gentry[2], and G. Scaglia[4], *[1]LSU AgCenter Hill Farm Research Station, Homer, LA, [2]LSU AgCenter School of Animal Sciences, Baton Rouge, LA, [3]Louisiana Tech University, Ruston, [4]LSU Iberia Research Station, Jeanerette, LA.*

Thirty-eight Angus cross lactating beef cows (BW = 582 ± 51.3 kg, BCS = 5.0 ± 0.5) were used to determine if differences in DMI and residual feed intake (RFI) exist based on cow size. Cows were housed in individual pens (2.2 × 9.1 m) equipped with 2.2 m of bunk space and fed a diet formulated to meet or exceed maintenance requirements consisting of 30% dry bermudagrass hay and 70% ryegrass baleage (DM = 49.3%, CP = 13.2%, NDF = 54.9%, TDN = 63%) for a 14 d adaption and 70 d feeding period. Individual daily feed intakes, BW, BCS, and hip height were recorded and cow was the experimental unit. Feed intakes were used to calculate RFI for each cow as the difference between actual and expected feed intake. Blood samples were obtained on d 0 and 70 and analyzed for glucose, insulin, and leptin. Cows were assigned to a light (L; 558 ± 23.6 kg) or heavy (H; 626 ± 38.6 kg) weight group based on d 0 BW adjusted to a 5 BCS for differences in DMI and RFI. Based on RFI, cows were classified as positive (POS; 1.65) or negative (NEG; −1.48) for first analysis and low (LOW; −2.28), medium (MED; −0.04), or high (HI; 2.35) for second analysis of d 0 BW, glucose, insulin, and leptin. Cows in the L group had a lower ($P < 0.01$) daily DMI (15.6 ± 1.2 kg) compared with cows in the H group (16.7 ± 1.1 kg); however, mean RFI was not different. Day 0 BW was similar for cows classified as POS (586 ± 50.4 kg) compared with NEG (580 ± 53.5 kg) RFI. Glucose and insulin levels were similar for both POS and NEG RFI groups; however, leptin levels tended to be higher ($P < 0.10$) on d 0 and 70 for cows classified as NEG (0.84 ng/mL) compared with POS (0.58 ng/mL) RFI. Day 0 BW was similar for cows classified as either HI (582 ± 51.7 kg), MED (593 ± 54 kg), or LOW (570 ± 50 kg) RFI. Glucose and leptin levels were similar among HI, MED, and LOW RFI groups; however, insulin levels were higher ($P < 0.01$) on d 0 for HI and LOW RFI groups compared with MED and tended ($P < 0.10$) to be higher on d 70 for HI compared with MED and LOW RFI groups. While differences in DMI were associated with cow size, mature BW is not a good predictor of feed efficiency in beef cows using RFI.

Key Words: cattle, residual feed intake, dry matter intake

431 Effects of feeding a natural biopolymer (chitosan) on methane emissions and performance in beef cattle. D. D. Henry*[1], M. J. Ruiz-Moreno[1], F. M. Ciriaco[1], M. Kohmann[2], V. R. G. Mercadante[1], G. C. Lamb[1], and N. DiLorenzo[1], *[1]North Florida Research and Education Center, University of Florida, Marianna, [2]Department of Agricultural and Biological Engineering, University of Florida, Gainesville.*

Recent in vitro experiments indicate that the natural biopolymer chitosan could modify ruminal fermentation and decrease methane production. Our objective was to evaluate the natural biopolymer chitosan as a feed additive to mitigate in vivo methane emissions and increase performance in beef cattle. Twenty-four crossbred heifers (BW = 252 ± 24 kg) were used in a randomized block design replicated in 2 periods. Heifers were randomly assigned to 12 pens (2 heifers/pen) and pens were randomly assigned to 1 of 6 treatments in a 2 × 3 factorial arrangement. Factors included diet [high concentrate (HC) or low concentrate (LC)] and either 0.0, 0.5 or 1.0% of chitosan dietary inclusion on a DM basis. Heifers were housed in the University of Florida-Feed Efficiency Facility in Marianna, FL. Diets were offered ad libitum and intake was recorded by a GrowSafe system (GrowSafe Systems, Airdrie, Alberta, Canada). After at least a 14-d adaptation period, methane emissions were measured using the SF_6 tracer technique for 5 consecutive d in each sampling period. Performance data were collected for the heifers. Data were analyzed using the MIXED procedure of SAS (SAS Institute, Cary, NC). No effects ($P > 0.10$) of chitosan or chitosan × diet interaction were found for DMI or methane emissions. A diet effect ($P < 0.01$) was found for methane emissions expressed as g/d, as g/kg of $BW^{0.75}$, and as g/kg of DMI. Heifers consuming a LC diet produced 130 g of CH_4/d vs. 45 g of CH_4/d in the HC diet. When adjusted for intake, heifers produced 18.2 and 7.1 g of CH_4/kg of DMI in LC and HC, respectively. The addition of up to 1% of chitosan did not affect ($P > 0.10$) methane emissions or growth performance in heifers consuming either diet. Heifers consuming a LC diet had decreased ($P < 0.01$) ADG and G:F and produced 2.9 times more methane per day than those fed a HC diet. However, when expressed as methane produced per kg of DM consumed, heifers consuming a LC diet produced 2.6 times more methane than those consuming a HC diet.

Key Words: beef, methane, chitosan

432 Ruminal methanogens in steers that are negative or positive for residual gain. H. Freetly*, J. Wells, M. Kim, K. Hales, and A. Lindholm-Perry, *USDA, ARS, US Meat Animal Research Center, Clay Center, NE.*

Cattle produce CH_4 in the rumen and it represents a loss of feed energy. A possible cause of variation in feed efficiency may be differences in capacity to produce CH_4. We hypothesized that cattle with a higher residual gain (RG) would have a lower abundance of methanogens in the rumen. Individual DMI and BW gain were determined on crossbred steers (n = 132, initial age = 348 ± 1 d and BW 444 ± 4 kg) for 56 d. Steers were offered feed ad libitum and individual intake was measured. The diet consisted of 82.75% rolled corn, 12.75% corn silage, and 4.5% supplement (0.066% monensin and 51% CP). Residual gain was calculated from the regression of BW on DMI; f(x) = (0.1262 ± 0.0128)x + (25.7 ± 9.9), $R^2 = 0.43$. The 7 animals with the most extreme positive and negative RG that were within 32% of the STD of the mean DMI (772 ± 90 kg) were sampled. Steers were slaughtered and mixed rumen fluid was strained through cheesecloth and frozen. DNA was isolated from rumen content, and bacterial DNA was quantified using PCR with unique amplicons and is expressed as the log of the DNA concentration. Total archaea bacteria standardized to total bacterial DNA (16S) did not differ between High and Low RG ($P = 0.96$). High and Low RG steers did not differ for *Methanobrevibacter* ruminantium + *Mbb. cuticularis* ($P = 0.56$), *Methanosarcina barkeri* ($P = 0.58$), or *Methanobacterium ruminantium* ($P = 0.54$) after standardizing for total archaea bacteria. The concentration of *Mbb. smithii* + *wolinii* + *thaueri* + *gottschalkii* + *woesii* tended to be greater in the High RG steers ($P = 0.06$). While species composition may shift between cattle with different RG, total methanogens did not differ suggesting that differences in feed efficiency may not be a function of rumen microbial capacity to produce methane. Partially funded by National Institute of Food and Agriculture Grant 2011–68004–30214 National Program for Genetic Improvement of Feed Efficiency in Beef Cattle.

Key Words: cattle, methane, methanogen

433 Assessing body fat chemical composition in F1 Nellore × Angus bulls and steers through the use of biometric measures. M. A. Fonseca*[1,2], L. O. Tedeschi[1], S. C. Valadares Filho[2], N. F. De Paula[3], H. J. Fernandes[4], and L. D. Silva[2], *[1]Texas A&M University, Department of Animal Science, College Station, [2]Federal University of Vicosa, Department of Animal Science, Vicosa, Minas Gerais, Brazil, [3]Federal University of Mato Grosso, Department of Animal Science, Cuiaba, Mato Grosso, Brazil, [4]Mato Grosso do Sul State University, Department of Animal Science, Aquidauana, Mato Grosso do Sul, Brazil.*

This study was conducted to assess the body fat chemical composition through the use of biometric (BM) and postmortem (PM) measurements taken in 40 F_1 Nellore × Angus bulls (B) and steers (S) under feedlot conditions. The animals had 12.5 ± 0.51 mo of age, and shrunk BW (SBW) of 233.03 ± 23.47 and 238 ± 24.58 kg for B and S, respectively. Animals were fed 60% corn silage and 40% concentrate. Eight animals were slaughtered at the beginning (4 B, 4 S), and the remaining animals were randomly assigned into a factorial 2 (gender) × 3 (slaughter weights) arrangement of treatments for the entire trial. The subsequent slaughters were performed when the group of animals reached an average BW of 380 (6 B, 5 S), 440 (6 B, 5 S), and 500 kg (5 B, 5 S). The day before the slaughter, the following BM were taken: hook bone width (HBW), pin bone width (PBW), abdomen width (AW), body length (BL), rump height (RH), height at withers (HW), pelvic girdle length (PGL), rib depth (RD), girth circumference (GC), rump depth (RuD), and thorax width (TW). The PM collected were empty BW (EBW) subcutaneous fat (SF), internal fat (InF), intermuscular fat (ImF), carcass and empty body physical fat, fat thickness at the 12th rib (FT), and 9 – 11th rib section fat (HHF). Additionally, the amount of carcass (CF_{ch}) and empty body (EBF_{ch}) chemical fat contents were estimated by ether extraction of the carcass and empty body constituents. The equations were developed using a stepwise procedure to select the variables with the best goodness-of-fit and the least root mean square error (RMSE). There was an effect of gender ($P < 0.05$) and the equations were developed separately: $EBF_{ch}(kg) = -8.7312 + 1.5672 \times CF_{ch} + 0.5599 \times RuD$ ($r^2 = 0.995$ and RMSE = 2.73) and $CF_{ch}(kg) = -123.8316 + 3.7369 \times AW$ ($r^2 = 0.901$ and RMSE = 6.92) for S, and $EBF_{ch}(kg) = 34.7554 + 0.3735 \times SBW - 2.4676 \times PGL$ ($r^2 = 0.952$ and RMSE = 6.70) and $CF_{ch}(kg) = 44.4023 - 0.3932 \times EBW - 2.5457 \times PGL$ ($r^2 = 0.959$ and RMSE = 6.21) for B. The observed BM that most affected the CF_{ch} and EBF_{ch} in this database were RuD and AW for S, and PGL for B, respectively.

Key Words: carcass fat estimation, empty body fat estimation, modeling

434 High energy diet enhances stearoyl-CoA desaturase (SCD) expression in Hanwoo skeletal muscle. K. Y. Chung*, S. H. Lee, S. S. Chang, Y. M. Cho, E. M. Lee, and H. S. Kang, *Hanwoo Experiment Station, NIAS, RDA, Pyeongchang, Korea.*

High energy diet has been used for enhancing intramuscular adipose tissue in high quality beef cattle. The aim of this experiment was to determine the effect of high energy diet on the level of SCD gene expressions and genotypes. We hypothesized that SCD expression is increased in beef cattle muscle tissue when fed a high energy diet and that this is related to SCD genotypes (CC, CT, TT). A 2 × 3 factorial arrangement (High, Control, vs. CC, CT, TT) in a completely random design was used to feed 24 Hanwoo steers. Two steers were fed in same pen and 12 pens were used for treatment. Blood was drawn from each steers on every first week from 11 to 28 mo. Longissimus dorsi (LD) muscle was collected within 10 min of harvest for analysis of mRNA SCD abundance. Overall ADG were not different between high energy diet and control diet ($P > 0.05$). However, 22 and 27th mo ADG were increased ($P < 0.05$) by high energy diet compare with control diet. Overall serum NEFA concentrations were not affected by high energy diet ($P > 0.05$), but 22nd and 26th mo NEFA concentrations were increased ($P < 0.05$) by high energy diet. Marbling score and yield grade were not affected by high energy diet ($P > 0.05$). There was a negative correlation ($R^2 = 0.7868$) between concentrations of stearic and palmitoleic acid. Palmitoleic acid was lowest in control-fed CT group and highest in control-fed TT group. Real-time quantitative PCR revealed that the mRNA content of SCD in muscle from high energy diet cattle increased ($P < 0.05$) as compared with the control group. These data indicated that high energy diet increased relative mRNA level of SCD, and these effects may be mediated monounsaturated fatty acid composition in Hanwoo LD muscle.

Key Words: genotype, Hanwoo, SCD

435 Metabolic imprinting effect during early growth on extra cellular matrix construction in Wagyu (Japanese Black steers). A. Nomura*[1], R. Fujimura[1], A. Saito[4], S. Khounsakunalath[1], K. Saito[2], K. Sakuma[2], T. Abe[2], H. Hasebe[2], S. Kaneda[2], T. Etoh[1], Y. Shiotsuka[1], S. Maak[3], E. Albrecht[3], H. Takahashi[1], T. Gotoh[1], *[1]Kuju Agricultural Research Center, Kyushu University, Taketa, Oita, Japan, [2]National Livestock Breeding Center, Nishigo, Fukushima, Japan, [3]Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany, [4]Zenrakuren, Tokyo, Japan.*

The extracellular matrix (ECM) physically supports tissue structures by forming junctions with surrounding macromolecules. In muscle, the ECM supports the contraction of myofibers and is an important factor affecting the tenderness of meat. A previous study reported that supplementation with ground maize increased the quantity of heat-soluble collagen and improved meat tenderness in beef produced from grazing Holstein bulls. This suggests that early nutrition may change the quantity of heat-soluble collagen in beef. This phenomenon is referred to as "metabolic imprinting or metabolic programming" based on medical research regarding "the developmental origins of health and disease (DOHaD)." We examined how metabolic imprinting during early nutrition affects the expression of genes related to the ECM in muscles of Japanese Black cattle fattened on grass. Twenty-three steers were divided into 2 feeding groups. One group was intensively nursed with milk replacer (maximum1800 g/d) and was fed concentrate and roughage after weaning (HE: n = 12). The other group was normally nursed with milk replacer (maximum 600 g/d) and was fed roughage alone after weaning (R: n = 11). The longissimus thoracis muscle (LT) was sampled by needle biopsy at 3 and 10 mo and DNA microarray analysis was performed. Expression levels of some of the genes related to the ECM were significantly different between the HE and R groups. In this study, we focused on 2 genes: (1) fibronectin, which connects cells to other macromolecules of the ECM, and (2) type IV collagen, which surrounds cells as a component of the endomysium and is a heat-soluble collagen. Gene expression for fibronectin was greater in the HE than in the R animals at both 3 and 10 mo. Conversely, gene expression of type IV collagen was greater in the R than in the HE animals at 3 mo, but this result was reversed at 10 mo. In conclusion, our data suggest that early nutrition may affect the formation of the ECM in the muscle of Japanese Black cattle.

Key Words: cattle, ECM, metabolic imprinting

436 Metabolic imprinting effect in beef production: Influence of nutrition manipulation during an early growth stage on adipogenesis in the longissimus muscle in Wagyu (Japanese Black). R.

Fujimura[1], K. Etoh[1], S. Khounsaknalath[1], K. Saito[2], K. Sakuma[2], K. Kaneda[2], T. Abe[2], T. Etoh[1], Y. Shiotsuka[1], H. Hasebe[2], H. Hasebe[2], S. Maak[3], A. Elke[3], H. Takahashi[1], T. Gotoh*[1], *[1]Kuju Agricultural Research Center, Kyushu University, Taketa, Oita, Japan, [2]National Livestock Breeding Center, Nishigo, Fukushima, Japan, [3]Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany, [4]Zenrakuren, Tokyo, Japan.*

Japanese Black cattle (Wagyu) are known to accumulate high levels of intramuscular fat. This experiment was conducted to clarify how early nutrition affected adipogenesis in Japanese Black steers fattened on roughage as metabolic imprinting effect. Japanese Black steers were randomly allocated into 2 groups. The high-energy group (Imp: n = 12) received intensified nursing until 3 mo of age and was then fed a high-concentrate diet from 4 to 10 mo of age. The roughage group (Cont: n = 11) received normal nursing until 3 mo of age and was then fed only roughage from 4 to 10 mo of age. From 10 mo of age, both groups were fed only roughage until slaughter at 31 mo of age. Muscle samples were biopsied from the longissimus muscle (LM) at 3, 10, 14, 20 and 30 mo of age. Three genes relating to glucose metabolism, PPARγ2, SCD, C/EBPα, Leptin, and FASN were investigated in each LM sample by qPCR analysis. The expression of PPARγ2 was significantly higher in group Imp than in group Cont at 3 and 10 mo of age ($P < 0.05$) and conversely significantly lower at 20,and 30 months of age ($P < 0.05$). The expression of C/EBPα was lower in group Imp than in group Cont at 30 mo of age ($P < 0.1$). The expression of SCD was significantly higher in group Imp than in group Cont at 10 mo of age ($P < 0.05$) and conversely significantly lower at 20 and 30 mo of age ($P < 0.05$). The expression of FASN was significantly higher in group Imp than in group Cont at 10 mo of age ($P < 0.01$) and conversely lower at 20 ($P < 0.1$) and 30 mo of age ($P < 0.05$). The expression of Leptin was significantly higher in group Imp than in group Cont at 14 mo of age ($P < 0.05$). These results indicate that the high energy treatment during the early growth phase would influence or disturb adipogenesis timing in grass-fattening of Japanese Black steers.

Key Words: cattle, metabolic imprinting, adipogenesis

Beef Species Symposium: Nutrient Requirements of the Beef Female in Extensive Grazing Systems—Considerations for Revising the Beef NRC

437 Difficulties associated with predicting forage intake by grazing beef cows. S. A. Gunter*[1], D. B. Faulkner[2], A. M. Meyer[3], E. J. Scholljegerdes[4], J. E. Sprinkle[5], S. A. Soto-Navarro[4], and S. W. Coleman[6], *[1]USDA-ARS, Woodward, OK, [2]University of Arizona, Oro Valley, [3]University of Wyoming, Laramie, [4]New Mexico State University, Las Cruces, [5]University of Arizona, Payson, [6]USDA-ARS, El Reno, OK.*

The current NRC model is based on a single equation that relates DMI to metabolic size and net energy density of the diet and was a significant improvement over previous models. However, observed DMI by grazing animals can be conceptualized by a function that includes animal demand, largely determined by metabolic or linear size, physiological state, genetics, or any combination. Forage DMI is really modified by its nutritive value and balance, herbage mass and structure, locomotion, climate, profitability of bites, the interaction with genetics, and level and type of supplementation. Even in the database used to generate the current NRC equation, DMI by cows is poorly predicted at the extremes. In fact, across the range of actual DMI, predicted DMI is rather flat indicating an insensitivity so further refinement of the model is needed. Also, it may be necessary to construct multiple models designed for various rangeland and pasture types. We would suggest that future models be based on multiple equations including functions for physiological state, previous plane of nutrition, animal suitability to the environment, and activity to modify the predicted DMI. Further, the model could possibly account for imbalances of protein to energy, particularly as it relates to ruminal function, and herbage distribution and accessibility as it influences grazing behavior and selectivity. The inclusion of some of these functions may render the model inputs too complex for many users, hence models must be evaluated for complexity as well as how well the model fits under multiple situations. Further, the issue of how reference data was collected (pen vs. pasture) and how the methods or constraints influence DMI must be evaluated. For instance, if DMI is greater under grazing, is it because of greater metabolic demand due to activity and climatic conditions, or to differences in direct measurement of DMI compared with indirect methods (e.g., internal and external markers). Overall, the new NRC model needs to be more robust in its ability to account for the wide variation in the environment, dietary characteristics, and metabolic demands.

Key Words: cow, grazing, intake

438 How well does the current metabolizable protein system account for protein supply and demand of beef females within extensive western grazing systems? R. C. Waterman*[1], J. S. Caton[2], and C. A. Loest[3], *[1]USDA-Agricultural Research Service, Fort Keogh LARRL, Miles City, MT, [2]North Dakota State University, Department of Animal Sciences, Fargo, [3]New Mexico State University, Department of Animal and Range Sciences, Las Cruces.*

Extensive western beef livestock production systems within the Southern and Northern Plains and Pacific West combined represent 60% (approximately 17.5 million) of total beef cows in the United States. The beef NRC is an important tool and excellent resource for both professionals and producers to use when implementing feeding practices and nutritional programs within these various production systems. Objectives of this symposium paper are to identify areas within the current beef NRC that could be refined so that future beef NRC models would have greater precision predicting protein supply and demand for beef cattle production within extensive western grazing systems. In western systems, a management protocol often implemented is strategic supplementation which may consist of supplying a prorated bolus dose of protein. An important addition to the current beef NRC model would be to allow users to describe supplement composition, and amount and frequency in which supplement is delivered. Beef NRC models would then need to be modified to account for N recycling that occurs throughout a supplementation interval and the impact that this would have on microbial efficiency and microbial protein supply. The beef NRC should also consider the role of ruminal and postruminal supply and demand of specific limiting amino acids. Additional considerations should include the partitioning effects of nutrients under different physiological production stages (e.g., lactation, pregnancy, and during periods of BW loss) and the role of metabolic modifiers or additives. Metabolic modifiers or additives can greatly influence partitioning of protein (i.e., amino acids) and redirect nutrients for different physiological needs. Our intention is that information provided by this symposium will aid in the revision of the beef NRC by providing supporting material for changes and identifying gaps in existing scientific literature where future research is needed to enhance the predictive precision and application of the beef NRC models.

Key Words: amino acid, ammonia, cow

439 Potential limitations of NRC in predicting energetic requirements of beef females within western U.S. grazing systems. M. K. Petersen*[1], C. Mueller[2], J. T. Mulliniks[3], A. J. Roberts[1], and T. Del Curto[2], *[1]USDA-ARS Ft Keogh Livestock & Range Research Laboratory, Miles City, MT, [2]OSU-Eastern Oregon Agricultural Research Center–Union Station, Union, [3]University of Tennessee, Knoxville.*

Assessment of cow energy balance and efficiency in extensive grazing settings have occurred on a nominal basis over short intervals and have not been used to model lifetime energy utilization (output Mcal/intake Mcal = lifetime energetic efficiency). Solis et al. (1988) demonstrated in pen-fed cows, differences ($P < 0.01$) in efficiency of weight change ranging from 135 to 58 g/Mcal ME intake. Furthermore, variation in efficiency of ME use for tissue gain or loss from 80 to 36%. Energy costs for maintenance, tissue accretion and mobilization were lower in some breeds. The most efficient may reflect the potential for cattle that fit semi-arid grazing environments with low input management. Successful range cattle are likely the result of natural selection for efficiency. Animals exposed to a variety of stressors may continually adapt so energy expenditure is reduced. Critical factors comprising cow lifetime achievement including reproductive success, disease resistance, and calf weaning weight maybe driven by cow caloric utilization in energy limiting environments. Therefore, ME adjustments for adapted cattle within these landscapes with seasonal BW changes can alter seasonal NEm requirements. Other than growth of replacement heifers, most retained energy is associated with fat storage. Evaluation of energy reserves have been implemented using BCS systems. Estimates of total and composition of BW change associated with plus and minus 1 BCS have been reviewed in the current NRC; depending on BW, breed, and maturity. The overall efficiencies associated with BCS changes are not only affected by composition of BW change, but partial efficiencies associated with tissues utilizing available energy and protein sources and the history of

recent gain or loss. Herd analysis questions as to whether NRC BCS descriptions accurately represent NEm requirements of adapted females utilizing western rangelands. A more complete understanding of greater productivity in the field than the current model proposes will help direct future research and inform models to simulate energetic accountability and subsequent female performance.

Key Words: energy requirement, NRC, beef cow

Breeding and Genetics: Genomic Selection in Dairy I

440 In vivo and in vitro heat shock proteins gene expression in cattle. A. C. A. P.M. Geraldo*[1], L. J. Oliveira[1], A. M. F. Pereira[2], F. Moreira da Silva[3], and E. A. L. Titto[1], *[1]Faculdade de Zootecnia e Engenharia de Alimentos-Universidade de Sao Paulo, Pirassununga, Sao Paulo, Brazil, [2]Universidade de Evora, Evora, Portugal, [3]Universidade dos Acores, Angra do Heroismo-Terceira, Acores, Portugal.*

The main purpose for this study was the quantification of the heat shock proteins HSPA1A and HSP90AA1, in cow lymphocytes, when subjected to heat stress directly - in vivo, or indirectly - in vitro. The aim was to identify differences between HSP expression in vitro and in vivo. The experiment was conducted in the Biometeorology and Ethology Laboratory of FZEA-USP. Were used 3 female Holstein Frisian, which were subjected to heat stress, by sun exposure. The blood samples were collected after sun exposure, with a temperature of 40 ± 2°C, during 3 d. For in vitro tests, blood of the same animals was collected and placed for a period of 4 h in a water bath at 40°C, thus simulating the thermal stress. Total RNA of lymphocytes was extracted, treated with DNase I and submitted to cDNA synthesis for gene expression quantification of HSPA1A and HSP90AA1, by real time PCR (qRT-PCR). The data were tested for normality by Kolmogorov-Smirnov test and for homocedasticity by Levene test. Data were analyzed according to a general linear model procedure with 2 fixed factors treatment and genes expression. Significantly different means were submitted to post-hoc comparisons of means (LSD test) and regarded as significantly different when $P \leq 0.05$. The results showed that there are no significant differences between the in vitro and the in vivo treatments, but there are significant differences in genes expression in the different treatments.

Key Words: cow, HSPA1A, HSP90AA1

441 Comparison of genomic inbreeding within a family-based structure in Holstein cattle. D. W. Bjelland*[1], K. A. Weigel[1], A. Coburn[2], R. D. Wilson[2], and A. Lasecki[2], *[1]University of Wisconsin-Madison, Madison, [2]Genex Cooperative Inc./CRI, Shawano, WI.*

Pedigree inbreeding estimates the percentage of alleles of individual which are identical by descent. With the use of genomic information, more accurate measures of inbreeding have been developed. These methods are utilized in this study to compare the expected genomic inbreeding derived from sire-dam mating pairs to the actual genomic inbreeding of their progeny as well as compare genomic inbreeding measures between full siblings. Genomic information consisting of 54,001 SNP markers for 3,601 Holstein cattle were available for this study. A total of 638 sire-dam-progeny trios and 3,906 full sibling pairs were available for analysis. The percent homozygosity of SNPs remaining after editing for minor allele frequency, call rate, and Hardy-Weinberg equilibrium (32,114 remaining SNPs) and the percentage of the genome contained within a run of homozygosity were utilized as the 2 measures of genomic inbreeding calculated for each animal. The expected percent homozygosity for progeny resulting from each sire-dam mating pair was also calculated. Average percent homozygosity for all animals was 62.6 ± 1.1% while average inbreeding calculated from runs of homozygosity was 6.2 ± 2.4%. The expected percent homozygosity between sire-dam mating pairs was 65.1 ± 0.9%, which was on average 2.4 ± 0.9% greater than the percent homozygosity of the actual progeny. When comparing one full sibling to another, measures of percent homozygosity had a correlation of 0.48 while genomic inbreeding derived from runs of homozygosity had a correlation of 0.52. The largest difference in percent homozygosity shown between 2 siblings was 4.8%, while the largest difference in inbreeding derived from runs of homozygosity was 10.7%. Results of this study indicate that the progeny produced have less overall homozygosity than what would be expected from their parents. This may indicate that the progeny which would have been more homozygous, were not viable and were lost early in development. Furthermore, while pedigree information has provided reasonable estimates of the alleles which are identical by descent, differences between full siblings reconfirm that the actual measure can vary greatly.

Key Words: inbreeding, genomics

442 Genomic selection of Sahiwal cattle: A developing country perspective. M. Moaeen ud Din*, G. Bilal, and H. M. Waheed, *Animal Breeding and Genetics Lab, Faculty of Veterinary and Animal Sciences PMAS-Arid Agriculture University, Rawalpindi, Pakistan.*

The objective of present study was to explore the potential application of genomic selection in a typical developing country situation using Sahiwal cattle of Pakistan as an example. Sahiwal breed of cattle is one of the top milk producers under harsh climatic conditions of tropics and sub-tropics owing to its characteristic of disease and parasitic resistance. A selection program to enhance the genetic potential for milk production of Sahiwal cattle using progeny testing program is going on in Pakistan. Traditional progeny testing program has made a remarkable improvement in the genetic potential of dairy animals in the developed world. However, progeny testing program faces severe implementation issues in the developing countries due to limitation of resources and lack of basic infrastructure. Simulated studies in developed countries have shown the potential of genomic selection in shortening generation interval and increasing the accuracy of selection (especially young bulls) that can bring a relatively rapid genetic improvement as compared traditional progeny testing approach. Based on the available genetic and phenotypic parameters of Sahiwal dairy cattle; a comparison was made between typical progeny testing program and genomic selection. The assumed size of the training population for genomic selection was 6962 cows registered with Research Centre for Conservation of Sahiwal Cattle. The results revealed that genomic selection can reduce the generation interval in the male to male selection pathway from 10.5 years down to 2.75 years along with a substantial reduction in generation interval of other selection pathways. Genomic selection resulted in a 2.5 times increase in response to selection compared with that in a progeny testing program. Furthermore, it reduced the costs of proving bulls up to 96%. The present study may encourage the researchers and policy makers to initiate the program of genomic selection for Sahiwal cattle in Pakistan and it may also serve as an example for other developing countries.

Key Words: developing country, genomic selection, Sahiwal cattle

443 Implementation of a routine genetic and genomic evaluation for mastitis resistance using producer-recorded health data and indicator traits in Canadian dairy cattle. J. Jamrozik[1], A. Koeck[1], G. J. Kistemaker[2], and F. Miglior*[2,3], *[1]CGIL, Dept. of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada, [2]Canadian Dairy Network, Guelph, ON, Canada, [3]Guelph Food Research Centre, Agriculture and Agri-Food Canada, Guelph, ON, Canada.*

Genetic evaluation model for mastitis resistance has been developed for Canadian dairy breeds. Traits were mastitis (MAST), mean SCS,

SD of SCS and excessive test-day SCC (>500,000 cells/mL) in the first 150 DIM of lactation, and 3 first-lactation conformation traits: udder depth (UD), fore udder attachment (FUA), and body condition score (BCS). Binary mastitis trait (0 = no case, 1 = at least one case) and 4 SCS related indicators were considered as different traits in first and later (up to the 5th) lactations, giving in total 11 traits in the multiple-trait animal linear model. Models for specific traits included fixed effects of herd-parity, year-season-parity and age-season-parity (MAST and SCS traits), and herd-round-classifier and age-season-time of classification (conformation traits). Random effects were animal additive genetic, permanent environmental and herd-year (MAST and SCS traits only). Genetic parameters for the Holstein breed were estimated using a sample data on 59,819 cows with 113,123 lactations and Bayesian methods via Gibbs sampling. Estimates of heritability for MAST were 0.03 and 0.05 for first and later lactations, respectively. Heritability for SCS traits ranged from 0.02 (SD of SCS) to 0.17 (average SCS). Conformation traits were moderately heritable, from 0.26 (BCS) to 0.50 (UD). Mastitis in 1st lactation was a different trait that mastitis in older cows (genetic correlation = 0.59) and it was relatively highly genetically correlated with SCS traits (from 0.51 to 0.71, and from 0.60 to 0.78 for first and later lactations, respectively). Genetic correlations between MAST and conformation based indicator traits were moderate and stronger for the 1st lactation (from −0.34 for BSC to −0.52 for UD) compared with later parities (from −0.09 for FUA to −0.27 for UD). The new model for mastitis resistance in Canadian dairy breeds will allow complementing currently used indicator traits with direct information on clinical mastitis and it is expected to generate more accurate genetic and genomic evaluations for this trait.

Key Words: mastitis resistance, genetic evaluation

444 Genetic analysis of leukosis incidence in a US Holstein population including phenotypes from relatives without genotypes. E. A. Abdalla*[1], G. J. M. Rosa[1], K. A. Weigel[2], T. Byrem[3], and Francisco Penagaricano[1], *[1]Department of Animal Sciences, University of Wisconsin-Madison, Madison, [2]Department of Dairy Science, University of Wisconsin-Madison, Madison, [3]Antel BioSystems Inc., Lansing, MI.*

Bovine leukosis virus (BLV), a retrovirus closely related to the human T cell leukemia virus type 1 (HTLV-1), is an oncogenic virus that infects bovine B cells causing bovine leukosis (BL) disease. Up to this point, no vaccine is available for the virus and BL has spread widely in dairy herds in the US and in several other countries. The economic impact of BL on the US dairy cattle industry has been reported in many studies and in official reports released by the US Department of Agriculture. In addition, BLV is suspected to be one possible cause of HTLV-1 and it has been found to be responsible for a significant worldwide proportion of breast cancer cases. The objectives of the study were to identify genomic regions and biologically relevant pathways potentially associated with BL incidence in dairy cattle. Milk ELISA test results were available for 11,554 Holsteins from 112 herds in 16 US states, which were daughters of 3,002 sires. The genomic information for 961 of those bulls as well as for 3,000 additional bulls was available. A single-step analysis combining phenotypic, pedigree and genomic information was performed using BLUPf90 family programs. Gene set enrichment analysis was conducted to find possible Gene Ontology (GO) and KEGG pathways related to this trait. Estimated SNP effects indicated some genomic regions that might be associated with BL incidence, such as in chromosomes 1, 14 and 17. Additionally, we found in total 12 GO terms and 2 KEGG pathways significantly enriched with genes associated with BL. Interestingly, several of these functional categories such as cytoskeleton, calcium ion homeostasis, intracellular signaling cascade and regulation of small GTPase mediated signal transduction are involved in biological process that could be associated with BL. Results of this study are in agreement with our previous findings and indicate a potential for selection improvement to decrease BL incidence in dairy cattle. In addition, these results could provide insight into the genetic architecture of this complex trait in cattle.

Key Words: bovine leukosis, ssGBLUP, GWAS

445 Identification of loci associated with fertility traits via genome-wide association studies in the Holstein breed. M. K. Abo-Ismail*[1], S. P. Miller[1,2], M. Sargolzaei[1,3], D. A. Grossi[1], S. S. Moore[3], G. Plastow[3], P. Stothard[3], S. Nayeri[3], and F. Schenkel[1], *[1]Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, [2]Livestock Gentec, University of Alberta, Edmonton, AB, Canada, [3]L'Alliance Boviteq, Saint-Hyacinthe, QC, Canada.*

Improving the accuracy of genomic selection for fertility traits could help reduce fertility problems in the Holstein breed. The objectives of this study were to identify significant genomic regions for 11 fertility traits, fine map these regions, and run an in-silico functional analysis for the corresponding genes. Genome-wide association studies (GWAS) were performed using a generalized quasi-likelihood score test, using genotypes from the BovineSNP50 Bead-Chip and imputed genotypes of the Illumina Bovine HD BeadChip (300,339 SNPs) with accuracy of about 99% from 9015 Holstein bulls with progeny proofs. The GWAS identified 1203, 835, 808, 553, 162, 214, 1410, 1008, 373, 380 and 36 SNPs associated with calving ability (CA), daughter calving ability (DCA), calving ease for heifer and cow (CEh and CEc), calf survival for heifer and cow (CSh and CSc), sire calving ease for heifer and cow (SCEh and SCEc), sire calf survival for heifer and cow (SCSh and SCSc) and sire conception rate (SCR) at 5% chromosome-wise significance level by Bonferroni correction. A total of 5425 genes were found to overlap with or to be nearby significant SNPs (within 5kbp) for the 11 fertility traits using UMD3.1 bovine genome assembly. Most of the genes were on chromosome 5 (13%), 18 (9%), 3 (6%), 19 (6%) and 23 (6%). The in-silico functional analysis for the genes holding significant SNPs using annotations from human orthologs suggested enrichment of 356 biological processes ($P < 0.05$) and 192 pathways, which included GnRH signaling, oocyte meiosis, and steroid hormone biosynthesis. Further research is underway to validate significant SNPs and assess their predictive ability for the genetic merit of fertility traits in dairy cattle.

Key Words: genome-wide association study, candidate gene, fertility trait

446 Analysis of health trait data from on-farm computer systems in the United States. I: Pedigree and genomic variance components estimation. K. L. Parker Gaddis*[1], J. B. Cole[2], J. S. Clay[3], and C. Maltecca[1], *[1]North Carolina State University, Raleigh, [2]Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD, [3]Dairy Records Management Systems, Raleigh, NC.*

With an emphasis on increasing profit through increased dairy cow production, a negative relationship with fitness traits such as health has become apparent. Decreased cow health can affect herd profitability through increased rates of involuntary culling and decreased or lost milk sales. Improvement of health traits through genetic selection is an appealing tool; however, there is no mandated or consistent recording system for health data in the US. Producer-recorded health information may provide a wealth of information for improvement of dairy

cow health, thus improving the profitability of a farm. The principal objective of this study was to use health data collected from on-farm computer systems to estimate variance components and heritability for health traits commonly experienced by dairy cows. The single-step method was then used to incorporate genomic data in a multiple trait analysis. Single-trait binomial analyses were performed for 9 health traits using a sire model. Health traits included cystic ovaries, digestive disorders, displaced abomasum, ketosis, lameness, mastitis, metritis, reproductive disorders, and retained placenta. Parity and year-season were included as fixed effects and herd-year and sire were included as random effects. Heritability estimates ranged from 0.03 (SE = 0.06) for cystic ovaries to 0.20 (SE = 0.02) for displaced abomasum. Variance component estimates were used in a multiple trait analysis including the aforementioned health traits. Heritability estimates calculated from the multiple trait model ranged from 0.02 [95% highest posterior density (HPD) = 0.01, 0.03] for lameness to 0.13 (95% HPD = 0.11, 0.16) for displaced abomasum. A strong genetic correlation was found between displaced abomasum and ketosis (0.81). The single-step genomic analysis calculated heritability estimates that ranged from 0.01 (95% HPD = 0.004, 0.014) for lameness to 0.09 (95% HPD = 0.073, 0.107) for mastitis as well as comparable genetic correlations. From the results of these analyses, it was concluded that genetic selection for health traits using producer-recorded data are feasible.

Key Words: dairy, health, variance component

447 Analysis of health trait data from on-farm computer systems in the United States. II: Comparison of genomic analyses including two-stage and single-step methods. K. L. Parker Gaddis*[1], J. B. Cole[2], J. S. Clay[3], and C. Maltecca[1], *[1]North Carolina State University, Raleigh, [2]Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD, [3]Dairy Records Management Systems, Raleigh, NC.*

The development of genomic selection methodology, with accompanying substantial gains in reliability for low-heritability traits, may dramatically improve the feasibility of genetic improvement of dairy cow health. Many methods for genomic analysis have now been developed, including the "Bayesian Alphabet" and single-step methods. However, little research has been conducted to analyze the performance of these methods when applied to lowly heritable traits, such as health events. This may be due in part to a lack of documented phenotypes for health events. Producer-recorded health information may be able to fill this gap and provide health-related phenotypes, allowing substantial improvements to be made in these traits. The principal objective of this study was to investigate various genomic methods applied to health data collected from on-farm computer systems in the US. A single-step analysis was conducted to estimate variance components and heritabilities of health traits commonly experienced by dairy cows including displaced abomasum, ketosis, lameness, mastitis, metritis, and retained placenta. A blended H-matrix was constructed for a one-step threshold model with fixed effects of parity and year-season and random effects of herd-year and sire. Two-stage Bayesian methods were also implemented including single-trait and multiple-trait Bayes A analyses using deregressed sire breeding values as pseudo-phenotypes. The deregressed breeding values were obtained from prior analyses using threshold sire models. The data were split into 4 groups for cross-validation using K-means clustering. Mean reliabilities of genomic estimated breeding values calculated with the single-step method ranged from 0.35 to 0.41. Mean reliability of genomic estimated breeding values, calculated using single-step methods, increased 33% from previous estimates calculated from pedigree information for all traits. Comparable increases in reliability were obtained using 2-stage methods. It was concluded that the addition of genomic information can improve the estimates of lowly heritable health traits.

Key Words: dairy health, genomic, single-step

George C. Fahey Companion Animal Nutrition Symposium II: Comparative Animal Nutrition

448 Comparative animal nutrition: An adaptive strategy within a changing environment. M. S. Edwards*, *California Polytechnic State University, San Luis Obispo.*

To survive within a changing environment, organisms adapt their behavior. The dynamics and demographics within animal science departments across the country are shifting along with human-animal interactions. More than 50% of incoming animal science undergraduates express interests in non-production animals including companion and wildlife species. These interests represent a unique opportunity to introduce and engage students to concepts using unique species models. The symposium objectives are to (1) explore the comparative nutrition relationships that exist between domestic and exotic species, and (2) encourage and promote the inclusion of comparative nutrition in animal science programs. The academic genealogy of research scientists and faculty in the field of comparative animal nutrition, as well as professionals practicing in applied programs clearly demonstrates connections to their animal science ancestry. Comparative nutritionists rely on research of animal scientists and others to understand and develop nutrition programs for nondomestic species. The Comparative Nutrition Society (http://www.cnsweb.org/) fosters communication among laboratory and field scientists from various disciplines with interests in comparative nutrition. Animal scientists have routinely invoked the comparative studies of Kleiber, Brody and others when introducing concepts of energy metabolism. These interspecific comparisons across a "mouse to elephant" scale help students visualize the relationships of body mass, surface area, heat production and metabolic rate. Similarly, hummingbirds maybe used as an example demonstrating the impact of expressing a species' nutrient requirements as a dietary concentration or as a function of the species body weight or energy intake. The uniqueness of the species is used to elevated the student's interest to teach a concept that applies across multiple species, production and non-production alike. By integrating these topics into courses, programs can transform students' specific animal interests into a passion for fields of comparative animal sciences.

Key Words: comparative, nutrition, teaching

449 A rhinoceros is not always like a horse: Case studies on using domestic animal nutrition models for zoo animal nutrition. M. L. Schlegel*, *San Diego Zoo Global, San Diego, CA.*

Zoo animal nutritionists rely on domestic animal nutrition to understand digestive physiology, energy requirements, and nutrient requirements. The foundation of animal nutrition applies to all animals, but zoo nutritionists are often formulating diets for a wider variety of species with diets that contain unique food items. While there are many cases when using the domestic animal model works well, there are circumstances when zoo animals differ from their domestic counterparts. Using mare's milk composition to develop a rhinoceros hand-rearing formula has been successful, but using estimates of mare milk production to estimate rhinoceros lactation has not. Estimates of the nutrient requirements of the horse are applicable to the rhinoceros, but there is evidence that black rhinoceros (*Diceros bicornis*) are sensitive to diets high in iron. Dietary nutrient requirements of beef cattle and small ruminants serve as good models for most zoo ruminants, and dealing with copper deficiency in zoo ruminants and dietary mineral interactions are the same. We are learning that ruminant browsers in zoos are prone to sub-clinical acidosis with even a small to moderate amount of dietary starch compared with their domestic cousins. It is difficult to extrapolate the energy requirement for zoo mammalian carnivores and omnivores (felids, canids, ursids) from domestic dogs and cats, but nutrient requirements are very similar. When evaluating nutritional health of zoo animals their serum mineral and vitamins concentrations are very similar to domestic animals, but there are exceptions. While animals are more similar than they are different with respect to nutrition there are individual species cases where zoo animals deviate from their expected domestic animal model.

Key Words: comparative nutrition, domestic models, zoo animal

450 Unraveling the nutritional cost of avian immunity: A comparative approach. K. C. Klasing*, V. J. Iseri, and K. A. Lee, *University of California, Davis.*

Immune systems must protect against pathogens but the nutritional costs of developing, maintaining and using this system impinge on the flow of nutrients to growth and reproduction. Thus immune systems have been selected to be efficient. We have used a combination of domestic, companion, and wild avian species (broiler and layer chickens, ducks, cockatiels, passerines, columbidae) to untangle the costs of immunity and the selective forces that modify these expenditures. To determine the major evolutionary forces that affect the investment in immunity we captured approximately 200 individuals of 40 bird species in tropical and temperate areas of the Americas. There was a direct positive association between body mass and the amount of energy expended and acute phase proteins produced during the acute phase response to *E. coli*. Smaller species invested more in constitutive aspects of immunity and less in pathogen-induced responses. We expected to find that longer lived species invested more, but this was not the case. In adult chickens, the systemic immune system (including all major leukocytes and protective proteins but excluding mucosal leukocytes) at maintenance has the same lysine content as 16% of a medium egg, 332 average sized feathers, or 5% of a pectoralis muscle. The increase in lysine accretion due to injection of *E. coli* was 113% during the acute phase (24 h) and 44% during the adaptive response (5 d). Acute phase proteins contributed 84% to the lysine used during the acute phase and Ig contributed 44% during the adaptive phase. The remainder was due to leukocyte proliferation. However, the lysine accreted in the expansion of the liver for support of the acute phase response was almost 3 times the lysine accreted for the cells and proteins of the immune system, indicating that the liver is the largest contributor to the acute phase response. The adaptive response was completely fueled by the decay of the acute phase response and did not have a net nutritional cost. This research approach illustrates the power of combining natural selection and artificial selection for understanding the basic principles of biology that underlie both.

Key Words: nutrition, immunity, cost

451 Comparative study of milk oligosaccharides in mammals. C. B. Lebrilla*, *Department of Chemistry and Department of Biochemistry and Molecular Medicine University of California, Davis.*

Human milk oligosaccharides are the third most abundant dry component in milk. It has been attributed several protective properties to the infants from acting as prebiotic to pathogen block. Milk oligosaccharides have

diverse structure with potentially hundreds in human milk. The analysis of other mammalian milk has provided better understanding of human milk. Primates have MOs more similar to human. However, within the primates the similarities do not necessarily follow phylogeny. Milks of primates who live in large social groups tend to be more similar compared with those who are solitary. Human milk is high in fucosylation but low in sialylation. Conversely, animals who are non-primate such as bovine and porcine tend to have very high sialylation and low fucosylation. Understanding the differences in the HMO will be key to understanding the relationship between the different groups and their respective microbiota.

Key Words: human milk oligosaccharide, milk, fucosylation

452 Comparative growth physiology on the land and in the sea: Animal science to marine mammal biology. J. P. Richmond*, *University of North Florida, Jacksonville.*

At first glance, the connection between animal science and marine science may not be obvious. However, the closest terrestrial relatives to cetaceans (whale and dolphin) are ungulates (deer and cattle), and most cetacean species maintain a multi-chambered stomach despite their pisciviorous diet. Other species including seals and sea lions are monogastrics closely related to terrestrial carnivores such as mink and bear. Studies in marine systems often limit access to animals due to remote locations of animals, small population size, endangered species status, or limited ability to capture and restrain animals for sample collection. Research in bovine and porcine systems provide valuable models to study the physiological mechanisms that regulate growth and nutrient partitioning that can then be used to evaluate and interpret physiological status of free-ranging wildlife. Metabolic hormones such as growth hormone (GH) and insulin-like growth factor (IGF)-I, are well studied in domestic species, and are a bridge between growth physiology, sex, developmental age, and nutritional status. Differences in tissue specific growth rate are mediated by changes in the magnitude and timing of the response of these hormones during development. For example, in most species GH concentrations are elevated in neonates and decline with age while IGF-I follows the opposite pattern. Relatively slow growing Steller sea lions follow this typical domestic animal pattern and accumulate approximately 1% of body mass per day while nursing (GH 10 to 20 ng/mL, IGF-I 150 to 200 ng/mL at 4 wk of age). In contrast, rapidly growing hooded seal gain 30% of their body mass per day in the 4 d nursing period. GH is reduced (<5 ng/mL) and IGF-I is elevated (>300 ng/mL) at birth. These concentrations are maintained during nursing and facilitate rapid deposition of adipose tissue. Comparison of the hormonal regulation of growth in species with distinct developmental patterns will enhance our knowledge of the link between physiology, nutrition and life history of diverse species. Animal science provides the foundation on which to build our understanding of comparative growth physiology.

Key Words: comparative growth physiology, marine species

453 Cattle to cats: Comparative carbohydrate nutrition of widely diverse animal species. G. Fahey*, *University of Illinois, Urbana.*

Dietary fiber (structural carbohydrates + lignin) no longer is considered to be merely roughage, or ballast, or filler. Indeed, in human nutrition, it is considered a "shortfall nutrient," one that is seriously lacking in human diets as evidenced by the diseases that result, in part, from its absence. Likewise, fiber is essential in the diet of ruminants and represents an important component of the diet of non-ruminants. Fiber is one of the more complicated substances studied in the fields of animal and human nutrition. Knowledge of the plant cell wall – its chemical composition, physical properties, structure, organization, potential fermentability, viscosity, density, intake potential, feeding value within select diet matrices, health outcomes related to select fiber fragments – is critical if advancements are to be made in improving its utilization and in understanding physiological and health outcomes associated with fiber inclusion in diets. But it is no longer just about plant cell walls – oligosaccharides, resistant starches, glycemic carbohydrates, novel carbohydrates made from starch, and select bioactive fiber fragments all fall under the "fiber umbrella." This presentation will briefly recount a 40 year career of using comparative nutrition approaches to the study of this complex ingredient so important to the physiology and health of animals and humans.

Key Words: comparative nutrition, carbohydrate

454 Design and validation of primers to access rumen *Treponema saccharophilum* population in both in vitro and in vivo systems. J. Liu*[1,2], W. Zhu[1,2], Y. Y. Pu[1], J. K. Wang[1,2], and J. X. Liu[1,2], *[1]Institute of Dairy Science, College of Animal Sciences, [2]MoE Key Laboratory of Molecular Animal Nutrition, Zhejiang University, Hangzhou, Zhejiang, China.*

Treponema saccharophilum was isolated in the early decades and described as highly preferred to utilize pectin for growth. Typically, alfalfa hay contains 10–15% pectin as a component of the cell wall matrix, whereas grass or corn stover has pectin content less than 5%. The objective of this study was to develop a set of PCR primers targeting the 16S rRNA gene of *T. saccharophilum* and to assess the relative abundance of *T. saccharophilum* associated with different forages that vary in pectin content using real-time PCR method. Fifteen 16S rRNA gene sequences having higher than 97% similarity with *T. sacchrophilum*, retrieved from our pyrosequencing data, were used as target templates along with type strain *T. saccharophilum* DSM2985 for primer designing. To confirm the specificity of our designed primers, 23 clones of the PCR amplicons amplifying from total rumen DNA were randomly picked and sequenced to build phylogenetic tree. Phylogenetic analysis revealed 2 closely-related clusters: 3 clones grouping with the type strain and the rest of clones grouping together with no cultivable representatives, suggesting the existence of a subspecies of *T. saccharophilum*. Growth of *T. saccharophilum* under in vitro system was compared among alfalfa hay (AH), Chinese wild rye hay (CW) or corn stover (CS) alone and in combination with pectin or corn starch as substrate, to investigate the efficiency of this method. After incubation for 24 h, *T. saccharophilum* grew better in AH or CW with pectin than CW or CS as sole fiber source ($P < 0.05$). Supplementation of corn starch did not enhance the growth of *T. saccharophilum*. The validation of this method was also investigated in vivo. Samples of rumen fluid were collected from 12 primiparous Chinese Holstein cows that were fed on diets with AH, CW or CS as main forage source. The results of real time-PCR showed that the relative abundance of *T. saccharophilum* in rumen of cows fed on AH as forage source was significantly higher than those on CW and CS ($P < 0.05$).

Key Words: *Treponema saccharophilum*, pectin, forage

455 Effect of yeast-derived microbial protein in low and high forage diets on lactation performance of dairy cows. A. K. Manthey*[1], K. F. Kalscheur[1], A. D. Garcia[1], and K. Mjoun[2], *[1]South Dakota State University, Brookings, [2]Alltech, Brookings, SD.*

The objective of this study was to investigate the effect of substituting soybean meal with yeast-derived microbial protein [(YMP) DEMP; Alltech Inc., Nicholasville, KY] in diets containing 2 forage concentrations. Sixteen Holstein cows (4 primiparous and 12 multiparous) were randomly assigned to a 4 × 4 Latin square in a 2 × 2 factorial arrangement of treatments. Diets contained low (LF; 45% of diet DM) or high forage (HF; 65% of diet DM) and YMP at 0 (NYMP) or 2.25% (WYMP) of the diet. Forage consisted of 67% corn silage and 33% alfalfa hay (DM basis). Cows fed LF consumed more DMI (28.3 vs. 26.8 kg; ($P < 0.007$) and produced more milk (39.9 vs. 39.7 kg; $P < 0.005$) than cows fed HF regardless of the addition of YMP (Table 1). Milk fat percentage was lower in cows fed LF compared with HF (3.76 vs. 3.94; $P < 0.04$), whereas fat yield tended to be lower ($P < 0.07$) in cows fed YMP than in those that were not. Although milk protein percentage did not differ between forage concentrations with or without the addition of YMP, protein yield and total solids were greater in cows fed LF. Cows fed LF produced more energy-corrected milk (ECM) than those fed HF (41.9 vs. 40.2; $P < 0.04$). Feed efficiency (ECM/DMI) was greater for cows fed NYMP compared with WYMP (1.52 vs. 1.45; $P < 0.02$). There were no interactions of forage and YMP for any of the parameters measured. Results suggested that the forage level as well as YMP affected cow performance. Cows fed LF diets produced more milk and ECM, yet resulted in a lower fat percentage.

Table 1.

	Low forage		High forage			
Item	NYMP	WYMP	NYMP	WYMP	SEM	*P*-value[1]
DMI, kg/d	28.3	28.2	26.0	27.2	0.97	F
Milk, kg/d	39.9	40.4	38.4	37.3	1.09	F
Fat, %	3.84	3.68	3.98	3.89	0.15	F
Fat, kg/d	1.52	1.47	1.52	1.43	0.05	NS
Protein, %	3.26	3.25	3.26	3.19	0.08	NS
Protein, kg/d	1.30	1.31	1.25	1.18	0.03	F
TS, kg/d	5.15	5.12	5.03	4.73	0.13	F
ECM, kg/d	42.1	41.7	41.2	39.2	0.98	F
ECM/DMI	1.50	1.47	1.54	1.44	0.04	D

[1]F = Forage effect ($P < 0.05$); D = YMP effect ($P < 0.05$); NS = no significant effect of forage, YMP, and forage × YMP interaction.

Key Words: dairy cow, forage concentration, yeast-derived microbial protein

456 Effects of subacute ruminal acidosis on fecal pH and starch digestibility of Holstein cows. C. S. Fox*, S. Luan, M. R. Murphy, and F. C. Cardoso, *University of Illinois, Urbana-Champaign.*

To investigate the association of subacute ruminal acidosis (SARA), fecal pH (FPH), and starch digestibility (SD), 6 rumen-cannulated Holstein cows (CAN, BW = 762 kg; 287 ± 45 d in milk) were used in a replicated 3 × 3 Latin square design balanced for carry-over effects. Periods (10 d) were divided into 4 stages (S): S1, baseline, d 1–3, ad libitum TMR; S2, restricted feeding, d 4, cows fed for 50% of S1 DMI; S3, challenge, d 5, treatments applied; S4, recovery, d 6–10, all cows were fed ad libitum TMR. Treatments were: CON, no top dress; MOD, 10% of S1 DMI as top dress (pelleted mixture of 50:50-wheat:barley); and HIG, 20% of S1 DMI as top dress. TMR samples were analyzed for starch and lignin contents weekly. Fecal samples were collected in 7 time points (TP): TP1, d 1-afternoon; TP2, d 5-morning; TP3, d 5-afternoon; TP4, d 5-night; TP5, d 6-morning; TP6, d 6-afternoon; and TP7, d 7-afternoon. Fecal pH was measured at sample collection. Fecal samples from TP1 to TP5 were analyzed for starch and lignin contents. Rumen pH was lower ($P < 0.0001$) for HIG (6.25 ± 0.09) than for CON (6.44 ± 0.09). Nadir time (hour relative to feeding) at rumen pH below 6 were 3, 5, and 7 h for CON, MOD and HIG, respectively. Fecal pH was similar ($P = 0.233$) for CON (6.48 ± 0.06), MOD (6.54 ± 0.07), and HIG (6.37 ± 0.07). At TP4 FPH was at its nadir (6.04 ± 0.09, $P < 0.001$). At S3 FPH had a tendency ($P = 0.102$) for a linear effect among CON, MOD, and HIG (6.54 ± 0.08, 6.50 ± 0.08, and 6.38 ± 0.08, respectively). Starch digestibility tended ($P = 0.102$) to be greater for CON then MOD and HIG (96.71% ± 0.8, 96.36% ± 0.8, and 94.15% ± 0.8, respectively).

Starch digestibility displayed a linear effect ($P = 0.048$) among CON, MOD, and HIG. At S3 there was a linear effect ($P = 0.014$) for SD among CON, MOD, and HIG (97.62% ± 1.5, 97.47% ± 1.5, and 91.84% ± 1.6, respectively). At TP4 SD was at its nadir (93.74% ± 1.2, $P < 0.053$). In conclusion, cows receiving HIG had lower SD than cows receiving MOD or CON. Linear effects for both SD and FPH with increasing challenge suggest a relationship that might be useful as a diagnostic tool for SARA.

Key Words: subacute ruminal acidosis, fecal pH, starch digestibility

457 Induction of subclinical ruminal acidosis leads to marked alterations in blood immunometabolic markers and minerals in lactating Jersey than Holstein cows file in response to. J. S. Osorio*[1], F. T. da Rosa[1], E. Trevisi[2], M. R. Murphy[1], F. Cardoso[1], and J. J. Loor[1], *[1]University of Illinois, Urbana, [2]Università Cattolica del Sacro Cuore, Piacenza, Italy.*

Subacute ruminal acidosis (SARA) has long been regarded as a major reason for economic losses in the dairy industry in the United States. SARA has been associated with decreased milk production and decreased efficiency of milk production, while it increases culling rate and death loss. Although Holstein and Jersey cows have inherent differences in terms of lactation potential their response to SARA in terms of immunometabolic alterations and their resilience to normal levels after induction of SARA are yet to be defined. Twelve lactating cows (>100 DIM; n = 12/breed) were used in a replicated 2 × 2 Latin square design of represented period and dietary treatment (control and challenge). Each period comprised 10 d divided into 4 stages: baseline (d 1–3), feed restriction (d 4), challenge (d 5), and recovery (d 6–10). In each period a control (CO) diet was offered during baseline and recovery stages. On d 4 cows were restricted to 50% of average baseline feed intake until d 5. The challenge on d 5 consisted of either a CO diet or the CO + 4.6 kg of a 50:50 wheat/barley pellet. Blood samples were collected on d 5 at 0, 3, 6, and 12 h relative to the challenge. Data from cows subjected to challenge were analyzed using the PROC MIXED procedure of SAS, where square, period, breed (b), and h were fixed effects, while cow nested within period was the random effect. An interaction of b × h ($P < 0.04$) was observed for Mg, Na, K, aspartate transaminase (AST), NEFA, and BHBA with Jerseys having greater concentrations of these biomarkers at either 3 or 6 h after challenge. Besides NEFA and Mg, Jerseys also had greater concentrations of other biomarkers at 0 h. Concentrations of Mg, ceruloplasmin, albumin, alkaline phosphate, haptoglobin, NEFA, and reactive oxygen metabolites (ROMt) were greater ($P < 0.04$) overall in Jersey cows regardless of h after challenge. Similarly, creatinine and myeloperoxidase were greater ($P < 0.03$) in Holstein cows. Overall, our results suggest that the profile of immunometabolic biomarkers and minerals in blood were more affected by SARA in Jerseys.

Key Words: breed, immunometabolite, SARA

458 Evaluation of OmniGen AF in heat-stressed Holstein cows in lactation. L. W. Hall*[1], S. D. Anderson[1], F. A. Rivera[1], F. Villar[1], J. D. Chapman[2], N. M. Long[3], and R. J. Collier[1], *[1]University of Arizona, Tucson, [2]Prince Agri, Quincy, IL, [3]Clemson University, Clemson, SC.*

OmnGen AF is a feed supplement containing yeast and B vitamins. A total of 60 cows on a commercial dairy in Arizona were balanced for DIM, parity and milk production and assigned to 1 of 2 treatment groups fed OmniGen AF (OG, 30 cows) or control (CON, 30 cows) diets for 52 d postcalving. At 52 d of lactation cows were randomly selected (n = 12) from both groups (6 OG and 6 CON) and housed in environmentally controlled modules for 21 d at the University of Arizona. The OG was top-dressed 2×/d with molasses as the carrier and the CON cows received the molasses carrier 2×/d. Both were mixed into the top one-third of the TMR. During the environmental room phase of the study cows fed OG had higher feed intake than CON during heat stress (HS) (46.8 kg vs. 42.9 kg, $P < 0.0001$) and no difference during thermoneutral (TN). A temperature-humidity index (THI) threshold of 68 or greater was used to achieve HS. Feeding OG maintained a numerical 1 kg milk yield advantage compared with CON (30.3 kg vs. 31.4 kg, $P = 0.26$) during HS but not during TN. Cows fed OG had lower milk fat (%) (4.2% vs. 3.8%, $P = 0.02$) and milk protein (%) ($P = 0.04$). There was no difference in 3.5% FCM between treatments. Water consumption was lower (12.4 l/d in OG treated cows, $P < 0.01$) than control cows. Respiration rates were lower in treated cows at 1400 h and 1700 h (4.7 and 8.4 less respirations/min, $P = 0.05, < 0.001$) and rectal temperatures were also lower (0.15°C and 0.25°C lower that CON, $P = 0.05, < 0.001$) in treated cows. Feeding OG reduced physiological responses to heat stress in lactating dairy cows.

Key Words: heat stress, nutrition

459 The effects of feeding time on the circadian pattern of feed intake, milk production, and plasma hormones and metabolites in dairy cows. M. Niu*, Y. Ying, P. A. Bartell, and K. J. Harvatine, *Penn State University, University Park.*

The timing of feed intake entrains circadian rhythms (24 h repeating cycles) in other mammals. The object of this study was to determine if the timing of feeding can entrain circadian rhythms in dairy cows. Nine Holstein cows were arranged in a replicated 3 × 3 Latin Square design with 14-d periods in an automated feed observation system that recorded feed weight every 10 s. Treatments were feeding 1 ×/d at 0830 h (AM) or 2030 h (PM) and feeding 2 ×/d in equal amounts at 0830 and 2030 h (AMPM). All treatments were fed at 110% of daily intake. Cows were milked 2 ×/d at 0500 and 1700 h. Daily measurements were analyzed by a mixed model that included the random effect of cow and period and the preplanned contrasts were AM vs. PM and AM vs. AMPM. Time course data were analyzed with mixed model procedures using repeated measures and the planned contrast were tested at each time point. Second, a cosine function was fit to time course data by nonlinear regression. There was no effect of treatment on DMI, digestible DMI, or total tract digestibility of DM, OM, and NDF. Over 16 and 24% of DMI was consumed in the first hour after feeding for the AM and PM, and 12 and 19% for AMPM in the morning and evening, respectively. Milk yield and composition did not differ among treatments. Milk yield at the 0500 h milking was 1.3 kg higher than the 1700 h milking ($P < 0.01$). Plasma BUN was increased 0.52 and 0.89 mg/dL by PM and AMPM compared with AM, respectively ($P < 0.05$). Treatment did not affect fecal NDF or plasma insulin, glucose, and NEFA, but there was an interaction of treatment and time ($P < 0.05$). Treatment modified the circadian pattern of fecal NDF ($P < 0.01$), plasma glucose ($P < 0.05$), and insulin ($P < 0.01$), but no effect on plasma BUN or NEFA was observed. Phase (time of peak) of fecal NDF was advanced 4.4 h by PM compared with AM ($P < 0.05$), and amplitude tended to be reduced by AMPM compared with AM ($P = 0.08$). In conclusion, feeding time entrains the circadian rhythms of fecal NDF, plasma glucose, and insulin, but has little effect on daily DMI and milk yield.

Key Words: feeding time, circadian rhythm, dairy cow

460 Effects of subacute ruminal acidosis on milk yield and milk composition of Holstein and Jersey dairy cows. K. J. Haerr*, S. Luan, M. R. Murphy, and F. C. Cardoso, *University of Illinois, Champaign-Urbana.*

To investigate the association between Subacute ruminal acidosis (SARA) on milk yield and milk composition, 6 Holstein cows (HOL, BW = 717 kg; 258 ± 16 d in milk), 6 rumen-cannulated Holstein cows (CAN, BW = 762 kg; 287 ± 45 d in milk), and 6 Jersey cows (JER, BW = 470 kg; 190 ± 86 d in milk) were used in a replicated 3 × 3 Latin square design to measure carry-over effects. Periods consisted of 10 d and were divided in 4 stages. Stage 1 (S1), baseline, d 1–3, ad libitum TMR; S2 restricted feeding, d 4, all cows fed for 50% of their S1 DMI; S3 challenge, d 5, treatments applied; S4, recovery, d 6–10, cows were fed ad libitum TMR. Cows were fed according to NRC (2001) recommendations. Treatments were: CON, no top dress (TD, pelleted mixture of 50:50 of wheat:barley); MOD, 10% of DMI in S1 as TD; and HIG, 20% of DMI in S1 as TD. Milk yield was recorded daily and milk composition was obtained for d 2, 4, 5, and 8. Dry matter intake was recorded daily. Body weight and BCS were measured at each period. Statistical analysis was performed using the MIXED procedure of SAS 9.2 (SAS Institute, Inc.). No treatments carry-over effects were observed for any outcome variable ($P > 0.30$). Milk yield was similar ($P = 0.141$) for CON (21.2 ± 35 kg/d), MOD (22.22 ± 35 kg/d), and HIG (21.85 ± 36 kg/d). Holstein milk yield was higher ($P < 0.001$) than JER (24.9 ± 49 and 19.2 ± 54 kg/d, respectively). There was no difference ($P = 0.486$) in milk fat (MF) among treatments. Holstein MF was lower ($P < 0.001$) than JER MF (3.64% ± 0.1 and 4.74% ± 0.1, respectively). There was no difference ($P = 0.615$) in milk protein (MP) among treatments. Holstein MP was lower ($P < 0.001$) than JER MP (3.08% ± 0.06 and 3.65% ± 0.02, respectively). Feed efficiency (FE = energy-corrected milk/DMI) was greater ($P < 0.001$) for S2 (3.34 ± 0.2) than for S1 (1.66 ± 0.2), S3 (1.16 ± 0.2), and S4 (1.65 ± 0.2). In conclusion, MOD and HIG did not result in greater milk fat depression or lower milk yield compared with cows receiving CON.

Key Words: milk, ruminal acidosis, SARA

461 Effects of *Saccharomyces cerevisiae* fermentation product on bacteria in the rumen and hindgut of lactating dairy cows during subacute ruminal acidosis (SARA). S. C. Li*[1], E. Khafipour[1], I. Yoon[2], M. Scott[2], and J. C. Plaizier[1], *[1]University of Manitoba, Winnipeg, MB, Canada, [2]Diamond V, Cedar Rapids, IA.*

The effects of *Saccharomyces cerevisiae* fermentation product (SCFP) on bacteria in the rumen and hindgut during normal feeding (first 4 wk) and subacute ruminal acidosis (SARA_ challenge (following 1 wk grain-based feeding) were studied using 8 rumen- and cecal-fistulated lactating dairy cows in a crossover experiment. A 3-wk washout period separated the experimental periods. During the SARA challenge, 22% of the corn silage in the diet was replaced with wheat/barley pellets. Cows were either supplemented with 14 g/d of Diamond V Original XPC mixed with 140 g/d ground corn (SCFP) or with 140 g/d of ground corn only (Control). During wk 4 and 5 of each period, ruminal, cecal, and rectal contents were sampled at 0 and 6 h after feeding. Genomic DNA was tested using a relative qPCR SYBR Green assay with the primers targeting the 16s rRNA gene of tested bacteria groups except *E. coli*, for which FimH gene was targeted. The challenge successfully induced SARA, and the time below pH 5.6 increased ($P < 0.01$) from 11 to 311 min/d. In the rumen, SARA increased ($P < 0.05$) *Lactobacillus* spp., *Megasphaera elsdenii*, and *Prevotella albensis*, and decreased ($P < 0.05$) *Prevotella brevis* and *Treponema bryantii*. Supplemental SCFP increased ($P < 0.05$) *P. brevis* and *Bifidobacterium* and showed the potential to alleviate changes caused by SARA. In the cecum, SARA reduced ($P < 0.05$) *P. brevis*, *Clostridium perfringens* while increasing ($P < 0.05$) *M. elsdenii* and *E. coli*. Supplemental SCFP tended to increase ($P = 0.11$) *Bifidobacterium* in the cecum under normal and SARA challenge conditions. In the rectum, SARA increased ($P < 0.05$) *Lactobacillus* spp., *M. elsdenii*, *T. bryantii*, and *E. coli*, and reduced ($P < 0.05$) *Bifidobacterium*. Supplemental SCFP tended ($P = 0.06$) to increase *T. bryantii*, *Bifidobacterium* and *Butyrivibrio fibrisolvens* in the rectum. Neither SARA nor SCFP affected *Streptococcus bovis* and *C. perfringens* in the rumen and hindgut. In conclusion, SCFP stabilized rumen conditions during SARA by alleviating the microbial population changes caused by SARA and increased bacterial populations with beneficial health effects, such as *Bifidobacterium*.

Key Words: bacteria, Original XPC, SARA

462 Factors associated with the type and levels of mastitis pathogens isolated from milk samples collected from milk of organically and conventionally managed dairy cattle. Z. Ullah*[1], J. K. Margerison[1], D. Simcock[2], and N. Lopez Villolobos[3], *[1]Institute of Agriculture and Environment, Massey University, Palmerston North, New Zealand, [2]Institute of Food Nutrition and Human Health, Massey University, Palmerston North, New Zealand, [3]Institute of Veterinary and Biological Sciences, Massey University, Palmerston North, New Zealand.*

This study assessed the factors associated with mastitis related pathogens isolated from individual quarter milk samples collected from 46 organically (Org) and 51 conventionally (Conv) managed dairy cows. The Rapid Mastitis Test and pathogen isolation were completed on milk samples collected at 1, 14, 130, 260 d in milk (DIM). Presence of mastitis pathogens was treated as a binomial trait (0 = absence, 1 = presence), and modeled, following a logit-transformation, using PROC GLM MIX (SAS version 9.3) including herd, lactation number, DIM and interaction between management type and lactation number as fixed effects and individual cow as a random effect. Monthly somatic cell count (Org: 145,000; Conv: 139,000/ml) did not differ between organic and conventional management. *Bacillus* spp. were isolated more frequently from organic than conventional quarters (Org: 8.6; Conv: 5.3 isolates) whereas coagulase-negative staphylococci (CNS) tended ($P = 0.055$) to be isolated more frequently in organically (Org: 24.3) than conventionally (Conv: 17.3) managed quarters. The CNS cases were greater in all cows at 1 DIM (CNS: Org: 35.6%; Conv 29.7%) compared with 130 DIM (CNS: Org: 24.9%; Conv: 11.8%). Conventional quarters had a higher incidence of *Bacillus* spp. and *Streptococcus uberis* at 1 DIM than organically managed quarters. *Bacillus* spp. was isolated more frequent in older (>5 lactations) conventionally managed quarters, while cases of *Streptococcus uberis* were greater in 3+4 lactation organically managed animals. Clinical mastitis (CM) and CNS were greater in organic cows in 1 and > 5 lactations, while conventional cows showed no significant differences between lactations. In conclusion, organically managed cows had a greater number of cases of *Streptococcus uberis* in 3+4 lactation and cases of animal culling were higher. Overall, mastitis pathogens were more frequent at 1 DIM and first lactation animals, indicating the opportunity to improve prevention in dry cows and prepartum heifers.

Key Words: mastitis, organic, dairy

463 Associations of subclinical endometritis with energy metabolism and inflammation during the periparturient period and early lactation in dairy cows. T. Yasui*, K. McCann, R. O. Gilbert, D. V. Nydam, and T. R. Overton, *Cornell University, Ithaca, NY.*

Multiparous Holstein cows (n = 108) were used to determine the associations of subclinical endometritis (SCE) with plasma nonesterified fatty acids (NEFA) and B-hydroxybutyrate (BHBA) as markers of energy metabolism, calculated energy balance (EB), and plasma haptoglobin (Hp) as a marker of inflammation during the periparturient period and early lactation. Evaluation of endometrial cytology by low volume uterine lavage was conducted on one day between 40 and 60 d postcalving. The incidence of SCE among cows sampled was 40%. Area under the curve (AUC) were calculated for both NEFA and BHBA using data collected from −3 to +3 wk relative to parturition. Overall, cows that developed SCE tended to have higher AUC for NEFA (7759 vs. 6602 μEq/L × d; $P = 0.08$) and BHBA (126.9 vs. 112.6 mg/dL × d; $P = 0.08$). Further stratification into prepartum (wk −3 to parturition) and postpartum (parturition to wk +3) revealed that prepartum AUC for both NEFA and BHBA were not associated with subsequent SCE, whereas postpartum AUC for NEFA (5391 vs. 4427; $P = 0.11$) tended to be increased and BHBA was increased (72.0 vs. 58.9; $P < 0.05$) for cows that developed SCE. Consistent with the results for plasma NEFA and BHBA, calculated EB during the prepartum period was not different in cows that did or did not develop SCE; however, cows with SCE had lower (−3.8 vs. −1.9 Mcal/d; $P = 0.02$) EB during the 6-wk postpartum period compared with cows without SCE. Analysis of EB by week (wk −3 to −1 before calving and wk 1 to 6 postcalving) indicated that EB in cows with SCE was lower at wk 1 (−8.1 vs. −4.9; $P = 0.01$), wk 2 (−7.9 vs. −5.5; $P = 0.04$), and wk 3 (−4.9 vs. −2.7; $P < 0.05$) and tended to be lower at wk 6 (0.9 vs. 2.5; $P = 0.10$) than cows without SCE. Plasma Hp concentrations were analyzed from wk 1 to 8 of lactation; concentrations of Hp were not different during either wk 1 or the entire postpartum period between cows that did or did not develop SCE. These results suggest that decreased energy status, particularly during the first 3 wk postpartum, predisposes dairy cows to subsequent SCE.

Key Words: subclinical endometritis, energy status, haptoglobin

464 Meta-genomics of rumen bacteria in cows exposed to different feeding strategies. H. M. Golder*[1,2], S. E. Denman[3], C. McSweeney[3], W. J. Wales[4], M. J. Auldist[4], A. R. Rabiee[1,2], P. Celi[2,5], and I. J. Lean[1,2], *[1]SBScibus, Camden, NSW, Australia, [2]University of Sydney, Faculty of Veterinary Science, Camden, NSW, Australia, [3]CSIRO Animal, Food and Health Services, Queensland Bioscience Precinct, St. Lucia, QLD, Australia, [4]Future Farming Systems Research Division, Department of Primary Industries, Ellinbank, VIC, Australia, [5]Melbourne School of Land and Environment, The University of Melbourne, Parkville, VIC, Australia.*

We hypothesized that distinct bacterial communities would result from different feeding strategies. Twenty-four rumen fistulated, lactating Holstein cows in a prospective cohort study grazed pasture that provided approximately 8 kg DM/cow per d and were offered 1 of 3 diets: (1) Control (10 cows); (2) partial mixed ration (PMR; 10 cows); or (3) PMR plus protein (PMR+P; 4 cows). The study compared feeding PMR with or without increased protein with controls. The control diet included wheat grain fed twice daily at milking and ryegrass silage fed on the pasture. The PMR comprised corn silage, corn grain, wheat grain and the same silage fed on a feedpad twice daily after milking. The PMR+P cows were managed similarly to the PMR cows, but the ration contained lucerne hay, no silage and 16% DM of the wheat grain was replaced with canola meal. Monensin (220 mg/hd/d), tylosin (220 mg/hd/d), vitamins and minerals were included in all diets. The diets were replicated at 5 rates: 8, 10, 12, 14 or 16 kg DM/cow per d (27:73 ryegrass silage:wheat DM; 2 cows/rate per diet). The PMR+P was offered at 14 or 16 kg only. Rate within diet comparison was isoenergetic. Three rumen fluid samples were collected over a 10 h period after AM milking. Genomic DNA 454 tag amplicon pyrosequence data was processed using QIIME software. Microbiomes were not different; however, distinct bacterial populations between diets ($P < 0.001$) and rates ($P < 0.001$) were evident on principal components between group analysis. Co-inertia analysis showed feeding rate was a larger influence on bacterial composition than time of sampling, individual rumen VFA, ammonia, lactate or pH. Rate had a large effect on bacterial composition for the Control and PMR groups fed the 8 or 10 kg rate. A strong positive association was present between ammonia and bacteria in 12 and 14 kg PMR groups and 14 kg PMR+P cattle. Bacteria populations of these 3 groups were positively associated with lactate, butyrate, acetate and pH. Bacteria in the control group fed at 12, 14 or 16 kg were strongly influenced by propionate concentrations. Feeding system and rate influenced rumen measures and bacterial populations.

Key Words: acidosis, meta-genomics

465 The influence of immunological stress on the limiting sequence and ratio of lysine, methionine and threonine in preruminant calves. N. Zhang*, H. Li, Y. Tu, C. Jiang, and Q. Diao, *Feed Research Institute, Chinese Academy of Agricultural Sciences, Beijing, China.*

The redistribution of nutrients from the growth process to support of immune system function suggests altered nutritional requirements during immune challenge. However, it is not clear how the amino acid requirements altered following immune stress. This study investigated the effect of immunological stress on the limiting sequence and ratio of Lys, Met, and Thr in preruminant calves. According to the method of amino acid deletion, 25% of Lys, Met or Thr was deleted from the milk replacers, which contained 22.00% CP, 1.60% Lys, 0.50% Met and 1.03% Thr, to form 4 kind of experimental diets. Forty male Chinese Holstein calves (between 6 and 8 d old, 40 ± 1 kg of body weight) were randomly divided into 8 groups with 5 replicates (1 calf per replicate). Per Four groups of calves feed 4 kinds of diets respectively. The first 4 groups injected intraperitoneally with 2.5 μg *E. coli* lipopolysaccharides (LPS) /kg BW at 24, 26 and 28 d of age. The other 4 groups injected with an equivalent volume of sterile saline as control. A total collection of feces and urine was conducted between 25 and 27 d for analysis of nitrogen metabolism. The average daily gain of calves was decreased (438.7 vs. 366.5 g/d, $P < 0.05$, for the Control and LPS group calves, respectively) and the ratio of feed to gain of calves was increased (1.89 vs. 2.21, $P < 0.01$)by the immunological stress. The nitrogen retention was suppressed by the immunological stress (0.54 vs. 0.49 g N /kg $BW^{0.75}$/d, $P < 0.05$). The ratio of the change of N retention (g /kg $BW^{0.75}$/d) to the change of Lys, Met, or Thr intake (g /kg $BW^{0.75}$/d) changed from 1.34, 1.07 and 0.71 to 0.92, 0.49 and 0.67, suggested that the limit sequence of Lys, Met, and Thr were changed from Lys > Met > Thr to Lys > Thr > Met, with the immunological stress. The ratio of Lys / Met / Thr for calves changed from 100/29/58 to 100/27/61 with the immunological stress. The results indicated that the immunological stress suppressed the growth performance and nitrogen balance, and changed the limit sequence and the optimum ratio of Lys, Met, and Thr.

Key Words: amino acid, immunological stress, limiting sequence and ratio

Ruminant Nutrition: Dairy: Starch, Amino Acids and By-Products Supplementation

466 The effect of arginine supplementation during pregnancy on uterine blood flow in dairy heifers. C. Yunta*[1], B. R. Mordhorst[2], K. A. Vonnahme[2], C. Parys[3], and A. Bach1,4, *[1]Department of Ruminant Production-IRTA, Caldes de Montbui, Barcelona, Spain, [2]Center for Nutrition and Pregnancy, Department of Animal Science, North Dakota State University, Fargo, [3]Evonik Industries AG, Hanau, Germany, [4]ICREA, Barcelona, Spain.*

We hypothesized that arginine (Arg) supplementation during early pregnancy would increase uterine blood flow. The objective of this study was to evaluate the effects of Arg supplementation on uterine artery hemodynamics from d 40 to 140 of gestation in dairy heifers. Catheters were surgically placed into the peritoneal cavity on d 41 of gestation in Holstein heifers (n = 17; 448 ± 73.9 kg) and every 12 h, infusions of 40 mg of Arg/kg of BW (ARG; n = 9) or an equivalent volume of buffered saline (CTRL; n = 8) were administered until d 146. Animals were fed ad libitum, and DM intake (DMI) was recorded daily. Blood samples were obtained, heifers were weighed, and uterine artery hemodynamics [flow volume (FV), heart rate, pulsatility index (PI), and resistance index (RI)] were recorded on d 41, 62, 83, 104, 125, and 146. Plasma concentrations of amino acids (AA) were analyzed. Data from d 41 of pregnancy were considered as a baseline and the remainders of the data were then analyzed using a mixed-effects model that accounted for the fixed effects of treatment, day of gestation, and their interaction, with age and BW at d 41 as covariates, plus the random effect of heifer within treatment. There were no differences in DMI. Overall, FV increased ($P < 0.001$) with pregnancy day (172 ± 44.5 mL/min on d 41; 954 ± 45.8 mL/min on d 146). Uterine blood FV evolved differently between treatments, with CTRL heifers having a greater ($P < 0.05$) FV (1104 ± 65.42 mL/min) at 146 d of pregnancy than ARG heifers (806 ± 65.3.2 mL/min). PI and RI decreased throughout pregnancy but did not differ between treatments. Heart rate was less ($P < 0.05$) in ARG (74 ± 1.4 beats/min) than CTRL heifers (81 ± 1.5 beats/min). Plasma concentrations of Arg tended ($P = 0.09$) to be greater in ARG than in CTRL heifers, but Car, Val, Ile, Leu, Phe and Trp were less ($P < 0.05$) in ARG than in CTRL heifers and so was the proportion of essential AA in plasma (65 ± 2.3 vs. 73 ± 2.4%). Contrary to our hypothesis, Arg did not increase uterine blood flow but did alter heart rate and maternal concentration of some plasma AA.

Key Words: arginine, blood flow, heifer

467 Protein source and amino acid balance for dairy calves fed milk replacer. G. H. Hwang*[1], J. J. Castro[1], A. Saito[2], D. A. Vermeire[3], and J. K. Drackley[1], *[1]University of Illinois, Urbana, [2]Zen-Raku-Ren, Tokyo, Japan, [3]Nouriche Nutrition Ltd., Lake St. Louis, MO.*

Amino acid (AA) balance and content of non-milk proteins may be important for calves fed milk replacers for intensified growth. Our objectives were to determine: 1) if essential AA might be limiting in milk replacers containing skim milk and whey proteins; 2) effects of replacing whey protein concentrate (WPC) with hydrolyzed wheat protein (HWP); and 3) if essential AA balance might limit growth in calves fed milk replacer formulated with skim milk proteins and HWP. Calves (12–13 females, 7–10 males per diet) were assigned randomly at d 2 of life to 5 milk replacer diets in a continuous design. Calves were fed only milk replacers (28.5% CP, 15% fat) to 28 d; then starter was introduced. Milk replacers were fed at 600 g/d in wk 1, 800 g/d in wk 2, and 1200 g/d in wk 3 and 4. Diet A was formulated to contain 2.6% Lys from skim milk and WPC; other diets were supplemented with Lys-HCl to 2.6% Lys. Diet B was as Diet A but with added Met, Thr, His, Phe, Val, and Leu to achieve a dietary AA profile suggested to optimize growth recommended by Van Amburgh (Cornell Univ.). Diets C and D contained 4.5% and 9.0% HWP, with Met, Thr, His, Phe, Val, Leu, Ile, and Trp added to meet diet B profile. Diet E was as diet D but with only Lys, Met, and Thr balanced. Skim milk protein was constant across diets; HWP replaced half (diet C) or all (diet D) of the WPC. Calves were weaned at 56 d, with final measurements at d 90. Data were subjected to ANOVA and regression analysis. Mean BW tended to be lower for calves fed diet E than for those fed diet B at 8 wk (77.8 vs. 80.7 kg, $P = 0.08$). The linear effect of age on BW from wk 1 to 13 was less ($P < 0.05$) for diet E than for diets A and C but did not differ from diet B ($P = 0.19$). Linear and quadratic effects of increasing MWP on ADG were not significant ($P = 0.78$, $P = 0.73$). Growth did not differ between diets A or B. Starter intake was lower for diet B than for diet A, but did not differ among other diets. In conclusion, addition of essential AA to a milk protein-based milk replacer did not increase growth. Inclusion of 4.5 or 9% HWP in milk replacer for intensified growth did not decrease growth when essential AA were balanced.

Key Words: calf, amino acid, modified wheat protein

468 Effect of dietary starch concentration in primiparous dairy cows in early lactation. H. Gencoglu*[1], G. Yilmazbas-Mecitoglu[2], A. Keskin[2], I. Cetin[1], C. Kara[1], A. Orman[3], E. Karakaya[2], G. Deniz[1], A. Gumen[2], I. I. Turkmen[1], and R. D. Shaver[4], *[1]Department of Animal Nutrition and Nutritional Diseases, Faculty of Veterinary Medicine University of Uludag, Bursa Turkey, [2]Department of Obstetrics and Gynecology, Faculty of Veterinary Medicine University of Uludag, Bursa, Turkey, [3]Department of Zootechnics, Faculty of Veterinary Medicine University of Uludag, Bursa, Turkey, [4]Department of Dairy Science, University of Wisconsin-Madison, Madison.*

The objective of this trial was to determine the effect of dietary starch concentration on locomotion and body condition scores and performance of early lactation dairy cows fed diets of different starch concentrations. Twenty-four primiparous Holstein cows were randomly assigned to 1 of 3 treatments in a completely randomized design from calving through 72 d DIM. Diets contained 30% corn silage, 20% chopped alfalfa hay, and 50% concentrate/mineral/vitamin/additive mixtures (on DM basis). The concentrate mixtures were formulated by partially replacing dry ground shelled corn with wheat bran. Cows were fed the low (LS), medium (MS) and high-starch (HS) diets as total mixed ration. The dietary starch contents were 16.2, 19.8, and 24.1% for low LS, MS, and HS, respectively (DM basis). Body condition score (BCS), body weight (BW) and locomotion scores were measured weekly throughout the trial. Dry matter intake and milk yield were recorded daily on individual cows milked 3×. Data were analyzed according mixed models procedure. There was a tendency ($P = 0.07$) for locomotion scores to be greater for MS compared with LS. Milk yield averaged 29.4 kg/d and was unaffected ($P > 0.10$) by treatment. Values for milk urea nitrogen ranged from 12.4 to 13.0 mg/ dL across the treatments and was lower for cows fed MS than for cows fed the LS. The BW, BCS, and milk fat and protein percentage measurements were unaffected ($P > 0.10$) by treatment. Dry matter intake for cows fed the LS diet was 1.1 and 2.3 kg/d greater than for cows fed the MS ($P < 0.05$) and HS ($P < 0.01$) diets, respectively. It was concluded that when partially replacing corn grain with wheat bran to formulate

reduced-starch diets, increased dry matter intake for dairy cows fed LS may reduce feed efficiency (kg of milk/kg of dry matter intake).

Key Words: dairy cow, milk production, starch

469 Milk fat depression caused by feeding distillers grains and corn oil to dairy cows was partially alleviated by supplementing potassium carbonate. K. C. Lamar* and W. P. Weiss, *The Ohio State University, Wooster.*

In vitro experiments have found that added K_2CO_3 decreased concentrations of biohydrogenation intermediates associated with milk fat depression, such as trans-10, cis-12 CLA. These intermediates are often produced when diets are fed to cows with high concentrations of polyunsaturated fatty acids such as those found in distiller's grains. We hypothesized that adding K_2CO_3 to a high fat diet based on distillers grains would alleviate milk fat depression. Sixteen Holstein cows averaging 157 DIM were placed into 4 blocks; each block comprised a 4 × 4 Latin square with 21-d periods and a 2 × 2 factorial arrangement of treatments. The basal diet (no added K or fat) contained 25% distillers grain with corn silage as the sole forage and contained 22% starch, 32% NDF, 3.4% long chain fatty acids, and 1.5% K (DM basis). Treatments were 0 or 1.9% added fat from corn oil (in high fat diets, distillers +corn gluten meal + corn oil = 25%) with 0 or 0.85% added K (from DCAD Plus; Church & Dwight Co., Inc., Princeton, NJ). Dry matter intake was reduced with supplemental K (20.9 vs. 22.3 kg/d; $P < 0.01$) and fat (21.1 vs. 22.2 kg/d; $P < 0.01$) but no interaction was observed. Likely in response to lower DMI, milk production tended to decrease with added K (31.1 vs. 32.2 kg/d $P < 0.09$). Added fat decreased milk fat percent (2.78 vs. 2.97%; $P < 0.01$) and added K increased it (3.00 vs. 2.75%; $P < 0.01$) but no interaction was observed. Milk fat yield was reduced by fat supplementation but an interaction between fat and K was observed ($P < 0.05$). Supplemental K increased fat yield with high fat (0.92 vs. 0.84 kg/d; $P < 0.01$) but had no effect with the lower fat diet (0.96 vs. 0.97 kg/d; $P > 0.1$). Milk protein percent (3.35 vs. 3.43% $P < 0.05$) and yield (1.04 vs. 1.10 kg/d; $P < 0.01$) decreased with added K, perhaps in response to reduced DMI. Dietary fat reduced milk protein concentration (3.43 vs. 3.36%; $P < 0.06$) but not yield. Supplemental K_2CO_3 overcame some of the negative effects of polyunsaturated fats on milk fat production but milk fat concentrations were still low compared with breed average.

Key Words: milk fat depression, potassium, distillers grains

470 Effects of replacing soybean meal with canola meal for lactating dairy cows fed three different ratios of alfalfa to corn silage. A. Faciola*[1] and G. Broderick[2], *[1]University of Nevada, Reno, [2]ARS, USDA, USDFRC, Madison, WI.*

Previous research suggested that CP from canola meal (CM) was used more efficiently that CP from solvent soybean meal (SBM) by lactating dairy cows. We wished to test whether CM was more effective than SBM on different ratios of alfalfa to corn silage. Forty-eight lactating Holstein cows were blocked by DIM and parity into 4 pairs of blocks of 6 cows each in a 3 × 2 arrangement of treatments in a cyclic changeover design trial with 6 experimental diets. Cows within blocks were randomly assigned to the experimental diets and fed for 4-wk periods before switching treatments over a total of 16 weeks. Treatments were 3 ratios of alfalfa to corn silage ratios (1:5, 1:1, and 5:1; DM basis), each supplemented with protein from SBM or CM. Diets contained (DM basis): 60% forage, 8–15% high moisture corn, 2–5% soy hulls, 1.3% mineral-vitamin premix, 16.5% CP, and 31–33% NDF. Data from the last week of each period were analyzed using the mixed procedure in SAS. Least squares means are reported in the table. When CM replaced SBM, improved yield of milk and milk protein ($P = 0.03$) and SNF ($P = 0.05$) was observed. There also was a trend for increased lactose yield ($P = 0.07$). Moreover, MUN decreased ($P < 0.01$) when CM replaced SBM. No significant interaction of protein source and forage source was observed. Production of milk and milk components was improved as alfalfa silage was replaced by corn silage.

Table 1. Production data

	Protein source		Alfalfa to corn silage ratio			*P*-value	
Item	SBM	CM	5:1	1:1	1:5	Protein source	Forage source
DMI, kg	23.5	23.8	23.7	24.0	23.4	0.4	0.42
Milk yield, kg/d	36.4	37.3	34.6	37.2	38.7	0.03	<0.01
ECM, kg/d	35.6	36.1	33.9	36.4	37.2	0.24	<0.01
Milk N/N intake, %	27.3	27.5	25.1	27.2	29.9	0.66	<0.01
Fat, %	4.0	3.94	4.09	3.99	3.82	0.25	<0.01
Fat, kg/d	1.45	1.46	1.41	1.49	1.47	0.69	0.02
Protein, %	3.02	3.02	2.96	3.02	3.07	0.92	<0.01
Protein, kg/d	1.1	1.12	1.02	1.12	1.19	0.03	<0.01
Lactose, %	4.85	4.84	4.81	4.86	4.87	0.86	0.03
Lactose, kg/d	1.77	1.81	1.66	1.81	1.89	0.07	<0.01
SNF, %	8.75	8.74	8.64	8.76	8.83	0.63	<0.01
SNF, kg/d	3.19	3.26	2.99	3.26	3.42	0.05	<0.01
MUN, mg/dL	14.0	12.9	13.8	13.2	13.4	<0.01	0.03

Key Words: alfalfa silage, canola meal, soybean meal

471 Milk production responses to a change in dietary starch concentration vary by production level in dairy cattle. J. C. Ploetz*, S. E. Burczynski, M. J. VandeHaar, M. S. Allen, and A. L. Lock, *Michigan State University, East Lansing.*

The effects of dietary starch concentration on yield of milk and milk components were evaluated in a crossover design experiment. Holstein cows (n = 32; 115 ± 22 DIM) with a wide range in milk yield (28 to 62 kg/d) were assigned randomly, within level of milk yield, to treatment sequence. Treatments were diets containing 30% dry ground corn (CORN) or 30% soyhull pellets (HULLS) on a DM basis. Cows were fed a diet intermediate to the treatments during a preliminary 14-d period. Diets containing corn silage and alfalfa silage were formulated to contain 16% CP, 27 or 44% NDF, and 30 or 12% starch for CORN and HULLS, respectively. Treatment periods were 28 d with the final 5 d used for data and sample collection. The statistical model included the random effect of cow, the fixed effect of treatment, period, and linear and quadratic interactions between treatment and preliminary milk yield. Compared with HULLS, CORN increased (all $P < 0.001$) DMI (26.6 vs. 28.0 kg/d), milk yield (36.0 vs. 40.2 kg/d), milk protein concentration (3.15 vs. 3.30%) and yield (1.11 vs. 1.31 kg/d), milk fat yield (1.32 vs. 1.47 kg/d), and ECM yield (36.9 vs. 41.4 kg/d). Treatment did not affect milk fat concentration ($P = 0.56$). Yields of de novo and preformed milk fatty acids increased with CORN ($P < 0.0001$ and $P = 0.02$, respectively), whereas yield of 16-carbon fatty acids increased with HULLS ($P < 0.0001$). Treatment interacted with level of preliminary milk yield for several response variables (yields of milk, milk

protein, milk fat, ECM, and 3.5% FCM). For ECM, lower producing cows benefited from the HULLS diet while there was an increasingly positive response to CORN as milk yield increased up to ~50 kg/d (quadratic interaction $P = 0.04$). CORN increased feed efficiency (ECM/DMI; 1.40 vs. 1.48, $P = 0.02$) and BW (697 vs. 704 kg, $P = 0.01$) compared with HULLS, however BCS was unaffected ($P = 0.23$). In conclusion, higher producing cows benefited from the high starch diet, and lower producing cows were better able to maintain production when fed the lower starch diet.

Key Words: feed efficiency, starch concentration, variation in response

472 Interactive effects between dietary grain source and oil supplement on feeding behavior and lactational performance of Holstein cows. S. Kargar*[1,3], G. R. Ghorbani[1], M. Khorvash[1], and D. J. Schingoethe[2], *[1]Isfahan University of Technology, Isfahan, Iran, [2]South Dakota State University, Brookings, [3]University of Wisconsin-Madison, Madison.*

Effects of grain source and dietary oil supplement on dry matter intake (DMI), feeding, chewing behavior, and productivity of lactating dairy cows were evaluated. Eight multiparous Holstein cows (77 ± 22.1 d in milk) were used in a duplicated 4 × 4 Latin square design with a 2 × 2 factorial arrangement of treatments. Experimental diets contained either ground barley or ground corn supplemented with either fish oil or soybean oil at 2% of dietary dry matter (DM). Geometric mean particle size of dietary treatments was 4.1 mm. Dry matter intake tended ($P < 0.09$) to be greater for barley- vs. corn-based diets (23.2 vs. 22.3 kg/d), but was reduced for the fish oil compared with soybean oil supplemented diets ($P < 0.01$; 21.1 vs. 24.3 kg/d). This reduction in DMI was attributed to smaller meal size ($P < 0.01$; 1.24 vs. 1.55 kg of DM) and slower eating rate ($P < 0.01$; 0.082 vs. 0.098 kg of DM/min) for fish oil compared with soybean oil supplemented diets. Sorting index was not influenced by dietary treatments, but grain source interacted by oil supplement to affect DMI of particles retained on 19 mm sieve ($P < 0.01$). Although not significant, milk yield tended to be greater when cows were fed barley- compared with corn-based diets (42.5 vs. 41.3 kg/d) with no changes in milk composition. Compared with soybean oil, fish oil negatively affected milk yield ($P < 0.01$; 40.4 vs. 43.4 kg/d), and thereby, milk fat ($P < 0.01$; 0.91 vs. 1.26 kg/d) and protein ($P < 0.01$; 1.23 vs. 1.33 kg/d) production. However, feed efficiency (milk yield/DMI) was greater in fish oil- compared with soybean oil supplemented diets ($P < 0.01$; 1.94 vs. 1.80). The grain source did not affect meal patterns, but rumination time was greater for barley- compared with corn-based diets as result of longer rumination duration ($P < 0.01$; 32.5 vs. 28.5 min/meal). Also, dietary grain source and oil supplement tended ($P < 0.09$) to interact for total chewing time. Results indicated that grain source and oil supplement can interact to affect intake and total chewing activity, but not productivity of lactating cows.

Key Words: grain, oil, dairy cow

473 Effects of starch level and monensin in fresh cow diets on subclinical endometritis and indices of immune function. T. Yasui*[1], M. M. McCarthy[1], C. M. Ryan[1], R. O. Gilbert[1], M. J. B. Felippe[1], G. D. Mechor[2], and T. R. Overton[1], *[1]Cornell University, Ithaca, NY, [2]Elanco Animal Health, Greenfield, IN.*

Primiparous and multiparous cows (n = 70) were used to determine the effects of starch level in the early postcalving diet (wk 1 to 3 postcalving) and monensin supplementation throughout the periparturient period and early lactation on subclinical endometritis and aspects of immune function. Cows were randomly assigned to one of the following postcalving dietary treatments: (1) High starch (HS), no monensin; (2) HS, monensin; (3) Low starch (LS), no monensin; (4) LS, monensin. Monensin was supplemented within a topdress pellet at 400 mg/d for 3 wk precalving period and 450 mg/d for 9 wk of lactation. Endometrial cytology as characterized by low volume uterine lavage at 7 d postcalving (7 d) and on one day between 40 and 60 d postcalving (40–60 d) was not affected by treatments. Phagocytosis (PHG) and oxidative burst (OB) activities at 7 d and 40–60 d were analyzed for blood neutrophils (PMN) and monocytes (MON). At 7 d, cows fed HS tended ($P = 0.06$) to have increased percentage of MON conducting PHG and had ($P = 0.05$) greater MON index [positive % × MFI (mean fluorescence intensity)] compared with cows fed LS. Cows fed monensin tended ($P = 0.10$) to have higher MFI in MON conducting PHG at 7 d. Effects of HS treatment on OB stimulated by PMA (phorbol myristate acetate) at 7 d showed a trend ($P = 0.07$) for increased MON index. For PHG activity at 40–60 d, MFI and index in PMN tended ($P = 0.09$ and 0.06) to have an interaction of starch and monensin such that cows that were previously fed LS and were concurrently being fed monensin had increased MFI and index. For OB activity at 40–60 d, monensin treatment increased the percentage of PMN ($P = 0.02$) and MON ($P = 0.03$) and the index of MON ($P = 0.05$) stimulated by *E. coli* and tended to increase the percentages of PMN ($P = 0.06$) and MON ($P = 0.07$) stimulated by PMA. Blood PMN glycogen content at 7 d was not affected by treatments; however, at 40–60 d cows previously fed high starch had higher ($P = 0.02$) glycogen content. The results suggest both starch level and monensin treatment can affect aspects of immune function in early lactation cows.

Key Words: immune function, monensin, starch

474 Effects of starch and rumen-protected amino acid supplementation on rumen microbial protein synthesis and milk performance in lactating dairy cows fed corn stover. W. Zhu*[1], C. H. Tang[1], X. P. Sun[1], J. X. Liu[1], Y. M. Wu[1], Y. M. Yuan[2], and X. K. Zhang[2], *[1]College of Animal Sciences, Zhejiang University, Hangzhou, China, [2]Shanghai Bright Holstan Co., Ltd., Shanghai, China.*

This study was conducted to evaluate the effects of supplementing starch and rumen-protected (RP) AA on lactation performance, rumen fermentation, and nitrogen (N) utilization efficiency of lactating dairy cows fed corn stover. Twelve multiparous (parity = 3.5 ± 1.0) Chinese Holstein dairy cows (BW = 661 ± 46.3 kg; DIM = 133 ± 13.5) were used in a 3 × 3 Latin square design. The basal diets were isonitrogenous and isocaloric, with a ratio of forage to concentrate of 45:55. The 3 diets contained the following forage ingredients (%, DM basis): alfalfa 19, and Chinese wild rye grass 6 (AH); corn stover 22, and alfalfa 6, supplemented with starch 8 (CSS); and CSS supplemented with RP Met and RP Lys (CSSAA). All the diets contained 17% corn silage (DM basis). The daily DMI ($P = 0.68$) and milk yield ($P = 0.20$) did not differ among the treatments. Compared with CSS, supplementation of RPAA increased the 4% FCM (26.9 vs. 28.6, $P = 0.06$) and milk efficiency (milk yield / DM intake) (1.34 vs. 1.43, $P = 0.08$), with no difference between AH and CSSAA or CSS. Contents of milk protein, fat, and lactose were not different among the treatments. Milk protein yield was greater ($P = 0.07$) for cows fed AH than those fed CSS (0.895 vs. 0.833kg), with CSSAA at an intermediate position (0.891kg). Rumen ammonia N concentration was lower ($P < 0.01$) for AH diet than for CSS and CSSAA. Rumen pH, volatile fatty acids, microbial protein yield, and MP did not differ among the treatments. The urinary urea N was greater ($P = 0.03$) for CSS than for AH, while feeding CSSAA diet resulted in a lower urea N concentration in milk ($P = 0.02$) and blood ($P = 0.03$) than CSS. Greater N conversion ($P < 0.01$) was

detected for CSSAA than for CSS (0.282 vs. 0.262), with no difference between CSSAA and AH. It is inferred that a sufficient supply of energy for microbial protein synthesis benefits lactation performance in lactating cows fed low-quality forage such as CS, and that RPAA supplementation would further improve the lactation performance and N utilization.

Key Words: corn stover, starch, amino acid

475 Effects of varying periparturient dietary starch amount on primiparous dairy cow performance, lipid metabolism and health. Z. Sawall*[1], W. Weich[1], D. Lobao da Silva[1], T. Parrott[2], and N. B. Litherland[1], *[1]University of Minnesota, St. Paul, [2]Dupont Industrial Biosciences, Waukesha, WI.*

Thirty Holstein and Holstein-cross primiparous dairy cows were used in a completely randomized design to determine if periparturient diets varying in starch content alter nutrient intake, lipid mobilization and milk production. Cows were balanced by breed and assigned to one of 4 treatments 42 d prepartum (PRE). Dietary treatments (low (LS) vs. high starch (HS)); low starch PRE 13.1% CP; 15.5% starch; 47.6% NDF) and postpartum (POST) 16.5% CP; 20.1% starch; 36.5% NDF) or 2) high starch PRE (13.2% CP; 26.7% starch; 39.2% NDF) and POST (16.8% CP; 29.7% starch; 27.7% NDF). Dietary starch was altered by replacing corn silage and soy hulls with ground corn. Data were analyzed using PROC MIXED in SAS as a completely randomized design with model including starch, week and breed. PRE and POST data were analyzed separately. We hypothesized that LS would have greater DMI resulting in greater milk production and reduced lipid mobilization. PRE DMI (starch, $P = 0.41$) averaged 11.6 and 12.1 ± 0.4 kg/d and POST DMI ($P = 0.91$) averaged 20.1 and 19.9 ± 0.8 kg/d for LS and HS respectively. HS tended ($P = 0.09$) to increase 3.5% FCM yield (31.8 vs. 28.9 ± 1.1 kg/d) and at wk 1 and 6 POST increased significantly ($P = 0.05$, $P < 0.01$). HS group had higher Serum NEFA at 12 h ($P = 0.02$) and on d 7 (starch × d, $P = 0.05$). On D 1 Serum BHBA was greater (starch × d, $P < 0.01$) for HS vs. LS and POST liver total lipids for the average of d 7 and d 14 ($P = 0.02$) averaging 4.8 and 6.8 ± 0.6% and were significantly greater on d 14 (starch x d, $P = 0.05$). Liver triacylglycerols in HS were greater ($P = 0.04$) than LS and averaged 0.9 and 1.9 ± 0.3%. Colostrum yield of HS group was higher than LS ($P = 0.07$) averaging 3.5 and 4.8 ± 0.5 kg for HS and LS group respectively. However, LS group colostrum had higher ($P < 0.01$) IgG concentration than HS (5487.1 and 3953.4 ± 343.5). In conclusion, increased dietary starch concentration did not alter PRE or POST DMI but tended to increase 3.5% FCM yield. Results indicate that higher dietary starch increased milk production, but not DMI, leading to greater lipid mobilization in primiparous cows.

Key Words: transition cow, starch, lipid

476 Bacteria populations in grain-, sugar-, and histidine-challenged cattle. H. M. Golder*[1,2], S. E. Denman[3], C. McSweeney[3], A. R. Rabiee[1,2], P. Celi[2,4], and I. J. Lean[1,2], *[1]SBScibus, Camden, NSW, Australia, [2]University of Sydney, Faculty of Veterinary Science, Camden, NSW, Australia, [3]CSIRO Animal, Food and Health Services, Queensland Bioscience Precinct, St. Lucia, QLD, Australia, [4]Melbourne School of Land and Environment, The University of Melbourne, Parkville, VIC, Australia.*

We hypothesized that distinct bacterial communities would develop among starch, fructose and/or histidine fed heifers during a single non-life threatening but substantial challenge. Holstein heifers (n = 30) were assigned to 5 grain-based groups: (1) control (no grain); (2) grain [fed at a dry matter intake (DMI) of 1.2% of bodyweight (BW)]; (3) grain (0.8% of BW DMI) + fructose (0.4% of BW DMI); (4) grain (1.2% of BW DMI) + histidine (6 g/head/d); and (5) grain (0.8% of BW DMI) + fructose (0.4% of BW DMI) + histidine (6 g/head/d). Rumen fluid samples were collected using a stomach tube 5, 115 and 215 min after ingestion of the rations. Genomic DNA 454 tag amplicon pyrosequence data were processed using QIIME software. Microbiomes were not different; however, distinct bacterial populations between substrate groups were evident in a principal components between-group analysis ($P < 0.001$). Bacterial diversity for the fructose or histidine treated heifers was large compared with changes in a tight group of *Bacteroidetes* for the grain only fed heifers. *Streptococcus bovis* had a median abundance of 0.25% in the fructose cattle and appeared to be the primary bacteria shifting in this short-term carbohydrate challenge. *Levilinea*, capable of lactate production, had a median relative abundance of 0.15% and was associated with the grain + fructose heifers. *Selenomonas* and *Lactobacillus* were present in only low abundances and were not distinctly associated with a particular substrate group. *Megasphaera elsdenii* were not closely associated with any groups. Co-inertia analysis showed a strong positive relationship between bacterial composition in the fructose fed groups and the percentage of offered fructose consumed, total lactate and butyrate concentrations and a negative relationship with rumen pH. Bacterial composition in the grain and grain + histidine groups had a positive relationship with the percentage of offered grain consumed and rumen ammonia, valerate and histamine concentrations. Rapid changes in bacterial populations can occur in a short period after a single substrate challenge and the nature of these changes may influence ruminal acidosis risk.

Key Words: fructose, lactate, rumen bacteria

477 Effect of supplementing sunflower cake in dairy diet on milk production and composition. G. Pirlo*, L. Migliorati, M. Capelletti, F. Abeni, L. Degano, A. Bruni, M. Povolo, G. Cabassi, and G. Contarini, *Consiglio per la ricerca e sperimentazione in agricoltura (CRA), Lodi, Italy.*

Economic valorization of by-products is critical for the sustainability of biodiesel production. There is little information about the use of sunflower cake (SC) in lactating dairy cow diet. Two groups of 16 Italian Holstein cows were kept in 2 experimental farms for evaluating the effect of partial substitution of soybean meal (SBM) with SC, obtained from mechanical squeezing (95.6% DM and 12.8% EE on DM). All cows were of second or third lactation and of early or late stage of lactation. In both farms cows were allotted to 2 groups, according to age and lactation stage; cows of half a group were fed SBM, and the others were fed SC. Diets were isoenergetic and isonitrogenous and 2 kg of SC substituted 1 kg of SBM. The experimental design was a change-over, replicated in 2 farms, with periods of 3 wk: the first 2 for adaptation and the third wk for sample collection. Data were processed with the GLM procedure of SAS. Partial substitution of SBM with SC did not influence milk production. However, SC decreased milk protein concentration (3.52 vs. 3.43, $P < 0.001$), percentage of palmitic acid (31.5 vs. 28.2, $P < 0.001$), and total saturated fatty acids (70.0 vs. 67.9, $P < 0.001$). Sunflower cake increased percentage of stearic acid (8.66 vs. 10.31, $P < 0.001$), oleic acid (21.3 vs. 22.9, $P < 0.001$), vaccenic acid (0.87 vs. 1.21, $P < 0.001$), CLA (0.47 vs. 0.63, $P < 0.001$), linoleic acid (2.59 vs. 2.95, $P < 0.001$), monounstatured and polyunsatured fatty acids (25.6 vs. 27.1 and 4.39 vs. 4.90 respectively, $P < 0.001$). Treatment did not influence proportion of arachidonic acid and n-3 fatty acids. Fat globule size was not affected. Introduction of SC has some beneficial effects on nutritional characteristics of milk, in particular CLA and polyunsaturated fatty acids concentration. This experiment is the first step for evaluating the suitability of diets containing SC for long-ripening cheese production.

Key Words: sunflower cake, milk fatty acid

478 Effects of different levels of 2 selected gums addition on textural properties of goat milk yogurts. B. P. Gupta*[1], Y. W. Park[1], J. Jones[1], and S. Ibrahim[2], *[1]Fort Valley State University, Fort Valley, GA, [2]North Carolina A&T State University, Greensboro.*

Sensory quality and consumer acceptability of yogurts are greatly influenced by textural characteristics of the products. Our previous work indicated that xanthan and locust bean were found to be the best choices among the 7 gums tested in improving the textural quality of goat milk yogurt. This present study was conducted to determine optimum levels of supplementation of the 2 gums in enhancing rheological quality of goat yogurts. Experimental yogurts were manufactured with addition of 0.2%, 0.3% and 0.5% of the 2 gums (wt/vol) to goat milk produced at the Georgia Small Ruminant Research & Extension Center, Fort Valley State University, Fort Valley, Georgia, and all gums treated yogurt products were stored for 0, 2 and 4 weeks in a 4°C refrigerator. Textural properties of all respective experimental goat yogurts were evaluated using a texture analyzer (Model TA.XT2i, Texture Technology Corp., Scarsdale, NY). Viscosity of yogurts was measured by firmness (g force) and consistency, and adhesiveness or stickiness was measured by cohesiveness (g force) and index of viscosity. Firmness and consistency for all yogurts made using 3 different concentrations of the 2 gums were generally higher than those of control samples, with a few exceptions. These results indicate that xanthan and locust bean fortifications to the goat milk had improved the textural qualities of the caprine yogurt products. Addition of 0.5% locust bean showed the highest firmness and that of 0.2% xanthan resulted in highest consistency among all treatments. Viscosity, cohesiveness and adhesiveness of 0.3% and 0.5% added locust bean showed higher and more consistent values than the other groups. It was concluded that the supplementations of 0.2% xanthan and 0.5% locust bean to the caprine milk improved the textural qualities of the goat milk yogurts.

Key Words: goat milk yogurt, gum, texture

479 Physico-chemical characteristics of fresh and corresponding pasteurized camel milks from intensive dairy farm in Saudi Arabia. E. Beaucher[1], N. Nogueira[1], B. Camier[1], J. Jardin[1], V. Briard-Bion[1], A. Musaad[2], G. Konuspayeva[2], B. Faye[2], and F. Gaucheron*[1], *[1]UMR 1253 Science et Technologie du Lait et de l'œuf, INRA-Agrocampus Ouest, Rennes, France, [2]Camel and Range Research Center, Al-Jouf, Sakaka, Saudi Arabia.*

Compared with cow milk, the knowledge concerning the physico-chemical characteristics of camel milk is confuse and sometimes discordant. Explanations concerning these discordances are differences in the geographical origin of camel milk and analytical methods used for the characterization. The objective of this study was to describe precisely the physico-chemical characteristics of fresh whole and corresponding camel milk from the Camel and Range Research Center located at Al-Jouf, Sakaka (Saudi Arabia).The analyses were performed to (1) Determine the global composition of this milk (total and whey proteins, main minerals, lactose and fat); (2) Identity of the main proteins by mass spectrometry previously separated by reversed phase chromatography (3) Characterize the micellar properties of casein micelle in terms of mineralization, size, charge and hydration. The collected milk came from 16 milking camels. The recovered volume, corresponding to 2 milking, was 150 L. One liter of raw milk and one liter of the corresponding pasteurized milk (70°C for 10 min) was sampled for the physico-chemical characterization. Experiments were performed in duplicate. For raw milk, the concentrations of dry matter, fat, lactose, total nitrogen, non-casein nitrogen, Ca, inorganic phosphate, Mg, Na, K, Cl and citrate were 110, 25.5, 49, 29, 9.6, 1.23, 1.52, 0.09, 1.07, 1.71, 1.54 and 1.67 g/kg. The chromatographic profiles of the main proteins were complex but the different caseins molecules were identified. No b-lactoglobulin was detected. Different molecular masses were also determined without identify precisely the corresponding proteins. Concerning the micellar characteristics, the zeta potential was about −15.5 mV, the hydration 1.70 g of water per g of dry pellet of ultracentrifugation and the average size of about 250 nm. These micelles contained Ca and inorganic phosphate with 0.04 and 0.04 g of these ions/g of casein. The mass ratio of micellar Ca/Pi was close to 1.0. All these parameters were not significantly affected by the pasteurization.

Key Words: camel milk, pasteurization, casein micelle

480 Changes and formation mechanisms of oxidized-flavor of milk powder during heat related processes. L. Zhang* and Y. Li, *Harbin Institute of Technology, College of Food Science and Engineering, Harbin Institute of Technology, Harbin, China.*

Oxidative deterioration of milk powder during processing and storage processes is a bottleneck in restricting application of milk powder. The aim of this work was study on the potential mechanism of formation in oxidized flavor of milk powder during heat-related processes. Solid-phase microextraction-gas chromatography-mass spectrometry was used to analyze the oxidized flavor during the raw milk heated process. Total antioxidant capacity (DPPH radicals scavenging activity) and peroxide value were used as the indicators of heated-induced changes in oxidative environment of milk. While the oxidized environment of milk fat and the exposure of flavor precursors were also analyzed by dynamic light scanning. The protein materials extracted from fat globule membrane were also analyzed by SDS-PAGE. The results showed the oxidized flavor, hexanal, heptanal, nonanal, 2-heptanone, 2-nonanone, were increased with the increasing the heat intensity among the range of heat temperature (70 to 90°C) and heat time (0.5 to 20 min). There was a good regression relationship between the oxidized flavor compounds and heat intensity. The correlation coefficients ranged from 0.868 to 0.936. For the antioxidant capacity, compared with the unheated samples, DPPH radicals scavenging activity of heated milk significantly decreased ($P < 0.05$), while peroxide value significantly increased ($P < 0.05$). The ranges of fat globule diameter d3,2 and specific surface area were 3.05 to 3.46 μm and 17038 to 20083 cm^2/mL respectively. Heat treatment at low intensity could not influence the distribution of milk fat globules. SDS-PAGE, which suggested the proteins, such as β-lactoglobulin, α-lactalbumin, xanthine oxidase and butyrophilin in fat globule membrane could be cross-linked through the molecular or intermolecular reactions. These results indicated that the formation of oxidized flavor compounds was improved due to the changes in oxidized status of milk during heat treatment.

Key Words: milk powder, heat process, oxidized flavor

481 Milk quality of Nguni cows of Southern Africa. M. Chimonyo*[1], M. Mapekula[2], and K. Dzama[3], *[1]University of KwaZulu-Natal, Pietermaritzburg, South Africa, [2]University of Fort Hare, Alice, South Africa, [3]University of Stellenbosch, Stellenbosch, South Africa.*

Efforts to produce milk in communal production systems of Southern Africa largely ignore the adapted indigenous Nguni cattle. The study was conducted to determine fatty acid, amino acid and mineral composition of milk from Nguni cows of Southern Africa. Milk samples from 16 Nguni cows grazing on rangeland were collected once per lactation phase, i.e., early lactation (January), mid lactation (April) and late lactation (June) in 2009 for milk composition analyses. Milk samples were analyzed for amino acids, fatty acids and mineral content. Data were analyzed using the PROC Mixed procedure with repeated measures analysis of SAS (2009). Least squares means were separated using the PDIFF option (SAS, 2009) when the F-test was significant at $P < 0.05$. Relative to crossbred cows, Nguni cows produced milk with higher ($P < 0.05$) protein content, essential amino acid levels, phosphorus and n-6:n-3 ratio. Milk yield, fat and total solids content, potassium levels and total mono-unsaturated fatty acids (MUFA) were, however, comparably low ($P < 0.05$). In the early and mid-lactation stages, milk from Nguni cows had higher ($P < 0.05$) essential amino acids (arginine, phenylalanine, histidine, isoleucine and leucine), calcium levels and polyunsaturated fatty acids to saturated fatty acids (PUFA/SFA) ratios than their crossbred counterparts. It was concluded that milk composition of Nguni cows is desirable for human consumption, especially in the early-to-mid lactation. The potential of improving milk production from Nguni cattle, widely considered to be beef-type cattle, is, therefore huge and deserves attention.

Key Words: fatty acids, food security, Nguni cattle

482 Physicochemical characteristics of nonfat dry milk and skim milk powder produced in the United States A. K. A. Ali*, K. E. Smith, K. J. Burrington, and J. A. Lucey, *Wisconsin Center for Dairy Research, University of Wisconsin-Madison, Madison.*

Nonfat dry milk powder (NFDM) is the most commonly produced dry milk product in the United States. It is a commonly used ingredient in many food applications to improve the body, texture, and flavor of products. Physicochemical properties, such as, moisture, color, particle size, and bulk density, can affect storage ability, handling and processing of milk powders. Objectives of this study were to determine physicochemical quality parameters of domestic NFDM and skim milk powder (SMP). In our study, 23 samples from 4 domestic producers of NFDM/SMP were obtained. Samples were 25 kg or 50 pound bags of low, medium and high heat NFDM/SMP that have not been agglomerated or instantized and were approximately 6 to 9 mo old. Moisture, color, particle size, and bulk density were determined. Accelerated storage testing of powder also was done at 70°C for one week. Moisture content of the samples varied from 3.90 to 4.59%. Samples had variations in lightness value L* (93.85–96.37) as well as b* value (12.32–17.99). Following accelerated storage DE* values, indicating total color change of the powders, ranged 46.53–90.13. DE* values showed significant positive correlation with the moisture content of the powders. The particle size in volume median diameter D (v, 0.5) of milk powders showed significant variations with a range of 21.05–73.92 µm. Significant differences in bulk density were not apparent between NFDM/SMP or between heat treatments. Differences were noted between one company versus the other 3 manufacturers indicating differences in processing conditions between manufacturers, rather than the actual type of milk powder product. The particle size and bulk density can influence the functional properties of powders (such as reconstitution ability, flowability, wettability, dispersibility, and compressibility) and there by influence the possible end use behavior of these products.

Key Words: NFDM/SMP, physicochemical properties

483 Impact of calcium reduction on the functional properties of milk protein concentrate 80. C. Marella*, A. Kommineni, P. Salunke, A. Biswas, and L. E. Metzger, *Midwest Dairy Foods Research Center, Dairy Science Department, South Dakota State University, Brookings.*

Ultrafiltration (UF)/Diafiltration (DF) are utilized in production of Milk protein concentrates (MPC). The UF process allows passage of soluble components such as lactose and some minerals. Previous research has demonstrated that partial removal of calcium from the product during UF process affects the functional properties of MPC. The objective of the present research was to determine the effect of calcium reduction as a result of CO_2 injection on functional properties of MPC. Three replicates of CO_2 injected reduced-calcium MPC and 3 replicates of control MPC were produced, using different lots of skim milk for each replicate. All the MPCs were stored at room and elevated temperatures for 2 mo. Solubility was measured at 20°C and at 4°C (cold solubility). Insolubility indices were also measured on 5% protein solutions. Heat stability of 5% protein solutions and viscosities of 5 and 10% protein solutions were also determined. Reduced-calcium MPC had a solubility of ~97% on d 1 and there was no significant loss ($P > 0.05$) in solubility during 60 d storage at room temperature and at 40 C. In contrast, the control MPC had a solubility of 91% at d 1 and significant reduction in solubility was observed during 60 d storage at 40 C. The significantly ($P < 0.05$) higher solubility of the reduced calcium MPC at d 1 indicates the calcium may play a role in protein aggregation during manufacturing. Reduced-calcium MPC also had a cold solubility of 92% while the control MPC had 74%. Insolubility indices were correlated with solubility data at room and cold temperatures and a model was developed for predicting solubility by measuring insolubility index. Reduced-calcium MPC had significant ($P < 0.05$) differences in heat stability and viscosity when compared with the control MPC. The present study quantified the effect of various levels of calcium reduction on functional properties of MPC powders.

Key Words: MPC, calcium reduction, solubility

484 Impact of retentate preheating on the functionalities of milk protein concentrate. L. Rupp*[1], M. Molitor[2], and J. A. Lucey[1,2], *[1]University of Wisconsin-Madison, Department of Food Science, Madison, [2]Wisconsin Center for Dairy Research, Madison.*

Processing conditions can influence the properties and functionalities of milk protein concentrate 80 (MPC80). Characteristics of nonfat dry milk are well known to be affected by pre-heating of the concentrate before spray drying, however it is not known how MPC powders are affected by heat treatment before drying. Increased levels of protein denaturation could affect foam stability, solubility and powder storage properties. Ultra- and diafiltered retentate (25% TS) was heated to 50, 60, or 70°C for 9 min immediately before spray drying. Outlet air temperatures were adjusted to maintain similar moisture contents. Four trials were conducted and fat contents in the powders were 2.8, 2.8, 2.0 and 1.4, respectively. Viscosity of the retentate, powder particle size, foam stability, foam overrun, and foam yield stress (5% wt/wt, pH 7, 20-min whipping time) of MPC80 were analyzed. The powders were stored at 30°C and tapped bulk density and solubility were determined every 30 d for 6 mo. Due to the lower viscosity of the concentrate at increased temperatures, the droplets produced during atomization caused significantly ($P < 0.05$) smaller powder particles. Foam stability and % overrun of the powders were extremely variable, ranging from 104 to 1041 s and 397 to 847%, respectively. Only powders with a low fat content (≤2%) were able to form stable foams, confirming that residual fat inhibits foaming. Foaming experiments are ongoing. Bulk density decreased during storage time but was not significantly affected by

pre-heating temperatures. Solubility slightly declined in all powders over time but pre-heating to 70°C for 9 min did not negatively affect solubility. It has been suggested that fat could shield powder particles from water during the rehydration process causing poor wettability, but no differences in solubility were found in powders with elevated fat contents. It was concluded that under the conditions we investigated, pre-heating of the concentrate before drying has no major effect on MPC80 properties.

Key Words: milk protein concentrate, processing, functionality

485 Interactions between acidified dispersions of milk proteins with dextran or dextran sulfate. U. Pachekrepapol*, D. Horne, and J. Lucey, *University of Wisconsin-Madison, Madison.*

Exopolysaccharides (EPS) produced by some starter cultures are often used to modify yogurt texture. Our goal was to study the effect of neutral and negatively charged EPS on acidified milks to better understand the possible interaction mechanisms. Acidified milks were used to better simulate yogurt conditions. Dextran (DX; MW 2×10^6 Da) and dextran sulfate (DS; MW 1.4×10^6 Da) were used as model examples of neutral and negatively charged EPS, respectively. Reconstituted skim milk (5–20% TS, w/w) was acidified to pH 4.4, 4.6, 4.8 or 4.9 at ~0°C (to prevent gelation) by addition of 3 *N* HCl. DX or DS was added to acidified milks to give concentrations of 0–2% (w/w) and 0–1% (w/w), respectively. Milks were observed for possible phase separation after storage at 0°C for 1 and 24 h. Any gelation of milk systems was determined by frequency sweep. The type of interactions between caseins and DX/DS was investigated by total carbohydrate analysis of supernatants from phase separated samples. At 5.0–7.5% TS, phase separation of milks occurred even without DX or DS addition due to destabilization of caseins in acid conditions. At higher milk solids content, phase separation was only detected after 24 h when DX or DS was added. Phase separation occurred when 1.5–2.0% DX was added to milk with >7.5% TS, or when 0.7–1.0% DS was added to milk with 10.0 to 12.5% TS. Similar results were observed at all pH levels. Gelation occurred with the addition of 1.5–2.0% DX or 0.4–1.0% DS to milk containing high TS (≥10%). Based on carbohydrate analysis of supernatants, we believe that DX interacted with milk proteins through a type of depletion flocculation mechanism, while DS appeared to interact via electrostatic type interactions with milk proteins. This study helps to better understand how different types of EPS interact with milk proteins, which should improve our control of cultured products made with these EPS-producing strains.

Key Words: dextran, dextran sulfate, depletion flocculation

Lactation Biology II

486 Using infrared thermography for detecting intramammary infections under practical and *E. coli* O55:B5 endotoxin challenge conditions in dairy ewes. A. Castro-Costa[1], G. Caja*[1], A. A. K. Salama[1], M. Rovai[1], C. Flores[1], and J. Aguiló[2], *[1]Ruminant Research Group (G2R), Department of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain. [2]Group of Biomedical Applications (GBA), Department of Microelectronics and Electronic Systems, Universitat Autònoma de Barcelona, Bellaterra, Spain.*

A total of 83 lactating dairy ewes from 2 breeds (Manchega, n = 48; Lacaune, n = 35) were used in 2 experiments for assessing on the use of infrared thermography (IRT) for detecting intramammary infections (IMI). In Exp. 1, ewes were milked twice-daily and IRT pictures taken with an IRI 4010 camera (Irysis, Northampton, UK; accuracy, ± 0.15°C) before and after milking at 46 and 56 DIM. Mean udder skin temperatures (UST) were measured from IRT pictures and IMI detected by bacterial culture of milk samples. A total of 85.5% udder halves were classified as healthy and 14.5% as IMI. No UST differences were detected by udder health (healthy vs. IMI; $P = 0.484$) nor side (left vs. right; $P = 0.879$), but UST varied by effect of breed ($P = 0.003$) and by milking moment ($P = 0.014$) and milking turn ($P < 0.001$). The UST increased linearly with ambient temperature (r = 0.88). In Exp. 2, 3 groups of 3 Lacaune ewes, milked once-daily in late lactation (155 DIM), were used for evaluating the response to an *E. coli* O55:B5 endotoxin challenge (0.083 µg/kg BW). Treatments were: 1) control (C00, both halves untreated), 2) half udder (T10 and C01, one udder half treated and the other untreated, respectively), and 3) treated (T11, both halves treated). Vaginal temperature, UST, milk yield and milk composition changes were monitored at different time intervals during 3 d. Local and systemic signs of IMI, as well as milk changes (flakes, CMT, SCC and composition) were observed from h 6 ($P < 0.05$ to 0.001). For all treatments, UST increased after challenge, peaking at h 6 in T11 ($P < 0.001$) and decreasing thereafter without treatment effects. No differences were detected in fat and protein milk contents, but lactose content and SCC in milk were different between treated vs. untreated udder halves ($P < 0.05$) throughout the challenge. Ambient temperature and UST correlated (r = 0.60). In conclusion, despite the accuracy of the camera and the SEM obtained for UST (±0.05 to ± 0.24°C), we were unable to discriminate between healthy and IMI udder halves (subclinically or clinically infected) in dairy ewes.

Key Words: endotoxin, infrared thermography, mastitis

487 Effect of corn grain and soybean meal with different processing methods on milk protein expression profiles in lactating dairy cow. S. S. Li*[1,2], J. S. Shen[1,2], D. X. Ren[1], and J. X. Liu[1,2], *[1]Institute of Dairy Science, College of Animal Sciences, [2]MOE Key Laboratory of Molecular Animal Nutrition, Zhejiang University, Hangzhou 310058, China.*

A proteomics approach was used to investigate the effects of feeding corn grain and soybean meal with different processing methods on milk protein expression profiles in lactating dairy cows. Twelve multiparous Holstein dairy cows were used in a 4 × 4 Latin square design with a 2 × 2 factorial arrangement. The main factors were corn [finely ground (FGC) and steam-flaked corn (SFC)] and soybean meal [solvent-extracted (SSBM) and heat-treated soybean meal (HSBM)], which were used to formulate 4 diets with a same basal ingredient: 27% FGC and 9% SSBM; 27% SFC and 9% SSBM; 27% FGC and 9% HSBM; and 27% SFC and 9% HSBM. Each period lasted for 21 d. Milk samples were collected on d 17, 18, 19 of each period, and changes in milk proteins were determined by 2-dimensional electrophoresis (2-DE) and Image-Master 2D Platinum 6.0 software. A total of 13 spots were detected with variations in protein spots abundance according to statistical analysis. These spots were identified by matrix-assisted laser desorption/ionization time of flight/ time of flight (MALDI TOF/TOF) mass spectrometry. The milk protein profiles on the gels were similar in cows fed FGC or SFC. However, abundance of α_{S2}-casein fragments were higher in the cows on HSBM than on SSBM, while fragments of β-casein, κ-casein, β-lactoglobulin, α-lactalbumin and zinc-α-2-glycoprotein were downregulated. The relative decrease in β-casein was validated by Western blot, and was in agreement with the mass spectrometry data. These results suggested that feeding diets differing in nitrogen supply principally change the synthesis and secretion of milk proteins in the mammary gland of lactating cows.

Key Words: corn grain, soybean meal, milk proteome

488 Dietary anion-cation difference and day length affect milk calcium content. A. Boudon[1], M. Johan[1], A. Narcy[2], and C. Hurtaud*[1], *[1]INRA-Agrocampus Ouest UMR 1348 PEGASE, Saint-Gilles, France, [2]INRA URA, Nouzilly, France.*

Milk and dairy products are an important source of calcium for humans but recent studies in France have shown a clear decrease in milk calcium content during May and June and with grass diets compared with corn silage diets. The aim of this study was to identify the reasons of this seasonal drop of milk calcium content by testing the effect of 2 levels of dietary anion-cation differences (DCAD; 0 mEq/kg DM for D0 and 400 mEq/kg for D400) and 2 d lengths (8 h of light/d for short days and 16 h/d for long days) on calcium balances of dairy cows. The DCAD treatments were conceive to mimic diets based either on maize silage or on herbage. The cows were only lightened by solarium lights providing UVA and UVB. The trial was carried out according to a Latin square design using 8 dairy cows averaging 103 ± 44 DIM with 4 periods of 14 d. Data were analyzed accordingly using Mixed procedure. The significance threshold was set at $P \leq 0.05$. There was no significant interaction between day length and DCAD level. With D400 compared with D0, blood pH increased and plasma ionized calcium content decreased, while the plasma total calcium content was not different between treatments. However, milk calcium content increased, in relation with a decrease of the amount of calcium excreted in urine. DCAD had no significant effect on protein and casein contents and D400 tended to decrease milk yield. This illustrates that the udder did not decrease Ca uptake from the blood at high DCAD even though high DACA decreased the availability of Ca by decreasing the proportion of blood ionized Ca. Milk calcium and casein contents were significantly lower with long compared with short days, whereas day length had no effect on milk yield. This work highlights that long and sunny days can explain a part of the seasonal decrease of milk calcium content in summer and refutes the hypothesis that low milk calcium contents at grazing could be due to the high DCAD of herbage.

Key Words: dairy cow, milk, calcium

489 Calf sex influences whole-lactation milk and component production in Holstein cows. A. J. Carpenter*[1], K. Hinde[2], J. S. Clay[3], and B. J. Bradford[1], *[1]Kansas State University, Manhattan, [2]Harvard*

University, Cambridge, MA, [3]Dairy Record Management Systems, Raleigh, NC.

Research in some animals has indicated that sex of progeny may influence milk production and composition in the ensuing lactation, and that this effect is influenced by parity. To investigate whether this phenomenon is observed in dairy cattle, data from 1995 to 1999 were obtained from Dairy Record Management Systems and analyzed by modeling the fixed effects of calf sex, parity, use of BST, and their interactions, and the random effect of year. Only Holsteins with lactations that began with a single heifer or bull calf were included in analysis. The lactation was considered BST positive if BST use was reported in any of the first 5 test days. Response variables analyzed were 305-d milk (305MILK), fat (305FAT), protein (305PROT), and peak milk (PEAK) production, and average somatic cell score (SCS). Over 2.5 million lactation records were used to assess all response variables except for PEAK (~1 million lactations). Cows beginning a lactation with the birth of a heifer had 1.01 ± 0.10% greater 305MILK, 1.02 ± 0.12% greater 305FAT, 0.82 ± 0.12% greater 305PROT, and 0.68 ± 0.15% greater PEAK, but 0.92 ± 0.17% lower SCS than cows with bulls (all $P < 0.001$). Significant sex by BST interactions were detected for all yield variables. For BST negative lactations, heifers resulted in greater yields ($P < 0.001$), but among BST positive lactations, there was no difference in 305MILK ($P = 0.09$), 305FAT ($P = 0.13$), 305PROT ($P = 0.41$), or PEAK ($P = 0.48$) as a function of calf sex, reflecting a ≥ 78% decrease in the marginal advantage of heifers. Sex effects were similar when data were analyzed without lactations involving dystocia, and were generally evident across all parities. Although the magnitudes of the differences are small, the highly significant effects of sex and the fact that BST administration negated these effects suggest that this analysis has revealed a real biological phenomenon. Based on these observations, we suggest that larger-magnitude sex bias in milk secretion observed in previous studies was likely due to postnatal signals (e.g., greater demand) rather than prenatal programming.

Key Words: lactation, sex effect, prenatal

490 The effect of induced involution on DNA methylation upstream of milk protein genes, α-lactalbumin and β-lactoglobulin. S. Pryor*, J. Dobson, and K. Singh, *AgResearch, Hamilton, New Zealand.*

Bovine mammary gland involution following termination of milking results in a decline in milk protein gene expression, including expression of major milk proteins α-lactalbumin (α-LA) and β-lactoglobulin (β-LG). Increased DNA methylation has previously been observed around a STAT5 binding site within the 10-kb region upstream of the α_{S1}-casein gene with cessation of milking. The aim of the present study was to determine if termination of milking has an effect on DNA methylation within the 10-kb region upstream of the α-LA and β-LG genes. Mammary alveolar tissue was obtained from non-pregnant cows in mid-lactation slaughtered at 6 h (lactating) or 7 and 28 d (n = 5/group) after the last milking. Following 7 d non-milking, quantitative RT-PCR analysis showed the level of α-LA and β-LG mRNA decreased 140-fold ($P < 0.001$) and 17-fold ($P < 0.01$), respectively, compared with lactating controls. After 28 d non-milking, α-LA and β-LG mRNA levels were downregulated 10-fold and 5-fold ($P < 0.05$) respectively, relative to lactation. Quantitative Sequenom MassARRAY analysis of DNA from mammary alveolar tissue revealed a similar level of methylation at analyzed sites within the 10 kb region upstream of the α-LA gene in lactating cows and those not milked for 7 or 28 d. In contrast, DNA methylation was increased around a putative STAT5 binding site directly upstream of the first β-LG exon with cessation of milking. In lactating cows, methylation of 35% was detected at a CpG dinucleotide located within this putative STAT5 binding site, which increased to 45% and 50% ($P < 0.05$) following 7 and 28 d non-milking, respectively. These results indicate that increased methylation within a putative STAT5 binding site upstream of the β-LG gene may be associated with the decline in β-LG expression occurring with termination of milking. However, despite the decreased level of α-LA mRNA with non-milking, methylation of analyzed sites upstream of the α-LA gene did not change, suggesting that the role DNA methylation plays in regulation of gene expression with involution may differ for each milk protein.

Key Words: lactation, epigenetics

491 Udder cistern size affects lactation persistency and ability to adapt to once-daily milking in dairy cows. A. Molenaar*[1], G. Caja[2], S. Leath[1], H. Henderson[1], C. Cameron[1], M. Challies[1], K. Taukiri[1], T. Chikazhe[3], S. Kaumoana[3], B. Lannou[1], A. Dorleac[1], A. Guy[1], C. Gavin1,4, and K. Singh[1], *[1]AgResearch Ruakura, Hamilton, New Zealand, [2]Group of Ruminant Research (G2R), Universitat Autonoma de Barcelona, Bellaterra, Spain, [3]AgResearch, Tokanui Dairy Research Farm, Te Awamutu, New Zealand, [4]Faculty of Science and Engineering, University of Waikato, Ruakura, New Zealand.*

Sixty NZ dairy cows (Holstein and Jersey crossbred; 505 ± 1 kg BW; 4.4 ± 0.3 yr) were allocated into 4 groups (n = 15) according to previous seasons lactation persistency (HP, high; LP, low) and milk yield (HY, high; LY, low) to study the relationship between udder cistern size and milk loss when moved from twice (2×) to once (1×) daily milking in late lactation. Groups had similar parity and half the cows remained at 2× as matched controls. Cows were grazed, feed supplemented, and milked on a rotary parlor with automatic data recording. At 16 to 21 h after last milking, cistern size of rear udder quarters was measured by ultrasonography (sectorial probe, 5 MHz) at 3 scanning sessions done in the rotary, as (1) distended cistern size (DCS) after inducing milk letdown (oxytocin, i.m. 20 IU/cow) on d −15 and +11 of start of 1×; and (2) natural cistern size (NCS) after blocking milk letdown (atosiban, i.v. 5 mg/cow, given before heading to the rotary), followed by DCS, on d +15. Milking was performed after DCS and NCS-DCS to obtain total, cisternal and alveolar milk volumes, respectively. A final scan was done after milking to detect residual milk. Cistern size was assessed using a linear scoring template (0 to 5; accuracy, ± 0.5). Milk yield at d −15 varied by group (HP, 12.6; LP, 11.0; HY, 13.1; LY, 10.5 L/d; SEM, ± 0.3; $P < 0.05$), but DCS only differed ($P < 0.05$) between HP and HY (3.29, 3.59, 3.93 and 3.69; SEM, ± 0.07, respectively). Post milking scans showed that cows left milking with 5 to15% residual milk. Changing to 1× produced 30% milk loss on average, being greater in LP cows ($P < 0.05$) than in other groups (27, 36, 29 and 29%). No DCS differences were observed after changing to 1×. Values of NCS (3.23, 3.14, 3.64 and 3.08; SEM, ± 0.10) were the greatest in HY and cisternal milk was lowest in LY cows (55, 54, 61 and 47% total milk) ($P < 0.05$), the rest being no different. Cisternal milk volume positively correlated with milk yield (2×, $r^2 = 0.48$; 1×, $r^2 = 0.67$). In conclusion, udder cistern size was related to lactational performances of dairy cows and could be used as a tool for dairy management decisions.

Key Words: atosiban, udder cistern, ultrasonography

492 The appearance of blood components in milk during the first hours of endotoxin induced mastitis follows two different chronological patterns. O. Wellnitz[1], C. Zbinden[1], J. Lüttgenau[2], H. Bollwein[2], and RM Bruckmaier*[1], *[1]Veterinary Physiology, Vetsuisse*

Faculty University of Bern, Bern, Switzerland, [2]Clinic of Reproductive Medicine, Vetsuisse Faculty University of Zurich, Zurich, Switzerland.

During mastitis considerable changes in milk composition occur. Besides an increase of somatic cells several blood components start to increase in milk within 2 to 4 h after endotoxin challenge. This study aimed to investigate the sequence and pattern of appearance of several blood components in milk during the first hours of an endotoxin induced mastitis. Eight Holstein dairy cows were challenged with 200 µg *E. coli* lipopolysaccharide (LPS) into one quarter. Milk samples (~10mL) were taken at 0, 1, and 2 h after challenge and then every 15 min until 5 h after challenge from the LPS treated and one control quarter. Somatic cell count (SCC; using DeLaval cell counter), Immunoglobulin (Ig)G1 and 2 (by ELISA), and lactate dehydrogenase (LDH), and L-lactate (enzymatically using commercial kits) were analyzed. Differences between LPS treated and control quarters were evaluated using mixed model procedure including cow as repeated subject with a Bonferroni correction and are considered significant if $P < 0.05$. SCC, L-lactate, immunoglobulin (Ig)G1, IgG2, and LDH increased in LPS challenged quarters until the end of the experiment but did not increase in control quarters. Milk IgG1, IgG2, and LDH were already significantly increased at 2 h after challenge. In contrast milk SCC and lactate remained at a basal level until 2 h after challenge. A significant increase was detected at 2.75 h (SCC) and at 2.25 h (L-lactate) after challenge. In conclusion, the blood components IgG1, IgG2 and LDH increase in milk in response to endotoxin challenge before an elevation of SCC and lactate can be detected. The increase of blood components in milk follows 2 different patterns: There is a fast increase within the second hour of challenge for IgG1, IgG2, or LDH, reaching a plateau within 3 h. On the other hand, SCC and L-lactate show a consistent increase not reaching a plateau within 5 h.

Key Words: mastitis, milk, blood-milk barrier

493 Milk production during the colostral period is not related to the later production level in dairy cows. E. C. Kessler, R. M. Bruckmaier, and J. J. Gross*, *Veterinary Physiology, Vetsuisse Faculty University of Bern, Bern, Switzerland.*

In dairy cows, milk yield increases after parturition to a peak at around wk 6 of lactation. Because milk is not sold during the colostral period, milk yield during the first few days after parturition is mostly not recorded. However this period is crucial for the development of metabolic diseases. For analysis of the evolution of milk production from parturition the first 10 milkings after parturition and daily milk yields from d 1 to 28 of lactation were analyzed in 17 primiparous and 39 multiparous cows milked twice daily. Milk yield of first milking after parturition ranged from 1.3 to 20.7 kg (Δ 19.4 kg) in cows and from 1.8 to 10.9 kg in heifers (Δ 9.1 kg). At the tenth milking production ranged from 9.2 to 21.5 kg in cows (Δ 12.3 kg), and from 7.0 to 15.2 kg in heifers (Δ 8.2 kg), resp. The correlation between the amount of first colostrum and daily milk production in cows decreased from r = 0.47 on d 5 to r = 0.32 on d 14 ($P < 0.05$) i.e. the effect of colostrum yield on milk production decreased with DIM. On d 28, all multiparous cows had a comparable production level independent of their first colostrum yield. However, in heifers the variation of the daily milk production was maintained until d 28 of lactation. Immediately after parturition, daily milk production increased exponentially, but after approximately 1 wk in lactation, the slope of the daily milk production curve flattened and continued more linear. A non-linear regression equation was used to determine the time point when the lactation curve passed into a linear slope. This turn occurred earlier in heifers (d 6.9 ± 0.3) than in multiparous cows (d 8.2 ± 0.2, $P < 0.01$). In conclusion, a lower milk production during the first days of lactation was not necessarily related to the lactational performance in multiparous cows. Considering a simultaneously lower metabolic load in cows giving less milk in the very beginning of lactation, this attribute might gain importance as a breeding objective.

Key Words: lactation curve, milk yield, dairy cow

494 Palmitate induces endoplasmic reticulum stress and oleate and sodium salicylate suppress oxidative stress in immortalized bovine mammary epithelial cells. L. K. Mamedova[1], S. R. Montgomery*[1], K. J. Harvatine[2], and B. J. Bradford[1], *[1]Kansas State University, Manhattan, [2]Pennsylvania State University, University Park.*

Palmitate has been shown to induce endoplasmic reticulum (ER) and oxidative stress in some cell types, whereas sodium salicylate (SS) and unsaturated fatty acids have been shown to mitigate these stresses. Therefore, we hypothesized that SS would counteract the effects of palmitate in immortalized bovine mammary epithelial (MAC-T) cells. In the first experiment, MAC-T cells were treated with SS (50 µ*M*), palmitate (250 µ*M*), or oleate (500 µ*M*) alone or in combination in DMEM with 10% fetal bovine serum, 1% penicillin streptomycin, 1% insulin, and 2% bovine serum albumin and incubated for 24 h. To determine if palmitate effects were due to ceramide (CER) synthesis, a second experiment was conducted where MAC-T cells were treated with palmitate (250 µM), myriocin (1 µ*M*; CER synthesis inhibitor), or both in the same basal media. Results from replicate wells (6 to 12/treatment) were analyzed by ANOVA and treatment effects were declared at $P < 0.05$. Palmitate increased mRNA abundance of the ER stress response targets XBP-1 (4-fold, $P < 0.01$), ATF3 (46-fold, $P < 0.001$) and CHOP (34-fold, $P < 0.001$) but neither SS nor oleate affected these transcripts ($P > 0.10$). The XBP-1 transcript is also spliced during the ER stress response. Palmitate increased the proportion of XBP-1 that was spliced (3.8 vs. 13.6 ± 2.2%, $P < 0.001$); this effect was not counteracted by SS or oleate. Myriocin treatment ablated the XBP-1 mRNA and XBP-1 splicing responses to palmitate (both $P < 0.05$), but surprisingly, further increased CHOP and ATF3 mRNA abundance (both $P < 0.001$). Palmitate had no effect on TBARS (a measure of oxidative products), but both SS and oleic acid decreased TBARS and acted synergistically when combined ($P < 0.001$ for direct effects and interaction). These results demonstrate that palmitate induces ER stress in MAC-T cells, in part through ceramide effects. Although palmitate did not induce oxidative stress, oleate and SS may function to alleviate oxidative stress in MAC-T cells.

Key Words: palmitate, mammary epithelial cell, ceramide

495 Spore incidence in individual cows and correlation with weather in California. V. Arechiga* and R. Jimenez-Flores, *Dairy Products Technology Center, California Polytechnic State University, San Luis Obispo.*

Thermophilic endospore-formers have created a growing concern in the maintenance of high quality milk products. The spores of these species can survive many processing environments and for many years. With the ability to germinate when a product is most vulnerable, they represent a variable source of contamination with difficult means of prediction measures or prevention. Therefore, it is ideal to learn the source of these spores to design preventative measures. Standards for spore counts have been established in other countries already, and with its long processing run times the United States stands to benefit from finding means to limit spore presence in milk products. Past studies have examined the various environmental factors in the pasture and the dairy and the effect on bulk tank spore counts. This study aims to look at the environmental factors that affect the milk of individual cows, eliminating equipment contact involved in bulk tank results. Thermophilic spore quantities, which are the most problematic in milk powder, were enumerated in fluid milk samples from individual cows in one herd over a 9-mo period (September through May) during the course of changing weather patterns in California. The milk samples were split and put through a mesophilic (80°C for 12 min) or thermophilic (100°C for 30 min) heat shock treatment, and plated on Tryptic Soy Agar with 1% starch. After incubating for 48 h at 55°C, the colony forming units were counted and recorded along with the weather conditions for the days of milk collection. Statistical analysis was done using Minitab at a significance level of 0.05. Mesophilic spores existed in nearly every milk sample collected ($n = 474$, $\hat{y} = 6.3$ cfu/mL), while the thermophilic spores existed in much smaller quantities and fewer cows ($\hat{y} = 3.0$ cfu/mL). Spore counts were significantly higher in both spore types in wet weather ($\hat{y} = 7.4$ cfu/mL) as compared with dry weather ($\hat{y} = 4.5$cfu/mL). Last, thermophilic spores were significantly decreased in colder months ($\hat{y} = 2.0$ cfu/mL).

Key Words: spore, milk, thermophile

496 Aroma development in relation to microbial growth in milk under Ragusano cheese-making conditions using different wooden vats (tina). S. Carpino*[1], T. Rapisarda[1], I. Schadt[1], G. Belvedere[1], and G. Licitra[1,2], *[1]CoRFiLaC, Regione Siciliana, Ragusa, Italy, [2]DISPA, Catania University, Catania, Italy.*

Ragusano cheese is a brine-salted pasta filata raw-milk cheese. Starters are not added, but the biofilm of the wooden vat (tina) and the natural milk flora are responsible for the milk acidification. The aim of this study was to investigate the development of volatiles' and odor active compounds in relation to microbial growth in milk which has been inoculated with biofilm from different tinas and which has undergone the usual cheese-making procedure except for the rennet addition step. Biofilm samples were obtained from the inner surface of 11 wooden tinas (A-K) with sterile swabs suspended in peptone water. Aliquots of a UHT milk sample were inoculated with the biofilm samples. tina surface area per volume milk was 1.5 times the usual exposure conditions. Incubated samples were first analyzed with Smart Nose®. Four (B, E, F, J) were selected as they were representing the greatest volatiles' variation (PC1 45%;PC2 25%). Samples E and F were similar in profile, but different from B and J. Profiles of B and J differed also. Samples B, E, F, and J were further analyzed by GC/O and GC/MS and for the total bacterial count (TBC), for counts of mesophilic lactobacilli (ME_LB), mesophilic lactococci (ME_LC), thermophilic lactobacilli (TH_LB), thermophilic lactococci (TH_LC) and enterococci (EC). Data were analyzed with principal component analysis. Odor active compounds, which distinguished samples, belonged to 3 groups of compounds that within group had the same presence/absence pattern. Group 1 was composed by pentanol,(Z)-2-nonenal, 2-nonanone and methyl thiophene, group 2 by 2-hexenol, ethyl hexanoate, dimethyl disulfide and (E)-limonene oxide, group 3 by (E)-2-nonenal, octane and methyl geranate. Samples B and E had odors of group 1 and 2, sample F had odors 1 and 3, whereas sample J had no odors of groups 1, 2 or 3. Odors of groups 1 and 2 were negatively associated with TBC and LC_TH. Odors of group 3 were positively associated with LC_ME and with lower effect on LC_ME and negatively with LB_TH. Levels of EC had low influence on odor or volatile differentiations (PC1 28%; PC2 20%).

Key Words: Ragusano, cheese, biofilm

497 Development of enzyme substrate assay for monitoring *E. coli*/*E. coli* O157:H7 in milk and milk products. R. Lawaniya*, N. Kumar, B. Arora, A. Khan, and M. Blahara, *National Dairy Research Institute, Department of Dairy Microbiology, Karnal, India.*

Monitoring the microbiological quality of milk relies largely on examination for indicator bacteria such as coliforms, *E. coli* and enterococci. *E. coli* is used as indicators of fecal contamination of water and food and is of most interest to clinical, food and water microbiologists. Detection of *E. coli*/*E. coli* O157:H7 in dairy products still relies on conventional method requiring at least 3 to 4 d for its identification. Alternative methods based on nucleic acid, fluorescent antibody techniques need expensive devices as well as long enrichment steps. Using chromogenic substrate against specific enzymes produced by *E. coli*/*E. coli* O157:H7 can be a rapid detection strategy and an alternative for conventional methods. Keeping this in mind, a selective enrichment medium with potential inhibition up to 5.6 log cfu/mL of contaminants such as *Salmonella*, *Shigella*, *Yersinia*, *Proteus*, *Citrobacter*, Staph. aureus, and *L. acidophilus* has been developed and MIC of selective agents used in the development of medium are determined at specific cell level; i.e., 3 to 6 log cell/mL based on chromogenic assay. The developed assay can detect the target bacteria i.e., *E. coli* / *E. coli* O157:H7 within 12 ± 1 h compared with a 3- to 4-d protocol of conventional method in ISO-5887 part-1 detection method.

Key Words: *E. coli*, enzyme substrate assay, rapid method

498 Effect of drying methods on microencapsulated bacteria on secondary protein structure and glass transition temperature as studied by FTIR and DSC. D. Dianawati[1] and N. P. Shah*[2], *[1]Victoria University, Melbourne, Australia, [2]The University of Hong Kong, Pokfulam Road, Hong Kong.*

The objective of this study was to examine the effect of drying methods on microencapsulated *L. acidophilus* and *L. cremoris* on secondary protein structure and glass transition temperature. Protective mechanism of casein-based microcapsule containing mannitol on *L. acidophilus* and *L. lactis* ssp. *cremoris* and glass transition of the microcapsules were studied after spray- or freeze-drying and after 10 week of storage in aluminum foil pouch containing different desiccants (NaOH, LiCl or silica gel) at 25°C. An in situ FTIR analysis was carried out to recognize any changes in fatty acids of bacterial cell envelopes; interaction between polar site of cell envelopes and microcapsules, as well as alteration of their secondary protein structures, whereas DSC was used to determine glass transition

(T_g) of microcapsules. Hierarchical cluster analysis based on functional groups of phospholipid bilayers of cell envelopes and secondary protein structures was also carried out to classify the microencapsulated bacteria. The results showed that drying process did not affect fatty acids and secondary protein structures of bacteria, however, those structures were affected during storage depending upon the type of desiccant. Interaction between bacterial cell envelopes and microencapsulant occurred after drying as shown by alteration of wavelength of $P = O$ symmetric of cell envelopes from 1075 cm^{-1} to 1047 and 1048 cm^{-1} (fresh L. acidophilus, freeze-dried and spray dried cells, respectively). Similar phenomenon was demonstrated by *L. cremoris*. However, these structures were maintained after storage in foil pouch containing NaOH. Method of drying and type of desiccants influenced the level of similarities of microencapsulated bacteria. Desiccants and method of drying affected glass transition; yet no $T_g \leq 25°C$ was detected. This study demonstrated that the changes in fatty acids and secondary structures of the microencapsulated bacteria still occurred during storage at T_g above the room temperature indicating that glass state did not completely prevent chemical activities.

Key Words: microencapsulation, FTIR, DSC

499 The relationship between *Streptococcus thermophilus* exopolysaccharide diversity and fermented milk viscosity. H. Yi*, L. Zhang, and L. Zhang, *College of Food Science and Engineering, Harbin Institute of Technology, Harbin, China.*

Exopolysaccharides produced by *Streptococcus thermophilus* fermented milk plays a crucial role in the viscosity of the fermented milk. In this work, the content of exopolysaccharides of 19 different *Streptococcus thermophilus* fermented milk and the corresponding viscosity were studied. Then the exopolysaccharides produced by *Streptococcus thermophilus* were purified by DEAE-52 cellulose chromatography and Superdex 200 chromatography purification. The purified exopolysaccharide were added to fermented milk to detect the effect of purified exopolysaccharide on the yogurt viscosity. And the compositions of exopolysaccharide were determined by Fourier transform infrared spectroscopy. The results showed that strains which produced large amount of exopolysaccharides could improve the viscosity of fermented milk. The exopolysaccharides of 3 *Streptococcus thermophilus*, zlwTM11-EPS, zlwB9–3-EPS and zlwSP1.1-EPS, were selected and detect the effect of exopolysaccharides on fermented milk viscosity. It showed that the contribution of the zlwTM11-EPS on the viscosity of the fermented milk is the largest. Four major purified components were obtained from zlwTM11-EPS: zlwTM11–1, zlwTM11–2, zlwTM11–3 and zlwTM11–4. The purity were 89.35%, 92.49%, 81.03% and 93.37% respectively. These 4 purified components were added to the *S. thermophilus* zlwSP1.1 fermented milk. The 4 purified components could all increase the viscosity of the fermented milk, but the effect of the zlwTM11–2 was significantly higher than the other components. The major structure of zlwTM11–2 produced exopolysaccharide was β-D-pyranose. And the exopolysaccharide of zlwTM11–2 were constituted by rhamnose, mannose, glucose and galactose with the ratio of 9.7: 4.87: 39.14: 46.29. The optimum exopolysaccharides production conditions of zlwTM11–2 in fermented milk were also determined that was 4.49% of the inoculum size, 6.74h of fermentation time, 43°C of fermentation temperature. At last, the actual production of the zlwTM11–2 was 42.947mg/L which was 11.87% higher than before.

Key Words: fermented milk, exopolysaccharide, *Streptococcus thermophilus*

500 The growth and interaction of yeasts and lactic acid bacteria in milk fermentation. X. Han*, L. Zhang, H. Yi, and Q. Yi, *College of Food Science and Engineering, Harbin Institute of Technology, Harbin, China.*

Yeasts affect the quality of fermented milk through the production of flavor compounds and other metabolites. As a specialty product, yeast and lactic acid bacteria combined fermented milk has its own niche in the special places in China. In present study, 5 yeasts were screened and isolated from traditional dairy products throughout the northwestern China according to their fermented milk characteristics. The yeasts which have higher production of CO_2 and acid rate were selected to combine with the yogurt starter culture to fermented milk. The fermented temperature, inoculate and the ratio of yeast and LAB were optimized. Then the changes of viable count of yeast and LAB, the content of CO_2, ethanol and pH were also detected during 10°C storage for 4 weeks. The results showed the total inoculate rate of starter was 4%, the ratio of yeast and LAB were 1:4, fermented temperature was 37°C. The storage test manifest the pH of fermented milk were decreased from 4.21 to 3.83. The counts of LAB were increased from 5.5×10^8 to 8.3×10^8 cfu/mL during the first week storage at 10°C. Then the counts were decreased to the 7.3×10^7 cfu/mL. The viable counts of yeast were increased from 6.8×10^5 to 9.6×10^6 cfu/mL. The content of CO_2 and ethanol produced by yeast was 22.9 mmol/l and 14.57 mg/ml respectively. For the texture of product were better than LAB fermented milk (yogurt). However the apparent viscosity of product was lower than yogurt. For the sensory evaluation, the product has the little milk taste and with the little fresh flavor. These results manifested that the yeast possesses stability enhancing effects on LAB and yeast combined yogurt could provide the new products to the Chinese dairy marketplaces.

Key Words: yeasts, lactic acid bacteria, viable count

813 Cytokine and regulatory T cell responses of lactic acid bacteria and probiotic organisms in human peripheral blood mononuclear cells R. Ashraf*[1], O. N. Donkor[1], S. C. Smith[2], T. Vasiljevic[1], *[1]Victoria University, School of Biomedical and Health Sciences, Werribee Campus, Melbourne, VIC, Australia, [2]Deakin University, School of Exercise and Nutrition Sciences, Faculty of Health, Gut Health SRC Molecular and Medical Research, Burwood, VIC, Australia*

Many strains of lactic acid bacteria (LAB) are believed to have probiotic properties and offer various health benefits. In the current study, the immuno-modulatory effects of probiotic organisms and LAB were assessed following stimulation of peripheral blood mononuclear cells (PBMCs) with seventeen strains of probiotic and lactic acid bacteria. The production of pro- and anti-inflammatory cytokines including interleukin (IL)-2, IL-4, IL-10, IL-12 p70, interferon (IFN)-γ, tumor necrosis factor (TNF)-α and transforming growth factor (TGF)-β, the expressions of CD25 marker and forkhead box P3 (FoxP3)–regulatory T cell (Treg) marker were examined after stimulation of PBMCs with seventeen LAB strains. The results show that (i) live strains stimulated significant production of all cytokines but in varying concentrations, (ii) the pattern of cytokine production was found strain specific, (iii) TNF-α, IFN-γ, IL-10 and TGF-β were stimulated at high concentrations (iv) the strains of Bifidobacterium stimulated highest levels of TGF-β, IL-10 and IL-4 whereas L. casei 290 gave the highest response for TNF-α and S. thermophilus M5 for IFN-γ, (v) CD3+CD4+CD25+ cell population was significantly increased for all tested strains except Lc. lactis R704 (vi) the number of Treg population was significantly increased for tested strains where S. thermophilus M5, B. animalis subsp. lactis BB12, L. casei 290 and S. thermophilus 1342 showed seven-fold more expression of FoxP3 than unstimulated PBMCs. The study suggests that probiotic bacterial strains differ in their immunomodulatory effects.

Key Words: probiotic bacteria, immunomodulation, cytokine

Nonruminant Nutrition Symposium: Breaking the Mold—Formulating Monogastric Diets Without Traditional Ingredients

501 Alternative ingredients for diets—A global perspective. R. G. Campbell*, *Pork CRC, Willaston SA, Australia.*

Global animal feed production approached 865 million tonne in 2012 with Asia the largest producer of compound feeds (170 million tonne) followed by the United States (161 million tonne). The USA has been reliant on corn as the main cereal in monogastric diets but alterative grains and in particular barley, sorghum and triticale are used throughout Asia and Europe. The by-products of wheat milling are also produced in large amounts and available globally as alternatives to cereals and will continue to be used in the future. Soybean meal is a by-product of the soybean crushing industry and can be regarded as the bench mark protein source for most livestock and is produced in large amounts in China, United States, Argentina and Brazil (total 142 million tonne) and will remain a staple ingredient into the future but it is not an essential component of animal diets and is rarely used in Australia. In Europe, Canada and parts of Asia, canola seed meal is widely and increasingly available as a cost effective alternative protein supplement for livestock diets. The alternative ingredient that has seen the greatest growth over the last 5–6 years is DDGS the production of which exceeded soybean meal in the USA in 2012. DDGS is used to replace both soybean meal and corn in livestock diets. Because they are produced in large amounts we will continue to rely on these alternatives or by-products and need to develop means of rapidly assessing their nutrient value, technologies for better utilizing each and define/extend the limits of inclusion in diets for different classes of livestock based on their cost effectiveness rather than animal performance per se. Potential new feeds are likely to become available in the form of biomass from algae systems used in bio fuel production and the sequestration of CO_2 and eventually from cellulosic ethanol production. There is also potential to use food waste as an animal feed though it carries with it some biosecurity and potential market/perception risks but a lot is available more consideration should be given to its potential use. At a local level liquid and dry by-products from various human-related manufacturing operations have long been used very successfully particularly by pork producers.

Key Words: alternative feedstuffs, global animal feed production, DDGS

502 Factors to consider when formulating diets with alternative ingredients. K. Adams*, *Akey/Cargill, Brookville, OH.*

Alternative ingredients can offer an opportunity to swine nutritionists to decrease feed costs. Nutritional valuation, cost, handling characteristics and other factors that affect usage need to be considered. By-products by nature are variable. Quality control processes may be lacking. Names are seldom descriptive of the nutritional value of alternative ingredients. It is imperative to determine percent moisture, protein, fat, ADF, NDF, calcium, phosphorus, sodium and ash. Amino acid analyses are also useful. NIR analysis offers a quick method of assessing nutrient content, but equations must be developed for each specific by-product. Distillers dried grains with solubles (DDGS) are one of the most common by-products fed to swine, but they can vary greatly in nutrient content and mycotoxin levels. Depending on the quality of DDGS, the level fed can also influence feed intake and carcass yield. Bakery by-products are another popular ingredient used in swine diets, but can contain up to 25% wheat middlings, DDGS, or corn germ, resulting in ADF levels ranging from 1 to 23%. Hominy and corn germ meal are highly variable in fat and ADF content. Pet food fines can be made up of changing portions of cat, puppy, adult and senior dog food. Nutritionists may often find themselves using a "best guess" analysis for formulation. Complete feed processing can affect the level of by-products used in swine diets. Pelleting allows higher inclusions of less dense ingredients, but it can also result in higher iodine values in carcass fat. Some alternative ingredients are only available as liquids and need to be fed using liquid feeding systems or through water lines. Disposal of liquid by- products in a land fill or drying them to sell into the marketplace are both costly options, so companies producing them may offer attractive pricing. Many by-product ingredients are available to nutritionists and can help reduce cost of production. However, nutritional value of alternative ingredients needs to be evaluated carefully and the products used appropriately to support acceptable growth performance.

Key Words: by-product, alternative ingredient, swine

503 Controlling feed cost by including alternative ingredients into swine diets. R. T. Zijlstra*[1] and E. Beltranena[1,2], *[1]University of Alberta, Edmonton, AB, Canada, [2]Alberta Agriculture and Rural Development, Edmonton, AB, Canada.*

Sustained price increases for traditional feedstuffs such as cereal grains, protein meals, and fats have forced the pork industry to consider dietary inclusion of alternative feedstuffs. The 2012 US drought reduced crop yields and escalated feed commodity prices beyond those triggered by the expansion of the biofuel industry. Crops may serve as feedstuffs but are also processed into human food, fuel, and bio-industrial products. Together with these products, feed co-products such as distillers dried grains with solubles (DDGS), canola meal (expeller-pressed, solvent-extracted), canola and camelina cake, and crude glycerol are produced. As omnivores, pigs are ideally suited to convert these non-human edible co-products into high quality food animal protein. Thereby, co-products can partially offset increases in feed cost provided their price is less per unit of energy (NE) or lysine (SID), but also present risks and feeding challenges. First, processing of co-products adds variability in macronutrient profile beyond the intrinsic variability of crops. Thus, feed quality evaluation to profile digestibility of energy, AA, and P is as important as the energy and AA system selected for feed formulation. Moreover, rapid evaluation (NIRS) is needed to manage the risk of variation among batches of individual feedstuffs. Second, fermentation and heat processing affect AA and P availability. Overheating reduces lysine availability due to Maillard reactions, reduces heat-labile anti-nutritional factors, but combined with fermentation, may increase mineral availability. Third, co-products may contain chemical residues and mycotoxins such as deoxynivalenol that survive or are augmented by processing that reduce voluntary feed intake. Finally, co-product use may affect carcass characteristics and pork quality. Inclusion of high fiber co-products reduces dressing percentage. Inclusion of high unsaturated fatty acid co-products softens pork fat. In conclusion, the feeding of co-products may reduce feed costs per unit of pork produced, but also provides challenges to achieve cost-effective, predictable growth performance, carcass characteristics, and pork quality.

Key Words: co-product, nutritional value, pig

504 Maintaining high quality swine and poultry diets with non-traditional ingredients. J. D. Hancock*, M. E. Morts, R. S. Beyer, and C. K. Jones, *Kansas State University, Manhattan.*

For decades, focus among US nutritionists has been on alternative protein sources, amino acid concentrations, and amino acid ratios that might be used to improve growth performance in swine and poultry. However, we are in unprecedented times. During the past 7 years energy costs for swine and poultry diets have soared in the US and abroad and this has ushered in a new emphasis on non-traditional feedstuffs that might be used to control diet costs while maintaining growth performance. Use of alternative cereal grains such as wheat and sorghum are commonplace in the United States and especially in the High Plains. Here at Kansas State University, we have experimented with use of rice flour, cassava, triticale, and molasses, having good success in swine diets. To further control diet costs, co-products from the milling, baking, and ethanol industries cannot be discounted. Of particular importance in global swine and poultry diets are co-products from the wheat flour and ethanol industries with use of 20 to 30% wheat middlings and 30 to 40% distillers dried grains with solubles (DDGS) being real possibilities. Use of such alternative ingredients is not without potentially problematic changes in feed manufacturing, diet flowability, feed intake, and carcass characteristics. Also, these products are in transition (e.g., low-oil DDGS) as these industries mature. However, the need for cheap sources of calories may finally have trumped the need for comfort allowed with feeding a simple corn-soybean meal diet. The challenge for nutritionists will be to stay abreast of changes in physical and nutritional characteristics of co-products and to stay open to use of new and alternative ingredients to formulate high quality, affordable diets.

Key Words: swine, poultry, diet ingredient

505 Algae, a by-product of the biofuel industry to replace soybean meal in swine and poultry diets. X. G. Lei*, *Cornell University, Ithaca, NY.*

The fast growing worldwide population and diminishing arable land have made food security and nutrition a major challenge. While animal agriculture provides 25% of total calorie intake, the traditional feeding regimen directly competes against human consumption of high energy and protein staples. Apparently, alternative ingredients are needed to replace corn and soybean meal for sustainable animal production. Microalgae have recently been explored as a new exciting source of biofuel, and the defatted residual biomass contains high levels of protein and other nutrients. Since 2009, our laboratory has conducted a total of 12 feeding experiments to determine whether the defatted microalgal biomass could replace a portion of soybean meal or a combination of corn and soybean meal in diets for laying hens, broilers, and weanling pigs. The defatted biomass derived from 3 different microalgal species (Cellana, Kailua-Kona, HI) was supplemented at 7.5 to 25% in corn-soybean meal diets for the 3 types of animals. The feeding experiments lasted as short as 3 wk for the starter period of broilers or as long as 15 wk for the full cycle of egg production of layer hens. With appropriate supplementations of amino acids and manipulations of other nutrients, inclusions of various levels of the defatted microalgal biomass to substitute for soybean meal did not alter growth performance or a series of plasma biochemical indicators of the animals. Intriguingly, animals fed the microalgal biomass appeared to have lower plasma uric acid or urea-nitrogen concentrations than those fed the control diets. In conclusion, our research has demonstrated the feasibility of using the defatted microalgal biomass from the biofuel production to replace a portion of soybean meal in diets for poultry and swine. Supported in part by a USDA/DOE Biomass R&D Initiative grant.

Key Words: microalgae, soybean meal, animal nutrition

506 Control of cow hypocalcemia: Field application of ion-selective field effect transistor technology. E. M. Rodríguez*[1], A. Bach[1,2], N. Abramova[3], A. Bratov[3], A. Ipatov[3], and A. Arís[1], *[1]Department of Ruminant Production, IRTA, Caldes de Montbui, Spain, [2]ICREA, Barcelona, Spain, [3]BioMEMS Group, IMB-CNM, CSIC, Bellaterra, Spain.*

The early detection of subclinical levels of blood calcium (Ca) in the cow can avoid later health and production problems. Therefore, a field Ca sensor could be a powerful tool. The aim of this study was to develop a reliable prototype to quantify blood Ca in the cow, to define its specifications and to determine the influence of blood Ca daily circadian fluctuations in the periparturient cow. An analytical system based on ion-selective field effect transistor (ISFET) with Ca selective photocurable membranes was developed to offer a semiautomatic Ca analysis of serum (obtained by thrombin coagulation or centrifugation), plasma or direct blood. The sensor Ca measurements were validated by comparing the results with those obtained using the ICP-OES reference method. Cleaning solutions based on proteolytic enzymes in a neutral solvent, detergent or HCl were tested. Twelve Holstein multiparous cows were sampled at 24–48 h postcalving to analyze daily blood Ca changes at 0700, 1400, and 2000 h. Data were analyzed with a mixed-effect model with repeated measures. The precision of the analysis by ISFET was greater than reported for double charged ions with a σ within 3–7%. A linear response in the $0.1–10^{-5}$ *M* Ca concentration range and a detection limit of 3×10^{-6} *M* were obtained. Each analysis takes <20 min and only 100 μL of sample is needed. The serum samples obtained after thrombin coagulation or centrifugation and the plasma samples did not differ from the total Ca concentration determined using the reference method. However, direct blood measures differed from the reference measures and shortened the life of the ISFET to a single use. The best way to recuperate the sensors' response was the cleaning of the system with the proteolytic solution, although the detergent yielded positive outcomes as well. Blood Ca levels were not affected by daily circadian fluctuations. In conclusion, the results demonstrate that ISFET technology can be applied efficiently to analyze serum or plasma Ca in the cow as a new fast, reliable and inexpensive method. Also, blood samples from the periparturient cow can be obtained any time of the day.

Key Words: cow, hypocalcemia, ion-selective field effect transistor (ISFET)

507 Calcium urinary excretion in dairy cows with different levels of glucose tolerance. E. Schwegler*[1], F. da Rosa[1], A. Silva[1], E. Oliveira[1], P. Montagner[1], M. Weschenfelder[1], A. Krause[1], C. Brauner[1], E. Schmitt[2], V. Rabassa[1], A. Schneider[1], E. Xavier[1], F. Del Pino[1], and M. Correa[1], *[1]Federal University of Pelotas, Pelotas, RS, Brazil, [2]Brazilian Agricultural Research Corporation, EMBRAPA-CPAFRO, Porto Velho, RO, Brazil.*

During the peripartum dairy cows experience a transitory period of insulin resistance. In humans, insulin resistance is associated with increased urinary excretion of calcium (Ca). Therefore, the aim of this study was to assess the Ca urinary excretion during the peripartum in dairy cows with different levels of glucose tolerance during the prepartum period. Nineteen pluriparous Holstein cows were enrolled in this study. Glucose tolerance tests (GTT) were conducted at 20d prepartum. The GTT was based on an infusion of 500 mg/kg body weight of glucose and posterior determination of serum glucose concentrations at several time points up to 180 min and the calculation of the glucose area under the curve (AUC). The cows were categorized according to the rate of glucose metabolism into sensitive group (GS: higher glucose metabolism, 8,194 ± 388.6 mg/dl), intermediate group (GI, 12,079 ± 528.2 mg/dL) and resistant group (GR: lower glucose metabolism, 15,507 ± 292.4 mg/dL). Blood and urine samples were collected on d −23, −14, −7, −3, 0, 3, 6, 9, 16 and 23 from calving. Concentrations of creatinine (Creat) and Ca were analyzed in serum (S) and urine (U). The Ca excretion in the urine was estimated by calculating the fractional excretion (EF) using the formula: (UCa/SCa) × (SCreat/UCreat) × 100. Statistical analysis was performed using the SAS. According with the AUC categorization, 6 cows were in the GS, 7 cows were in the GI and 6 cows in the GR. The GR had higher fractional excretion of calcium in the prepartum (96.3 ± 10.4%) than the GS (59.2 ± 8.8%) ($P < 0.01$). Calcium excretion in GI (59.5 ± 7.6%) was similar to GS ($P > 0.05$), but lower than GR ($P < 0.05$). In the postpartum period the GR (27.7 ± 3.7%) had an increased Ca excretion than GS (16.1 ± 3.3%) ($P = 0.02$), although GI similar between GR and GS (21.9 ± 3.0%) ($P > 0.05$). In summary, the present study indicates that prepartum cows less tolerant to glucose excrete more urinary calcium in the pre and postpartum periods. More studies to understand the potential effects of these results on the etiology of hypocalcemia are necessary.

Key Words: glucose tolerance, peripartum, calcium urinary excretion

508 The association of postpartum calcium concentration with body weight change and milk production in dairy herds with automatic milking systems during the first 30 days in milk. L. S. Caixeta*[1], P. A. Ospina[1], S. K. Johnson[1], M. Capel[2], and D. V. Nydam[1], *[1]Cornell University, Ithaca, NY, [2]Perry Veterinary Clinic, Perry, NY.*

The objectives were to characterize calcium concentration variability and evaluate the association between subclinical hypocalcemia (HPC) and changes in body weight (BW) and milk production (MP) within the first 30 d in milk (DIM) in herds with automatic milking systems. In a prospective cohort study of 3 herds, 105 dry cows were enrolled and followed until 30 DIM. Serum samples were analyzed for calcium at 1, 2 and 3 DIM. Based on previous reports, HPC was defined as having at least one reading between 6 and 8 mg/dL and treated as a dichotomous variable in the analysis. Daily measurements of BW and MP were used to estimate BW change over time and total MP in the first 30 DIM. Occurrence of any disorders: displaced abomasum, ketosis, milk fever, retained placenta or metritis, was also included in the analysis as a dichotomous covariate. The Mixed procedure in SAS was used to evaluate the association between HPC, disease, herd, and any biologically relevant interactions with BW and MP. HPC was found in 17% of primiparous and 65% of multiparous animals. Both disease and HPC status were significant predictor variables ($P < 0.01$), thus the result of the interaction between them is reported in Table 1. Subclinical hypocalcemia was not a significant predictor of milk production in primiparous animals, but multiparous cows with HPC produced 45.5 kg ($P < 0.01$) less milk than those without HPC during the first 30 DIM. Mature animals with HPC exhibited more rapid weight loss and produced less milk than their normocalcemic counterparts.

Table 1. Body weight change (kg) per day over the first 30 DIM and the interaction between disease (Dz) and subclinical hypocalcemia (HPC) by parity group; ll interactions had $P < 0.01$.

	Parity 1	Parity 2	Parity ≥3
No Dz × No HPC	−0.42	−1.44	−1.25
No Dz × HPC	−1.35	−1.22	−1.75
Dz × No HPC	−1.67	−2.40	−0.75
Dz × HPC	−1.10	−0.66	−2.13

Key Words: hypocalcemia, body weight, milk

509 Effects of protein supplementation of fall calving cows during breeding and lactation on growth and concentrations of IGF-I in plasma of beef calves. K. J. McLean*, B. H. Boehmer, L. J. Spicer, and R. P. Wettemann, *Oklahoma Agricultural Experiment Station, Stillwater.*

Fall calving cows grazing dormant native grass pasture were used to evaluate effects of protein supplementation during breeding and the first trimester of gestation on postnatal growth and concentrations of insulin and IGF-I in plasma of calves. Cows calved in Sept-Oct, grazed in one pasture, and were individually fed control (C, 1.82 kg/d of 38% CP supplement, n = 22) or low (L, 0.2 kg/d of 8% CP supplement, n = 21) from Nov 17 to March 20. Cows were exposed to bulls for 60 d commencing Dec 1. During lactation the subsequent year, half of the cows on C and L prenatal treatments was assigned to C and the other half was assigned to L. Birth weight, weaning weight, insulin, IGF-I, and plasma proteins were analyzed as a 2 × 2 factorial using the MIXED procedure of SAS. Birth weight and BW at weaning (205 d) were not influenced ($P = 0.76$) by prenatal treatment. Weaning weight (205 d) was greater ($P = 0.02$) for calves on postnatal C (200 ± 5 kg) compared with L (184 ± 5 kg). Neither prenatal nor postnatal treatment of dams influenced preweaning concentrations of insulin in plasma of calves ($P > 0.14$). Plasma concentrations of proteins and IGF-I were not influenced by prenatal or postnatal treatment in Dec ($P > 0.50$ and $P > 0.22$, respectively). Postnatal C calves had greater ($P = 0.03$) concentrations of IGF-I (21.5 ± 2.1 and 14.8 ± 2.1 ng/mL, respectively) and less plasma proteins (6.6 ± 0.1 and 6.8 ± 0.1 g/100 mL, respectively, $P = 0.05$) compared with L calves in Jan. Steer calves tended to have greater ($P = 0.06$) concentrations of IGF-I compared with heifers at weaning (29.9 ± 2.6 and 22.1 ± 2.9 ng/mL, respectively). Calves with L dams both prenatally and postnatally, had less plasma proteins at weaning ($P = 0.02$) compared with the other treatments. Postnatal performance of calves was not influenced when dams were supplemented with protein during breeding and early gestation that resulted in less BW loss and greater plasma IGF-I concentrations (J. Anim. Sci. 90 (E-Suppl. 3): 325, 2012), however, protein supplementation of dams during lactation increased growth of calves.

Key Words: nutrition, IGF-I, calf

510 Lipogenic-associated gene activity of adipose tissue from beef heifers and relation to production and reproductive traits. L. A. Rempel*, R. A. Cushman, T. G. McDaneld, J. R. Miles, L. A. Kuehn, and A. K. Lindholm-Perry, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Transition from adolescence to puberty is marked by changes in metabolic activity. Fatty acid synthase (FASN) catalyzes the de novo synthesis of fatty acids and increased expression has been linked to excess energy intake and obesity. The enzyme, DNA-protein kinase (DNA-PK) plays a role in DNA damage repair, but can also influence transcription of lipogenic genes, including FASN. The objectives of our study were to (1) evaluate the expression of these lipogenic-affiliated genes, FASN and DNA-PK, at one year of age and (2) evaluate their association with production and reproductive traits in crossbred heifers. Subcutaneous adipose tissue was collected at approximately one year of age from 130 crossbred beef heifers. Total RNA was extracted from adipose tissue and reverse transcribed to generate cDNA for real-time PCR. Raw expression data was log-transformed and normalized against 2 housekeeping genes. Relative expression of FASN and DNA-PK were not correlated ($P = 0.6148$) with each other. The relationship between gene expression and growth and reproductive traits was modeled using a regression analysis with covariates heterosis and breed included. Relative expression of adipose FASN in beef heifers at one year of age had a positive association ($P \leq 0.0019$) with ADG (0.08 ± 0.024 kg) and weight at puberty (85.3 ± 25.86 kg). Similarly, relative DNA-PK expression was also positively associated ($P \leq 0.0042$) with ADG (0.12 ± 0.041 kg) and weight at puberty (146.7 ± 40.75 kg). Moreover relative DNA-PK expression at one year of age in beef heifers was positively associated ($P = 0.0004$) with age at puberty (75.8 ± 20.94 d) while a negative association ($P = 0.0610$) was observed with weight at first breeding (−37.7 ± 19.94 kg). Relative expression of FASN and DNA-PK in adipose from heifers at 1 yr of age was related to growth parameters; however, age at puberty and weight at first breeding were affiliated with DNA-PK expression only. DNA-PK may be contributing to metabolic gene activation, which influences growth and puberty.

Key Words: heifer, adipose, pubertal

511 Endocrine profile and hepatic gene expression in Holstein cows with different nutritional managements during early lactation. A. L. Astessiano*[1], P. Chilibroste[2], M. Fajardo[2], J. Laporta[1], J. Gil[3], D. Mattiauda[2], A. Meikle[4], and M. Carriquiry[1], *[1]School of Agronomy, UDELAR, Montevideo, Uruguay, [2]School of Agronomy, UDELAR, Paysandú (EEMAC), Uruguay, [3]School of Veterinary Medicine, UDELAR, Paysandú (EEMAC), Uruguay, [4]School of Veterinary Medicine, UDELAR, Montevideo, Uruguay.*

Multiparous cows (n = 25) were used in a randomized block design to study the effects of nutrition during the first 60 d postpartum on endocrine profiles and hepatic gene expression. Cows were assigned to 3 treatments (TREAT): TMR = total mixed rations (30 kg DM/d offered; 45% forage, 55% concentrate); G1 = 50% pasture in one (am) grazing session (6 h; pasture allowance = 15 kg DM/d) + 50% TMR (15 kg DM/d offered); and G2 = 50% pasture in 2 (am/pm) grazing sessions (9 h; pasture allowance = 15 kg DM/d) + 50% TMR (15 kg DM/d offered). Plasma and liver biopsies were collected at −40, −20, +10 and +55 DPP. Gene expression was quantified by real time PCR. Means from a repeated measures analysis differed when $P < 0.05$. Insulin decreased around calving in G1 and G2 cows and in early lactation tended to be greater ($P = 0.06$) for TMR than G1 cows (19.4, 15.1 and 17.3 ± 1.3 uIU/mL for TMR, G1 and G2). Adiponectin increased from pre to postpartum (77%) and during postpartum was greater in G2 than G1 cows (52.5, 87.1 and 132.7 ± 18.2 ng/mL for TMR, G1 and G2). Leptin decreased from −40 to +10 d and increased thereafter recovering values of prepartum, and during the postpartum were greater in G2 than G1 cows (4.1, 3.1 and 4.5 ± 0.4 ng/mL for TMR, G1 and G2). Hepatic INSR mRNA increased 1.5-fold at +55 d for all TREAT. The LEPR-b mRNA was greater in G2 than G1 cows during early lactation (1.57, 1.10 and 1.91 ± 0.3 for TMR, G1 and G2) as its expression increased from pre to postpartum in TMR and G2 but not in G1 cows. Although ADIPOR1 mRNA did not vary due to TREAT or days of lactation, ADIPOR2 mRNA increased 2.5-fold from pre to postpartum in all TREAT. Expression of ANGPTL4 mRNA tended ($P = 0.07$) to be affected by TREAT being greater in TMR than G2 cows during the postpartum (2.36, 1.97 and 1.05 ± 0.4 for TMR, G1 and G2) as it increased from pre to postpartum in TMR and G2 but remained stable in G1 cows. Cows fed TMR showed better metabolic status (greater BCS, insulin and, ANGPLT4 mRNA) while G2 showed a differential partitioning of energy (body reserves vs. activity) during early lactation associated with the feeding strategy postpartum

Key Words: nutrition, dairy cattle

512 Effects of maintenance energy requirements of gestating beef cows on plasma concentrations thyroxine, triiodothyronine, and rectal temperature. B. H. Boehmer*, K. J. McLean, and R. P. Wettemann, *Oklahoma Agricultural Experiment Station, Stillwater.*

Spring-calving, Angus cows (n = 29) were used to evaluate the effects of maintenance energy requirements on plasma concentrations of thyroxine (T_4), triiodothyronine (T_3), and rectal temperature (RT). Nonlactating cows (5 to 10 yr of age, 144 ± 2 d of gestation) with a BW of 552 ± 8 kg and BCS of 4.3 ± 0.1 were individually fed a maintenance diet (Ne_m, Model 1, NRC 1996) for 31 d. Body weights were obtained twice weekly and daily feed intake was adjusted every 2 wk until constant BW was achieved (maintenance, MR). Mean MR of cows was 83.4 kcal/kg $BW^{0.75}$/d. Cows (n = 20) were infused with TRH (0.33 μg/kg BW) after consuming maintenance diets for 21 d. Blood plasma was collected at 0, 30, 60, 90, 120, 150, 180, and 240 min after TRH challenge and T_3 and T_4 were quantified in plasma by RIA. Maintenance energy requirements were used to classify cows as low (L; >0.5 SD less than mean, 79.4 kcal/kg $BW^{0.75}$/d), moderate (M; ± 0.5 SD of mean, 83.4 kcal/kg $BW^{0.75}$/d) or high (H; > 0.5 SD more than mean, 86.8 kcal/kg BW $^{0.75}$/d). Thyroxine, T_3 and RT were analyzed with PROC MIXED (SAS Inst. Inc.) and BW was analyzed with PROC GLM (SAS Inst. Inc.). Plasma concentrations of T_3 were greater in H and M cows (P = 0.04; 0.63 and 0.66 ng/mL, respectively) compared with L cows (0.58 ng/mL). Plasma T_3 increased after TRH to a maximum at 180 min in H (0.74 ng/mL) and M cows (0.78 ng/mL) and at 120 min in L cows (0.63 ng/mL). There was a MR × time effect ($P < 0.05$) for T_4 in plasma. Maintenance requirement of cows did not influence T_3:T_4 in plasma (P = 0.59) or RT (P = 0.46). Thyroid hormones influence metabolism and may be useful in determining maintenance requirements of beef cows. Production efficiency of beef cows may be improved by identifying cows that require less energy input while retaining performance.

Key Words: beef cattle, maintenance, thyroid

513 Comparisons of the transcriptome profiles of adipose tissue from beef and dairy cattle. J. Thomson*[1,2], P. Stothard[2], and J. P. McNamara[3], *[1]Montana State University, Bozeman, [2]University of Alberta, Edmonton, AB, Canada, [3]Washington State University, Pullman.*

RNA-seq, an application of next-gen nucleic acid sequencing technologies has enabled us to look at the transcriptomes of tissues at a given point of time with extremely high resolution. This technique has been used with great success to evaluate the effect of perturbations or treatments on gene expression. In this study we evaluated the functional and metabolic differences in transcriptome profile of 2 breeds of cattle with a history of divergent selective pressure and resulting differences in metabolism and gene expression: Holstein dairy cows and crossbred beef cows of Hereford and Angus genetics. RNA was isolated from 8 Holstein animals and 10 beef animals. The RNA was pooled within breed, enriched using poly-T oligo attached beads, and then cDNA libraries were synthesized and sequenced. Reads were aligned to UMD 3.1 and normalized read counts were used to calculate expression values for coding genes, alternative splice variants, and non-coding RNA transcripts. Functional analysis was conducted using Genesifter software from Geospiza and DAVID bioinformatics software version 6.7. Over 10 million reads were mapped to the reference sequence and expression values were generated for over 15,000 genes and over 30,000 potential splice variants in each breed. Differentially expressed genes were determined using Genesifter software pairwise *t*-test and Bonferroni correction for multiple comparisons with a significance threshold of adjusted $P < 0.05$. As expected the adipose tissue in both beef and dairy highly expresses genes associated with lipid transport and metabolism such as fatty acid binding protein 4 (FABP4) and perilipin (PLIN) both not statistically different. Definite differences were observed with dairy transcripts being enriched for oxidative phosphorylation (113 transcripts, $P < 0.005$) and cell cycle pathways (109 transcripts, $P <$ 0.005) while beef adipose transcripts were enriched for insulin signaling (105 transcripts, $P = 0.01$) and adipocytokine signaling (58 transcripts, $P = 0.003$). This may provide insight into the different roles of adipose tissue in breeds of cattle selected for different purposes.

Key Words: RNA-seq, genomics, physiology

514 Alterations in body mass and inflammometabolic indices in Holstein cows fed different levels of energy and receiving 2,4-thiazolidinedione. A. Hosseini*[1], E. Trevisi[2], F. T. da Rosa[1], G. Bertoni[2], J. K. Drackley[1], and J. J. Loor[1], *[1]University of Illinois, Urbana, [2]Università Cattolica del Sacro Cuore, Piacenza, Italy.*

Overfeeding energy during the dry period increases the incidence of metabolic disease postpartum. Dry matter intake (DMI), body condition score (BCS) and blood inflammometabolic markers can serve as reliable indicator of health, inflammation and liver function. We evaluated DMI, BCS, metabolism, inflammation, and liver function in response to level of dietary energy and 2,4-thiazolidinedione (TZD) administration. Fourteen dry non-pregnant Holstein cows were assigned to treatments in a randomized block design. All cows were fed a control diet (CON; NEL = 1.32 Mcal/kg) to meet 100% of NRC requirements for 3 wk, after which half of the cows were assigned to a moderate-energy diet (OVE; NEL = 1.54 Mcal/kg) and half of the cows continued on CON for 6 wk. The OVE diet was fed ad libitum and resulted in cows consuming ~180% of NRC. CON cows were fed to consume only to 100% of NRC. All cows received 4 mg TZD/kg of BW daily starting 2 wk after the initiation of treatments and for 2 additional wk. The last 2 wk of the study served as the washout period. BW and BCS were recorded twice a week, while DMI was recorded daily during the entire study. Blood was harvested frequently during wk −1 to 6 for measurement of metabolites and hormones. Data were analyzed using PROC MIXED of SAS. In OVE compared with CON, the BW, DMI and DMI as a percentage of BW increased over time ($P < 0.001$), while BCS remained unchanged. The concentration of glucose, hydroxybutyrate (BHBA), cholesterol and aspartate aminotransferase-oxaloacetic transaminase (AST-GOT) increased ($P \leq 0.04$) in OVE, but paraoxonase (PON) decreased ($P \leq$ 0.03) over time compared with CON. Overall concentration of NEFA and haptoglobin was lower ($P < 0.05$) in OVE than CON. An improvement of energy balance status in OVE cows was observed without a negative effect of TZD on DMI. The changes in AST-GOT and PON might reflect the effects of OVE on hepatic function. Excess dietary energy did not enhance inflammation and oxidative stress. In contrast with previous studies, TZD did not improve insulin sensitivity beyond what was observed with OVE alone.

Key Words: dairy cow, metabolic adaptation, 2,4-thiazolidinedione (TZD)

515 Adipose tissue insulin sensitivity in response to level of dietary energy and 2,4-thiazolidinedione in Holstein cows. A. Hosseini*, J. S. Osorio, F. T. da Rosa, J. K. Drackley, and J. J. Loor, *University of Illinois, Urbana.*

Mechanisms regulating insulin sensitivity in subcutaneous adipose tissue (SAT) of dairy cattle fed different levels of dietary energy during the prepartal period remain largely unknown. In monogastric SAT, 2,4-thia-

zolidinedione (TZD), a ligand of peroxisome proliferator-activated receptor-g (PPARG), has insulin-sensitizing effects. The specific aim of our study was to examine mechanisms whereby feeding a control or moderate-energy diet alter insulin sensitivity before, during, and after injection of TZD by evaluating insulin signaling-related genes in SAT. Fourteen dry non-pregnant Holstein cows were assigned to treatments in a randomized block design. All cows were fed a control diet (CON; NEL = 1.32 Mcal/kg) to meet 100% of NRC requirements for 3 wk, after which half of the cows were assigned to a moderate-energy diet (OVE; NEL = 1.54 Mcal/kg) and half of the cows continued on CON for 6 wk. The OVE diet was fed ad libitum and resulted in cows consuming ~180% of NRC. CON cows were fed to consume only to 100% of NRC. All cows received an intravenous injection of 4 mg TZD/kg of BW daily into the jugular vein starting 2 wk after the initiation of treatments and for 2 additional wk. The last 2 wk of the study served as the washout period. Biopsies of SAT were harvested at 2 (before TZD injection), 3, 4 (end of TZD), and 5 wk. Genes chosen for study included insulin signaling-related (INSR, IRS1, SLC2A4) and adipogenic/lipogenic enzymes/inducers (CEBPA, ADIPOQ, ADIPOR1, PPARG, SREBF1, FASN, SCD, DGAT2, INSIG1). Data were analyzed using PROC MIXED of SAS. In OVE cows, expression of PPARG and FASN was greater ($P < 0.05$) before and at the end of TZD injection. However, TZD injection decreased expression of IRS1 ($P = 0.04$), PPARG ($P = 0.05$), FASN ($P < 0.001$) and SREBF1 ($P = 0.02$) in OVE but not in CON cows. Results indicated that OVE did not decrease insulin sensitivity, and TZD actually decreased it.

Key Words: insulin sensitivity, 2,4-thiazolidinedione (TZD), dairy cattle

516 Overfeeding energy increases visceral fat deposition and alters metabolic indices in Holstein cows. A. Hosseini*[1], E. F. Garrett[3], E. Trevisi[2], F. T. da Rosa[1], G. Bertoni[2], J. K. Drackley[1], and J. J. Loor[1], *[1]University of Illinois, Urbana, [2]Università Cattolica del Sacro Cuore, Piacenza, Italy, [3]Department of Veterinary Clinical Medicine, University of Illinois, Urbana.*

Our objective was to examine the effect of overfeeding a moderate-energy diet on performance, visceral depot weights, body condition score (BCS), body weight (BW), and blood metabolites in dry non-pregnant cows. Fourteen Holstein cows (BCS = 3.31 ± 0.14) were assigned to treatments in a randomized block design. All cows were fed individually a control diet (CON; NEL = 1.32 Mcal/kg) to meet 100% of NRC requirements for 3 wk, after which half of the cows were assigned to a moderate-energy diet (OVE; NEL = 1.54 Mcal/kg) and half of the cows continued on CON for 6 wk. The OVE diet was fed ad libitum and resulted in cows consuming energy at ~180% of NRC. CON cows were fed to consume only to 100% of NRC. The BW and BCS were measured from wk −3 to 6, while the blood samples were collected before slaughter and several metabolites and hormones were measured. The DMI was recorded from −1 wk through slaughter on a daily basis. The wk before slaughter, OVE cows had greater concentration of BHBA (0.43 vs. 0.22; $P < 0.001$), cholesterol (3.77 vs. 2.65; $P = 0.008$) and AST-GOT (78.77 vs. 64.33; $P = 0.04$); whereas, the concentration of NEFA (0.07 vs. 0.17; $P = 0.002$) and bilirubin (0.89 vs. 1.5; $P = 0.005$) was lower in OVE cows. OVE cows had greater ($P < 0.001$) BW (757.5 vs. 692.5), DMI (kg/d; 17.20 vs. 8.02) and DMI as a percentage of BW (2.20 vs. 1.18); whereas, the BCS (3.4 vs. 3.6) and empty carcass weight (468.43 vs. 525.91) remained unchanged. In OVE cows, weight of the mesenteric (15.49 vs. 8.1; $P \leq 0.01$) and perirenal fat mass (11.17 vs. 3.39; $P \leq 0.04$), and liver (11.4 vs. 7.82; $P < 0.001$) was greater. Omental fat mass (15.16 vs. 23.41) did not differ. The similar BCS between the 2 diets and the fact that OVE cows had greater internal fat deposition suggests that BCS provided little information on visceral fat mass. Overfeeding energy did not impair insulin sensitivity but seemed to affect hepatic function.

Key Words: dairy cow, plane of energy, visceral fat

517 Level of dietary energy alters in vitro bovine adipose tissue insulin sensitivity and inflammatory response to TNF-α. A. Hosseini*[1], K. M. Moyes[2], F. T. da Rosa[1], J. K. Drackley[1], and J. J. Loor[1], *[1]University of Illinois, Urbana, [2]University of Maryland, College Park.*

Exogenous TNF-α increases liver triacylglycerol accumulation in late-lactation dairy cattle. In rats, an acute food deprivation resulted in greater periepididymal adipose TNF-α production. The objective of this study was to determine the acute in vitro effects of bovine insulin, recombinant bovine TNF-α, and their combination on subcutaneous adipose tissue (SAT) insulin sensitivity in dairy cattle fed different levels of dietary energy. Adipose tissue from the tail head was obtained at slaughter from 7 cows fed a control diet to meet 100% of NRC requirements and 7 cows fed a moderate-energy diet (OVE; ~180% of NRC requirements) for 6 wk. Tissue was transported on ice to the laboratory in an endotoxin free DMEM/Ham's F-12, L-Glutamine medium supplemented with Pen/Streptomycin as basal medium. After removing blood and connective tissue, 500 mg were dissected and cut to smaller pieces. Incubations were performed at 37°C and 5% CO_2 in duplicate for 2 h using 4 mL of basal media (control) or control with 1 μmol/L of bovine insulin (INS), 5 ng/mL of bovine recombinant TNF-α (TNF), or the same concentration of INS and TNF (IN-TNF). Data were analyzed using PROC MIXED of SAS. Genes chosen for study included insulin signaling-related (INSR, IRS1, SLC2A4), inflammatory and anti-inflammatory regulators (NFKB1, TNF, IL-1, IL-6, IL-10, SAA3 and HP) and adipogenic/lipogenic enzymes/inducers (CEBPA, ADIPOQ, ADIPOR1, PPARG, SREBF1, FASN, SCD, DGAT2, INSIG1). In CON cows, TNF and IN-TNF reduced ($P < 0.05$) the mRNA of IRS1. In OVE cows, TNF and IN-TNF led to greater ($P < 0.001$) mRNA of NFKB1 compared with control cultures; whereas, in CON cows the mRNA of TNF was lower ($P < 0.05$) in cultures with INS than control. Compared with control cultures, the mRNA of NFKB1 increased ($P < 0.001$) with TNF, and IN-TNF in CON cows. Our results indicate that SAT of OVE cows is more responsive to inflammatory cytokines. Moreover, exogenous insulin did not seem to improve its sensitivity in SAT during the inflammatory insult.

Key Words: subcutaneous adipose tissue, TNF-α, explant

518 Production traits of Montbéliarde-sired crossbreds compared to pure Holsteins in both high-input and low-input research herds. A. R. Hazel*, B. J. Heins, and L. B. Hansen, *University of Minnesota, St. Paul.*

Montbéliarde × Holstein crossbred cows (MH, n = 59) and Montbéliarde × Jersey/Holstein crossbred cows (MJH, n = 91) were compared with pure Holstein cows (HO, n = 163) for 305-d milk, fat, and protein production, and SCS during the first 5 lactations. Cows were in 2 research herds of the University of Minnesota, the high-input dairy at St. Paul and the low-input dairy at Morris, and calved from October 2005 to November 2012. Best Prediction was used to calculate production and SCS 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 of all traits included the fixed effects of herd, parity group (first, second, or third through fifth), breed, interaction of herd and parity group, herd-year of calving nested within interaction of herd and parity group, interaction of herd and breed, interaction of parity group and breed, interaction of herd, parity group, and breed, and random cow nested within breed. The MH and HO, respectively, were not significantly different ($P > 0.05$) for fat plus protein production (CFP) during first (509 kg vs. 518 kg), second (603 kg vs. 596 kg), nor third through fifth parities (643 kg vs. 641 kg). However, the MJH had significantly less ($P < 0.05$) CFP in first parity (−22 kg) compared with HO. For the low-input herd, the MJH had similar ($P > 0.05$) CFP in first (−2 kg) and third through fifth (+1 kg) parities, and tended ($P < 0.10$) to have greater CFP in second parity (+31 kg) compared with HO. Across herds, the MH (2.37) had lower ($P < 0.05$) SCS than MJH (2.57) and HO (2.87) during second parity. For the low-input herd, MH (3.05) and MJH (3.08) had lower ($P < 0.05$) SCS than HO (3.72) during third through fifth parities. The CFP of MH was similar to HO in both research herds; however, production for the MJH was more competitive with HO and MH for low-input production than high-input production.

Key Words: crossbreeding, heterosis, Montbéliarde

519 Fertility, survival, and mortality of Montbéliarde-sired crossbreds compared to pure Holsteins in two research herds. A. R. Hazel, B. J. Heins, and L. B. Hansen*, *University of Minnesota, St. Paul.*

Montbéliarde × Holstein crossbred cows (MH, n = 57) and Montbéliarde × Jersey/Holstein crossbred cows (MJH, n = 86) were compared with pure Holstein cows (HO, n = 153) for days open (DO), survival, and mortality rate. Cows calved in one of 2 research herds of the University of Minnesota, the high-input dairy at St. Paul and the low-input dairy at Morris, from October 2005 to May 2010. Cows were required to have at least 250 DIM for DO, and cows with DO greater than 250 d were truncated to 250 d. Cows were required to have 5 yr of opportunity for herd life (HL), and HL greater than 1,826 d was truncated to 1,826 d. Independent variables for statistical analysis of DO included the fixed effects of herd, parity group (first, second, or third through fifth), breed, interaction of herd and parity group, herd-year of calving nested within interaction of herd and parity group, interaction of herd and breed, interaction of parity group and breed, interaction of herd, parity group, and breed, and random cow nested within breed. The analyses of survival to subsequent calving, HL, and mortality rate included the independent variables of herd, breed, and interaction of herd and breed. The MH and MJH had significantly lower ($P < 0.01$) DO than HO, respectively, in first (127 d, 115 d, 161 d), second (135 d, 132 d, and 178 d) and third through fifth (122 d, 124 d, and 161 d) parities. Across parity and breed groups, Montbéliarde-sired crossbred cows had 41 d fewer DO than HO. For survival to third, fourth, and fifth calving, respectively, MH (58%, 43%, and 27%) and MJH (51%, 35%, and 20%) were significantly greater ($P < 0.01$) than HO (31%, 14%, and 6%). The HL was significantly longer ($P < 0.05$) for MH (1,050 d) and MJH (1,078 d) compared with HO (837 d). Mortality rate was significantly lower ($P < 0.05$) for MH (5.1%) compared with HO (17.7%). Data suggest Montbéliarde-sired crossbreds have superior fertility, longer HL, and lower mortality compared with HO, which may result in greater profitability for dairying.

Key Words: crossbreeding, survival, Montbéliarde

520 Association between stall surface and some dairy welfare measurements on farms using automatic milking systems. J. A. Salfer* and M. I. Endres, *University of Minnesota, St.Paul.*

The objective of this study was to evaluate the association between stall surface and some animal welfare measurements on farms using automatic milking systems (AMS) in Minnesota and Wisconsin. Fifty-one farms using AMS were visited once from June to September 2012. A random sample of a minimum of 30% of the cows in each pen were scored for locomotion (1–5 scale, 1 = normal, 5 = severely lame) and hygiene (1–5 scale, 1 = very clean and 5 = very dirty), and severe (swollen or open sores) hock lesions were recorded. Lying surface and number of farms were: mattresses (M; 22), sand (S; 14), waterbeds (W; 7), mattress and pasture (P; 5) and bedded pack (BP; 3). Lameness prevalence (% locomotion score = >3) was higher for M (40.9) than P (21.5; $P < 0.001$), S (22.5; $P < 0.001$) and BP (19.0; $P = 0.006$), but similar to W (35.3). Lameness prevalence was similar for BP, P and S. Severe lameness prevalence (% locomotion score = >4) was lower for P (2.7) than M (8.5; $P < 0.05$) and W (10.2; $P = 0.03$). Severe lameness prevalence tended to be lower for S (4.3) than M and W ($P = 0.07$; $P = 0.06$) and also tended to be lower for BP (1.7) than M and W ($P = 0.09$; $P = 0.06$). Prevalence of dirty cows (hygiene score >3) was lower for S (16.8) than BP (45.3; $P < 0.05$), M (41.9; $P = 0.001$), P (39.5; $P < 0.03$) and W (46.3; $P = 0.004$). Mattress, S, W and P were all similar. Prevalence of severely dirty (hygiene score > 4) cows was lower for S (1.8) than BP (14.6; $P < 0.05$) and W (11.1; $P < 0.05$) and tended to be lower than M (8.5; $P = 0.06$) and P (10.6; $P = 0.06$). Severe hock lesion prevalence was greater for M (17.2) than S (3.8; $P < 0.001$), W (7.8; $P = 0.02$) and BP (1.7; $P = 0.006$), and tended ($P = 0.06$) to be greater than P (9.9). Sand, W, BP, and P were similar. Results indicate that compared with previous studies in the Midwest, cows on AMS farms had higher lameness prevalence than cows housed in similar stall surfaces in other types of barns. This could be due to reduced footbath use on these AMS farms. Results also showed that cows on mattresses had greater prevalence of hock lesions compared with other surfaces.

Key Words: automatic milking system, lameness, hygiene

521 Environmental bioburden attributable to super-shedders in freestall pens. S. S. Aly*[1,2], A. D. Glover[2], J. D. Champagne[2], R. H. Whitlock[3], R. Anderson[4], and J. M. Adaska[5], *[1]Department of Population Health and Reproduction, School of Veterinary Medicine, University of California-Davis, Davis, [2]Veterinary Medicine Teaching and Research Center, School of Veterinary Medicine, University of California-Davis, Tulare, [3]Johne's Research Laboratory, New Bolton*

Center, School of Veterinary Medicine, University of Pennsylvania, Kennett Square, [4]California Department of Food and Agriculture, Animal Health Branch, Sacramento, [5]California Animal Health and Food Safety Laboratory, Tulare Branch, Tulare.

Environmental sampling can be used to reliably quantify *Mycobacterium avium* ssp. *paratuberculosis* (MAP) in fecal slurry from freestall pens. The amount of MAP in a pen's environment attributable to super-shedders (SS) is not known. In addition, it is not known whether the MAP bioburden in pens housing super-shedders significantly differs from those without SS or how movement of SS into and out of pens affects pen MAP bioburden. The objective of this study was to estimate the MAP bioburden in fecal slurry from freestall pens using quantitative real-time polymerase chain reaction (qrt PCR). MAP SS identified from a whole herd test were moved between 2 pens in a double crossover study design. Environmental samples were collected daily for 15 d with SS cows introduced to the first pen at d 4 through d 6 and in the second pen at d 9 through d 12 allowing for a washout period of 3 d in between and while holding pen population otherwise fixed. MAP bioburden of environmental slurry before introducing SS was not significantly different compared with after the washout period following removal of the SS (P value 0.13 and 0.59, pens 1 and 2 respectively). Map bioburden significantly increased upon introduction of SS cows ($P < 0.001$) with an estimated decrease of 9.1 cycles-to-threshold of qrt-PCR. Results of this study show that SS cows introduced to freestall pens can contribute significantly to pen MAP bioburden and within as short a time period as 3 d from introduction.

Key Words: Johne's, environmental bioburden, PCR

522 Influence of breed, milk yield, and temperature humidity index on dairy cow reticulorumen temperature, lying time, and rumination behavior. A. E. Sterrett*, B. A. Wadsworth, J. D. Clark, and J. M. Bewley, *University of Kentucky, Department of Animal and Food Sciences, Lexington.*

The objective of this study, conducted from October 8, 2012 to January 23, 2013 at the University of Kentucky Coldstream Dairy, was to compare daily lying time (LT), reticulorumen temperature (RT), and rumination time (RU) between 3 breed groups. Cows (n = 36; 12 Holstein (H), 12 crossbred (C), and 12 Jersey (J)) were matched by parity group (PG, 1 or ≥2 lactations), DIM, and milk yield (MY). Lying time, RU, RT, MY, and maximum temperature-humidity index (THI) were recorded and summarized for each cow day. At least 75 d per cow of recorded LT, RU, and RT data was required for study inclusion. The MIXED Procedure of SAS (Cary, NC) was used to evaluate fixed effects of breed, MY, PG, THI, and their interactions on LT, RT, and RU, with cow within breed as subject. Mean (±SD) daily DIM, LT, MY, RT, RU, THI were 198 ± 106 d, 11 ± 2 h, 28 ± 8 kg, 39 ± 1°C, 369 ± 99 min, and 63 ± 17, respectively. Breed × PG, breed × MY, and THI were significant predictors of LT ($P < 0.01$). Primiparous H cow LT was 1.28 ± 0.24 h lower than multiparous H cow LT ($P < 0.01$). Breed × PG and MY were significant predictors of RU ($P < 0.01$). Primiparous H cows ruminated 27.19 ± 9.97 ($P = 0.04$) and 33.00 ± 11.20 ($P < 0.01$) minutes longer than primiparous J and C cows, respectively. Milk yield × THI, THI × PG, and breed × PG were significant predictors of RT ($P < 0.01$). Reticulorumen temperatures for primiparous H cows were 0.94 ± 0.01 and 0.28 ± 0.09°C higher than primiparous J and C cows, respectively ($P < 0.01$), suggesting that J and C cows may be more heat-tolerant. Rumination time was highly correlated with MY (r = 0.90, $P < 0.01$), but weakly correlated with THI (r = 0.03, $P < 0.01$). Lying time was moderately correlated with MY and THI (r = −0.32 and −0.21, respectively, $P < 0.01$). Reticulorumen temperature was moderately correlated with THI (r = 0.30, $P < 0.01$). The physiological and behavioral differences between H, J, and C cows observed in this study provide new insight into breed differences that can be useful for interpreting LT, RT, and RU data in future studies.

Key Words: reticulorumen temperature, rumination, lying time

523 Effect of milking frequency on the behavior and productivity of lactating dairy cows. K. D. Hart*[1], B. W. McBride[2], T. F. Duffield[3], and T. J. DeVries[1], *[1]Dept. of Animal and Poultry Science, University of Guelph, Kemptville Campus, Kemptville, ON, Canada, [2]Dept. of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada, [3]Dept. of Population Medicine, University of Guelph, Guelph, ON, Canada.*

The objective of this study was to determine the effect of milking frequency on the behavioral patterns and productivity of lactating dairy cows. Twelve free-stall housed, lactating Holstein dairy cows, including 7 primiparous (PP) and 5 multiparous (MP), were exposed to each of 2 treatments (over 21-d periods) in a replicated crossover design. Treatments were milking frequency: (1) 2×/d (at 0600 and 1800 h) and (2) 3×/d (at 0600, 1400, and 2200 h). Milk production, feeding, lying, and rumination behavior were electronically monitored for each animal for the last 7 d of each treatment period. Milk samples were collected for the last 3 d of each period for milk component analysis. Data were analyzed in a general linear mixed model. Cows produced more milk when milked 3×/d compared with 2×/d (37.7 vs. 34.9 kg/d; SE = 1.2; $P = 0.002$). Primiparous cows produced less milk (32.1 vs. 40.3 kg/d; SE = 1.7; $P = 0.004$) and consumed less DM (24.2 vs. 28.0 kg/d; SE = 0.5; $P < 0.001$) than MP cows. The extra time required for milking 3×/d altered the distribution of cow behavioral activity throughout the day. While this did not affect total daily lying (694.7 min/d) or rumination (506.1 min/d) time, there was a tendency for cows milked 2×/d to spend less time (224.6 vs. 237.5 min/d; SE = 17.6; $P = 0.1$) feeding and, thus, consume their feed at a faster rate (0.13 vs. 0.12 kg DM/min; SE = 0.02; $P = 0.07$) than cows milked 3×/d. For MP cows, the increase in feeding activity was facilitated through having longer (40.1 vs. 36.8 min/meal; SE = 3.3; $P = 0.004$), and slightly larger meals (4.8 vs. 4.6 kg DM/meal; SE = 0.7; $P = 0.05$) when milked 3×/d. Alternatively, PP cows consumed smaller (2.9 vs. 3.2 kg DM/meal; SE = 0.7; $P = 0.05$), more frequent meals (9.1 vs. 7.7 meals/d; SE = 1.1; $P = 0.04$) throughout the day when milked 3×/d, resulting in a tendency for greater DMI (24.7 vs. 23.6 kg/d; SE = 0.5; $P = 0.08$). These results indicate that under 3×/d milking schedules, PP cows will positively adjust their feeding behavior to achieve similar production increases as MP cows.

Key Words: milking frequency, behavior, parity

524 Periconceptional heat stress of Holstein cows affects subsequent milk production and composition. B. Brown*, J. Stallings, and M. Rhoads, *Virginia Polytechnic Institute and State University, Blacksburg.*

The fertility of lactating Holstein cows is severely reduced during periods of heat stress (HS). Of course, some inseminations conducted during HS result in successful pregnancies from which heifer calves are born; many of these heifer calves are retained and raised to enter the milking herd as replacements. We hypothesized that the HS experienced by these females around the time they were conceived conferred long-lasting effects that could potentially alter milk production and composition during adulthood. Therefore, the objective of the current study was to examine the relationship between periconceptional HS and

measurements of milk production and composition. National Dairy Herd Improvement Association data was obtained from Dairy Records Management Systems. Records (n = 704,419) included Holstein cows born between 2000 and 2011 in FL, GA, SC, MS, LA, AL, and TX. Conception dates were calculated by subtracting 276 d from the recorded birth date. Records for cows conceived within the months of June, July, and August were retained as "HS-conceived" (HSC) cows; cows conceived within the months of December, January, and February were retained as contemporaries. Adjusted 305-d mature equivalent milk, protein, and fat yields were evaluated by ANOVA using PROC HPMIXED of SAS. Heat stress-conceived cows produced less milk than contemporaries in the following states: FL ($P < 0.01$), GA ($P < 0.01$), MS ($P = 0.02$), LA ($P < 0.01$), AL ($P < 0.01$), and TX ($P < 0.01$). Periconceptional HS reduced fat yield in FL ($P < 0.01$), GA ($P < 0.01$), MS ($P < 0.01$), LA ($P < 0.01$), AL ($P < 0.01$), and TX ($P < 0.01$) and tended to decrease fat yield in SC ($P = 0.08$). Protein yield was significantly reduced in FL ($P < 0.01$), SC ($P < 0.05$), LA ($P < 0.01$), AL ($P < 0.01$), MS ($P = 0.05$), and TX ($P < 0.01$). The relationship between HSC and adjusted 305-d mature equivalent milk production variables suggests that HS at the time of conception and during early pregnancy impairs cow performance throughout her lifetime. Further studies are needed to explore the mechanisms responsible for this relationship and resulting effect on dairy production efficiency.

Key Words: milk, dairy cow, heat stress

525 Use of urine as a diagnostic tool for subacute ruminal acidosis (SARA) in lactating Holstein and Jersey cows. S. Luan*, M. R. Murphy, F. C. Cardoso, and J. K. Drackley, *University of Illinois, Urbana.*

Subacute ruminal acidosis (SARA) is a common digestive disorder in high producing dairy cows that decreases production efficiency. Methods for early diagnosis of SARA could help prevent potential losses. To investigate the association between SARA and urine pH (UPH) and rumen pH (RPH), 6 Holstein cows (HOL, BW = 717 kg; 258 ± 16 d in milk), 6 rumen-cannulated Holstein cows (CAN, BW = 762 kg; 287 ± 45 d in milk), and 6 Jersey cows (JER, BW = 470 kg; 190 ± 86 d in milk) were used in a replicated 3 × 3 Latin square design balanced to measure carry-over effects. Periods (10 d) were divided into 4 stages (S): S1, baseline, d 1–3, ad libitum TMR; S2, restricted feeding, d 4, cows fed for 50% of S1 DMI; S3, challenge, d 5, treatments applied; S4, recovery, d 6–10, all cows fed ad libitum TMR. Treatments were CON, no top dress; MOD, 10% of S1 DMI as top dress (pelleted mixture of 50:50 of wheat:barley); and HIG, 20% of S1 DMI as top dress. Rumen pH (CAN) and UPH (all cows) were recorded at −2 to 22 h relative to feeding during S3. No treatment carry-over effect was observed for any outcome variable ($P > 0.30$). Mean RPH was lower ($P < 0.001$) for HIG (6.25 ± 0.09) than for CON (6.44 ± 0.09). Nadir time (h) for RPH below 6 was 3, 5, and 7 h for CON, MOD, and HIG, respectively. The linear effect among CON, MOD, and HIG was significant for RPH ($P < 0.001$) and UPH ($P < 0.007$). During S3, UPH was lower ($P < 0.05$) for HIG (8.43 ± 0.08) than for CON (8.49 ± 0.08) in Holsteins, but did not differ for JER. The DMI was lower for during S2 as designed, but did not differ among S1, S3, and S4. The quadratic effect among CON, MOD, and HIG was significant ($P < 0.007$) for DMI. Holstein cows had higher ($P < 0.001$) DMI than JER (17.0 ± 0.48 vs. 12.1 ± 0.68 kg/d, respectively). In conclusion, cows receiving HIG had lower RPH and UPH than cows receiving CON. The UPH of Jersey cows was not as affected by SARA as UPH of HOL. Linear effects for both UPH and RPH with increasing challenge suggest a relationship that might be useful as a diagnostic tool for SARA.

Key Words: subacute ruminal acidosis, urine pH, rumen pH

526 Potential of mid-infrared spectrum of milk to detect changes in the physiological status of dairy cows. A. Laine*[1], A. Goubau[1], H. Hammami[1,2], C. Bastin[1], and N. Gengler[1], *[1]University of Liege, Gembloux Agro-Bio Tech, Animal Science Unit, Gembloux, Belgium, [2]National Fund for Scientific Research, Brussels, Belgium.*

Fertility and health problems are causing large economic losses to the dairy industry. Early identification of pregnant cows and early detection of mastitis are key elements to improve reproductive, health, and animal welfare and reduce costs for the farmer. The mid-infrared (MIR) spectrum obtained from milk recording routines measure the absorbance over a large number of wavelengths. Two studies, based on spectral data and extra phenotypes (pregnancy diagnosis and mastitis) from Luxembourg and Wallonia (Belgium) milk recordings, were conducted to investigate the potential use of the entire spectrum in the identification of animal status. In the first study, a total of 9,717 spectral records coupled with pregnancy status coming from milk recording in Luxembourg were used. A subset of MIR spectrum from non-pregnant cows was retained and a multivariate mixed model was applied to obtain predicted MIR spectral values for all test-days, prediction errors (residuals) representing the factors not present in the model (reproductive status, unaccounted factors, and error). A quadratic discriminant function was then constructed on the residual spectra to predict the pregnancy status. Leave one out cross-validation showed promising results with an error rate of cross-validation equal to 3.1% for non-pregnant cow and an error rate of cross-validation equal to 7.4% for pregnant cow. In the second study, a total of 4,126 test-days from cows with at least one mastitis detected during its lactation and coming from the Walloon milk recording were used. Significant differences ($P < 0.05$) were observed between milk MIR spectra considered related to mastitis (in an interval of 10 d around this test-day) and the other spectra for 23.8% of the analyzed MIR spectral data points. Results from both studies showed that MIR milk spectrum could be very useful to detect changes in the physiological status of dairy cows and could be potentially used in routine management decision tools.

Key Words: milk MIR spectrum, pregnancy diagnosis, mastitis

527 Evaluation of a novel system to measure enteric methane emissions from beef cattle on pasture. S. Zimmerman*[1], J. J. Michal[2], R. White[2], K. A. Johnson[2], A. Guerouali[3], and P. Zimmerman[1], *[1]C-Lock Incorperated, Rapid City, SD, [2]Washington State University, Pullman, [3]Hassan II Agronomic and Veterinary Institute, Rabat, Morocco.*

The GreenFeed system (GF; patent 8,307,785, C-Lock Inc., Rapid City, SD) is a new system to quantitatively measure CH_4 mass fluxes (emissions) from cattle while individual animals visit GF to receive a small feed reward several times per day. The objectives of this study were to determine how beef cattle adapt to using GF, determine the consistency of GF CH_4 emissions measures, and compare CH_4 emissions with those obtained using the sulfur hexafluoride tracer technique (SF_6). Over 20 wk, cattle were fed 4 diets: good quality pasture (P1), low quality pasture (P2), low quality pasture plus bluegrass straw (BGS) (P3), and BGS (P4). Seven Angus cows (BW = 706 ± 51 kg) and 1 Angus heifer were introduced to GF in staggered groups to test GF adoption rates. In P2 and P3, CH_4 emissions with SF_6 were simultaneously measured with 51 12-h canister samples from 6 cows. Individual animal ranking stability of GF measured CH_4 emissions across diets was determined by calculating the correlation coefficient (r) of individual animal averaged

CH_4 emissions between each of the diets. Then the P-value was determined based on r and number of animals. A similar correlation analysis was completed for time of day ranking stability. P-values of differences between GF and SF_6 were determined using the 2-tailed student *t*-test. All cattle used GF an average of 2.5 ± 1.1 times/d and received 1.2 ± 0.5 kg/d of alfalfa-based pellets. Herd averaged GF CH_4 emissions were 300 ± 2.0, 292 ± 1.4, 309 ± 1.0, and 297 ± 1.0 g/d in P1, P2, P3, and P4, respectively. The overall between-animal coefficient of variation (CV) of CH_4 emissions was 9.1%; the weekly within-animal CV was 6.5%. The relative CH_4 emission ranking for the 8 animals was consistent and significant ($P < 0.05$) across diets and across the day. GF and SF_6 herd averaged CH_4 emissions were not significantly different in P2 or P3 ($P = 0.41$ and $P = 0.27$, respectively) and not significantly different ($P < 0.05$) for 9 of 12 individual animal comparisons. Overall, GF CH_4 emissions for outdoor-grazing animals were consistent, repeatable and in general, agreed with CH_4 emissions estimated with the SF_6 technique.

Key Words: methane, GreenFeed, beef cattle

528 Pasture-derived greenhouse gases emissions in cow-calf production systems. M. B. Chiavegato*, W. Powers, S. A. Utsumi, and J. Rowntree, *Michigan State University, East Lansing.*

The effects of stocking rates on pasture-derived greenhouse gas (GHG) flux are rarely reported for cow-calf production systems. This study aimed to compare GHG fluxes from cow-calf herds grazing under different stocking rates. During 2011 and 2012, methane (CH_4) and nitrous oxide (N_2O) fluxes from grazed pastures were quantified. Pastures were grazed with cow-calf herds at high stocking rate (2.5 cow/ha; 520 ± 50.4 kg, 30 d grazing return; HI), low stocking rate (1 cow/ha; 521 ± 40.4 kg, 60–90 d grazing return; LO), or excluded from grazing for several years (Control). Each year, 10 randomly deployed static chambers per paddock (750 m^2; n = 3 paddocks/treatment) were used to determine daily CH_4 and N_2O fluxes over 14-d post-grazing in early (May–June) and late (August–September) growing seasons. Soil (ST) and ambient temperature (AT) and soil water content (SWC) were monitored. Gas flux was analyzed using ANOVA for a completely randomized design ($\alpha = 0.05$) although restrictions to randomization existed due to farm logistics and management. In early season, negative CH_4 flux (i.e., sink) was detected for Control and HI (−20.3 ± 6.1 and −13.3 ± 3.8 g C-CH_4 ha^{-1} d^{-1}, respectively), however LO was a source of CH_4 (4.2 ± 5.8 g C-CH_4 ha^{-1} d^{-1}; $P < 0.01$). In late season, HI and LO were sources (10.1 ± 2.7 and 5.7 ± 4.1 g C-CH_4 ha^{-1} d^{-1}, respectively) and Control remained a sink (−7.1 ± 4.0 g C-CH_4 ha^{-1} d^{-1}; $P = 0.02$). Soil temperature, AT and SWC did not influence CH_4 fluxes ($P = 0.11$, $P = 0.08$ and $P = 0.82$, respectively). Nitrous oxide flux did not change from early to late season ($P = 0.11$). Fluxes from HI, LO and Control were not significantly different (6.8 ± 0.5, 6.6 ± 0.8 and 5.7 ± 0.8 g N-N_2O ha^{-1} d^{-1}, respectively; $P = 0.47$). Soil temperature, AT and SWC influenced N_2O fluxes ($P < 0.01$). The net flux of C-equivalent for HI, LO and Control were 0.86 ± 0.06, 0.91 ± 0.1 and 0.64 ± 0.1 kg C ha^{-1} d^{-1}, respectively and were not significantly different ($P = 0.08$). Although grazed pastures are net sources of GHG, our results indicate potential opportunities to reduce GHG fluxes by CH_4 consumption in pastures soils grazed at high stocking rates.

Key Words: methane, mitigation, nitrous oxide

Small Ruminant Symposium: Sustainable Meat Goat Production

529 Sustainable health management for meat goats. J. Miller*, *Louisiana State University, Baton Rouge.*

Small ruminant (specifically goat) production has steadily increased in the US over the past few years. The objective of profitable production is to efficiently manage an operation to grow healthy animals that can be marketed in a timely manner. Issues with health are a major constraint to such production. It is important to maintain an overall balance in providing overall health care. This balance should include pregnancy and neonatal care, regular vaccination programs, parasite control and nutrition among other aspects of management. The one health issue that is always present is parasites, especially nematodes (worms). Appropriate worm control based on local/regional conditions may in some cases be the deciding factor on whether farms can stay in business. There are many sources of information available to the producer, and input from local veterinarians should be included where ever possible. For sustainable meat goat production, it is very important for the producer to be well-informed and to be willing to implement appropriate practices for worm control and other health management concerns.

Key Words: goat, health, sustainable

530 Sustainable feed and forage management for meat goats. J.-M. Luginbuhl*, *North Carolina State University, Raleigh.*

Meat goats (*Capra hircus*) offer an opportunity to effectively convert pasture nutrients to goat meat, a product currently marketable and in demand by a growing segment of the US population. The "generalist" feeding behavior of goats gives them a clear advantage in their ability to utilize a variety of landscapes and plant communities. Managed to match their nutritional demands, plant communities, represented by pasture and browse species, can provide an abundant, lost-cost feed supply, supplanting the need for expensive concentrates. Classified as intermediate feeders preferring browse or forbs, meat goats perform well grazing cultivated pastures if grazing management practices match their grazing behavior. The primary goal is to have control of the animal grazing pattern so that one can dictate the degree of defoliation and the frequency of defoliation. In addition, the needs of the plants as well as the needs of the animals must be taken into consideration to obtain efficient animal production over several years. Therefore, research focusing on forage evaluation and animal performance, aiming at developing year-round forage feeding programs which allow for as much grazing as possible throughout the year, was conducted to meet the needs of this emerging industry. Depending on the environment, a year-round forage system may consist only of perennial and(or) annual grasses and legumes and browse, or a more complex system that includes a mixture of temperate perennial and(or) annual grasses and legumes as well as summer or sub-tropical perennial and(or) annual grasses and legumes, and browse. The potential of Sericea lespedeza [*Lespedeza cuneata* (Dum.-Cours) G. Don], a highly drought tolerant warm-season legume containing tannins, was also investigated as an alternative to the use of traditional anthelmintics to control the gastrointestinal barber pole nematode (*Haemonchus contortus*). In conclusion, the foraging habits of goats have important environmental implications by ultimately increasing the sustainability of production systems.

Key Words: controlled grazing, forage system, meat goat

531 Live animal and carcass evaluation of market goats. K. W. McMillin*[1], K. W. Braden[2], J. C. Gregorie[1], M. A. Persica III[1], and J. N. Maynard[1], *[1]Louisiana State University Agricultural Center, Baton Rouge, [2]Angelo State University, San Angelo, TX.*

Official grades and standards establish the criteria and levels of traits to distinguish among products which allow for communication of terminology, price, and specifications between buyers and sellers in the market. The beef, pork, and lamb industries have well established criteria for live evaluations and meat carcass grading systems that facilitated centralized locations for slaughter, shipment of boxed primal cuts, and longer product shelf life. The meat goat industry is currently less organized, lacking pictorial standards for market goat selection criteria terminology, transporting live goats rather than meat to consumption locations, selling carcasses instead of cuts, and losing market opportunities with ethnic or health conscious consumers due to unavailability of goat in most retail stores. Goat consumers have expressed interest in purchasing smaller portions of goat than carcasses or half carcasses and desire to use lean color and meatiness in their purchase decisions. Yield grades estimate amounts of lean meat based on accurate evaluation of the relative ratios of lean, fat, and bone tissues. Kid goats deposit minimal fat covering over the longissimus dorsi, which is often too small in meat goats, averaging 29 kg with 14 kg carcasses, to accurately measure for estimation of carcass muscling. Differences from other red meat have necessitated use of other indicators of fat, lean, and bone proportions. Correspondingly, results from 725 goats and their carcasses will be used to determine relationships of traits such as fatness over the ribs, in the flank regions and leg conformation with yield of lean goat. Quality or estimated palatability must be defined with terms and traits that can be objectively measured to facilitate communication, product transactions, and trust in the meat chain. The live animal, carcass, and muscle composition traits that contribute to tenderness, juiciness, and flavor of goat meat are being determined on Semimembranosus muscles from the same goat population samples. Development of suitable live animal and carcass evaluation standards will facilitate advancement of marketing and logistical technologies to benefit the meat goat industry.

Key Words: goat, evaluation, grading

532 Current trends and future strategies for marketing goat meat. M. Ibrahim*, *Fort Valley State University, Fort Valley, GA.*

Goat meat is one of the most widely consumed meats in the world, especially, in developing countries. Although goats have been in the United States for centuries, they were mostly produced for milk and fiber. It was only in the early 1990s that the United States developed serious interest in meat goat production. Prior to the early 1990s, goat meat came mostly from culled milk and fiber goats. Today, meat goat numbers are far greater than all the other types of goats in the United States. Since the early 1990s, both demand and supply of goat meat have increased tremendously. Much of this has been attributed to the influx of recent immigrants from non-European countries where goat meat is widely consumed. For example, the US 2010 census data shows that of the 40 million foreign born population, 85% of them were from non-European countries. The demand for goat meat surpassed the supply in the early 1990s. This resulted in an increase in goat meat importation, making the United States the world leading and net importer of goat meat. Over 90% of US goat meat imports come from Australia. The US goat meat market is very informal and segmented. Some of the market segments

include Hispanic, African, Asian, various religious groups (Muslims, Hindus, Christians, and Jews) and the health-conscious consumer. None of these groups is homogeneous. For example, Muslims are permitted to eat goat meat but not all Muslims consume goat meat. Some are very strict about the method of slaughter (Halal) and others are not. The future of the meat goat industry and goat meat market depends on increasing the availability and visibility of goat meat to the wider American consumers by adopting various marketing strategies such as making goat meat available in grocery stores. In a recent consumer study in Georgia, many respondents said that they did not have access to goat meat. The survey results also indicated that 85% of the respondents said they had never tasted or eaten goat meat. When asked whether they would be willing to buy goat meat if it was made available in their local store, about 54% responded in the affirmative.

Key Words: goat meat, demand, supply

533 Effect of microfiltration concentration factor on serum protein removal from skim milk using polymeric spiral-wound membranes. S. L. Beckman* and D. M. Barbano, *Cornell University, Ithaca, NY.*

The objective of this research was to determine the effect of concentration factor (CF) on the removal of serum protein (SP) from skim milk during 50°C microfiltration (MF) using a 0.3-µm polyvinylidene fluoride spiral-wound (SW) membrane. Pasteurized (72°C, 16 s) skim was MF at 3 CF, 1.50, 2.25, and 3.00×, each on a separate day of processing starting with skim milk. Two phases of MF were used at each CF, with an initial startup-stabilization phase (40 min, full recycle) to achieve desired CF, followed by a steady-state phase (90 min, feed-and-bleed) for data collection. The experiment was replicated 3 times, and SP removal from skim was quantified at each CF. System pressures, flow rates, and fluxes were monitored during the 90 min run. Permeate flux increased ($P < 0.05$) (12.8 15.3, and 19.0 kg/m^2 per h) with decreasing CF from 3.00 to 1.50×, while fouled water flux did not differ ($P > 0.05$) among CF indicating that the effect of membrane fouling on hydraulic resistance of the membrane was similar at all CF. However, the CF used during skim SW MF (0.3 µm) did affect the percentage of SP removed. As CF increased, from 1.50 to 3.00×, the percentage of SP removed increased ($P < 0.05$) from 10.6 to 35.6%, in a single stage feed-and-bleed MF system. Rejection of SP during polymeric SW MF of skim was caused by fouling of the membrane, not by the membrane itself and differences in the foulant characteristic among CF influenced SP rejection more than it influenced hydraulic resistance. We hypothesize that differences in the conditions near the surface of the membrane and within the pores during the first few minutes of processing, influenced the rejection of SP protein because more pore size narrowing and plugging occurred at low CF than at high CF due to a slower rate of gel layer formation at low CF. It is possible that SP removal from skim milk at 50°C could be improved by optimizing the membrane pore size, feed composition, and controlling the formation rate of concentration polarization derived gel layer at the membrane surface during the first few minutes of processing.

Key Words: microfiltration, concentration factor, spiral-wound

534 Modification of milk fat fatty acid profile by a combination of microfiltration and dry crystallization. K. E. Kaylegian*[1], J. Choi[1], K. Harvatine[2], J. N. Coupland[1], and R. J. Elias[1], *[1]Dept. of Food Science, Pennsylvania State University, University Park, [2]Dept. of Animal Science, Pennsylvania State University, University Park.*

A reduction in the saturated content of milk fat is desired to improve its healthfulness. Preserving the flavor and premium image of milk fat is paramount when evaluating technologies to change the fatty acid profile. The objective of this study was to combine microfiltration and dry crystallization to produce milk fat fractions with reduced saturated fat contents. Pasteurized milk was microfiltered through a 5 µ ceramic membrane using conditions that were optimized for the separation of large fat globules ($D_{32} > 4.5$ µm) and small fat globules ($D_{32} < 3.7$ µm) with minimal processing time, to protect the fat. The control milk, permeate and retentate streams were separated into cream, churned into butter, and clarified to produce anhydrous milkfat (AMF). Each AMF was fractionated using bench-scale dry crystallization with vacuum filtration and a 2-step process to produce solid (S) and liquid (L) fractions at 25 and 15°C. The experiment was repeated in triplicate. Fatty acid analysis (by GLC) showed no significant differences ($P > 0.05$) in total saturated fat between the control, permeate and retentate streams when comparing similar fractions (i.e., AMF, 25S, 25L, 15S, 15L). A shift in the fatty acid profile was observed when the liquid and solid fraction obtained at the same temperature were compared, and when the 15°C fractions were compared with the 25°C fractions. A decrease in long chain saturated fatty acids and an increase in short chain saturated and long chain unsaturated fatty acids were observed among these fractions. These changes counteracted each other, resulting in a 5% reduction of the total saturated fat content in the 15L fractions compared with the control. The 15L fraction showed a 16% increase in CLA 9–11 compared with the control AMF. The total saturated fat content was approximately 65.4% for the AMFs, 71.7% for 25S, 63.2% for 25L, 68.7% for 15S, and 62.3% for the 15L fractions. In conclusion, the use of dry crystallization produced milk fat fractions with small reductions in saturated fat content, and the addition of microfiltration did not result in additional benefits.

Key Words: milk fat, fatty acid, fractionation

535 Production of milk protein concentrate with a modified mineral content. C. Marella*, P. Salunke, A. Biswas, and L. E. Metzger, *Midwest Dairy Foods Research Center, Dairy Science Department, South Dakota State University, Brookings.*

Milk protein concentrates (MPC) are products obtained from ultrafiltration (UF) of skim milk. It is well established that MPC powders can have a loss of solubility during storage as a result of protein-protein interactions, and formation of insoluble complexes. Previous studies have shown that partial replacement of calcium with sodium improves MPC functionality and prevent the loss in solubility during storage. These studies have utilized pH adjustment with addition of acids, addition of monovalent salts or ion exchange treatment of UF retentate. The objective of this study was to utilize carbon dioxide to produce MPC with improved functionality. Preliminary studies were conducted with injection of CO_2 into skim milk that determined 1500, 1850 and 2200 ppm of dissolved CO_2 before UF for obtaining MPCs with 20, 30 and 40% reduced calcium content, respectively. From these preliminary results, a CO_2 injection level of 2200 ppm was selected for further study. In this study reduced-calcium MPC from 189.25 L of skim milk subjecting to injection of 2200 ppm of CO_2 before UF along with additional injection during UF. A control MPC was also produced from same lot of skim milk without injection of CO_2. The above processes were replicated 3 times, using different lots of skim milk for each replication. The reduced calcium UF retentates (17% TS) had a viscosity of 11 cP at 100/s shear rate, while the control UF retentates had a viscosity of 24 cP, a 2-fold higher in viscosity. Injection of CO_2 and the resultant solubilization of calcium phosphate had a significant ($P < 0.05$) effect on UF performance, resulting in a 10 and a 20% loss in initial and average flux, respectively. Processing of skim milk with injection of CO_2 resulted into higher irreversible fouling resistances (Rfi), a 48% increase in Rfi. As compared with the control, the reduced-calcium powders had 28 and 34% lower ash and calcium contents, respectively. This study demonstrates that MPCs with a modified mineral content can be produced with injection of CO_2 before and during UF of skim milk.

Key Words: MPC, reduced calcium, mineral modified

536 Direct capture membrane adsorption chromatography with crude whey at pilot scale. L. Voswinkel* and U. Kulozik, *Technische Universität München, Freising, Germany.*

This study aimed at the development of a chromatographic process for whey protein isolation from crude whey as unit operation in the dairy industry. There is a demand for purified protein fractions such as lactoferrin (Lf) or lactoperoxidase (LPO) as well as for a specific protein composition in whey; e.g., depletion of β-Lactoglobulin (β-LG) for baby food. During the last decade several attempts and solutions for whey protein isolation have been published, including large scale packed columns and membrane adsorption technology. These processes resulted in fractions with high purity and recovery, but still required pretreatment steps, such as crossflow filtration, to avoid blocking of the stationary phase. Sartorius Stedim Biotech (Göttingen, Germany) has developed a spiral wound membrane device for ion exchange chromatography for the handling of crude feedstocks. Some industrial applications with direct capture-membrane adsorption chromatography (MAC) are proposed in this work. Using unfiltered buffers and cheese whey without adjusting its pH (if it is between pH 6–7) β-LG binds to an anion exchanger (AEC). The bind and elute process takes 30 min and yields 40 g protein with 99.5% purity at 5 L bed volume. This method is useful for β-LG depleted fresh whey keeping it as native as possible. Another unit operation is as simple. Unfiltered whey with no pH-adjustment is loaded onto a cation exchanger. Within 90 min, 1 ton of whey can be processed to gain pure Lf and LPO. The flowthrough from the AEC-step can also be used as substrate. The third application is the isolation of CMP resulting in 92% purity. In this case adjustment of conductivity to 3 mS/cm and pH-value to 4.9 is necessary. The loss of binding capacity in all studies was <10% over 5 cycles. A cleaning procedure with acid and NaOH recovered the initial binding capacity. The experiments showed that the processes are easy to handle and technical equipment does not require high pressure systems and special chemical stability. Therefore, direct capture-MAC is a fast, simple and reliable method convenient as a unit operation, not least for dairy SMEs.

Key Words: direct capture-membrane adsorption chromatography (MAC), whey protein fractionation, crude feedstock

537 Effect of operating conditions on particle size of milk protein concentrates during ultrafiltration. X. Luo, L. Ramchandran, and T. Vasiljevic*, *Advanced Food Systems Research Unit, College of Health and Biomedicine, Victoria University, Melbourne, Victoria, Australia.*

Various processing conditions during concentration of milk are known to affect their physical functionalities. To be useful as functional ingredients, milk protein concentrates (MPC) should possess desirable physical properties. For example emulsifying properties of MPC are believed to be influenced by the particle size. The present work investigated the effect of processing temperature as well as varying pH on particle size and membrane performance during a 5-fold concentration of skim milk by ultrafiltration (UF) using polyethersulfone membrane (molecular cut-off 20 kDa) with the aim to establish foundation for optimizing a process regimen for production of MPC with targeted functionalities. The skim milk was concentrated by ultrafiltration operated first at 3 temperatures (15, 30 or 50°C) and then at a constant temperature of 15°C but with varying pH (6.3, 5.9 or 5.5). Particle size and zeta potential of skim milk, retentate and permeate samples were measured immediately after the collection of samples using a Malvern Zetasizer while calcium content was determined by AAS. Membrane performance was evaluated by measuring the permeate flux (every 30 min) and SEM examination of membrane surface and its cross section. The operation temperature of UF influenced the calcium removal and change in casein micelle size. More ($P < 0.05$) calcium was removed from skim milk into the permeate at lower temperature (15°C) of UF, resulting in smaller casein micelle size. However, pH did not ($P > 0.05$) apparently influence particle size; although calcium removal was significantly higher ($P < 0.05$) at pH 5.5. The absolute value of zeta potential decreased with increase in UF operation temperature and decreasing pH. Membrane fouling occurred more rapidly at 50°C than at 15 or 30°C. At 15°C, fouling occurred more rapidly at pH 5.5. UF of skim milk at 15°C and pH 6.3–5.9 favored the production of milk concentrate with smaller casein micelles and less membrane fouling and thus can be preferred during MPC production.

Key Words: milk protein concentrate, ultrafiltration, particle size

Animal Health: Immune Response Patterns

TH1 Fatty acid catabolism modifies hypothalamic metabolome to suppress inflammation and appetite. J. W. McFadden*[1,2], E. Kim[3], Q. Li[2], S. Aja[2], V. V. Bandaru[2], N. J. Haughey[2], F. P. Kuhajda[2], and G. V. Ronnett[2], *[1]West Virginia University, Morgantown, [2]Johns Hopkins University, Baltimore, MD, [3]Daegu Gyeongbuk Institute of Science and Technology, Daegu, South Korea.*

Overnutrition causes hypothalamic lipotoxicity, reduced fatty acid (FA) oxidation (FAO), and inflammation to support hyperphagia. Increasing neuronal FAO with C75, a carnitine palmitoyltransferase-1 stimulator, suppresses appetite during overnutrition. The objective was to define this mechanism in primary hypothalamic neurons (PHN) collected from embryonic Sprague-Dawley rats. Following differentiation, 9 d in vitro, PHN (cultured in 3 mM glucose, 5% O_2, 5% CO_2) were treated with vehicle, 200 μM palmitate (C16:0), 70 μM C75, or C75 with C16:0 for 3, 4, or 18 h. For targeted metabolomics, lipid extracts were analyzed by a liquid chromatograph electrospray ionization tandem mass spectrometer (LC/ESI/MS/MS). For untargeted metabolomics, methanol extracted metabolites were independently analyzed on a gas chromatograph/MS and an ultrahigh performance LC/MS/MS. Data were analyzed by ANOVA and Tukey's test. For metabolomics data, statistics were performed on the log of the normalized, median-scaled data. Treatment with C75 for 4 h increased ($P < 0.01$) [^{14}C]-palmitate oxidation and ATP levels, and decreased ($P < 0.05$) AMP-activated protein kinase activation in PHN. From targeted and untargeted profiling, 96 and 185 metabolites were detected, respectively. Of interest, levels of palmitate, as well as palmitoyl-linked ceramide, dihydroceramide, monohexosylceramide, cholesterol, and fatty acylglycerol increased ($P < 0.05$) in PHN treated with C16:0 for 3 h; outcomes reversed ($P < 0.05$) by augmented FAO with C75. Untargeted metabolomics revealed decreased ($P < 0.10$) acetyl-CoA and propionylcarnitine levels, and increased ($P < 0.05$) oxidized nicotinamide adenine dinucleotide and citrate levels in PHN treated with C75 for 18 h, indicative of increased tricarboxylic acid cycle flux and oxidative phosphorylation caused by upregulated FAO. Treatment with C16:0 for 18 h increased ($P < 0.01$) tumor necrosis factor-α and interleukin-1β mRNA in PHN, pro-inflammatory effects inhibited by C75. Increasing hypothalamic FAO prevents lipotoxicity and inflammation to improve energy sensing, a potential means to prevent hyperphagia during overnutrition.

Key Words: fat metabolism, hypothalamus, metabolomics

TH2 Effect of subcutaneous fat stores on fatty acid content of serum phospholipids fraction in periparturient dairy cows. C. M. Scholte*, K. C. Ramsey, S. L. Shields, and P. Rezamand, *University of Idaho, Moscow.*

During early lactation, the diet does not meet the elevated energy requirements of high producing dairy cows. This leads to elevated lipid mobilization and thus release of fat into the blood in the form of nonesterified fatty acids (NEFA). Large quantities of NEFA have shown to alter the profile of the phospholipids (PL) fraction of the serum fatty acids (FA). The PL fraction is involved in cellular plasma membrane integrity, lipoprotein synthesis and intercellular signaling. The objective of this study was to determine how the changes in lipomobilization, as assessed by body condition score (BCS) around time of calving, affect the FA profile of serum PL fraction. Twenty-two primiparous and multiparous cows were monitored from 4 wk prepartum through 4 wk postpartum. Based on BCS around calving, cows were dichotomized into 2 groups of over-conditioned (BCS ≥3.25) or control (BCS ≤3.0). Blood samples were obtained at −28, −7, +8, +18, and +28d relative to parturition. Serum PL fraction was separated and analyzed for the FA profile. Data were analyzed as repeated measures by using PROC MIXED (SAS 9.2) and significance was declared at $P < 0.05$. Several FA in the PL fraction of serum lipids varied significantly by BCS around the time of parturition, including palmitic (C16:0), sapienic (C16:1), margaric (C17:0), linoleic (C18:2), and eicosadienoic (C20:2) acids. Further investigation is warranted to fully understand the relationship between over-conditioning and FA profiles of serum and circulating immune cells and their response to pathogens.

Key Words: dairy cow, lipid mobilization, phospholipid

TH3 Productive performance and risk of fat cow syndrome of cows at peak lactation with or without clinical mastitis. C. F. Qin[1,2], P. H. Zhang*[1], J. Q. Wang[2], P. Sun[2], D. P. Bu[2], D. Zhu[1], Y. G. Chai[1,2], and T. Zhang[1], *[1]Hunan Provincial Key Laboratory for Genetic Improvement of Domestic Animal, College of Animal Science and Technology, Hunan Agricultural University, Changsha, Hunan, China, [2]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Mastitis affects milk quality and quantity and induces metabolic disorders, causing great economic loss. This study evaluated the effects of clinical mastitis (CM) on productive performance and risk of fat cow syndrome in cows at peak lactation. Four Holstein cows without mastitis and another 4 diagnosed with CM were used in this study. All cows were from the same farm and with the same days in milk (57 DIM) and similar parities (1 to 3). Dry matter intake (DMI) and milk yield were recorded daily and body condition scoring (BCS) was conducted twice weekly. On 77 DIM, serum was sampled via jugular vein before morning feeding and milk samples were obtained. Data were analyzed using the MIXED procedure (SAS 9.1). In cows with CM, BCS increased ($R^2 = 0.87$) and milk yield decreased linearly ($R^2 = 0.94$) by DIM. Milk fat percentage (3.87 and 6.70%; $P > 0.05$) and yield (1.08 and 0.86 kg/d; $P > 0.05$), total solids proportion (12.48 and 15.13%; $P > 0.05$) and yield (3.50 and 2.19 kg/d; $P > 0.05$) and fat to protein ratio (1.34 and 1.90; $P > 0.05$) were not affected by CM. Composition of milk protein (2.94 and 3.50%; $P < 0.05$) and free fatty acid (1.46 and 2.75%; $P < 0.05$) increased when cows suffered from CM. DMI (20.78 and 12.55 kg/d; $P < 0.01$), milk yield (27.89 and 11.09 kg/d; $P < 0.01$), 4.0% fat corrected milk yield (27.38 and 19.09 kg/d; $P < 0.05$), energy corrected milk yield (29.11 and 20.11 kg/d; $P < 0.05$) and feed conversion rate (1.36 and 0.90; $P < 0.05$) decreased in cows with CM. In serum, level of total calcium (2.35 and 2.40 mmol/L; $P > 0.05$) and 25-hydroxyvitamin D_3 (31.28 and 25.67 ng/mL; $P > 0.05$) were not affected by suffering from CM. Albumin composition (35.43 and 29.43 g/L; $P < 0.05$) was lower and glucose level (2.86 and 4.48 mmol/L; $P < 0.05$) increased in serum of cows with CM, and concentration of serum β-hydroxybutyric acid (0.41 and 0.62 mmol/L; $P = 0.08$) tended to be higher in cows suffered from CM. Results indicated that productive performance was depressed and risk of fat cow syndrome increased when cows at peak lactation suffered from clinical mastitis.

Key Words: clinical mastitis, productive performance, fat cow syndrome

TH4 Association between hematological parameters and gender upon arrival with clinical bovine respiratory disease (BRD) risk in newly received beef calves. J. T. Richeson*[1], P. J. Pinedo[2], E. B. Kegley[3], J. G. Powell[3], M. S. Gadberry[3], P. A. Beck[3], and S. M. Falkenberg[4], *[1]Department of Agricultural Sciences, West Texas A&M University, Canyon, [2]Texas A&M AgriLife Research & Extension Center-College of Veterinary Medicine & Biomedical Sciences, Texas A&M University System, Amarillo, [3]Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville, [4]Ruminant Diseases and Immunology Research Unit, National Animal Disease Center, USDA-ARS, Ames, IA.*

The primary objective of this study was to analyze the association between complete blood count (CBC) parameters and gender upon arrival at a stocker receiving facility with the risk of subsequent clinical BRD. A secondary objective was to evaluate the accuracy of CBC parameter thresholds on predicting the risk of BRD. A retrospective cohort model was designed using 1,179 crossbred bull and steer calves (initial BW = 197 ± 2.4 kg) participating in 4 studies at 2 University of Arkansas cattle facilities. Gender (bull or steer) was determined and whole blood samples were collected and analyzed for concentration and/or percentage of total and differential leukocytes, red blood cells (RBC), hemoglobin, and platelets using an automated hemocytometer. Calves were monitored daily for signs of respiratory illness and were considered morbid based upon the BRD case definition specific to each trial. For statistical analyses, area under the curve (AUC) values were determined to measure the accuracy of each CBC parameter in predicting BRD and for assessing sensitivity and specificity thresholds. Then, a chi-squared test and multivariable logistic regression models were used for BRD prediction and results were categorized into low, medium, or high quartiles. Individual animal was experimental unit for all analyses and after removal of outliers, 943 animals were included in the final model. The resulting AUC values for the CBC parameters showing significant contrasts were low to moderate, and ranged from 0.51 (neutrophils; $P = 0.69$) to 0.67 (eosinophils; EOS; $P < 0.001$). The only CBC parameters showing a consistent predictive value for BRD were EOS ($P \leq 0.002$) and RBC ($P \leq 0.007$). Bull calves upon arrival were at greater ($P < 0.001$) risk of developing subsequent clinical BRD than steers; the odds of being initially diagnosed with BRD for bulls were 3.32 times the odds for steer cohorts. Arrival gender, along with the combination of reduced EOS and increased RBC concentrations in peripheral blood could be useful in identifying animals at greater risk for BRD.

Key Words: biomarker, bovine respiratory disease, complete blood count

TH5 Relationship between lying behavior and metritis in Holstein dairy cows. J. M. Huzzey*, A. Itle, D. M. Weary, and M. A. G. von Keyserlingk, *University of British Columbia, Animal Welfare Program, Vancouver, BC, Canada.*

Sick animals are often lethargic, as energy conservation helps facilitate recovery. The aim of this study was to test the prediction that Holstein cows with metritis would spend more time lying down. Data loggers were used to measure postpartum lying behavior (lying time, number of lying bouts, average lying bout duration) of cows on 2 commercial farms from d+1 to d+20 relative to calving: 150 cows from Farm 1 and 69 cows from Farm 2. Vaginal exams occurred twice per week from calving until 20 d in milk (DIM) and cases of metritis were diagnosed based on the presence of purulent and/or fetid vaginal discharge. Among cows diagnosed with metritis, 13 animals had at least 2-d of lying data recorded before the first observed clinical signs of infection; this data was used to create baseline data from which within-cow changes in lying activity could be described during the days following diagnosis. Lying behavior following diagnosis was averaged into 2 3-d periods for analyses: d 0 to 2 and d 3 to 5 post-diagnosis. Differences from baseline were analyzed using one sample *t*-tests. Clinical signs of metritis first appeared at 5.9 ± 2.4 DIM and the severity of the infection peaked at 7.5 ± 3.1 DIM (mean ± SD). The lying time (±SD) of metritic cows during the baseline period averaged 11.63 ± 2.87 h/d. Lying time tended to decrease by 1.08 ± 0.54 h/d from baseline during the first 3-d post-diagnosis and was 2.15 ± 0.75 h/d lower than baseline between d 3 to 5 post-diagnosis; the increased difference in lying time during the later days may have been associated with an increasing severity in the infection. Prior to metritis diagnosis the average (±SD) number of lying bouts and lying bout duration was 11.04 ± 2.15 bouts/d and 1.10 ± 0.34 h/d, respectively. These measures of lying activity did not change after metritis diagnosis. The reduction in lying times following metritis diagnosis is opposite to the lethargy-induced change originally predicted and may be due to animal discomfort and pain associated with the uterine infection.

Key Words: health, activity, welfare

TH6 Depleted serum vitamin E concentrations precede retained placenta in multiparous dairy cows. Y. Qu*, A. N. Fadden, M. G. Traber, and G. Bobe, *Oregon State University, Corvallis.*

Retained placenta (RP), defined as fetal membranes not being expelled within 24 h after calving, is a costly disease in multiparous dairy cows that is associated with perturbations in arachidonic acid metabolism. Vitamin E is an antioxidant that limits lipid peroxidation and has been shown to be lower one week before calving. We hypothesized that serum vitamin E (α-tocopherol) concentrations are depleted weeks before calving in cows that will develop RP. The objective of this study was to evaluate vitamin E status of multiparous dairy cows from a commercial dairy herd using a nested case-control design to compare cows that (a) were healthy after calving, (b) developed RP, or (c) developed in the first 28 d after calving other diseases, such as mastitis, metritis, laminitis, or ketosis. Blood samples were taken at postpartum d −21, −14, −7, −3, −1, and 0 from 96 multiparous Holstein cows (32 cows per group) and serum α-tocopherol and cholesterol concentrations were analyzed. Cows that later developed RP had 24% lower prepartal serum α-tocopherol concentrations (8.3 ± 0.6 vs. 10.9 ± 0.4 μ*M*; $P < 0.001$) and 17% lower α-tocopherol to cholesterol molar ratios (2.91 vs. 3.50 μ*M*/m*M*; $P = 0.003$) compared with cows that did not develop RP. Differences between cows that developed RP and those that did not were apparent as early as 3 wk before calving [α-tocopherol concentrations (8.0 ± 0.7 vs. 10.9 ± 0.5 μ*M*; $P = 0.002$) and α-tocopherol to cholesterol molar ratios (2.84 vs. 3.49 μ*M*/m*M*; $P = 0.003$)]. Healthy cows (concentration:12.3 ± 0.5 μ*M*, $P_{\text{Healthy vs. RP}} < 0.001$; ratio: 3.97 μ*M*/m*M*, $P_{\text{Healthy vs. RP}} < 0.001$) had the highest prepartal vitamin E status, whereas cows with other diseases had an intermediate vitamin E status (concentration: 9.5 ± 0.5 μ*M*, $P_{\text{Other Disease vs. RP}} = 0.10$; ratio: 3.45 μ*M*/m*M*, $P_{\text{Other Disease vs. RP}} = 0.66$). These findings suggest decreased vitamin E status is an early indicator for the development of RP in multiparous cows.

Key Words: dairy cow, retained placenta, vitamin E

TH7 Elevated serum visfatin concentrations precede retained placenta in multiparous dairy cows. A. N. Fadden, M. G. Traber, and G. Bobe*, *Oregon State University, Corvallis.*

Visfatin (also known as "pre-B colony enhancing factor" or "nicotinamide phosphoribosyl transferase") is a multifunctional protein associated with immune function and glucose homeostasis, which has not been previously examined in dairy cows. Visfatin is expressed in humans in fetal membranes and placenta and is elevated in serum during placental infections. Retained placenta (RP), defined as fetal membranes not being expelled within 24 h after calving, is a costly disease in multiparous dairy cows that is associated with placental inflammation. We hypothesized that serum visfatin concentrations are elevated in dairy cows that will develop RP. The objective of this study was to compare prepartal serum visfatin concentrations of multiparous dairy cows that either were healthy after calving (control) or developed RP (cases) on a commercial dairy herd. Using a nested case-control design, blood samples, taken at d −21 (−25 to −18), −14 (−17 to −11), −7 (−10 to −5), −3 (−4 to −3), −1 (−2 to −1), and 0 postpartum from multiparous Holstein cows that (a) were not treated for diseases within the first 4 weeks after calving (healthy cows, n = 22) or (b) developed RP (RP cows, n = 28) were analyzed for serum concentrations of visfatin. The RP cows had on average 26% lower prepartal serum visfatin concentrations (8.4 ± 0.6 vs. 6.2 ± 0.7 μg/L; $P = 0.009$) compared with healthy cows. Three weeks before calving, serum visfatin concentrations were significantly higher in RP compared with healthy cows (9.5 ± 0.7 vs. 7.5 ± 0.8 μ*M*; $P = 0.04$). Thus, elevated serum visfatin concentrations precede calving and suggest that serum visfatin concentrations could be used as a biomarker of the development of RP in multiparous cows.

Key Words: dairy cow, retained placenta, visfatin

TH8 Depleted serum vitamin E concentrations precede milk fever in multiparous dairy cows. Y. Qu*, A. N. Fadden, M. G. Traber, and G. Bobe, *Oregon State University, Corvallis.*

Milk fever (MF), defined as the clinical manifestation of hypocalcemia within the first 48 h after calving, is a costly disease in multiparous dairy cows that is associated with perturbations in calcium transport. We previously documented that depleted serum vitamin E (α-tocopherol) concentrations precede left displaced abomasum. We hypothesized that serum α-tocopherol concentrations are depleted before calving in cows that will develop MF, a gateway disorder for left displaced abomasum. Our objective was to compare prepartal serum α-tocopherol concentrations of multiparous dairy cows that (a) were healthy after calving, (b) developed MF, or (c) developed after calving other diseases on a commercial dairy herd. Using a nested case-control design, blood samples, taken on d −21, −14, −7, −3, −1, and 0 postpartum from 105 multiparous Holstein cows (35 cows per group) that (a) were not treated for diseases within the first 4 weeks after calving, (b) developed clinical signs of MF, or (c) developed in the first 28 d after calving other diseases, such as mastitis, metritis, laminitis, or ketosis, were analyzed for serum concentrations of α-tocopherol and cholesterol. Cows that later developed MF had on average 17% lower prepartal serum α-tocopherol concentrations (9.0 ± 0.5 vs. 10.8 ± 0.4 μ*M*; $P = 0.005$) and 15% lower α-tocopherol to cholesterol molar ratios (2.91 vs. 3.44 μ*M*/m*M*; $P = 0.002$) compared with cows that did not develop MF. These group differences were already significant 3 weeks before calving for α-tocopherol (8.6 ± 0.7 vs. 10.7 ± 0.5 μ*M*; $P = 0.01$) and α-tocopherol to cholesterol molar ratios (2.97 vs. 3.48 μ*M*/m*M*; $P = 0.03$). Healthy cows (concentration: 12.1 ± 0.5 μ*M*, $P_{\text{Healthy vs. MF}} < 0.001$; ratio: 3.91 μ*M*/m*M*, $P_{\text{Healthy vs. MF}} < 0.001$) had the highest prepartal vitamin E status, whereas cows with other diseases had an intermediate vitamin E status (concentration: 9.6 ± 0.5 μ*M*, $P_{\text{Other Disease vs. MF}} = 0.39$; ratio: 3.02 μ*M*/m*M*, $P_{\text{Other Disease vs. MF}} = 0.55$). These findings suggest lower serum α-tocopherol concentrations as potential early indicator for developing of MF in multiparous cows.

Key Words: dairy cow, milk fever, vitamin E

TH9 Assessment of shedding of *Mycobacterium avium* ssp. *paratuberculosis* into milk and colostrum of naturally infected dairy cows over complete lactation cycles. J. R. Stabel*[1,2], L. Bradner[1], S. Robbe-Austerman[3], and D. C. Beitz[2], *[1]USDA-ARS-NADC, Ames, IA, [2]Iowa State University, Ames, [3]USDA-ARS-VS, Ames, IA.*

Mycobacterium avium ssp. *paratuberculosis* (MAP) is the causative agent of Johne's disease (JD). One mode of transmission of MAP is through ingestion of contaminated milk and colostrum by susceptible calves. The objective of this study was to determine if the amount of MAP shed into the milk and colostrum of infected cows was affected by severity of infection, as well as the number of days in milk (DIM). Milk was collected over the 305-d lactation period from 24 asymptomatic cows in the subclinical stage of disease, 20 symptomatic cows demonstrating clinical signs, and 6 noninfected control cows. Milk was assayed for MAP by culture with BACTEC 12B and Herrold's egg yolk (HEY) media and by direct PCR for IS900 target gene. MAP was detected in 1.1, 2.7, and 7.6% of milk samples collected from cows with subclinical JD and 9.5, 11.2, and 38.8% of milk samples collected from cows with clinical JD by culture in HEY medium, Bactec 12B medium, and direct PCR, respectively. None of the milk samples collected from control cows were positive for MAP by any detection method. Viable MAP was primarily isolated from milk and colostrum of subclinically and clinically infected cows collected in early lactation (DIM 0–60); with decreased incidence in mid (DIM 60–240) and late (DIM 240–305) lactation. This study demonstrates that shedding of MAP into milk is affected by infection status of the cow as well as DIM, providing useful information to producers to help break the cycle of infection within a herd.

Key Words: *Mycobacterium avium* ssp. *paratuberculosis*, Johne's disease, milk

TH10 Monitoring response to vaccination with an inactivated BVDV vaccine by RNAseq transcriptome analysis in cattle. W. Demasius[1], R. Weikard[1], F. Hadlich[1], K. Müller[2], and Ch. Kühn*[1], *[1]Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, [2]Freie Universität Berlin, Department of Veterinary Medicine, Berlin, Germany.*

Bovine neonatal pancytopenia (BNP) is a fatal disease of newborn calves that is characterized by severe hemorrhages and a depletion of thrombocytes, leucocytes and myeloid stem cells. Epidemiological studies confirmed an association between BNP and a specific inactivated Bovine virus diarrhea virus (BVDV) vaccine. Genetically preconditioned cows vaccinated with this vaccine elicit BNP in newborn calves via colostrum. Although alloantigens against MHC class I molecules have been detected in the serum and colostrum of the respective cows, the pathogenesis of BNP is still not fully clear. Deep RNA sequencing (RNaseq) offers the opportunity of holistic monitoring of quantitative and structural differences between whole transcriptomes of a cell or tissue. In our analyses, we included 12 lactating and nonlactating cows, all except one from a German Holstein × Charolais crossbred population. Blood samples for RNA isolation were taken prior and 2 weeks after vaccination with the BVDV vaccine associated with BNP. RNaseq of transcript libraries was performed in a paired-end 61-bp multiplexed run. The reads obtained were demultiplexed, evaluated for quality and aligned to the bovine reference genome with the Bowtie/Tophat software package. Cufflinks options were used to assemble transcripts and to obtain read counts per transcribed locus. Read counts of loci were tested for differential expression in response to vaccination applying

a threshold of q < 0.05. Our experiment yielded 57.8 to 79.7 million mapped reads/sample. Transcript assembly showed that 4,596 of the 18,181 loci expressed in all samples had not been identified before. Bioinformatic enrichment analyses of transcripts differentially expressed due to vaccination identified the pathways of allograft rejection, graft-versus-host disease, cytokine-cytokine receptor interaction, natural killer cell mediated cytotoxicity, and RIG-I-like receptor signaling as significantly affected by vaccination, which indicates a major immune response to an alloantigen and to RNA virus infection.

Key Words: RNAseq, vaccination, cattle

TH11 *Cryptosporidium parvum* in Holstein calves at the State of Jalisco, México. I. Vitela-Mendoza[1], L. Medina-Esparza[1], C. Cruz-Vazquez[1], M. Ramos-Parra[1], I. Mejía-Haro[1], and S. S. González-Muñoz*[2], *[1]Instituto Tecnológico El Llano, Aguascalientes, Aguascalientes, México, [2]Colegio de Postgraduados, Montecillo, Estado de México, México.*

Cryptosporidium parvum, a parasite that causes diarrheas in young calves, is typically spread by ingestion of oocysts excreted in feces. Therefore, the objective of this study was to detect *Cryptosporidium* species in Holstein calves in Los Altos Norte, State of Jalisco. Between July and December 2012, 400 samples of feces were taken: 200 from 7- to 14-d-old male calves and 200 from 4- to 6-mo-old heifers. These samples were individually analyzed using a microscope (Leica LCD Digital) to identify *Cryptosporidium* oocysts, using Kinyoun staining. We also carried out molecular diagnosis to further characterize the species in samples identified as positive by the microscope analysis. *Cryptosporidium parvum* was found in 80% of 7- to 14-d-old male calves, and in 20% of 4- to 6-mo-old heifers. Nested PCR was used in 50 samples, in which 830-bp fragment corresponding to the 18S rRNA gene *Cryptosporidium* was identified in 36 samples (76%) of 7- to 14-d-old male calves, and in 14 samples (28%) of 4- to –mo-old heifers. Genetic analysis allowed to determining that isolates have 99 to 100% similarity with *C. parvum* bovine genotype. The high prevalence of cryptosporidiosis detected in this study is the first report of genetically identified *C. parvum* in Holstein calves in the State of Jalisco.

Key Words: *Cryptosporidium parvum*, nested PCR, Holstein calf

TH12 Evidence of seasonality and birth clusters of *Mycobacterium avium* subspecies *paratuberculosis* infection in US dairy herds. Y. Zare*[1], G. E. Shook[2], M. T. Collins[3], and B. W. Kirkpatrick[1,2], *[1]College of Agricultural and Life Sciences, Department of Animal Science, University of Wisconsin-Madison, Madison, [2]College of Agricultural and Life Sciences, Department of Dairy Science, University of Wisconsin-Madison, Madison, [3]School of Veterinary Medicine, Department of Pathobiological Sciences, University of Wisconsin-Madison, Madison.*

Paratuberculosis (Johne's disease) is a contagious intestinal infection of ruminants caused by *Mycobacterium avium* subspecies *paratuberculosis* (MAP). Young calves are at the highest risk for acquiring the infection mainly through ingestion of MAP from contaminated milk, colostrum, and feces or environmental contacts. The objectives were to assess (1) seasonality of MAP infection incidence and (2) whether MAP-infected animals were randomly distributed or clustered by date of birth within herds. Data consisted of ELISA and fecal culture test results of 9,200 mature cows from 30 US Jersey herds and 4 Wisconsin Holstein herds. ELISA results were available for all animals; however, fecal cultures were performed selectively. Within-herd apparent prevalence of MAP infection ranged from 0.01 to 0.30. Two definitions for infected animals were utilized. In the first infection (case) definition (CD1) animals testing positive and negative to ELISA were considered as infected and non-infected, respectively. In the second case definition (CD2) animals testing positive to either test were considered infected and cows testing negative to ELISA or to both ELISA and fecal culture were regarded as non-infected. For objective 1, 28 herds for CD1 and 24 herds for CD2 met specific criteria and were pooled for analysis. The effects of age, breed, herd, and season of birth were examined using logistic regression analysis. Season of birth was significant for both CDs; highest incidence was in summer ($P < 0.05$). For objective 2, 14 herds for CD1 and 2 herds for CD2 met specific criteria. A temporal clustering approach implemented in SaTScan software v 9.1 was used to detect clusters of birth cohorts using animals' birthdates and windows of 4, 10, 60, 90 and 120 d. Significant clustering of MAP-infected animals occurred in multiple herds. Existence of clusters necessitates matching cases and controls on birthdates to control for non-uniform exposure to MAP in genome wide association, candidate gene studies, or on-farm disease intervention trials.

Key Words: Johne's disease, dairy cattle, temporal clustering

TH13 Association between bovine viral diarrhea virus (BVDV) vaccine response and birth and weaning weights in crossbred beef calves. X. Sheng*, J. Walker, and M. Gonda, *South Dakota State University, Brookings.*

Antibody response following bovine viral diarrhea virus (BVDV) vaccination varies among individuals in beef herds. Some of this variation could be caused by genetic differences among individuals. If genetic selection were to be used to improve individual antibody response to vaccination, we must first understand whether BVDV vaccine response associates with other economically important traits in beef production. Our objective was to estimate the phenotypic correlation between BVDV-specific antibodies post-vaccination and birth and weaning weights in crossbred beef cattle. Crossbred calves (n = 208) raised at Antelope Range and Livestock Research Station in Buffalo, SD were vaccinated with Bovi-Shield GOLD 5 (Pfizer Inc., NY). Blood samples were collected at 3 time points: time of initial vaccination (d 0; $\mu = 193$ d of age), booster vaccination (d 34), and 50 d after the booster vaccination (d 84). Weights were recorded within 48 h of birth and when weaned (time of booster vaccination). A BVDV-specific antibody ELISA was used to measure BVDV-specific antibodies. The BVDV vaccine response was defined as (1) final BVDV-specific antibody concentration (d 84) subtracted from initial BVDV-specific antibody concentration (d 0) and (2) booster BVDV-specific antibody concentration (d 34) subtracted from initial BVDV-specific antibody concentration. A regression model including effects of gender and age was applied to estimate the association between BVDV-specific antibody response to vaccination and birth and weaning weights. Gender and age was significantly correlated with weaning weight and birth weight ($P < 0.0001$). Higher final BVDV vaccine responses (d 84 – d 0) were significantly correlated with heavier birth weights ($P = 0.0176$). Neither final nor booster BVDV vaccine response was significantly correlated with weaning weight. Our results suggested that no unfavorable phenotypic correlation between BVDV-specific antibodies post-vaccination and weaning weight existed in cattle. However, a significant, unfavorable phenotypic correlation between BVDV vaccine response and birth weight was found.

Key Words: BVDV, vaccine response, beef cattle

TH14 The effect of feeding endophyte-infected fescue on the acute phase response to lipopolysaccharide in beef heifers. A. W.

Altman*[1], N. C. Burdick Sanchez[2], J. A. Carroll[2], T. B. Schmidt[3], E. S. Vanzant[1], and K. R. McLeod[1], *[1]Department of Animal and Food Sciences, University of Kentucky, Lexington, [2]Livestock Issues Research Unit, USDA-ARS, Lubbock, TX, [3]Department of Animal Science, University of Nebraska-Lincoln, Lincoln.*

Angus heifers (n = 22; 292 ± 9.0 kg BW) were paired by BW and randomly placed on either an endophyte-infected (E+) or endophyte-free (E−) diet for 10 d to determine the influence of feeding endophyte-infected fescue on the physiological and acute phase responses of beef heifers to a lipopolysaccharide (LPS) challenge. Heifers were individually penned (thermoneutral; 3.0 × 3.7 m stalls) and fed at 1.8 × NEm. Diets contained 20% fescue seed, 30% cottonseed hulls, 36% cracked corn, 10% supplement, and 4% molasses, and were balanced to meet protein and mineral requirements. On d −16, heifers were fitted with vaginal temperature probes and on d −1 heifers were fitted with indwelling jugular cannulas. On the day of challenge, sickness behavior scores were recorded and blood samples were collected from heifers at 0.5 h intervals from −2 to 8 h, and again at 24 h relative to LPS administration (0.5 μg/kg BW at time 0 h). Serum was isolated and analyzed for cortisol, interferon-γ (IFN-γ), tumor necrosis factor-α (TNF-α), and interleukin-6 (IL-6) concentrations. Data were analyzed separately within pre- and post-challenge periods with the Mixed Procedure of SAS, using repeated measures in a completely randomized design. Within period, no treatment by time interactions were detected ($P > 0.10$). Cortisol, IFN-γ, TNF-α, and IL-6 concentrations increased for both groups from pre-LPS to post-LPS. Basal cortisol concentrations were unaffected ($P = 0.31$) by endophyte treatment pre-LPS, but were greater ($P = 0.01$) in E+ heifers during the post-LPS period (50.1 vs 55.0 ng/mL). TNF-α was greater in E+ heifers during both the pre- ($P < 0.01$; 6.2 vs. 6.0 pg/mL) and post-LPS periods ($P < 0.01$; 102.0 vs. 62.7 pg/mL). Neither IFN-γ nor IL-6 was affected by endophyte treatment during either period ($P \geq 0.13$). Sickness behavior scores were greater for E+ post-LPS ($P < 0.01$). Vaginal temperatures were greater for E- heifers pre-LPS ($P < 0.01$; 38.70 vs. 38.61°C) and greater for E+ heifers post-LPS ($P < 0.01$; 38.98 vs. 39.05°C). These data indicate that endophyte status affects the acute phase response when heifers are challenged with LPS.

Key Words: endophyte, cytokine, LPS

TH15 Oronasal administration of lipopolysaccharide and oral administration of lipopolysaccharide along with lipoteichoic acid enhanced salivary immunoglobulin A in periparturient dairy cows. S. Iqbal*[1], Q. Zebeli[1,2], D. A. Mansmann[1], S. M. Dunn[1], and B. N. Ametaj[1], *[1]University of Alberta, Edmonton, AB, Canada, [2]University of Veterinary Medicine, Vienna, Austria.*

The objective of this study was to evaluate whether repeated oronasal or oral administration of dairy cows to increasing doses of lipopolysaccharide (LPS) or a combination of LPS with lipotechoic acid (LTA) prepartum, respectively, would improve their mucosal immune responses. Two experiments were conducted. In experiment 1, 100 dairy cows were treated oronasally with increasing doses (0.01, 0.05, and 0.1 μg/kg BW) of LPS from *Escherichia coli* 0111:B4 dissolved in saline solution (TRT), or with saline solution alone (CTR). In experiment 2, 30 dairy cows were treated orally either with saline solution alone (CTR), or saline solution containing 3 increasing doses of LPS from *E. coli* 0111:B4 (0.01, 0.05, and 0.1 μg/kg BW) along with a flat dose of LTA from *Bacillus subtilis* (i.e., 120 μg/animal; TRT). Both treatments were applied for 3 consecutive weeks started at d −28, and then applied on d −25, −21, −18, and −14 prepartum. Saliva samples were collected on d −28, −7, +7, and +28 around parturition and analyzed for total IgA antibodies. Data was analyzed by the mixed procedure of SAS. Overall results indicated that TRT group in experiment 1 had greater concentrations of salivary total IgA antibodies ($P < 0.01$), with higher values started at d −7, and peak levels attained at d +7 compared with CTR group. Cows in experiment 1 had no treatment by wk interaction ($P > 0.05$); however measurement wk alone showed an influence for salivary IgA antibodies ($P < 0.01$). Interestingly, salivary total IgA antibodies were 2-fold greater in TRT cows in experiment 2 ($P < 0.01$), with higher values starting from d −7 until d +28 compared with CTR group. Cows in experiment 2 also showed an effect of measurement wk, as well as a treatment by wk interaction for salivary IgA antibodies ($P < 0.05$). In conclusion, periparturient dairy cows treated with repeated oronasal LPS alone or oral LPS along with LTA before calving enhanced concentrations of saliva total IgA antibodies against the 2 main bacterial endotoxins.

Key Words: lipopolysaccharide, lipoteichoic acid, saliva immunoglobulin A

TH16 Repeated oral exposure to lipopolysaccharide and lipoteichoic acid prepartum decreased uterine horn fluctuation and the incidence of abnormal discharges in postparturient dairy cows. S. Iqbal*[1], Q. Zebeli[1,2], D. A. Mansmann[1], S. M. Dunn[1], and B. N. Ametaj[1], *[1]University of Alberta, Edmonton, AB, Canada, [2]University of Veterinary Medicine, Vienna, Austria.*

The postpartum uterus of the transition dairy cow is highly susceptible to infection with numerous bacterial strains. The aim of this study was to evaluate whether repeated oral administration of lipopolysaccharide (LPS) along with a flat dose of lipoteichoic acid (LTA) to dairy cows would affect uterine horn fluctuation and the incidence of abnormal discharges. Thirty pregnant Holstein cows received orally either 2 mL of saline solution alone (CTR), or saline solution containing 3 increasing doses of LPS from *E. coli* 0111:B4 (0.01, 0.05, and 0.1 μg/kg BW) along with a flat dose of LTA from *Bacillus subtilis* (i.e., 120 μg/animal; TRT) on d −28 −25, −21, −18, and −14 before the expected day of parturition. Cows were monitored for rectal temperature starting 2 wk before until 2 wk after the expected day of parturition. Examination of the reproductive tract of each cow was conducted via rectal palpation on a weekly basis until +28 d postpartum. Data was analyzed by categorical modeling procedure of SAS. Results indicated that uterine horn fluctuations were present in CTR cows in a greater number of cases (8 vs. 1) compared with the TRT cows ($P < 0.01$). The symmetry of the uterine horns was not uniform in 4 cows in the CTR group vs. 1 cow in the TRT group; although data was not significant ($P > 0.05$). The number of cows with uterine discharges also tended to be greater in the CTR cows (6 vs. 1) compared with the TRT group ($P = 0.08$); although both groups had only 1 cow with bad odor of uterine discharge ($P > 0.05$). No difference in the cervix size and rectal temperature was evidenced between the 2 treated groups ($P > 0.05$). In a companion abstract we are reporting greater total salivary IgA antibody in cows treated with LPS and LTA. In conclusion, cows administered orally with LPS and LTA showed lower cases with uterine horn fluctuations and uterine discharges suggesting that the treatment might confer some protection against bacterial infections. More research is warranted to prove these preliminary findings.

Key Words: lipopolysaccharide, lipoteichoic acid, uterine horn fluctuation

TH17 Environmental heat stress modulates thyroid status and its response to repeated endotoxin (LPS) challenge in steers. S.

Kahl*[1], T. H. Elsasser[1], R. P. Rhoads[2], R. J. Collier[3], and L. H. Baumgard[4], *[1]USDA-ARS, Beltsville, MD, [2]Virginia Polytechnic Institute and State University, Blacksburg, [3]University of Arizona, Tucson, [4]Iowa State University, Ames.*

Thyroid hormones are important in the adaptation to heat stress, allowing the adjustment of metabolic rates in favor of decreased energy utilization and heat production. Thyroid status is compromised in a variety of acute and chronic infections and toxin-mediated disease states. Our objective was to evaluate in cattle, the activity of pituitary-thyroid axis during adaptation to heat stress and the response of this thyroid status to immune stress modeled by LPS challenge. 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 9 d. To minimize confounding effects of altered plane of nutrition, TN were pair-fed to HS. On d 4 and 7, steers received a LPS challenge (LPS1 and LPS2; E. Coli 055:B5, 0.2 µg/kg BW, i.v.) with blood samples collected at 0, 1, 2, 4, 7, and 24 h relative to the start of each challenge. Plasma concentrations of thyrotropin (TSH), thyroxine (T_4), triiodothyronine (T_3), and reverse-triiodothyronine (rT_3) were measured by RIA. Before the start of LPS1, HS decreased ($P < 0.01$ vs. TN) plasma TSH (40%), T_4 (45.4%), and T_3 (25.9%), but did not affect rT_3 concentrations. In TN group, LPS1 challenge decreased ($P < 0.01$ vs. 0 h) plasma concentrations of TSH between 1 and 7 h and T_4 and T_3 at 7 and 24 h. In HS steers, LPS1 injection reduced plasma TSH at 2 h only ($P < 0.05$), decreased plasma T_3 at 7 and 24 h ($P < 0.01$) but did not affect already depressed plasma T_4. In all steers, LPS1 increased ($P < 0.01$) plasma rT_3 concentrations at 4, 7, and 24 h. The patterns of T_4, T_3, and rT_3 changes during LPS2 were similar to those in LPS1 with less evident response in plasma TSH after LPS2. The data are consistent with the concept that HS adaptation in cattle results in the depression of pituitary-thyroid axis with preserved normal extrathyroidal T_3 production. The data also suggest that LPS challenge suppresses both pituitary-thyroid axis and peripheral T_3 generation, responses that are more apparent in steers subjected to previous HS exposure.

Key Words: endotoxin, heat stress, thyroid hormone

TH18 Proinflammatory responses to repeated endotoxin (LPS) challenges are augmented in Brahman cattle compared to Angus cattle following the second LPS challenge. T. H. Elsasser*[1], C. Chase[2], and S. Kahl[1], *[1]USDA-ARS, Beltsville, MD, [2]USDA-ARS, Clay Center, NE.*

The ability to express a robust proinflammatory response (PIR) to a pathogen is essential in protecting against pathogen proliferation. However, failure to actively terminate PIR in due course can lead to excessive tissue damage from the overproduction of reactive compounds being generated in responding cells. *Bos taurus* and *Bos indicus* cattle are known to present different sensitivities to pathogen susceptibility. However, few data if any specifically address the characteristics of their respective host PIR after exposure. To determine whether *Bos taurus* and *Bos indicus* cattle differ in their PIR characteristics, a validated repeated LPS challenge procedure was performed with the respective biomarkers assessed specifically in regard to the degree to which the respective breeds mounted a tolerance response to the second LPS challenge. Healthy Brahman (BR) and Angus (AN) steers (n = 4/breed; 312 kg Av BW) were fed ad libitum and group housed by breed. Each animal was challenged twice with LPS (LPS-1, LPS-2; *E. coli* 055:B5, 0.2 µg/kg BW) with challenges separated by 3 d. Blood samples were obtained by venipuncture before and at 1, 2, 3, 4, 6 and 24 h following LPS. Concentrations of tumor necrosis factor-α (TNF), nitric oxide response ([nitrate + nitrite], NOx) and xanthine oxidase (XO) were measured in plasma. Rectal temperatures (RT) were recorded at the times of blood sampling. After LPS-1, TNF responses (AUC, area under the concentration × time curve) were greater in AN than BR but decreased only in AN after LPS-2 ($P < 0.05$). The total NOx response after both LPS challenges were significantly greater in BR than AN ($P < 0.05$) and augmented in BR after LPS-2. Mean XO concentrations were more than twice as high in BR then XO at any time before or after LPS ($P < 0.001$, breed), marginally increased after LPS-1 in both breeds, and only attenuated in response afterLPS-2 in AN. Increases in RT did not abate in BR following the LPS-2 ($P < 0.03$ vs. AN). The data indicate that fundamental differences in tolerance development in PIR were apparent between BR and AN.

Key Words: proinflammatory response, breed, acute phase response

TH19 Effects of intrauterine infusion of endometritic cows with *E. coli* lipopolysaccharide on endometrial gene expression and reproductive performance. J. Moraes*[1], P. Silva[2], A. Scanavez[1], L. Mendonca[1], J. Silva[1], K. Galvao[3], and R. Chebel[1], *[1]Department of Veterinary Population Medicine, University of Minnesota, St Paul, [2]Department of Animal Science, University of Minnesota, St Paul, [3]Department of Large Animal Clinical Sciences, University of Florida, Gainesville.*

Objectives were to evaluate the effects of intrauterine infusion of endometritic cows with *E. coli* lipopolysaccharide (LPS) on endometrial gene expression, cortisol and haptoglobin concentration, and reproductive performance. Cows (n = 2931) were examined for clinical endometritis at 31 ± 3 d postpartum using the Metricheck. Endometritic cows (n = 267) were assigned to receive intrauterine infusion of 20 mL of phosphate-buffered saline with 0µg (NC, n = 87), 150µg (150LPS, n = 91), or 300µg (300LPS, n = 89) of *E. coli* LPS. Healthy cows (CON = 2664) were used as positive control. A sub-sample of cows (NC, n = 16; 150LPS, n = 17; 300LPS, n = 17) had uterus biopsied 6h after infusion and another sub-sample of cows (NC, n = 18; 150LPS, n = 17; 300LPS, n = 14) had uterus biopsied 24h after infusion. Blood from all endometritic cows was collected before treatment (0h) and 24, 48 and 168h after treatment for determination of haptoglobin concentration. A sub-sample of endometritic cows (NC, n = 43; 150LPS, n = 45; 300LPS, n = 42) had blood sampled at 0, 2, 4, 6 and 24 h for determination of cortisol concentration. Binary data were analyzed by SAS PROC LOGISTIC, rate at which cows became pregnant was analyzed by Cox proportional hazard ratio using SAS PROC PHREG, and fold-change in expression of endometrial genes was analyzed by a non-parametric method (Kruskal-Wallis). Treatment affected ($P < 0.01$) the rate at which cows became pregnant. Pregnancy rate of CON cows was greater than that of NC cows [AHR (95% CI) = 0.59 (0.41, 0.84); $P < 0.01$] and pregnancy rate of CON tended to be greater than that of 300LPS cows [AHR (95% CI) = 0.75 (0.54, 1.05); $P = 0.09$]. The rate at which CON and 150LPS cows became pregnant was not different ($P = 0.15$). Interestingly, the expressions of mRNA for IL1-beta, IL-6, IL-8, IL-10, TLR-4, TNF-alpha at 6 h and 24 h after treatment were not ($P > 0.15$) affected by treatment. Treatment with 150 µg of LPS improved reproductive performance, but had no effect on endometrial gene expression.

Key Words: lipopolysaccharide, uterus, endometritis

TH20 Phagocytic activities of leukocytes, monocytes and neutrophils of dairy cows fed with n-3 and n-6 fatty acids sources in the transition period and early lactation. L. C. Verdurico*, J. R.

Gandra, R. D. Mingoti, R. V. Barletta, T. S. Canaes, L. Oliveira, G. D. Calomeni, R. Gardinal, C. S. Takyia, T. H. Vendramini, and F. P. Renno, *Universidade de Sao Paulo, Universidade de Sao Paulo, Pirassununga, Sao Paulo, Brazil.*

The aim of this study was to evaluate effect of omega 3 and omega 6 supplementation, on expression of adhesion molecules of Holstein cows during transition period and early lactation. Forty-eight Holstein cows were divided in 4 experimental groups in randomized design. Animals were assigned to receive one of 4 treatments: (1) control (C; n = 12), without fat sources in pre and postpartum; (2) flaxseed (FS; n = 12), fed 60 and 80 g/kg of DM of flaxseed in pre and postpartum; (3) whole raw soybeans (WS; n = 12), fed 120 and 160 g/kg of DM of whole raw soybeans in pre and postpartum; (4) calcium salts of unsaturated fatty acids (CSFA; n = 12; Megalac-E), fed 24 and 32 g/kg of DM of calcium salts of unsaturated fatty acids in pre and postpartum. Experimental diets were fed from 35 d before the estimate calving until 84 d of lactation, formulated to meet nutritional requirements of each period. Blood samples were taken −21, −14, −7 d in relation to prediction of birth, at birth and +7, +14, +21, +42, +84 d postpartum. Data were analyzed using the PROC MIXED of SAS 9.1 with fixed dietary effect, time effect, interaction between diet and time. Data were analyzed by orthogonal contrasts C vs. WS+CSFA+FS (C1); FS vs. WS+CSFA (C2); and WS vs. CSFA (C3). We measured phagocytic activities of leukocytes, monocytes and neutrophils of dairy cows. There was a higher percentage of leukocytes and monocytes positive for phagocytosis for diets FS, WS, and CSFA compared with the C diet, (36.0; 33.1; 30.2 vs. 21.3), (37.2; 31.4; 29.5 vs. 32.6) respectively for leukocytes in pre and postpartum; and (64.6; 61.4; 48.2 vs. 32.7), (51.2; 49.1; 47.6 vs. 41.2) respectively for monocytes in pre and postpartum. For neutrophils in pre and postpartum and postpartum monocytes was observed higher percentage of positive cells for FS diet compared with diets CSFA and WS. The inclusion of sources of fatty acids n-3 and n-6 in the diet of dairy cows improved the phagocytic activity in the transition period.

Key Words: dairy cow, fat source, immune function

TH21 Effect of IgG binding on expression of Fc receptors and SYK activation in bovine neutrophils. J. Williams*, M. Worku, A. Alston, R. Noble, and T. Hanner, *North Carolina Agricultural & Technical State University, Greensboro.*

In cattle the immunoglobulin G (IgG) binding FcR (FcγRI, -II, and -III) plays an important role in clearance of mastitis causing bacteria. Activating (CD32a) and inhibitory (CD32b) isoforms of Fcγ receptors, FcγRII (CD32) have been identified. Variation in FcRs may impact gene expression and downstream intracellular signaling. The objective of this study was to evaluate the effect of IgG binding on transcription of FcRI, FcRII and its sub isoforms and to evaluate changes in endogenous levels of phosphorylated Syk kinase. Blood was collected from 6 lactating cows (3 Holstein Friesian and 3 Holstein × Jersey). Isolated blood neutrophils were incubated with IgG or maintained in PBS. Total RNA was then isolated and cell lysates prepared. Real time PCR was used to evaluate changes in the expression profile of FcRI, FcRII and FcRII sub-isoforms using GAPDH as a reference control. Amplified products were separated on a 1% agarose gel and observed following staining with ethidium bromide. All genes were transcribed. Variable gene expression was observed. A significant (80-fold) increase in FcRII transcript was observed in Holstein × Jersey as compared with Holstein Friesian breeds. Binding of IgG to neutrophils for Holstein × Jersey cows significantly increased expression of SYK ($P < 0.007$). Following the binding of IgG to neutrophil variation in the transcription of immunoreceptors and activation of intracellular signal mediator SYK may play a role in the resolution of infection. Further characterization using a larger sample size is needed.

Key Words: Fc receptor, neutrophil, transcription

TH22 Modulation of the intestinal immune response of calves by *Bacillus cereus* var. *toyoi* (Toyocerin). A. Aris*[1], F. Fabregas[1], S. Pares[1], M. Terre[1], M. Castillo[3], and A. Bach[1,2], *[1]IRTA, Caldes de Montbui, Spain, [2]ICREA, Barcelona, Spain, [3]Rubinum SA, Rubi, Spain.*

It has been previously shown that *Bacillus cereus* var. *toyoi* (Toyocerin) improves the humoral response to vaccination in calves. The objective of this study was to further evaluate the effects of Toyocerin on the immune system response of calves. Twenty-four Holstein calves (75.2 ± 1.87 kg of BW and 77 ± 0.7 d of age), were randomly distributed according to BW in 2 groups: 12 calves were assigned to a conventional concentrate feed (CTR), and the other 12 calves were fed the same concentrate feed supplemented with 2×10^8 cfu *Bacillus cereus* var. *toyoi*/kg of concentrate (TOY). Animals were euthanized at 60–67 d of the study. Immediately after sacrifice, calves were abdomen-opened, and the whole gastrointestinal tract was removed. Jejune fragments were sampled to quantify cytokine and enzyme expression by qPCR and intestinal contents were processed to quantify production of IgA by ELISA. Data were analyzed by ANOVA using the treatment as the main effect. The TOY calves presented a greater ($P < 0.05$) amount of secretory IgA in jejune content than CTR animals (6434 ± 478 mg/mL vs. 4673 ± 499 mg/mL, respectively); whereas no differences in IgA were observed at cecum level. Calves in the TOY group showed a clear increase ($P < 0.05$) in the expression level of Th1 cytokines such as IFN-γ ($3.49 \times 10^{-3} \pm 0.519 \times 10^{-3}$) compared with calves in the CTR group ($1.34 \times 10^{-3} \pm 0.519 \times 10^{-3}$), which would explain an improvement in cellular activity. Accordingly, gene expression of nitric oxide synthase increased ($P < 0.05$) and that of myeloperoxidase tended ($P < 0.1$) to increase in TOY ($3.21 \times 10^{-3} \pm 0.398 \times 10^{-3}$ and $6.53 \times 10^{-4} \pm 0{,}68 \times 10^{-4}$, respectively) compared with CTR calves ($2.12 \times 10^{-3} \pm 0.382 \times 10^{-3}$ and $3.06 \times 10^{-4} \pm 0.65 \times 10^{-4}$,respectively). In conclusion, these results confirm the positive effects of Toyocerin in enhancing the humoral response of calves, expanding its modulatory effects at both the cellular and humoral level of intestinal immune response.

Key Words: immunity, inflammation, gut

TH23 Decomposing between-cow and within-cow variation in hematology and leukocyte responses in dairy cows during the periparturient period. M. D. Sellers*, C. R. Nightingale, A. R. Pepper-Yowell, T. L. Harris, and M. A. Ballou, *Department of Animal and Food Sciences, Texas Tech University, Lubbock.*

Previous research has shown that most variation in immune variables following calving is residual, within-cohort variation. The objective of the current study was to decompose total variation in hematology and leukocyte responses into time, between-cow, and residual (within-cow) variation. Twenty-five Holstein cows were sampled at −60 (end of previous lactation), −30, 0, 15, and 30 d relative to parturition for hematology and various leukocyte responses. A linear model was fitted with the effects of cow and time, with within-cow variation being a major source of residual variation. Percentage of variation attributable to a given effect was estimated by dividing the sums of squares attributable to any effect by the total sums of squares and is reported as η^2. Bootstrapped resampling was used to estimate confidence intervals around η^2 estimates. Time effects were observed for all variables except TNF ($P = 0.148$) and lymphocyte count ($P = 0.704$). Between-cow effects

were observed for percentage of neutrophils positive for and intensity of oxidative burst response ($P < 0.007$ and $P < 0.0142$, respectively.), and total leukocyte count ($P < 0.003$). Across all variables, within-cow variation was higher than variation between cows or due to time (Table 1). Variation due to time was highest in plasma haptoglobin concentration ($\eta^2 = 0.345$), which elevated following parturition (Table). High within-cow variation may indicate that cows with high or low values at certain time points likely do not maintain high or low values for the duration of the peripartum period.

Table 1.

	η^2 - Time		η^2 - Cow		η^2 - Residual	
	Estimate	Interval	Estimate	Interval	Estimate	Interval
Oxidative burst intensity	0.181	[0.128–0.285]	0.271	[0.191–0.370]	0.548	[0.434–0.621]
L-Selectin expression	0.246	[0.102–0.505]	0.169	[0.089–0.229]	0.585	[0.363–0.713]
Plasma haptoglobin	0.345	[0.203–0.546]	0.083	[0.047–0.122]	0.572	[0.398–0.687]
Tumor necrosis factor-α	0.045	[0.018–0.159]	0.274	[0.161–0.373]	0.681	[0.558–0.758]
Total leukocytes	0.208	[0.146–0.322]	0.283	[0.191–0.366]	0.509	[0.395–0.600]
Neutrophil count	0.247	[0.160–0.387]	0.186	[0.079–0.283]	0.567	[0.421–0.705]

Key Words: peripartum, immune, variation

TH24 Leukocyte responses immediately following calving are not predictive of first test day milk yield or somatic cell count in multiparous Holstein cows. M. D. Sellers, C. R. Nightingale, R. Y. Liang*, T. L. Harris, A. R. Pepper-Yowell, B. S. Obeidat, and M. A. Ballou, *Department of Animal and Food Sciences, Texas Tech University, Lubbock.*

The objective of the current study was to determine if hematology or leukocyte responses immediately following calving were predictive of first test day milk yield or somatic cell count (SCC). Twenty-four multiparous Holstein cows within 72 h post-calving were sampled for measurement of hematology and many leukocyte responses, which included: neutrophil expression of the adhesion protein L-selectin, neutrophil oxidative burst capacity against an *Escherichia coli*, plasma concentrations of the acute phase protein haptoglobin, and whole blood secretion of tumor necrosis factor-α and interferon-γ when stimulated with lipopolysaccharide and phytohemagglutinin-P, respectively. At 29 ± 5 d in milk, milk was collected and analyzed for yield and somatic cell count. First test day milk (mean ± SD) was 47.4 ± 6.72 kg and SCC was 2.6 ± 1.69 Log_2(SCC/100,000). Regression analysis with stepwise backward elimination was utilized to estimate the best-fitting predictive model based on the lowest AIC. The best-fitting predictive model for first test day milk production included the dependent variables: percentage of neutrophils positive for producing an oxidative burst as well as tumor necrosis factor-α and interferon-γ secretion from whole blood cultures, but there were no nonzero coefficients ($P > 0.077$). The multiple R^2 for the model was 0.370 ± 0.181. The best-fitting model for first test day SCC included the dependent variables: percentage of neutrophils positive for producing an oxidative burst, mean fluorescence intensity of oxidative-burst positive neutrophils, and tumor necrosis factor-α and interferon- γ secretion from whole blood cultures. There was a tendency for secretion of interferon-γ secretion to have a nonzero slope ($P = 0.058$). The multiple R^2 for the model was 0.278 ± 0.190. These data suggest that measures of hematology or leukocyte responses obtained immediately following calving are not largely predictive of first test day milk yield or somatic cell count.

Key Words: immune, performance, peripartum

TH25 Differential effects of stimulation on ruminant neutrophils. K. Gyenai* and M. Worku, *North Carolina Agricultural and Technical State University, Greensboro.*

Plants and their extracts have traditionally been used to improve animal health and welfare. Research is needed to determine the effectiveness and toxicity of traditionally used plants and other natural substances. In this study, we investigated the effects of *Moringa oleifera* leaf powder, bacterial LPS and peptidoglycan (PGN) on ovine, caprine and bovine neutrophils. Six animals each, treatment (n = 3) and control (n = 3) from the 3 different species were used. Isolated neutrophils were treated and incubated at 37°C, with 85% humidity and 5% CO_2 for 15 min with 100 μg PGN, 100 μg LPS or 100 μg of *Moringa* either individually or in combinations and PBS as control. Pro-inflammatory cytokine levels were evaluated in supernatants from treated neutrophils using commercial assays. Real time PCR using 84 different innate and adaptive immune markers was conducted using arrays. In ovine *Moringa*-treated samples, interferon gamma-γ and granulocyte-colony stimulating factor were (300 and 600% fold) increased compared with other cytokines and treatment respectively, ($P < 0.05$). Bovine neutrophil supernatants cytokine levels were significantly (1 to 3 fold) increased in tumor necrosis factor-α for LP, PGN and LPS in combination; PGN and *Moringa* in combination. However, in caprine neutrophils a 10 to 600% fold reduction was observed for all cytokines when compared with the other 2 species. Real-time analysis of innate and adaptive immune markers showed differential responses to each treatment. *Moringa*-treated ovine neutrophils had the highest expression profile with 16 genes up and 25 genes downregulated respectively. Treatment with Lps resulted to the least expression in all species, with ovine having smallest expression 3 genes down and 3 upregulated. Differential effects of stimulation were observed on ruminant neutrophils. Species-dependent effects may affect the use of plants such as *Moringa* and their extracts for animal health.

Key Words: *Moringa*, neutrophil, ovine

TH26 Evaluation of TLR2 surface expression on blood mononuclear cells (BMC) in high immune response (HIR) biased cows. L. Wagter-Lesperance*, M. Paibomesai, R. Opsteen, and B. Mallard, *University of Guelph, Guelph, ON, Canada.*

Dairy cattle with high immune response (HIR) following immunization with specified test antigens have been shown to be at a lower risk for developing disease compared with average and low responding animals. The host relies on both the first-line innate response and long-lasting adaptive immune response to effectively recognize and eliminate pathogens. Innate mechanisms of host defense are important in the initiation of adaptive immune responses and consist of a variety of cells and proteins. Cells express pattern recognition receptors (PRRs) such as toll-like receptor (TLR) that recognize pathogen-associated molecular patterns (PAMPs). Toll-like receptors recognize several PAMPs from both intracellular and extracellular pathogens. Blood mononuclear cells (BMC) from 8 cows were evaluated to identify differences in the expression of TLR2, in addition to CD3, CD5, CD14, and Anti-B cell receptor using flow cytometric analysis. Four of the 8 cows were previously classified as high for cell-mediated immune response (CMIR) and low for antibody-mediated immune response (AMIR) and the other 4 cows were classified as high for AMIR and low for CMIR. Descriptive

statistics and a Student's *t*-test of TLR2+ expression between HIR-biased groups was performed. Data will be analyzed using GLM SAS with significance at $P < 0.05$. Results (reported as the mean percent ± standard error) for all 8 cows were 19.85% ± 2.25 for TLR2+, 16.03% ± 1.37 for TLR2+CD14+, 18.69% ± 1.12 for TLR2+AntiBcell+, 9.015% ± 1.15 for TLR2+CD3+, and 3.065 ± 0.71 for TLR2+CD5+. Cows with a high AMIR bias (H-AMIR), had higher percentage of BMC expressing TLR2, in contrast to cows with a high CMIR bias (H-CMIR). H-AMIR bias cows tended to have more double stained cells in contrast to H-CMIR cows, but this was not significant. The sample size for this study was small, and so the evaluation of more cows may more clearly identify differences in the expression of TLR2 on BMC and specific subpopulations among cattle classified with high or low adaptive immune response.

Key Words: HIR, innate, toll-like receptor

TH27 Effects of an immunomodulatory dietary supplement on the global gene expression profile of neutrophils from periparturient dairy cows. X. S. Revelo[1], J. W. Davis[2], R. D. Schnabel[2], A. L. Kenny[2], N. M. Barkley[2], and M. R. Waldron*[2], *[1]University Health Network, Toronto, ON, Canada, [2]University of Missouri, Columbia.*

The importance of dietary strategies to improve the immune competency of periparturient dairy cows is well-recognized. We investigated the effects of a dietary supplement containing B-vitamins, dehydrated yeast, and *Trichoderma longibrachiatum* fermentation products on the global gene expression profile of neutrophils (PMNL). Cows received 56 g/day of OmniGen-AF (n = 5) or sham control (n = 5) mixed into total mixed rations from d 46 ± 1 prepartum until d 31 postpartum. Blood PMNL were harvested on d 7 postpartum and incubated with 0 or 50 μg/mL of *Escherichia coli* lipopolysaccharide (LPS) for 120 min. Poly-A enriched mRNA from the PMNL was converted into library templates, sequenced and mapped to the bovine reference genome. Digital count data was then analyzed to determine the effects of dietary supplementation and LPS incubation on PMNL gene expression. Feeding OmniGen-AF altered mRNA contents of 43 genes (7↑ and 36↓; $P < 0.05$, 20% FDR) in LPS-activated PMNL. Functional annotation analysis indicated that the genes with lower expression enriched the lysosome pathway. Independent from LPS activation, OmniGen-AF altered the expression of 53 transcripts (12↑ and 41↓; $P < 0.05$, 20% FDR) relative to non-supplemented controls. Genes with lower expression due to OmniGen-AF enriched the oxidative phosphorylation pathway. Gene ontology terms for this pathway included oxidation-reduction, electron transport chain, mitochondrial electron transport, ATP synthesis coupled electron transport, and cellular respiration. These results suggest potential mechanisms by which OmniGen-AF may influence the activity of PMNL in periparturient dairy cows. The effect of LPS incubation on PMNL gene expression was also tested independent of dietary supplementation. Regardless of dietary treatment, 50 μg/mL of LPS altered the mRNA contents of 333 genes (211↑ and 122↓; $P < 0.05$, 20% FDR), relative to 0 μg/mL. Genes with increased expression enriched the TOLL-like receptor signaling and hematopoietic cell lineage pathways. These results highlight molecular mechanisms involved in the PMNL response to LPS.

Key Words: neutrophil, gene expression, OmniGen-AF

TH28 Effects of recombinant bovine somatotropin (rbST) treatment during the peripartum period on innate immune responses and hemogram parameters. P. Silva*[1], J. Moraes[2], A. Dresch[2], K. Machado[2], and R. Chebel[2], *[1]Department of Animal Science, University of Minnesota, St Paul, [2]Department of Veterinary Population Medicine, University of Minnesota, St Paul.*

Objectives were to evaluate the effect of peripartum treatment with rbST on innate immune responses and hemogram parameters of Holstein cows. Holstein cows (256 ± 3 d of gestation and body condition score >3.5) were enrolled in this study and randomly assigned to one of 3: CON-0 mg/d rbST (n = 21), 35%-12.5 mg/d rbST (n = 21), or 50%-17.9 mg/d rbST (n = 23). Cows assigned to the 35% and 50% were treated every 7 d. Cows received a body condition score and were weighed at −28, −14, and 0 d prepartum. Blood was sampled weekly from 14 d pre to 21 d postpartum. Polymorphonuclear leukocyte (PMNL) phagocytosis (PHAGO) and oxidative burst (OB) was determined by flow cytometry after an ex vivo challenge with *E. coli*. Furthermore, expression of CD18 and L-selectin were determined by flow cytometry and complete blood count was performed. Cows were examined daily for metritis daily until 14 d postpartum. Dichotomous data were analyzed by logistic regression using the PROC GLIMMIX and continuous data were analyzed by ANOVA using the PROC MIXED procedure. Body condition score ($P = 0.42$) and weight ($P = 0.85$) were not affected by treatment. Incidence of metritis tended ($P = 0.06$) to be different among treatments (CON = 14.3, 35% = 14.3, 50% = 4.4%). There was no effect of treatment on percentage of PMNL PHAGO+ ($P = 0.60$), OB+ ($P = 0.15$), and PHAGO+OB+ ($P = 0.60$). Treatment, however, tended to increase PHAGO intensity of PHAGO+ PMNL (CON = 3,159.3 ± 129.6 GMFI; 35% = 3,505.6 ± 136.6; 50% = 3,559.4 ± 134.5; $P = 0.07$) and affected OB intensity of OB+ PMNL (CON = 5,321.4 ± 489.1; 35% = 6,712.3 ± 515.6; 50% = 7,131.3 ± 507.8; $P = 0.03$). Similarly, among PHAGO+OB+ PMNL, treatment tended to affect PHAGO intensity (CON = 3119.4 ± 132.8; 35% = 3465.1 ± 140.0, 50% = 3536.8 ± 137.8, $P = 0.07$) and affected OB intensity (CON = 9991.7 ± 776.5, 35% = 12216 ± 819.3, 50% = 12581 ± 806.0; $P = 0.05$). Treatment did not affect percentage of PMNL CD18+ ($P = 0.34$) and L-selectin+ ($P = 0.26$) and intensity of CD18 ($P = 0.80$) and L-selectin ($P = 0.33$) expression. Treatment did not affect granulocyte:lymphocyte ratio ($P = 0.91$). Treatment of cows with rbST resulted in improved PMNL activity that led to reduced incidence of metritis.

Key Words: bovine somatotropin, prepartum cow

TH29 Immune status of dairy calves in the Northern Plains of Costa Rica: Year 2. J. A. Elizondo-Salazar*[1], D. Benavides-Varela[1], and A. J. Heinrichs[2], *[1]Estacion Experimental Alfredo Volio Mata, Facultad de Ciencias Agroalimentarias, Universidad de Costa Rica, San Rafael, Costa Rica. [2]The Pennsylvania State University, University Park.*

The objective of this study was to characterize for the second consecutive year the immune status of dairy calves in the Northern Plains of Costa Rica. The data correspond to total serum protein measurements (TSP) obtained during the period of August and November 2011 in 33 dairy farms. 671 female and 47 male calves were sampled. Dam breeds were classified into Holstein, Jersey, Holstein × Jersey crosses and other. For the purpose of this study, failure of passive immunity was considered when TSP concentration was less than 5.5 g/dL. TSP concentration ranged from 2.0 to 10.0, with an overall mean of 5.7 g/dL. Of all the animals evaluated, 43.7% had failure of passive transfer. When sex of the calves was considered, 44.1% of females and 38.3% of males failed to obtain adequate levels of immunity and concentration of TSP showed no significant differences (6.0 vs. 6.1 g/dL, respectively). Calves born to Holstein × Jersey crosses had significantly higher TSP concentrations than calves born to other breeds. When considering calving of the dam, offspring born to first-time heifers had TSP concentrations of 6.3 g/dL and showed the lowest percentage of animals with inadequate transfer of immunity. The findings of this study suggest that colostrum

management practices should be placed to minimize the risk of failure of passive transfer in dairy herds in the Northern Plains of Costa Rica.

Key Words: total serum protein, immunoglobulin, passive immunity

TH30 Effect of disease in one lactation on the incidence of disease in the subsequent lactation in dairy cows. A. Vieira-Neto*[2], C. A. Risco[1], J. E. Santos[1], and K. N. Galvão[1], *[1]University of Florida, Gainesville, [2]Universidade do Estado de Santa Catarina, Lages, SC, Brazil.*

Objective was to evaluate if having disease in one lactation (Lac1) would affect the risk of developing disease in the subsequent lactation (Lac2). Five hundred forty-four lactation pairs were created from 1088 lactations from 303 Holstein cows from a 500-cow herd from 2006 to 2012. Data on calving related problems (abortion, dystocia, stillbirth, twins, retained placenta), metabolic diseases [clinical hypocalcemia, ketosis, displaced abomasum (DA)], metritis, and mastitis were collected from the farm management software. Data was evaluated using chi-squared when no other variables could logically affect the outcome or using the LOGISTIC procedure of SAS when more than one variable could affect the outcome. Having calving related problems in Lac1 increased the likelihood of having it in Lac2 (29.3 vs. 20.7%; $P = 0.04$). Having clinical hypocalcemia in Lac1 increased the likelihood of having it in Lac2 (45.5 vs. 3.7%; $P < 0.001$). Having calving related problems in Lac2 also increased the likelihood of having clinical hypocalcemia in Lac2 (10.5 vs. 2.9%; $P < 0.001$). Having ketosis in Lac1 increased the likelihood of having ketosis in Lac2 (52.5 vs. 34.6; $P < 0.001$). Having calving related problems in Lac2 also increased the likelihood of having ketosis in Lac2 (46.8 vs. 36.2; $P = 0.04$). Having metritis in Lac1 increased the likelihood of having it in Lac2 (26.3 vs. 18.4%; $P = 0.02$). Other factors affecting the incidence of metritis in Lac2 were induced parturition (42.1 vs. 18.8%; $P = 0.005$), retained placenta (85.0 vs. 17.9%; $P < 0.001$), twins (76.9 vs. 19.0%; $P < 0.01$), stillbirth (46.2 vs. 19.1%; $P = 0.01$), clinical hypocalcemia (44.0 vs. 19.3%; $P = 0.01$), and ketosis (30.5 vs. 14.1%; $P < 0.001$). Having DA in Lac1 increased the likelihood of having it in Lac2 (23.5 vs. 3.8%; $P = 0.01$). Ketosis in Lac2 also increased the likelihood of having DA in Lac2 (11.0 vs. 0.3%; $P < 0.001$). Mastitis in Lac1 did not affect the likelihood of having it in Lac2. In conclusion, with the exception of mastitis, disease in Lac1 affected the incidence of disease in Lac2.

Key Words: disease incidence, disease recurrence, dairy cow

TH31 Cortisol, interleukin 8, and immunoglobulin G ratios predict treatment for bovine respiratory disease in feedlot cattle. S. E. Speidel[1], R. R. Cockrum*[1], J. L. Salak-Johnson[2], C. C. L. Chase[3], M. G. Thomas[1], K. G. Prayaga[6], R. K. Peel[1], R. L. Weaber[4], H. Van Campen[1], G. H. Loneragan[5], J. J. Wagner[1], and R. M. Enns[1], *[1]Colorado State University, Fort Collins, [2]University of Illinois, Urbana, [3]South Dakota State University, Brookings,, [4]Kansas State University, Manhattan, [5]Texas Tech University, Lubbock, [6]Zoetis, Kalamazoo, MI.*

Bovine respiratory disease (BRD) is one of the most harmful illnesses affecting the beef industry in North America. Factors such as antibodies, chemokines and glucocorticoids can be used to assess the immune status of individual animals. We hypothesized that these factors could be used as indicators of BRD in feedlot cattle. The objective of this study was to determine if these parameters were predictive of the incidence of BRD as determined by treatment of individual animals. Crossbred steers (n = 2869) group housed in a commercial feedlot in Southeastern Colorado were used in the evaluation. Jugular blood samples were collected upon receiving for immune response parameter analyses. Data included feedlot treatment records (TRT), cortisol, immunoglobulin G (IgG), immunoglobulin G1 (IgG1), immunoglobulin G2 (IgG2), IgG1 to IgG2 ratio (IgG1:IgG2), and interleukin 8 (IL8). Six fixed logistic regression models were used to determine relationships between immune response parameters and BRD treatment in R. Binomial observations were used for TRT (0 = no treatment and 1 = treatment for BRD). Predictor variables included the fixed effects of sire, receiving weight, a feedlot pen by ranch interaction, and each individual immune response parameter. Results indicated that unit increases in cortisol and IL8 increased the odds of being treated for BRD by 0.83% ($P = 0.079$) and 0.054% ($P = 0.039$), respectively. Alternately, a unit increase in IgG1:IgG2 decreased the odds of being treated for BRD 3.67% ($P = 0.038$). A weak trend was found with IgG2 showing an increased probability (0.79%, $P = 0.155$) of being treated for BRD. No relationships between treatment for BRD and IgG or IgG1 were detected. These results indicate a relationship exists between cortisol, IL8, IgG1:IgG2 and treatment for BRD.

Key Words: bovine respiratory disease, cattle, immunity

TH32 Citrus-derived oil (CDO) kills both *Staphylococcus aureus* and *Escherichia coli* in bovine MAC-T mammary epithelial cell lines in vitro. K. M. Moyes*, J. A. Almario, S. Salaheen, D. Hewes, and D. Biswas, *University of Maryland, College Park.*

Both *E. coli* and *S. aureus* are major mastitis-causing pathogens in dairy herds and are associated with reduced animal health and economic losses to farmers. Management strategies to prevent and control *E. coli* mastitis are lacking whereas cure rates using antibiotics for *S. aureus* mastitis vary considerably. However, antibiotic use is coming under increasing public scrutiny due to the possible development of resistant pathogens and risk of residues appearing in the milk. Therefore, new strategies to control or treat mastitis are warranted. Recent studies have shown that 0.1% and 0.2% CDO inhibited growth of both *S. aureus* and *E. coli* bacteria. Therefore, our objective was to determine the effect of CDO on the inhibition of *S. aureus* and *E. coli* in bovine MAC-T mammary epithelial cell lines in vitro as a potential new strategy to control bovine mastitis. MAC-T cells (n = 6 replicates/treatment) were seeded into cell culture plates and then inoculated with ~10^7 cfu/ml of either *E. coli* or *S. aureus*. After infection, cells were washed and treated with CDO (Control [0%], 0.025, 0.05, 0.1 or 0.2% CDO) for 1 h. MAC-T cells were subject to lysis after treatment and bacteria were enumerated. When compared with control, treatment with either 0.05% 0.1% and 0.2% CDO decreased association of *S. aureus* by 4 log whereas 0.025% CDO decreased association by 2 log in MAC-T cells. Results were similar for *E. coli* where treatment with 0.1% and 0.2% CDO decreased the number of cells associated *E. coli* by 4.5 log whereas 0.05%; and 0.025% decreased *E. coli* by 3 log and 1 log, respectively, compared with control. Our results clearly show that CDO kill mastitis-causing pathogens in bovine MAC-T mammary epithelial cell lines in vitro. The use of CDO may be a promising new therapeutic option for improving control and treatment of *E. coli* and *S. aureus* mastitis of dairy cows during lactation.

Key Words: citrus oil, MAC-T, mastitis

TH33 Evaluation of on-farm colostrum quality measurement tools. A. Bartier*, C. Windeyer, and L. Doepel, *University of Calgary, Calgary, AB, Canada.*

Newborn calves acquire immunity passively through consumption of colostral IgG. The colostrometer and Brix refractometer are both

available as on-farm tools to indirectly assess colostral IgG content. The objective of this study was to determine which of these tools is a more accurate predictor of colostral IgG content compared with that determined by RID. Fourteen commercial dairy farms in central Alberta, Canada, with herd sizes ranging from 60 to 300 lactating cows were used. 572 colostrum samples were collected by the producers between February and July, 2012. These samples were from the cows' first milking and represented the colostrum that was fed to the calves at their first feeding. Colostrum quality was measured with a colostrometer (specific gravity measurement) and a digital Brix refractometer (dissolved solids content). IgG content was determined using RID at a commercial laboratory. The minimum, maximum and mean ± SEM for the Brix refractometer, colostrometer, and RID were 6.8, 41.4, 25.5 ± 0.21° Brix; 0, 140, 82 ± 1.3 mg/mL; and 8.3, 128.6, 55.3 ± 1.1 mg/mL, respectively. Spearman correlation was used for the colostrometer data due to a non-normal distribution whereas Pearson correlation was used for the Brix refractometer. The colostrometer data were better correlated with RID results (r = 0.77, $P < 0.01$) than were the Brix refractometer data (r = 0.62, $P < 0.01$). The proportion of samples that each tool correctly identified as good quality (≥50 mg/mL IgG) or poor quality (<50 mg/mL) at different tool cut-off values were evaluated using chi-squared tables. Intervals of 10 mg/mL from 40 to 100 mg/mL for the colostrometer and 2° from 16 to 28° Brix were tested. The highest proportion of correctly identified good and poor quality samples occurred at 80 mg/mL for the colostrometer (84.1% sensitivity and 77.0% specificity, $P < 0.01$), and at 23° Brix (66.9% sensitivity and 82.4% specificity, $P < 0.01$). At these cut-offs the positive and negative predictive values were 60.6% and 92.0% for the colostrometer ($P < 0.01$), and 61.1% and 85.8% ($P < 0.01$) for the refractometer. This study indicates that both tools are adequate at indirectly determining colostrum IgG content.

Key Words: IgG, Brix, colostrometer

TH34 The Wnt/Frizzled pathway in bovine neutrophils. H. Ismael and M. Worku*, *North Carolina Agricultural and Technical State University, Greensboro.*

The Wnt proteins are secreted members of the wingless family of signaling molecules. These proteins bind to 2 receptors on the cell surface, single transmembrane low density lipoprotein receptor-related proteins 5 and 6 (LRP5/6) and 7 transmembrane Frizzled receptors. There is accumulating evidence that the Wnt/Frizzled pathway may play a distinct role in inflammation. Expression of these genes in bovine neutrophils may play a role in mastitis related losses. The objectives of this study were to determine expression of members of Wnt signaling pathway in bovine neutrophils for long-term definition of their role in mastitis. Blood was collected from 3 Holstein Friesian cows. Neutrophils were isolated by differential centrifugation and hypotonic lysis of red blood cells. RNA was isolated using Tri-reagent. RNA samples were reverse-transcribed and the cDNA was obtained using the Ambion-Retroscript as per the manufacturer's protocol. Specific primers for Wnt1, Frizzled, secreted frizzeled and LRP were used for PCR amplification. Amplified products were run on a 1% agarose gel with PCR markers. Gels were stained with ethidium bromide and visualized using a Gel documentation system. GAPDH was used as loading control and primers in the absence of DNA were used as negative controls. Genes encoding Wnt(100–800bp), Frizzled (600bp) and LRP (400bp) were expressed in neutrophils from 3 cows. A larger sample size would allow statistical evaluation and significance in combating mastitis causing pathogens.

Key Words: gene, neutrophil, wingless

TH35 Genome-wide association of white blood cell types during vaccination. R. J. Leach*, C. G. Chitko-McKown, G. L. Bennet, S. A. Jones, J. W. Keele, W. M. Snelling, R. M. Thallman, and L. A. Kuehn, *U.S. Meat Animal Research Center, Clay Center, NE.*

Infectious disease of livestock continues to be a cause of substantial economic loss and adverse welfare. Breeding for disease resistant livestock could improve both the economic burden and animal welfare. We aim to identify key genes and pathways that control variation in immune response; knowledge that may aid both breeders and vaccinologists. The herd used during this investigation (n = 3500) were the product of multiple-sire matings of crossbred cows to F1 bulls of varying half-blood composition. The resulting animals consisted of variable fractions of 9 breeds: Angus, Hereford, Red Angus, Brahman, Charolais, Gelbvieh, Limousin, Simmental, and MARCIII composite (1/4 Angus, 1/4 Hereford, 1/4 Red Poll, 1/4 Pinzgauer). Each animal was vaccinated for the 5 major viral causes of BRD: BRSV, PI3, BVDVI/II and IBR. Multiple immune related phenotypes (counts of: white blood cells, neutrophils, lymphocytes, monocytes, eosinophils and basophils) were measured pre and post booster vaccination (a delta measurement was also calculated [post-pre]). Every animal in the herd was also genotyped with 50K SNP, with founding sires genotyped with 770k SNP, allowing the imputation of every animal to density of 770k SNP. After a genome wide association study was conducted, regions associated with the immune responses were discovered. Twenty-two SNP in the current study were associated with levels pre, post and delta basophils and post eosinophils, at the genome wide significance level. These SNP were located on 11 separate chromosomes, at least in part, highlighting the complexity of eliciting an immune response. Further, each trait had at least one SNP associated with it at the chromosome wide significance level. In addition, the estimation of SNP effects in different breeds was possible due to the multi-breed composition of the herd. We conclude that key pivotal pathways may be shared in eliciting and maintaining an immune response to differing types of antigens. The USDA is an equal opportunity provider and employer.

Key Words: immune response, beef cattle, GWAS

TH36 Associations among vaginal-vulvar laceration, vaginal discharge early postpartum, and prevalence of uterine disease. A. Vieira-Neto*[2], F. S. Lima[1], J. E. Santos[1], R. D. Mingoti[3], G. S. Vasconcellos[3], C. A. Risco[1], and K. N. Galvão[1], *[1]University of Florida, Gainesville, [2]Universidade do Estado de Santa Catarina, Lages, SC, Brazil, [3]Universidade de São Paulo, São Paulo, SP, Brazil.*

Objective was to evaluate the associations among vaginal-vulvar laceration score (VLS), vaginal discharge score (VDS) early postpartum and prevalence of clinical endometritis (CE). Holstein cows (n = 1028) had VLS (0: no laceration; 1: laceration <2 cm at dorsal commissure or internal vaginal wall; 2: vaginal-vulvar laceration >2cm) evaluated at 4 DIM. Cows had VDS (1: clear; 2: flecks of pus; 3: <50% pus; 4: >50% pus; 5: watery, reddish/brownish foul smelling) evaluated at 4, 6 and 8 DIM. The highest score identified on d 4, 6 or 8 was the final classification for each cow. Metritis was diagnosed between 4 and 8 DIM when VDS = 5 and CE at 32 DIM when VDS ≥ 3. Data were analyzed using PROC LOGISTIC of SAS, and models were adjusted for the effects of parity, calving problems (dystocia, twin, stillbirth, retained placenta), and calf sex. Metritis incidence was increased ($P \leq 0.02$) in cows having VLS1 (43.3%) and VLS2 (63.0%) compared with VLS0 (35.2%). Metritis was also increased in cows having calving problems (78.9 vs. 45.7%; $P < 0.001$) and primiparous cows (59.0 vs. 47.8%; $P = 0.05$). Prevalence of CE was increased ($P \leq 0.04$) in cows with VDS3 (25.4%), VDS4 (34.7%), and VDS5 (61.1%), compared with VDS2 (9.3%). Only

one cow had VDS1, so it was combined with VDS2. Prevalence of CE was also increased in cows with calving problems (65.1 vs. 40.3%; $P < 0.001$). Based on the strong association between VLS and metritis and CE, and the association between VDS and CE, VLS and VDS can be considered risk factors for the development of uterine disease.

Key Words: vaginal-vulvar laceration, vaginal discharge, metritis

Ruminant Nutrition: Fats, Fatty Acids, Oils, and Glycerin Supplementation II

TH37 Comparison of direct transesterification and extraction procedures to analysis the fatty acid composition in the rumen contents. S. P. Alves*[1,2], A. R. J. Cabrita[3], A. J. M. Fonseca[4], J. A. M. Prates[1], and R. J. B. Bessa[1], *[1]CIISA, Faculdade de Medicina Veterinária, Lisbon, Portugal, [2]UIPA, Instituto Nacional de Investigacao Agrária e Veterinária, Santarem, Portugal, [3]REQUIMTE, Faculdade de Ciências, Universidade do Porto, Porto, Portugal, [4]REQUIMTE, ICBAS, Universidade do Porto, Porto, Portugal.*

The information about rumen fatty acid (FA) composition is essential to understand the effects of ruminant diets on the composition of meat and milk. The aim of this work was to compare the FA composition in rumen content using a transesterification procedure, which directly produces FA methyl esters (FAME) from intact sample, and a 2-step extraction procedure followed by transesterification. Freeze-dried rumen samples from lambs were used. In the direct transesterification method (DT), the FAME were prepared by the addition of sodium methoxide in methanol followed by HCl in methanol. In the extraction methods, 2 subsequent extractions were carry out, first with 3× dichloromethane:methanol (2:1) (DMM) followed by a second extraction of the residue with methanol:water:HCl (5:4:1) (MWH). Both extracts were transesterified and the FAME were analyzed by GLC. The DT method produced 41 ± 1.1 mg/g DM of FAME in rumen samples, whereas the DMM plus MWH produced 32 ± 0.7 mg/g DM. These lost FAME were found in the aqueous phase of the DM extraction, which was then re-extracted (RE) 2× to recover more 9.9 ± 0.2 mg/g DM of FAME. Thus, the combined fractions accounted 42 ± 0.9 mg/g DM of FAME, which showed to be similar ($P = 0.708$) to the FAME produced by the DT method. Despite the saving of time and solvents compared with the extraction methods, the DT does not give information about the FAME composition of the different fractions (DMM, MWH and RE). Indeed, the FAME composition of the MWH and RE showed that the dimethylacetals and OBCFA are almost absent in these fractions suggesting that the microbial lipids are almost completed extracted with DMM. In contrast, the highest proportion of the total C18 FA was observed in the RE fraction, mainly because of the highest proportions of the C18:1trans, suggesting that *trans* FA are more retained in the aqueous phases and less extractable. As conclusion, both DT and combined extraction methods generate similar final results, given the extraction methods more information, although to produce reliable results the extractions should be checked to ensure complete lipid extraction.

Key Words: rumen, fatty acid, lipid

TH38 Delayed feeding of fat enriched protein supplement alleviates postprandial suppression of in vitro rumen metabolism. Q. Baptiste*, E. Nestor, S. Chavez, S. Rastle-Simpson, K. D'Souza, A. Redhead, M. Knights, and E. Felton, *West Virginia University, Morgantown.*

The effects of time of feeding a fat enriched protein supplement on postprandial rumen metabolism were investigated with in vitro rumen fermenters. All fermenters were fed a basal diet of orchard grass hay in unequal portions throughout the day, with the largest meals being fed at 0600 and 1800 h. The supplement of soybean oil mixed with soybean meal was fed to fermenters at 10% of total daily dry matter. Control (C) fermenters did not receive any supplement at any time. Three supplementation times were tested. Supplement was fed to fermenters at 0600 h (AM), 1800 h (PM), or in evenly divided doses at both times (AP). Fermenter effluent samples were collected at eight 3-h intervals over a 24-h period and were analyzed to determine concentrations of ammonia nitrogen [NH_3-N] and total volatile fatty acid [TVFA]. Fermenter pH was measured at each collection time. A quadratic treatment × postprandial time interaction ($P < 0.01$) was observed for pH, [NH_3-N] and [TVFA]. Postprandial [TVFA] of AP fermenters tended to increase ($P = 0.08$) at 6 h, was elevated ($P = 0.04$) by 9 h and had a peak value at 21 h which did not differ ($P = 0.10$) from that of C fermenters at 21 h. Contrastingly, AM fermenters [TVFA] were similar ($P = 0.11$) to PM and ($P = 0.48$) C fermenters but lower ($P = 0.02$) than that of AP fermenters at 21 h postprandial. Similarly, AP treatment elevated ($P \leq 0.05$) postprandial [NH_3-N] at 6, 18 and 21 h. There was also a tendency for PM treatment to elevate postprandial [NH_3-N] at 6 h ($P = 0.09$) and [NH_3-N] was higher in AP and PM ($P \leq 0.01$) than in AM at 21 h. Postprandial [NH_3-N] profiles were similar ($P \geq 0.05$) in AM and C fermenters. Postprandial pH was flatlined in C and AM but fluctuated greatest with AP and PM treatments. In AP treatment, postprandial pH peaked at 6 h ($P = 0.02$) and was numerically lower than other treatment pH values between 3 and 24 h. Fermenter pH increased ($P < 0.03$) between 15 and 21 h with PM treatment. Therefore, delayed feeding (AP, PM) of a fat enriched protein supplement alleviates postprandial suppression of in vitro rumen metabolism.

Key Words: in vitro, rumen, metabolism

TH39 Estimation of energy content and short-chain fatty acid for microwave irradiated sorghum grain by in vitro gas production technique. F. P. Khajehdizaj*, A. Taghizadeh, B. B. Nobari, and H.Paya, *Dept of Animal Science, Faculty of Agriculture, University of Tabriz, Tabriz, Eastern Azarbaijan, Iran.*

There is an interest in the industrial application of microwaves to improve conventional drying processes, with the intent of taking advantage of its lower startup time, faster heating, greater energy efficiency, space savings, precise process control, selective heating and yielding final products with improved nutritive quality. Objective of this study was to elucidate the effect of different irradiation times of microwave on estimated nutritive values of sorghum grain. The DM of sorghum grain was evaluated and water was added to increase the moisture content up to 30%. Three samples were subjected to microwave irradiation (Butane microwave BC380W) at a power of 900w for 3, 5 and 7 min. Gas production was measured by Fedorak and Hrudy method. Rumen liquor samples were obtained from the 2 wethers that were fed on a diet comprising (DM basis), 55% forage and 45% commercial concentrate. Rumen fluid was collected after the morning feeding. ME, NEl and SCFA values were calculated from the amount of gas produced at 24 h of incubation with chemical composition of sorghum grain using equations of Menke and Steingass and Getachew. The ME, NEl and SCFA were affected ($P < 0.05$) by microwave treatment (Table 1). As can be seen microwave treatments increased ($P < 0.05$) ME and NEl of sorghum grain. But there was no significant difference between time periods of treatment. The higher ME, NEl and SCFA predicted from gas production in microwave treated sorghum, due to a high absolute gas production at 24 h of incubation can be resulted from changes in chemical composition of treated sorghum. Gelatinization led to chemical and physical changes in the starch granules and facilitated starch availability for microorganisms to ferment them.

Table 1. Gas production estimated characteristics of untreated and microwave-treated sorghum grain

		Microwave treated			
Parameter	Untreated	3 min	5 min	7 min	SEM
ME (MJ/kg DM)	7.15[b]	8.06[a]	8.38[a]	7.93[a]	0.215
NEl (MJ/kg DM)	4.08[b]	4.75[a]	4.98[a]	4.66[a]	0.157
SCFA (mM)	0.84[b]	0.96[a]	1.01[a]	0.95[a]	0.030

[a–d]Means within a row with different subscripts differ ($P < 0.05$).

Key Words: in vitro gas production, microwave irradiation, sorghum grain

TH40 Effects of microwave irradiation on in vitro gas production characteristics of wheat grain. F. P. Khajehdizaj*, A. Taghizadeh, and B. B. Nobari, *Dept. of Animal Science, Faculty of Agriculture, University of Tabriz, Tabriz, Eastern Azarbaijan, Iran.*

Microwave energy penetrates a food or feed material and produces a volumetrically distributed heat source, due to molecular friction resulting from dipolar rotation of polar solvents and from the conductive migration of dissolved ions. The purpose of this study was to evaluate effects of microwave irradiation on gas production estimated kinetic parameters of wheat grain using gas production technique. The DM of 1 g sample in duplicate was determined and water was added to increase the moisture content of 1 kg wheat grain to 300 g/kg. Three samples (100 g each) were subjected to microwave irradiation (Butane microwave BC380W) at a power of 900w for 3, 5 and 7 min. Gas production was measured by Fedorak and Hrudy method. Rate and extent of gas production was determined for each feed by fitting gas production data with the one component model: $Y = A(1 - e^{-ct})$, where Y is the volume of gas produced at time t (h), A the potential gas production (mL g^{-1} DM), and *c* the fractional rate of gas production (h^{-1}). Parameters A and c were estimated by an iterative least square method using a non-linear regression procedure of SAS. Microwave treatments for 5 and 7 min increased ($P < 0.05$) the A fraction and decreased ($P < 0.05$) the rate of gas production (*c*) of wheat grain (Table 1). Irradiated for long times of wheat grain had a rise in parameters. It seems that microwave irradiation improved gelatinization of starch and led to chemical and physical changes in the starch granule. Disruption of linkages between protein matrix and starch granule, hydrogen bonds and water absorption facilitated microbial or enzyme degradation of the starch granule.

Table 1. In vitro gas production characteristics of untreated and microwave treated wheat grain

		Microwave treated			
Parameter[1]	Untreated	3 min	5 min	7 min	SEM
A	303.1[b]	294.2[b]	325.4[a]	336.6[a]	4.380
c	0.121[a]	0.120[a]	0.091[b]	0.083[b]	0.00278

[a–d]Means within a column with different subscripts differ ($P < 0.05$).
[1]A = potential gas production (mL/g DM); c = fractional rate of gas production (h^{-1}).

Key Words: microwave irradiation, gas production, rumen

TH41 Effect of alkaline pretreatment on in vitro volatile fatty acid production of sorghum grain. F. P. Khajehdizaj*, A. Taghizadeh, and B. B. Nobari, *Dept of Animal Science, Faculty of Agriculture, University of Tabriz, Tabriz, Eastern Azarbaijan, Iran.*

Sorghum grain (milo) is an excellent model for studying volatile fatty acid production during fermentation because sorghum has a resistant protein matrix and corneous endosperm in which starch (a major ingredient) has been embedded. Three types of chemical processing were used to monitor effects of alkaline pre-treatment on sorghum grain. Wood from an Elaeagnusan gastifolial tree was made and prepared by dissolving 500 of wood ash in 10 L of distilled water in plastic buckets. The mixture was stirred for 5 min and was allowed to settle for 15 h. The resulting supernatant was carefully removed and filtered through cotton cloth. A 500 g whole sorghum grain was soaked in 1 L of wood ash extract for 12 h. For NaOH and NaHCO3 processing, sorghum grain was mixed with 20 g/L of each of their solution in the proportion of 1 L of solution to 1 kg of grain and settled for 12 h. Untreated and alkaline pre-treated samples (300 mg) were weighed into 50 mL serum vial. Each feed sample was incubated in triplicate with 20 mL of rumen liquor and McDougall buffer solution (1:2) for each time of incubation. There were no differences for VFA production between Untreated and alkaline pre-treated sorghum at 12h ($P > 0.05$). This study revealed significant increase in VFA production of sorghum grain at time 4h of incubation by NaOH pre-treatment. It seems that the exact mechanism by which alkali improves digestibility of sorghum grain is not known, part of the improvement probably results from solubilization of hemicellulose in the seed coat, which renders the starch portion of the kernel more available for microbial attack

Table 1. The effect of alkaline pre-treatment of sorghum grain on in vitro total volatile fatty acids (mmol/L)

		Alkaline pretreated			
Time	Untreated	Wood ash	NaOH	$NaHCO_3$	SEM
4 h	5.3[b]	8.0[b]	14.7[a]	6.0[b]	1.34
12 h	23.3	22.0	25.7	19.0	3.06
24 h	58.0[a]	49.3[ab]	48.0[ab]	40.0[b]	5.49
48 h	82.0[a]	61.6[b]	57.6[b]	73.3[c]	2.16

[a–c]Means within a rows without common letter differ ($P < 0.05$).

Key Words: chemical treatment, sorghum grain, volatile fatty acids

TH42 Effect of essential oils on rumen fermentation and methanogenesis by in vitro gas production technique. E. W. Jin[1,2], J. Q. Wang*[1], Y. H. Jiang[1], D. P. Bu[1], W. J. Shen[1], H. T. Shi[1], W. H. Bao[1], and F. D. Li[2], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Gansu Agricultural University, Lanzhou, China.*

The objective of this study was to evaluate the effect of essential oil on rumen fermentation and methanogenesis by in vitro gas production technique. Ruminal fluid was obtained approximately 2 h before feeding from 3 dairy cows in mid-lactation fed total mixed ration (C:F = 40:60). Diet substrates is consistent with the donor cow, and approximately 0.5 g substrates were incubated with 75 mL of a 1:2 McDougall's buffer-to-ruminal fluid mixture for 72 h at 39°C. A randomized factorial design was used and there were 5 replicates in each treatment. The treatments were: cinnamon oil at the dose level of 0, 100, 300, 500 and 1500 mg/L, tea tree oil and clove bud oil with concentrations of 0, 50, 100, 300 and 1000 mg/L, respectively. The experiment was repeated 3 times. In vitro rumen fermentation parameters and dynamic gas production parameters were evaluated. Dynamic gas production data were obtained using automatic recording system of the AGRS-III in vitro gas production (China Agricultural University, Beijing, China). Data were analyzed using the PROC MIXED Model of SAS. The concentrations of ammonia N were decreased ($P < 0.05$) with adding cinnamon oil at the dose level of 300 and 1500 mg/L. The addition of tea tree oil with a level of 1000 mg/L and cinnamon oil with a level of 1500 mg/L decreased ($P < 0.05$)

concentration of total volatile fatty acid and proportion of propionate. The addition of tea tree oil and clove bud oil at a level of 100 mg/L significantly ($P < 0.05$) increased in the theory maximum gas production. Compared with the control groups, the proportion of methane were decreased ($P < 0.05$) by 47.4, 40.2, 51.5, and 67.5% with adding tea tree oil and clove bud oil at the 1000 mg/L, and cinnamon oil at a level of 500 mg/L and 1500 mg/L individually. The extent of tea tree oil, cinnamon oil, and clove bud oil reducing methane and dose showed a positive linear correlation ($R^2 = 0.96$,0.77, and 0.99, respectively). It was concluded that the addition of tea tree oil at the level of 100 mg/L and cinnamon oil at the 100~300 mg/L may be beneficial to manipulate rumen microbial fermentation.

Key Words: essential oil, in vitro gas production

TH43 Effect of C18 unsaturated fatty acid and rumen temperature on rumen fermentation and methane emission. Y. H. Jiang[1,2], J. Q. Wang[1], D. P. Bu*[1], H. J. Yang[2], L. H. Baumgard[3], E. W. Jin[1], H. T. Shi[1], and W. H. Bao[1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]College of Animal Science and Technology, China Agricultural University, Beijing, China, [3]Department of Animal Science, Iowa State University, Ames.*

Study objective were to evaluate the effect of high ruminal temperature on biohydrogenation and methane production using a dual-flow continuous culture system. The design of the experiment was a 2 × 4 factorial arrangement with 3 replicated independent runs, and a fermenter in continuous culture was considered an experimental unit. Oleic acid (OL), linoleic acid (LA), and linolenic acid (LNA) were added to the diet (3% of DM basis) and incubated with a normal ruminal temperature (39°C, RT) or high ruminal temperature (41°C, HT). Each fermenter was incubated in 1000 ± 10 mL filter rumen fluid and artificial saliva was continuously delivered to yield a fractional dilution rate of 6.0%/h by injection pump. Each independent period consisted of 5 d of adaptation and 3 d of sample collections. The samples for VFA, NH_3-N, and methane were obtained from the fermenter during the last 3 d. Data were analyzed using the GLM procedure of SAS. Compared with RT incubation, propionate concentration was decreased under HT incubation under HT ($P < 0.01$), but increased HT tended to increase concentration of isobutyrate ($P < 0.01$), butyrate ($P < 0.01$). The rumen fermentation would be changed in high ruminal temperature according to the value of ratio of non-glucogenic to glucogenic acids (NGR) ($P < 0.01$). The concentration of acetate and propionate were also lower in the OL compared with LA, LNA, and control ($P < 0.01$), the OL under HT increased the acetate: propionate (HT vs. RT, 2.68 vs. 2.40; $P < 0.01$) and the NGR ($P < 0.01$). The production of methane was not affected by the unsaturated fatty acid, but high ruminal temperature tended to decrease the production of methane ($P > 0.05$). The data suggests that rumen fermentation changes during heat stress.

Key Words: biohydrogenation, high ruminal temperature, rumen simulation system

TH44 Screening and characterization of *trans*-11 18:1 hydrogenating bacteria from rumen of dairy cows. Y. F. Lu[1,2], D. P. Bu*[1], S. G. Zhao[1], D. Jin[1], G. Q. Zhao[2], X. L. Hu[1], and J. W. Zhao[1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Sciences, Beijing, China, [2]College of Animal Science and Technology, Yangzhou University, Yangzhou, China.*

Trans-vaccenic acid (*trans*-11 C18:1, t-VA) serves as a precursor for the synthesis of unsaturated fatty acid and conjugated linoleic acid in the rumen. The purpose of this study was to isolate and identify t-VA hydrogenating bacteria in vitro and further to analyze their biochemical characteristics and phylogenetic position. The ruminal samples were collected from Holstein cows and inoculated into Hungate tubes in 3 triplicates with basal medium containing t-VA (50 μg mL^{-1}) under anaerobe chamber. 87 clones were picked by numerous transfers of spread plate cultivation ($n \geq 5$) at 39°C for 12h after enrichment incubation. Samples were collected at 0 and 12 h of clones' reenrichment. Fatty acids profiles were detected by gas chromatograph. The biochemical characterization of the isolated strain RV the highest t-VA hydrogenation bacteria was analyzed by VITEK 2 compact system. Data were analyzed using SAS. The 16S rDNA and functional genes, sodA, rpoB and recN, were sequenced and used for phylogenic tree building using neighbor joining method. The isolated bacterium was named RV. It was strictly anaerobic, gram-positive, globose or oval shaped, and had optimum growth at 39°Cand pH 6.0–7.8. The carbon or energy sources of RV can be from D-xylose, D-maltose, D-cellobiose, D-ribose, pullulan. It contained some enzyme activities (e.g., α-galactosidase, aginine dihydrolase1, α-glucosidase and arylamidase) and resistant phylotpye to bacitracin, novobiocin, polymixin B. RV significantly reduced T11C18:1 at 12 h of incubation ($P < 0.01$). The t-VA hydrogenating efficiency of RV is 82.1%. The 16S rDNA of RV had high identity to *Streptococcus equinus* and *Streptococcus bovis* (99–100%). However, observed from the phylogenetic tree of functional genes, the RV had the highest homology to *S. bovis*. One t-VA hydrogenating bacterium named RV which is a strain from *S. bovis* was isolated from bovine rumen. To our knowledge, this is the first study showing that *S. bovis* has t-VA hydrogenating activity and this study would provide a strain for the research of biohydrogenation mechanisms in the future.

Key Words: biohydrogenating bacteria, *Streptococcus bovis*, *trans*-vaccenic acid

TH45 Effects of rumen-protected γ-aminobutyric acid on performance and health status in heat-stressed dairy cows. J. B. Cheng[1,2], D. P. Bu[1], J. Q. Wang*[1], X. Z. Sun[1,2], L. Pan[1], and W. Liu[1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]College of Animal Science and Technology, Anhui Agricultural University, Hefei, China.*

This experiment was conducted to investigate the effects of rumen-protected γ-aminobutyric acid (GABA) on lactational performance and health status in heat-stressed dairy cows. Sixty Holstein dairy cows (141 ± 15 DIM, 35.9 ± 4.3 kg of milk/d) were randomly assigned to 1 of 4 treatments in a completely randomized design (n = 15). Treatments consisted of 0 (control), 40, 80, or 120 mg GABA/kg DM from rumen protected GABA. The experimental period lasted 70 d. The average temperature-humidity index (THI) at 0700, 1400 and 2200h was 78.4, 80.2 and 78.7, respectively. Compared with control cows, cows fed 40 or 80 mg/kg GABA had decreased ($P < 0.05$) rectal temperatures at 0700, 1400 and 2200h, but 120 mg/kg GABA had no effect ($P > 0.05$) on rectal temperature. Cows supplemented with GABA had no effect ($P > 0.05$) on respiration rates at any time point. Cows fed 40 mg/kg GABA had increased dry matter intake (DMI) (22.71 vs. 21.13 kg/d; $P < 0.05$), milk yield (33.23 vs. 31.15 kg/d; $P < 0.05$), energy-corrected milk (ECM) (32.76 vs. 29.84 kg/d; $P < 0.01$) and 4% fat corrected milk (FCM) (30.38 vs. 27.89 kg/d; $P < 0.05$) compared with control cows. DMI (22.16 vs. 21.13 kg/d), Milk yield (31.97 vs. 31.15 kg/d), ECM (31.32 vs. 29.84 kg/d) and FCM (29.27 vs. 27.89 kg/d) tended ($P <$

0.10) to be higher for cows fed 80 mg/kg GABA compared with controls, but milk yield and ECM were not affected ($P > 0.05$) in cows fed 120 mg/kg GABA. Dietary treatment had no effect ($P > 0.05$) on milk fat content, milk SCC and feed efficiency, but milk fat yield (1.14 and 1.10 vs. 1.03 kg/d; $P < 0.01$) was increased in cows fed 40 or 80 mg/kg GABA than those in controls. Milk protein content (3.01%) and yield (0.99 kg/d) were increased ($P < 0.01$) for cows fed 40 mg/kg GABA than for other treatments. Milk lactose and total solid content, and milk urea nitrogen were increased ($P < 0.05$) by GABA supplementation. In conclusion, rumen-protected GABA supplementation could alleviate heat stress, increase feed intake, improve milk performance, and the optimal supplemental GABA level for heat-stressed dairy cows would be 40 mg/kg DM.

Key Words: γ-aminobutyric acid, milk performance, heat stress

TH46 Effects of rumen-protected γ-aminobutyric acid on rumen fermentation of dairy cows under heat stress. J. B. Cheng[1,2], J. Q. Wang*[1], D. P. Bu[1], X. Z. Sun[1,2], L. Pan[1], and W. Liu[1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]College of Animal Science and Technology, Anhui Agricultural University, Hefei, China.*

γ-Aminobutyric acid (GABA) is an inhibitory neurotransmitter in the central nervous system, and has some physiological functions. The objective of this study was to determine the effects of rumen-protected GABA on rumen fermentation in heat-stressed dairy cows. Sixty Holstein dairy cows (141 ± 15 DIM, 35.9 ± 4.3 kg of milk/d) were randomly assigned to 1 of 4 treatments (n = 15 cows/group). Treatments were (1) control (no supplemental GABA), (2) 40mg GABA/kg DM from rumen protected GABA, (3) 80mg GABA/kg DM, and (4) 120mg GABA/kg DM. Cows were exposed to heat stress in the experimental period, during which time average temperature-humidity index (THI) at 0700, 1400 and 2200 h was 78.4, 80.2 and 78.7, respectively. The experimental period consisted of 2 wk for adaptation to the diet and 8 wk for sampling. Ruminal fluid samples were collected at 2 h after the morning feeding on d 70 of experimental period. Fecal samples were collected from the rectum or the ground, when fresh, at the end of experimental period: at 0900, 1500, and 2100 h (d 67), and at 0300, 0600, 1200, 1800 h (d 68), and at 0000 h (d 69). Compared with control, cows supplemented with GABA had higher concentrations of ammonia nitrogen (6.46, 7.13 and 7.64 vs. 4.94 mmol/L; $P < 0.01$), total volatile fatty acid (112.20, 112.61 and 115.25 vs. 100.96 mmol/L; $P < 0.05$), acetate (76.36, 74.67 and 78.41 vs. 68.45 mmol/L; $P < 0.01$), propionate (21.14, 21.80 and 21.73 vs. 18.83 mmol/L; $P < 0.01$), and microbial protein (0.49, 0.54 and 0.54 vs. 0.34 mg/mL; $P < 0.01$), but ruminal pH, concentrations of butyrate and valerate, ratio of acetate to propionate, enzyme activities of carboxymethylcellulase and xylanase were not different ($P > 0.05$) among treatments. Concentrations of iso-butyrate (0.99 and 0.91 vs. 0.76 mmol/L; $P < 0.01$) and iso-valerate (1.65 and 1.51 vs. 1.14 mmol/L; $P < 0.05$) in ruminal fluid were increased by 80 or 120 mg/kg GABA supplementation compared with control. These results indicate that rumen-protected GABA supplementation improved rumen fermentation in heat-stressed dairy cows.

Key Words: γ-aminobutyric acid, rumen fermentation, heat stress

TH47 Rumen biohydrogenation of polyunsaturated fatty acids differs between herb species. M. B. Petersen*[1] and S. K. Jensen[2], *[1]AgroTech, Institute for Agri Technology and Food innovation, Aarhus, Denmark, [2]Aarhus University, Department of Animal Science, Tjele, Denmark.*

Feeding species-rich herbage to dairy cows has been shown to alter ruminal biohydrogenation (BH) of polyunsaturated fatty acids (PUFA) and to lead to a higher content of beneficial PUFAs in milk, but little is known on how single plant species affect BH. In this study BH of PUFAs from 5 different plant species: chicory (*Cihorium intybus*), English plantain (*Plantago lanceolata*), salad burnet (*Poterium sangusisorba*), birds foot trefoil (*Lotus corniculatus*), alfalfa (*Meticago sativa*), and a clover grass mixture [on DM basis: 21% white clover (*Trifolium repens*) and 78% perennial ryegrass (*Lolium perenne*)] was investigated. The samples were incubated in 3 replicas in ruminal fluid from cows fed 3 different diets; a TMR based on corn- and grass silage, herbs silage composed of 10 herbs species and a ryegrass silage. Each feeding period lasted 21 d with collection of fluid at d 21. Twenty-two milliliters of strained rumen fluid, 22 mL buffer, and 1 g freeze-dried plant material were transferred to tubes, and incubated for 0, 2, 4, 6, 12, 24, and 30 h. Though BH occurred faster when samples were incubated in TMR rumen fluid, the overall BH pattern for PUFA was not dependent on the cows' diet. Differences in BH of the main PUFAs, C18:3n-3 (ALA) and C18:2n-6 (LA), was observed between single species. The lowest BH rate for both ALA and LA after 30 hours incubation was seen in salad burnet (51 and 37 percent ($P < 0.05$) for ALA and LA, respectively). Highest BH of ALA after 30 hours incubation was seen in birds foot trefoil (82 and 57%, $P < 0.05$) for ALA and LA, respectively). The highest content of c9,t11 C18:2 after 30 hours was observed for birds foot trefoil (0.007 g/ kg DM, $P < 0.05$) whereas no differences in content of C18:1t11 between species was seen. These results indicate that ALA and LA from salad burnet inhibit BH. The effect of herb silage on milk fat composition is currently studied in large scale on organic farms.

Key Words: biohydrogenation, fatty acid, herb

TH48 Microbiological and fermentative indicators in response to the inclusion of yeast *Candida norvegensis* on in vitro and in vivo experiments. O. Enriquez*[1], N. Madera[1], O. Ruiz[1], Y. Marrero[2,1], C. Arzola[1], C. Rodriguez[1], and A. Corral[1], *[1]Universidad Autonoma de Chihuahua, Chihuahua, Mexico, [2]Instituto de Ciencia Animal, La Habana, Cuba.*

Two experiments were made to compare the effect of yeast *Candida norvegensis* on utilization of fibrous feeds. The objective of these 2 studies were to evaluate, in vitro and in vivo, the response to the inclusion of doses of *Candida norvegensis* of corn stover. In the in vitro experiment 3 treatments were tested: 0 (0%), 30 (1.5%) and 60mL (3%) within 4 measuring times: 0, 24, 48 and 72h. On the other hand, the in vivo experiment was made with repeated measures over time evaluating the effect of 2 treatments of yeast: 0mL (0%) and 750 mL animal^{-1} day^{-1} (3.75%), at 0 4 8 and 12h; in both experiments a completely randomized design was used. Differences exist for measuring time, except pH showed no variation. A reduced production of ammonia nitrogen was presented at 0h ($P \leq 0.01$) with 0.42 mL mmol^{-1}; also showed a decrease in NDF on dry matter and ADF of dry matter while the time passed ($P \leq 0.01$). However, true digestibility of dry matter and NDF digestibility increased in the in vitro experiment ($P \leq 0.01$). In the in vivo experiment, a bigger population of total and cellulolytic bacteria were found with (6.22 and 8.10 cfu mL^{-1} log 10, respectively) in response to yeast doses, also higher pH and lower ammonia nitrogen values (6.95 and 0.51 mM ml^{-1} respectively). For measurement times, differences were found ($P \leq 0.05$) in total bacteria count, pH and ammonia nitrogen, showing the highest values of total bacteria at 0h, the highest pH value and the lowest of ammonia nitrogen at 12h. In conclusion there was no effect of yeast on the measuring parameters of the in vitro study, however the inclusion of 750 mL animal^{-1} day^{-1} of yeast in vivo, increases the

microorganisms population and reduces the ruminal concentration of ammonia nitrogen in sheep; so it can say that *Candida norvegensis* can be considered as an alternative additive for improving the use of fibrous feeds on ruminant feeding.

Key Words: additive, ruminant, yeast

TH49 Effects of purified n-6 and n-3 fatty acid on rumen fermentation indices and greenhouse gas emission in relation to bio-hydrogenation. S. M. Amanullah[1], S. C. Kim*[1], D. H. Kim[2], H. J. Lee[2], Y. J. Jae[2], Y. H. Joo[2], E. T. Kim[2], S. S. Lee[2], and I. H. Choi[3], *[1]Department of Animal Science (Inst. Agric. & Life Sci.), Gyeongsang National University, Jinju, South Korea, [2]Division of Applied Life Science, Gyeongsang National University, Jinju, South Korea, [3]Department of Companion Animal & Animal Resource Sciences, Joongbu University, Geumsan, South Korea.*

An in vitro experiment was conducted to estimate the effect of n-6 and n-3 fatty acid on rumen fermentation indices, fatty acid profile and greenhouse gas (GHG) emission. The treatments contained either pure C18:2n-6 (T1), C18:3n-3 (T2) or mixture of these fatty acids at 1:1 ratio (T3). Rumen fluid was collected from 2 cannulated Hanwoo steers fed rice straw and concentrate mixture in 2:8 ratio. Incubation was performed in 50 mL glass serum bottles containing 2 mg of fatty acid, 15 mL of incubation medium (rumen fluid + Van Soest medium = 1:2) and 150 mg of synthetic diet (411 g cellulose, 411 g starch, and 178 g casein/kg DM) at 37°C for 0, 1, 2, 4 and 8 h with 5 replications and 3 blanks. It was observed that the rate of bio-hydrogenation of n-6 and n-3 fatty acid (FA) is comparatively lower in T3 than others, characterized by higher C18:2n-6 and/or C18:3n-3 ($P < 0.0001$), PUFA ($P = 0.002$) and PUFA/SFA ratio ($P = 0.002$), but lower C18:0 ($P = 0.002$) and SFA contents ($P = 0.006$). The pH was not affected by the treatments in any incubation periods ($P > 0.05$). The concentrations of ammonia-N ($P = 0.002$), total VFA ($P = 0.039$) and iso-butyrate ($P < 0.001$) were higher in T1 than in the other treatments after 8 h of incubation. Methane production observed significantly lower ($P = 0.033$) in T2 than other treatments at 4 h of incubation. Concomitantly, propionate concentration also increased numerically in T2 at that period. Total gas volume and carbon dioxide content remained unaffected throughout the periods ($P > 0.05$). The results suggested that the mixture of pure n-6 and n-3 fatty acid is more effective to resist bio-hydrogenation partially to improve n-6 or n-3 fatty acid concentration in rumen rather than solely.

Key Words: fatty acid biohydrogenation, greenhouse gas, rumen fermentation

TH51 Effects of different forage profiles diets on key genes expression of fatty acid synthesis in the mammary gland of lactating dairy goats. H. Zhang, C. J. Ao*, L. W. Song, E. Khas, and X. F. Zhang, *Department of Animal Science of Inner Mongolia Agricultural University, Huhhot, Inner Mongolia, China.*

The objective was to investigate the effects of 2 forage profiles diets on the key gene expression of enzymes related to fatty acid synthesis in the mammary gland of goats. Analysis of mRNA expression for stearoyl coA desaturase (SCD), acetyl-coenzyme A carboxylase- α (ACACA), fatty acid synthesis (FASN) and lipoprotein lipase (LPL) were performed. Eight multiparous lactating goats (BW = 45.6 ± 2.5 kg, DIM = 90 ± 12 d) were assigned to 2 treatments in a crossover design. Animals were fed diets with different forage profiles, the concentrate-roughage ratio in the treatments were 40:60. Treatments were (1) hay (30%), corn straw (30%) with additional 40% of concentrate (HCS; CP: 14.2%, NDF: 39.7% and ME: 2.39Mcal/kg); (2) hay (30%), corn silage (20%) and alfalfa (10%) with additional 40% of concentrate (HCA; CP: 10.6%, NDF: 50.4% and ME: 2.24Mcal/kg), on DM base. Mammary gland biopsies were performed after milking on the last day of each period. The mammary tissue biopsy (50 mg/animal) was immediately frozen in liquid nitrogen and stored at −80°C until RNA isolation. Samples of total RNA were reverse transcribed to cDNA to determine the expression of key genes for fatty acid synthesis by the method of RT-PCR. Statistical analysis was performed using a paired *t*-test on the difference between treatments. Mammary mRNA abundance of SCD, which is involved in fatty acid desaturation, in animals fed HCA was increased by 50% ($P > 0.05$), ACACA and FASN, which are involved in de novo fatty acid synthesis were increased by 18 and 20%, respectively ($P > 0.05$) and LPL, which is involved in fatty acid uptake, was increased by 39% ($P > 0.05$) when compared with HCS. The data demonstrated that diet with high quality roughage (HCA) can increase the gene expression of enzymes that are related to milk fat synthesis in the mammary gland of dairy goats.

Key Words: dairy goat, fatty acid synthesis, mammary gland

TH52 Roughage quality affects mammary gland uptake of major milk fat precursors in lactating dairy cows. L. W. Song, C. J. Ao*, E. Khas, and H. Zhang, *Department of Animal Science, Inner Mongolia Agricultural University, Huhhot, Inner Mongolia, China.*

The objectives of this study were to determine the effects of roughage quality on fatty ACID metabolism in mammary gland and their transfer into milk fat in lactating dairy cows. Nine multiparous Holstein cows (BW = 617 ± 21; DIM = 120 ± 20) were used in a replicated 3 × 3 Latin square design with 21 d of diet adaptation and 7 d of data collection. Blood was collected from external pudendal artery and subskin abdominal vein. Treatments (DM basis) were (1) 40% corn straw plus 60% commercial concentrate supplement A (CSA; CP: 16.55%, NDF: 37.06%, NEL: 1.50 Mcal/kg); (2) 40% corn straw plus 60% commercial concentrate B (CSB; CP: 15.57%, NDF: 41.84%, NEL: 1.46 Mcal/kg); (3) 3.7% hay, 26.7% corn silage, 28.4% alfalfa plus 41.2% concentrate (Mixed Forage as MF; CP: 15.50%, NDF: 41.39%, NEL: 1.44 Mcal/kg). Fatty acids were analyzed by gas chromatography and data were analyzed by the PROC MIXED procedure of SAS 9.0. Results showed that DMI were lower for animals in MF group (13.69 kg/d) when compared with those in CSA and CSB groups (15.66 and 15.24 Kg/d, $P = 0.004$). No differences in milk yield and composition were observed among treatments, the MF group significantly increased the dairy efficiency (1.43) compared with the CSA (1.26) and CSB (1.26, $P = 0.05$) groups. The concentrations of most LCFAs (C16 to C18) and total FA in plasma of both artery and vein from animals in the MF group were higher than CSA and CSB groups. Particularly, plasma concentration of linolenic acid (C18:3n3) was significantly higher ($P < 0.0001$) in the MF group compared with CSA and CSB groups, and the plasma FA profiles were reflected in milk. Animals in the MF group had the highest milk concentration of linolenic acid (0.38g/100g vs. 0.26 and 0.20g/100g, $P = 0.04$). The MF group tended to increase the mammary extraction rate of total LCFAs than CSA and CSB ($P = 0.17$); however, no significant difference was found on the uptake ratio of mammary gland between treatments. We inferred that the different roughages sources could not change the FA extraction rate in mammary gland, and high quality roughages tended to adjust the milk fat composition to be better for human health.

Key Words: dairy cows, fatty acid, mammary uptake

TH53 Effect on fatty acids metabolism in mammary gland by two different diets of lactating dairy goats. L. W. Song, C. J. Ao*, E. Khas, H. Zhang, and S. W. Liu, *Department of Animal Science, Inner Mongolia Agricultural University, Huhhot, Inner Mongolia, China.*

Our objective was to determine the effects of different diets on the changes of the milk fat percentage, milk fat yields and the fatty acids metabolism in mammary gland. Eight multiparous Lactating goats(BW = 45.56 ± 2.5 kg, DIM = 90 ± 12 d) fitted with blood vessel intubation in external pudendal artery (EPA) and subskin abdominal vein (SAV) were administered 2 treatments in a crossover design. The diets used same concentrate but different roughage, Concentrate-roughage ratio was 40:60. Treatments were (1) hay (30%), corn silage (20%) and alfalfa (10%) as roughage on dry matter basis (HCA; 10.57% CP, 50.37% NDF and ME 2.24 Mcal/kg); (2) hay (30%), corn straw (30%) (HCS; 14.25% CP, 39.69% NDF and ME 2.39 Mcal/kg). Each period lasted 3 wk. At the last 3 d of each period, we collected the blood of EPA and SAV via the blood vessel intubation for FA detection. All data were analyzed by the PROC MIXED procedure of SAS9.0. The milk fat percentage of HCA group (3.04%) was significantly higher ($P = 0.01$) than HCS group (2.84%). But the differences of milk fat yields between 2 treatments (15.28 vs. 14.51g/d) were not significant ($P = 0.22$). HCA treatment increased the percentage of long-chain FA (>16C) that can be absorbed by mammary gland compared with HCS (35.03 vs. 33.03%, $P = 0.16$), the concentration of FA composition in the blood of EPA and SAV and in the milk were not significantly different, but the total percentage of SFA by HCA was lower than HCS (71.71% vs. 73.41, $P = 0.15$), UFA by HCA was higher than HCS (28.29 vs. 26.59%, $P = 0.15$). HCA tended to increase the concentration of total FA of EPA plasma than HCS (0.73 vs. 0.57, $P = 0.32$), significantly different in SAV plasma (0.62 vs. 0.44, $P = 0.02$), especially the concentration of C18:0 and C18:2c6 (0.1 vs. 0.08, $P = 0.12$; 0.12 vs. 0.09, $P = 0.11$, respectively). HCA treatment contrast to HCS, the milk fat percentage increased probably because of the increase in total exogenetic FA in milk fat flow through EPA and SAV of mammary gland.

Key Words: dairy goat, fatty acid composition, milk fat percentage

TH54 Study of effects of conjugated linoleic acid (CLA) on feed intake, milk yield and composition, and milk fatty acid profile of Holstein dairy cows in early lactation. A. Mahdavi*, K. Rezayazdi, A. Z. Shahneh, and M. Dehghan-Banadaky, *Department of Animal Science, College of Agriculture and Natural Resources, University of Tehran, Karaj, Tehran, Iran.*

The aim of this experiment was to determine the effects of conjugated linoleic acid (CLA) supplement on feed intake, milk yield and composition, and milk fatty acid profile of Holstein cows in early lactation. Fifteen multiparous lactating Holstein cows (20 ± 3 DIM; mean ± SD) were blocked by milk production, and assigned in a completely randomized block design for 2 wk of adaptation followed by 5 wk of supplementation. Treatments were (1) control (115 g/d Ca salts of palm fatty acids), (2) rumen-protected CLA (120 g/d of lipid-encapsulated CLA), and (3) rumen-unprotected CLA (40g/d rumen unprotected CLA that replacing and balancing by Ca salts of palm fatty acids). Each dose provided 96 g/d fatty acids. Both of CLA supplements provided 12 g/d of *trans*-10, *cis*-12 CLA. Individual milk yield and DMI were recorded daily and milk composition was determined weekly. Data were analyzed by MIXED procedure of SAS. DMI was not affected by CLA supplements. There was a significant increase in milk yield in rumen-protected CLA compared with other treatments ($P < 0.01$), which were 44.6, 42.0, and 41.7 kg/d for rumen-protected CLA, rumen-unprotected CLA and control, respectively. The rumen protected CLA reduced milk fat content compared with other treatments ($P < 0.01$), which were 2.76, 3.29, and 3.36% for rumen-protected CLA, rumen-unprotected CLA and control, respectively. In contrast, there were no significant differences in content of milk protein and lactose between treatments. The proportion of short- and medium-chain fatty acids decreased in rumen-protected CLA compared with other treatments whereas the proportion of long-chain fatty acids increased in rumen-protected CLA. There was a significant increase in milk fat content of *trans*-10, *cis*-12 in rumen-protected CLA compared with control ($P < 0.01$). The Δ^9-desaturase index was not affected by CLA supplements. The results of this experiment indicated that rumen-protected CLA could increase milk yield, decrease milk fat content, and alter milk fatty acid profile of Holstein dairy cows in early lactation.

Key Words: conjugated linoleic acid, Holstein cow, milk fat

TH55 High levels of crude glycerin in the diets of lambs finished in feedlot: ruminal fermentation. V. B. Carvalho*, J. M. B. Ezequiel, V. R. Fávaro, R. F. Leite, E. M. de Oliveira, É. H. Fernandes, L. F. Cremasco, J. R. Paschoaloto, M. T. C. Almeida, and B. H. F. Araújo, *FCAV, São Paulo State University - UNESP, Jaboticabal, São Paulo, Brazil.*

In most studies crude glycerin (CG) has been evaluated as a partial replacement of corn in the diet. This trial aimed to evaluate the effects of inclusion of high levels of CG (83% glycerol) in diets of feedlot lambs, replacing the corn until the whole, in ruminal fermentation: rumen pH and rumen ammonia concentration. Five rumen-cannulated Santa Inês lambs were used in a 5 × 5 Latin square design and were housed in individual pens. Diets were isonitrogenous and concentrate:forage ratio of 82:18 and were fed to the animals twice per day amounting 0.880 kg of DM (restricted intake). Five experimental diets were consisted of Tifton hay, corn, crude glycerin, corn gluten meal, corn oil, urea, sunflower meal, soybean hulls and mineral salt. Treatments were used: Without inclusion of CG, including 7.5% of CG, 15% of inclusion CG, 22.5% of CG inclusion and 30% CG inclusion of dry matter. To determine pH and ammonia concentration, rumen fluid samples were taken through the rumen cannula at the time of feeding (0) and, 1, 2, 4, 6 and 8 h after feeding. Statistical analysis was performed using the MIXED procedure of SAS and data were compared using orthogonal contrasts (linear and quadratic). The time of harvest was included as a repeated measure. The rumen pH and ammonia concentrations were not influenced by treatments ($P = 0.6881$) and ($P = 0.2819$), respectively. The mean values of pH and ammonia concentration were respectively 6.21 and 28.38 mg/dL. These data suggest that the use of crude glycerin in high levels not affect the rumen pH and ammonia concentration.

Key Words: ammonia, glycerol, pH

TH56 Lactation performance of dairy cows grazing a tropical pasture supplemented with sources of rumen protected fat. J. De Souza*[1], F. Batistel[1], K. C. Welter[2], M. M. V. Silva[1], C. Sitta[1], M. G. M. F. Santos[1], L. J. Chagas[1], D. F. A. Costa[1], and F. A. P. Santos[1], *[1]University of Sao Paulo, Piracicaba, SP, Brazil, [2]University of Sao Paulo, Pirassununga, SP, Brazil.*

The objective of this experiment was to investigate the effects of supplementation of early lactation dairy cows grazing a tropical pasture with diets containing calcium salts of palm oil (CSPO) or calcium salts of soybean oil (CSSO) on milk production and composition. Twenty-seven cows (15 ± 3 DIM) were used in a randomized block design and subjected to the following treatments: (a) control (no fat); (b) 400 g

CSSO cow^{-1} d^{-1}; (c) 400 g CSPO cow^{-1} d^{-1}. Treatment periods were 90 d in length followed by cows staying in the same diet to evaluated residual effect until the end of lactation period (280 DIM). Cows grazed paddocks of *Pennisetum purpureum* and received 8 kg cow^{-1} d^{-1} (DM) of concentrate twice daily. Milk yield was measured every 2 d and milk composition was analyzed every 6 d. Data were analyzed as repeated measures using a mixed model with block as random effect. The means were compared by Tukey test at 5%. Both sources of fat increased milk yield during the supplementation period (24.2; 26.8 and 29.0 kg d^{-1} for control, CSSO and CSPO, respectively). Milk yield was higher for CSPO than for CSSO. CSPO did not affect milk fat content in comparison with control (3.3 vs. 3.5% for CSPO and control, respectively), while CSSO reduced milk fat content (2.8%). Both fat sources decreased milk protein content (3.3; 3.1 and 3.1% for control, CSSO and CSPO, respectively), but did not affect lactose content (4.6; 4.5 and 4.6% for control CSSO and CSPO, respectively). Cows receiving CSSO lost less body weight (−5.4 vs. −18.3 kg $^{-1}$) and BCS (2.85 vs. 2.65) than cows receiving CSPO. After the supplementation period milk yield remained higher for CSPO in comparison to control and CSSO (21.0 vs. 18.4 and 19.3 kg d^{-1}, respectively). Milk composition was not affected after the supplementation period. CSPO increased total milk yield during lactation compared with control (7300 vs. 6100 kg $^{-1}$) and CSSO (7300 vs. 6600 kg $^{-1}$) treatments. Grazing dairy cows in early lactation supplemented with fat had a pronounced positive effect on performance throughout the whole lactation.

Key Words: palm oil, soybean oil, tropical pasture

TH57 Concentrate levels and supplemental fat for grazing mid-lactating dairy cows on milk fatty acids profile. F. L. Macedo, J. De Souza*, F. Batistel, W. F. Angolini, S. F. Angolini, and F. A. P. Santos, *University of Sao Paulo, Piracicaba, SP, Brazil.*

The objective of this experiment was to evaluate the interactions between the association of concentrate levels and fat supplementation on fatty acid profile in milk of dairy cows grazing a tropical pasture. Twenty-four Holstein × Jersey crossbred cows were assigned to randomized blocks according to number of lactation (primiparous or multiparous), DIM (132d ± 60) and milk yield (20.9 kg d^{-1} ± 2.22) in a 2 × 2 factorial arrangement. Treatments were (1) HS: High supplementation (1 kg of concentrate for every 2.5 kg of milk); (2) LS: Low supplementation (1 kg for every 5 kg of milk); (3) HSCS: HS with 2.78% of calcium salt of soybean oil (CS, Megalac-E); (4) LSCS:LS with 5.76% CS. Cows grazed fertilized Elephant grass pastures during 90 d. Milk samples were collected at 30, 60 and 90 d. Data were analyzed using MIXED procedure with statistical significance at $P < 0.05$ using Tukey test. The main saturated fatty acids (SFA) present in pasture and CS was C16:0 (18.4 and 17.6%), while unsaturated FA (UFA) were C18:2 c-9, c-12 (12.29 and 40.33%) and 18:3 n-3 (51.9 and 3%). The association of a possibly high dissociation of CS of soybean oil, rich in UFA, in the rumen along with a higher pasture DMI of treatments with low supplementation compared with the high supplementation (9.3 vs. 12.2 kg d^{-1}) most likely increased intake of C18:2 and C18:3. This may explain the increase in UFA, mono unsaturated FA (MUFA) and PUFA in milk of cows from CS treatment. Increasing UFA, particularly some PUFA (C18:2 isomers and CLA), may cause depression in milk fat, but they are also known for their human health related benefits.

Table 1. Fatty acids profile in milk of dairy cows supplemented or not with fat and different concentrate levels (CL)

	Treatment				*P*-value		
Fatty acids, %	HS	LS	HSCS	LSCS	CL	Fat	CL × Fat
SFA	64.7	61.3	59.9	58.0	0.008	0.001	0.43
UFA	33.0	36.1	37.8	39.4	0.01	0.001	0.46
MUFA	30.2	33.1	34.3	35.6	0.02	0.002	0.35
PUFA	2.79	2.98	3.45	3.83	0.02	0.001	0.44
18:2 c9,c12	0.28	0.15	0.65	0.56	0.01	0.001	0.10
18:2 c9,t11	0.19	0.42	0.09	0.051	0.001	0.001	0.18
18:2 t10, c12	0.003	0.002	0.003	0.01	0.09	0.04	0.04

Key Words: milk fatty acid, soybean oil, tropical pasture

TH58 Mathematical model for cheese yield prediction using nutritional composition of diets for dairy cows. E. Chávez-Delgadillo, D. Hernández-Sánchez, L. M. Vargas-Villamil, M. M. Crosby-Galván, O. Hernández-Mendo, S. S. González-Muñoz*, and R. Pinto-Ruiz, *Colegio de Postgraduados, Montecillo, Estado de México, México.*

The objective of this study was to develop a mathematical model to predict cheese yield using dairy cow live weight and composition of the diet as inputs. First, a systematic analysis of data from papers published by the *Journal of Dairy Science* (between 1980 and 2011) was carried out. Selection of papers and variables for the model was aimed to obtain 6 least squares linear regressions for predicting dry matter intake ($R^2 = 0.625$), milk production ($R^2 = 0.906$), milk protein yield ($R^2 = 0.904$), milk fat yield ($R^2 = 0.835$), lactose yield ($R^2 = 0.948$) and casein yield ($R^2 = 0.999$). Normal distribution of residuals for each linear regression was verified using Anderson-Darling test (P-value ≥ 0.05), with mean equal to zero and constant variance. Besides, each equation was validated using the new data for calculating the average predicted squared errors and the percentage of variability, to explain the model with the new data (R^2 prediction). The Van Slyke and Publow equation was used to predict cheese yield, which was also validated using the variability for the mathematical model here developed. According to this model, cheese yield and feed efficiency are sensible to changes in diet composition. Thus, both variables will be improved by increasing non-fiber carbohydrates and hemicellulose concentration in the diet but they will be reduced by increasing rumen degradable protein, whereas increasing ether extract in the diet will decrease cheese yield and improve feed efficiency.

Key Words: mathematical model, cheese yield, diet composition

TH59 Microbial nitrogen synthesis in lambs fed corn silage inoculated with *Lactobacillus buchneri* associated with levels of concentrate. F. C. Basso*, C. H. S. Rabelo, E. C. Lara, L. G. O. Jorge, G. R. Siqueira, and R. A. Reis, *Department of Animal Science, UNESP/FCAV, Jaboticabal, SP, Brazil.*

This study aimed to evaluate microbial N synthesis in lambs fed corn silage inoculated with *L. buchneri* associated to levels of concentrate. Corn hybrid was harvested at 31% DM, chopped and treated without (control) or with 1×10^5cfu of *L. buchneri* 40788 (LB) per gram of forage. Two bunker silos were filled with 60 t of forage each, remaining closed for 70 d. Twenty-eight crossbreed lambs (BW = 25.7 ± 4.3 kg), males, were divided in 7 blocks into 4 treatments: control and LB silages associated with 40 and 60% of concentrate (corn meal, soybean meal, wheat meal and mineral supplement, DM basis). Lambs were housed in individual pens and fed ad libitum twice daily (0700 and 1700 h). Orts were weighed daily and DMI was determined. Silage, ingredients of concentrate and orts were collected twice per week and analyzed for DM, CP, NDF and NSC. On d 36 of trial, spot urine samples were collected from all animals (BW = 32 ± 4.1 kg; 4 h after feeding) for later analysis of purine derivatives (PD: allantoin, uric acid, xanthine and hypoxanthine). Microbial N supply and microbial N synthesis were estimated and analyzed as randomized block design in a 2 × 2 factorial arrangement by ANOVA using MIXED procedure of SAS. Inoculation of corn silage reduced concentrations of NDF (361 vs. 390 g/kg of DM) and increased the NSC content (514 vs. 491 g/kg of MS). Lambs fed with control silage and 40% of concentrate consumed less that to animals fed with control silage and 60% of concentrate ($P < 0.05$), observing similar nutrients intake between lambs fed LB silage. Lambs fed LB silage and 40% of concentrate had higher microbial N supply (7.6 vs. 6.5 g/d) than those fed LB silage and 60% of concentrate; however microbial N synthesis was similar between levels (13.6 vs. 12.4 g of N/ kg of DOMR). Otherwise, lambs fed with control silage and 40% of concentrate had a lower microbial N supply (5.8 vs. 8.3 g/d) and microbial N synthesis that to those fed with control silage and 60% of concentrate (12.1 vs. 16.1 g of N/ kg of DOMR) in the diet ($P < 0.05$). Inoculation of corn silage increased the efficiency of diet utilization. Financial support by Fundacao de Amparo a Pesquisa do Estado de Sao Paulo– FAPESP, Sao Paulo, SP, Brazil.

Key Words: fiber composition, purine derivative

TH60 Influence of endotoxin and thermolysin on claw explants in an ex vivo laminitis model. S. Schaumberger*, M. Penner, N. Reisinger, and G. Schatzmayr, *Biomin Research Center, Tulln, Austria.*

Laminitis in ruminants has a multifactorial etiology. As a key factor feeding of increased fermentable carbohydrate has been identified. This feed change may lead to rumen acidosis. Coincident with the change in the rumen pH is the release of endotoxin from gram-negative bacteria. An enhanced absorption of bacteria, endotoxins, exotoxins, lactic acid and histamine through the rumen, leads to a direct or indirect disruption in the micro-circulation of the corium and later to the lesions observed in laminitis. Objective of our ex vivo study was to test the influence of endotoxins and thermolysin on the lamellar separation, which is observed during laminitis. Claws were obtained from the slaughter house and dissected. Claw explants consisted of inner claw wall, epidermal lamellae and of connective tissue. Explants were cultured with 1 mL culture medium and with different concentrations (200 – 50 µg/mL) of lipopolysaccharides (LPS) from *Escherichia coli* O55:B5 and thermolysin (100 – 1 µg/mL) from *Bacillus thermoproteolyticus rokko* for 24 h at 37°C and 5% CO_2. Explants cultured only in medium were used as a negative control. After incubation explants were tested for their integrity with a force transducer. Explants cultured in medium remained intact and were viable. Thermolysin showed a concentration-dependent separation. Separation force was significantly decreased in explants treated with 50 and 100 µg/mL thermolysin ($P = 0.004$ and $P = 0.006$) compared with control. In explants treated with 50 µg/mL LPS a separation force of 30 ± 6 N was necessary. For an unknown reason, separation force increased (35 ± 3 N and 36 ± 3 N) at 100 and 200 µg/mL LPS. In all runs, average separation force in the control group was 35 ± 11 N. No significant differences in separation force were revealed for explants incubated in LPS. Further experiments will be carried out to elucidate the contribution of LPS on the lamellar separation.

Key Words: laminitis, endotoxin, ruminant

TH61 Evaluation of a protocol to measure endotoxin activity in rumen fluid. S. Schaumberger*, C. Kalteis, N. Reisinger, and G. Schatzmayr, *Biomin Research Center, Tulln, Austria.*

Ruminants are fed high-grain diets to maximize their energy intake and productivity. These high fermentable diets often cause excess fermentation and lead to an acidotic state in the. During low rumen pH gram-negative bacteria lyse more rapidly and endotoxin concentration increases. The complexity of this imbalance leads to a reduced barrier function in the rumen. Endotoxin is translocated into blood and stimulates an inflammatory cell response. Clinical outcomes of a (sub-) acidotic state are, for example, rumenitis, metabolic acidosis, laminitis, reduced feed intake, abomasal displacement and others. Objective of our investigations was, to evaluate a reproducible method for detecting endotoxins in rumen fluid via kinetic chromogen Limulus-Amebocyte-Lysate assay (LAL). Following a literature search, 2 methods for sample preparation were compared: Thawed rumen fluid samples were heat inactivated and then either centrifuged or filtered (0.45 µm), before diluted and tested. Additionally tests were performed with and without Beta-Glucan buffer (Glucashield). LAL test was performed according to producers' guidelines. Best results (lowest standard deviations within repetitions) were recovered with the combination of filtering and the use of glucan buffer. Values recovered in rumen fluid were around 2.960 ± 110 EU/mL. Compared with this method, highest values were recovered with the method of combined centrifugation and Glucan buffer (5.680 ± 1.350 EU/mL). Tests methods with the use of glucan buffer revealed significant differences in their endotoxin activity ($P = 0.05$) in rumen fluid. Further tests will be performed to explain the differences in endotoxin activity in treatments with filters and centrifugation.

Key Words: acidosis, endotoxin, rumen fluid

TH62 Effect of corn silage with microbial inoculants on performance of feedlot lambs. F. C. Basso*, E. C. Lara, C. H. S. Rabelo, M. F. C. Miranda, G. S. Goncalves, L. G. O. Jorge, and R. A. Reis, *Department of Animal Science, UNESP/FCAV, Jaboticabal, SP, Brazil.*

This study aimed to evaluate the lambs performance fed corn silage inoculated with microbial inoculants. Corn hybrid was harvested at 40.4% DM, chopped, treated and ensiled in 3 stack silos with 40 t of forage each (closed for 85 d). The treatments were 1×10^5 cfu of

Lactobacillus plantarum MA18/5U combined with 1×10^5 cfu of *L. buchneri* CNCM I-4323 (LPLB) or combined with 1×10^5 cfu of *B. subtilis* AT553098 (LPBS) per gram of fresh forage, remaining a treatment uninoculated (control silage). Thirty crossbred lambs (BW = 29 ± 3.0 kg), males, were divided in 10 blocks into 3 treatments. Diet was composed of 60% of silage and 40% of concentrate (ingredients: corn meal, soybean meal, urea and mineral supplement, DM basis) and was formulated to daily gain of 200 g/d. Lambs were housed in individual pens and fed ad libitum twice daily (0700 and 1700 h). Orts were weighed daily and DMI was determined. Animals were weighed after fasting (16 h) at the beginning and end of the experimental period to obtain the ADG and feed conversion (FC). Animals were harvested with 40 kg (approximately 53 d of feedlot), then, carcasses were weighed to find the hot carcass weight (HCW), stored at −4°C for 24 h and weighed again to find the cold carcass weight (CCW). Thus, losses by cooling (LC), hot and cold carcass yield (HCY and CCY) were calculated. Subcutaneous fat thickness (FT) was measured over the loin eye between the 12th and 13th rib. Data were analyzed as randomized block by ANOVA using MIXED procedure of SAS (version 9.0). Lambs fed control silage showed higher DMI (1.5 kg/d) than those fed control silage (LPLB: 1.3 kg/d; LPBS: 1.4 kg/d; $P < 0.05$), whereas ADG was similar among animals (219 g/d). However, FC improved ($P < 0.05$) in lambs fed LPLB silage (6.0; Control: 6.5; LPBS: 6.8). The HCW (19.0 kg), CCW (18.3 kg), LC (2.8%), HCY (46.7%), CCY (45.0%) and FT (2.1 mm) were similar among animals fed different silages ($P > 0.05$). Inoculation in corn silage did not promote improvements on carcass characteristics, but feed conversion was enhanced in the lambs fed corn silage inoculated with *L. plantarum* combined *L. buchneri*. Financial support by Fundacao de Amparo a Pesquisa do Estado de Sao Paulo – FAPESP, $$Sao Paulo, SP, Brazil.

Key Words: *Bacillus subtilis*, *Lactobacillus buchneri*, *Lactobacillus plantarum*

TH63 Influence of yeast viability on rumen fermentation parameters and nutrient digestibility in beef heifers. D. Vyas*[1], A. Uwijeye[1], R. Mohammed[1], W. Z. Yang[1], K. A. Beauchemin[1], and N. Walker[2], *[1]Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [2]AB Vista, Marlborough, Wiltshire, UK.*

The study was aimed at determining the importance of yeast viability for reducing the incidence of subacute ruminal acidosis (SARA) and improving total tract nutrient digestibility in cattle. Six ruminally cannulated beef heifers (680 ± 50 kg BW) were used in a replicated 3 × 3 Latin square design and were fed a diet consisting of 40% barley silage, 10% chopped grass hay, and 50% barley grain based concentrate. Treatments were (1) control (no yeast); (2) active dried yeast (ADY; 4 g providing 10^{10} cfu/g; AB Vista, UK); and (3) killed dried yeast (KDY; 4 g autoclaved ADY). The treatments were directly dosed via the rumen cannula daily at the time of feeding. The periods consisted of 2 wk of adaptation (d1–14) and 6 d of measurements (d15–20). Ruminal pH was continuously measured (d14–20) using an indwelling system. Rumen contents were sampled on d15 and d17 at 0, 3, 6, 9 and 12 h after feeding. Total-tract nutrient digestibility was measured using an external marker ($YbCl_3$) from d15–20. Dry matter intake tended to be higher with KDY ($P = 0.07$) while no treatment effects were observed for apparent total-tract nutrient digestibility. Both ADY and KDY elevated minimum and mean rumen pH ($P = 0.07$) while no effects were observed on maximum pH ($P = 0.17$). Both treatments were effective in reducing time that ruminal pH was below 5.8 ($P < 0.01$) and 5.6 ($P < 0.01$) compared with the control. No treatment differences were observed in the ruminal VFA profile and lactate concentration; however, NH_3-N was significantly higher with ADY compared with the other treatments. The relative population size of *S. bovis* was higher with both yeast treatments ($P < 0.01$) while *R. flavifaciens* tended to be higher with KDY ($P = 0.05$). However, *F. succinogenes*, *S. ruminantium*, and *M. elsdenii* remained similar for all the treatments. The study demonstrates the positive effects of yeast treatments in reducing the incidences of SARA irrespective of its viability. However, further studies are required to evaluate the importance of yeast viability for other dietary conditions, particularly when the risk of acidosis is high.

Key Words: active dry yeast, rumen acidosis, ruminal pH

TH64 Influence of tannins extract supplementation at low level on feedlot performance of Katahdin × Pelibuey hair-lambs. B. Ortiz*[1], A. Camacho[2], N. E. Villalba[3], L. R. Flores[2], M. A. Mariezcurrena[1], M. D. Mariezcurrena[1], and R. Barajas[2], *[1]Universidad Autonoma del Estado de Mexico, Toluca, Edo. de Mexico, Mexico, [2]Facultad de Medicina Veterinaria y Zootecnia, Universidad Autonoma de Sinaloa, Culiacan, Sinaloa, Mexico, [3]Agricola Ganadera Mojolo, Culiacan, Sinaloa, Mexico.*

Twenty-four hair lambs (3/4 Katahdin and 1/4 Pelibuey breed) with a mean weight of 24.07 ± 2.09 kg were involved in an experiment with the objective of determine the influence of tannins extract supplementation at low level on feedlot performance of Katahdin × Pelibuey hair-lambs. Lambs were weighed and in groups of 3, were placed in 8 elevated (0.6 m) plastic floor pens (0.9 × 1.9 m). In a completely randomized block design lambs were assigned to next treatments: (1) Feeding with a 95% concentrate corn-canola meal based diet (14.2% CP; 2.0 Mcal NEm/kg DM) without additional tannins extract (CTRL), or (2) Control diet plus 0.3% (DM basis) of tannins extract supplementation (TE). Tannins extract were obtained from a Condensed and hydrolysable tannins blend (BYPRO; Inudor, S.A., Argentina), that contains 72% of tannins. Lambs were weighed at starting experiment and when each block accomplishes the target final weight (35 to 40 kg), the block of heavy lambs required 42 d to reach the market weight, and the block of light lambs required 56 d to arrive at the target weight. Experiment was analyzed by ANOVA as a randomized complete block design, with 4 replicates for treatment, pen was considered as the experimental unit. Final weight was not influenced by treatments ($P = 0.32$). The average daily gain was improved 18% ($P < 0.05$) by TE supplementation, with means of 245 and 290 g/day for lambs in the CTRL and TE treatments, respectively. Dry matter intake and feed efficiency were not modified by treatments ($P > 0.90$). It is concluded that low tannins extract supplementation at level close to 0.3% of dietary DM, improves weight gain of Katahdin × Pelibuey hair-lambs.

Key Words: lamb, feedlot performance, tannin

TH65 Effects of dietary phytogenic feed additives on in vivo rumen fermentation, enzyme profile, and microbial ecology of crossbred cattles. S. L. Ingale*[1], A. K. Pattanaik[2], D. N. Kamra[2], and K. Sharma[2], *[1]: College of Animal Life Sciences, Kangwon National University, Chuncheon, Republic of Korea, [2]Clinical & Pet Nutrition Laboratory, Division of Animal Nutrition, Indian Veterinary Research Institute, Izatnagar, India.*

An experiment was conducted to investigate the effects of dietary phytogenic feed additives on in vivo rumen fermentation, enzyme profile, and microbial ecology of crossbred cattle. Three rumen-fistulated Holstein-Frisian males (260 ± 14.8 kg) were arranged in a 3 × 3 switchover design involving 3 periods of 21 d duration each. Dietary treatments were

basal diet (CON) and basal diet supplemented with either 2.5% herbal combination comprising of *Withania somnifera*, *Boerhavia diffusa*, and *Holarrhena antidysentericum* (1:1:1; WiBH) or *Woodfordia fruticosa*, *Solanum nigrum*, and *Trigonelia-foenum-graceum* (1:1:1; WoST). The animals were fed on wheat straw:concentrate (60:40). In each of the 3 phases, at the end of 21d of feeding rumen liquor was sampled on 3 consecutive days, at 0, 2, 4, 6, and 8 h post-feeding and analyzed for pH, short chain fatty acids, nitrogen fractions, and protozoa population. For analysis of rumen enzymes activity and microbial quantification, whole rumen content was collected before feeding for 3 consecutive days. Dietary treatments had no effects ($P > 0.05$) on postprandial pH, short chain fatty acids, nitrogen fractions, and protozoa count of rumen liquor at any time of collection. The activity of rumen avicelase and xylanase were greater ($P < 0.05$) in animal fed diet supplemented with WoST compared with animal fed control and WiBH supplemented diets. Animals fed diets supplemented with WiBH or WoST had greater ($P < 0.05$) population of rumen *R. flavefaciens* and *F. succinogenes* and fungi compared with animals fed control diet. Moreover, *F. succinogenes* and fungi population were greater ($P < 0.05$) in WiBH supplemented groups than WoST supplemented group, whereas *R. flavefaciens* population was greater in WoST supplemented group than WiBH supplemented group. Results obtained in present study indicate that dietary supplementations of combination of phytogenic feed additives have potential to improve the fiber degrading bacteria, fungi populations and hydrolytic enzyme activity.

Key Words: crossbred cattle, enzyme profile, microbial ecology

TH66 Effect of tannin extract supplementation on apparent digestibility of crude protein and plasma urea nitrogen of implanted and non-implanted finishing hair-lambs. L. R. Flores*[1], J. J. Lomeli[1], J. I. Macias[1], E. A. Velazquez[1], N. E. Villalba[2], A. Camacho[1], E. Vazquez[1], I. Quintero[1], and R. Barajas[1], *[1]Facultad de Medicina Veterinaria y Zootecnia, Universidad Autonoma de Sinaloa, Culiacan, Sinaloa, Mexico, [2]Agricola y Ganadera Mojolo, S.A. de C.V., Culiacan, Sinaloa, Mexico.*

Twenty-four Katahdin lambs (25.05 ± 3.08 kg) were involved in a total feces collection experiment to evaluate the effect of tannin extract supplementation on apparent digestibility of crude protein and plasma urea nitrogen of implanted and non-implanted finishing hair-lambs. In groups of 3, lambs were placed in 8 plastic floor elevated pens (1.5 × 1.6 m). In agreement with a replicated cross over design were assigned to receive follows treatments: (1) Feeding a 95% concentrate diet based in whole corn grain and canola meal (CTRL); (2) Control and ear anabolic-implant (IM); (3) Control added with 0.3% (DM basis) of tannin extract (TE); and (4) Control added with 0.3% (DM basis) of tannin extract and ear anabolic-implant (IMTE). Experiment was divided in two 14-d periods; within a period, the first 10 d for adaptation and last 4 d for sample collection. Last day of each period blood samples were taken from jugular vein. Each cross over was integrated by 4 pens; lambs from 2 pens were ear implanted with 2 pellets of commercial implant Component (Elanco) equivalent to a dose of 40 mg of trenbolone and 8 mg of estradiol. One pen with implanted lambs and another with no implanted animals receiving TE supplementation, remainder pen were assigned to basal control diet. Once completed 14 d of first period, diets were switched. Experiment was analyzed by ANOVA for a replicated crossover design. Treatments had not effect ($P > 0.15$) on intake, fecal excretion and apparent digestibility of dry matter, organic matter or crude protein. Mean values of plasma urea nitrogen (PUN) concentration were 8.29, 5.91, 6.45, and 6.24 mg/dL for CTRL, IM, TE, and IMTE treatments, respectively. Both, IM and TE decreased ($P = 0.02$) PUN values compared with CTRL. PUN values were similar between IM and TE treatments. Results suggest than supplementation of tannin extract had no effect on apparent digestibility of crude protein and decreases PUN values in nonimplanted lambs, whereas in implanted lambs tannin supplementation did not affect PUN values.

Key Words: lamb, PUN, tannin

TH67 Effects of bismuth subsalicylate and dietary sulfur level on in vitro rumen fermentation in continuous culture. S. W. Fessenden*, A. J. Carpenter, M. Ruiz Moreno, and M. D. Stern, *Department of Animal Science, University of Minnesota, St. Paul, MN, USA.*

In ruminants, excess dietary sulfur is associated with reduced DM intake, poor feedlot performance, and sulfur-associated polioencephalomalacia. Bismuth subsalicylate (BSS) has been shown to decrease hydrogen sulfide in vitro; however, negative effects on fermentation were reported when BSS was included at 1% of diet DM. The objective of this experiment was to evaluate effects of BSS inclusion at 0.5% of diet DM on microbial fermentation in continuous culture when provided with differing levels of dietary sulfur. Eight dual-flow continuous culture fermenters were used during 2 consecutive 10-d periods consisting of 7 d for stabilization followed by 3 d of sampling. Treatments were arranged in a 2 × 2 factorial design, with 2 levels of BSS (0 and 0.5% of DM) and 2 levels of dietary sulfur (0.21% and 0.42% of DM). A pelleted feedlot diet containing 39% dry rolled corn, 32% earlage, 21% wet distillers grains, 3.2% corn silage, 1.5% soybean meal, 0.6% urea, and 2.7% mineral premix was provided to the fermenters at a rate of 75 g of DM/fermenter/d. Effluents from sampling days were composited by fermenter within period, resulting in 4 reps/treatment. BSS inclusion decreased ($P < 0.01$) true OM digestion, while no effects were observed for NDF and ADF digestion. Total VFA concentrations, molar proportions of acetic, propionic, and branched-chained VFAs decreased ($P < 0.01$) with BSS addition. The ratio of acetic to propionic acid and the molar proportion of butyric acid increased ($P < 0.01$) with BSS addition. In regard to nitrogen metabolism, BSS increased NH_3-N concentration, NH_3-N, and dietary-N flows ($P < 0.01$), and decreased non-NH_3-N flow, microbial-N flow and CP degradation ($P < 0.01$). Inclusion of BSS increased mean, minimum, and maximum fermentation pH ($P < 0.01$). Dietary sulfur level and the interaction of BSS and dietary sulfur had no effects ($P > 0.05$) on any measured parameter of fermentation. Results from this experiment indicate that BSS included at 0.5% of diet DM has detrimental effects on in vitro rumen fermentation in continuous culture. These effects are not dependent on level of dietary sulfur.

Key Words: bismuth subsalicylate, rumen

TH68 Effect of an exogenous phytase on digestibility, performance and phosphorus balance of Holstein steers. G. Buendía-Rodríguez[1], S. S. González-Muñoz*[2], M. D. Montoya-Flores[1], N. I. Ortega-Álvarez[1], and C. Aceves-Hacebe[1], *[1]CENIDFyMA, INIFAP, Ajuchitlán, Querétaro, México, [2]Colegio de Postgraduados, Montecillo, Estado de México, México.*

Phytase added to diets for ruminants may increase bioavailability of inorganic phosphorus (P). Therefore, the objective of this experiment was to evaluate the effect of an exogenous phytase on digestibility, performance and P balance of 24 Holstein steers (215.45 ± 12.26 kg initial body weight) individually fed a concentrate diet (14% CP and 3.1 Mcal ME). The experimental design was completely randomized with 3 treatments: 0, 12 and 24 g/t phytase (FINASE, AB Enzymes, Darmstadt, Germany; from *Trichoderma reesei*; 40,000 FTU/g) in the

diet. The experiment lasted 60 d and the variables recorded were: average daily gain (ADG), dry matter intake (DMI), feed conversion (FC), dry matter digestibility (DMD), P excretion and P retention (phosphorus balance). Data were analyzed using MIXED procedure of SAS and treatment means were compared with the Tukey test ($P \leq 0.05$). Treatments affected ($P \leq 0.05$) ADG (1119b, 1292a, 1130b; g) and DMI (5997^{ab}, 6307^{a}, 5933^{b}; g), but did not change FC (5.39, 4.92, 5.29) and DMD (65.38, 66.52, 64.65%). Besides, daily fecal P excretion was decreased (13.45^{a}, 13.08^{a}, 10.89^{b}; g) and as a consequence average P retention was increased (6.49^{c}, 7.89^{b}, 8.80^{a}; g/animal) ($P \leq 0.05$). Thus, it may be concluded that an exogenous phytase changed average daily gain and DMI of Holstein steers, whereas fecal P excretion was reduced, which may decrease soil contamination.

Key Words: phytase, steer performance, fecal P excretion.

TH69 Effects of supplementing *Propionibacterium freudenreichii* on lipid biohydrogenation of beef finishing diets containing flax oils using a semi-continuous fermentation system (RUSITEC). S. Ding*[1,2], M. L. He[2], G. O. Ribeiro Junior[3,2], A. Y. Alazzeh[2], H. Holo[4,5], O. M. Harstad[6], T. A. McAllister[2], S. J. Meale[1,2], and A. V. Chaves[1], *[1]Faculty of Veterinary Science, University of Sydney, Sydney, NSW, Australia, [2]Lethbridge Research Center, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [3]Veterinary School, Federal University of Minas Gerais, Belo Horizonte, MG, Brazil, [4]Department of Chemistry, Biotechnology and Food Science, Norwegian University of Life Sciences, Ås, Norway, [5]TINE SA, Oslo, Norway, [6]Department of Animal and Aquacultural Sciences, Norwegian University of Life Sciences, Ås, Norway.*

Propionibacteria has been shown to play a role in the ruminal biohydrogenation (BH) of polyunsaturated fatty acids (PUFA). However, to-date, no studies have been undertaken regarding the ability of propionibacteria to alter lipid BH patterns in diets supplemented with flax oil using the artificial rumen simulation technique (RUSITEC). Thus, a 23 d RUSITEC was conducted to examine the effects of supplementing *Propionibacterium freudenreichii* (strain T54) or T54 and flax oil in a beef finishing diet (TMR), on BH. The experiment consisted of an 8 d adaptation period and 15 d of inoculation with T54. Treatments were: 1) CON [10 g TMR + 23 mL autoclaved mixture of sodium lactate broth (SLB) with T54 (10^9 cfu/mL)]; 2) PB [10 g TMR + 23 mL inoculated SLB with T54 (10^9 cfu/mL)]; 3) FO (6% DM flax oil with autoclaved T54) FOPB (6% DM flax oil with T54). In situ DMD was determined at 48 h, and VFA concentrations were measured at 24 h on d 10 to 13. Proportions of individual fatty acids (FA) in feed residues were determined at 48 h and fatty acids profiles in the effluent was measured daily on d 20 to 23. Data were analyzed using the PROC Mixed SAS procedures. Within each run (n = 2), treatments were replicated twice. In situ DMD (%) at 48 h was not affected ($P > 0.10$) by either oil or T54. Flax oil resulted in higher ($P < 0.01$) total VFA production (m*M*) in comparison with non-oil groups. T54 or flax oil alone, or in combination, decreased ($P < 0.02$) acetate production. T54 increased ($P < 0.01$) propionic acid (%) by 14% compared with the control. Oil increased ($P < 0.01$) the percentages of PUFA and C18:3, yet decreased ($P < 0.01$) total saturated fatty acid content (SFA, %) in feed residues. Conversely, in the effluent, oil decreased PUFA (%) and C18:3 (%), while increasing SFA (%). T54 did not affect ($P > 0.05$) BH, except a slight decrease ($P < 0.01$) in PUFA (%) in the oil-based diet. Overall, it was determined that *P. freudenreichii* (T54) does not alter the fatty acid profiles in the effluent through changes in the biohydrogenation patterns of PUFA in flax oil.

Key Words: biohydrogenation, lipids, RUSITEC

TH73 Effects of probiotics supplementation on milk performance of late lactation dairy cows. L. C. Huang[1,3], N. Zheng[1,2], J. Q. Wang*[1,2], J. B. Cheng[1,3], and D. P. Bu[1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Ministry of Agriculture - Milk and Dairy Product Inspection Center (Beijing), Beijing, China, [3]College of Animal Science and Technology, Anhui Agricultural University, Hefei, China.*

The supplementation of probiotics, including yeast, lactic acid bacteria and *Bacillus subtilis* natto, were evaluated in 48 late lactation dairy cows with similar milk yield (27.34 ± 4.92kg/d) and DIM (230.63 ± 31.59 d). Cows were allocated to 4 treatments, blocked by average daily milk yield in the previous weeks. Four treatments were control (C, no supplemental probiotics), 15 g/(cow·d) of yeast (YC), 1 g/(cow·d) of lactic acid bacteria (LC), and 1 g/(cow·d) of *Bacillus subtilis* natto (NT). The research lasted 9 wk, including 2 wk of diet adaptation and 7 wk of experimental period. The experimental data were analyzed by SAS 8.0 via the mixed model. Milk yield of LC (26.51 kg/d) and NT (25.65 kg/d) was greater than C (24.24 kg/d) and YC (24.68 kg/d) ($P < 0.0001$). LC was also greater than NT, however, YC was not different with C. Fat corrected milk (4%), milk fat and protein yield of LC (25.90 kg/d, $P < 0.0001$; 1019.12 g/d, $P = 0.0046$; 920.14g/d, $P < 0.0001$) and NT (25.56 kg/d, 1016.72 g/d and 905.36 g/d) were greater than C (24.21 kg/d, 970.89 g/d and 849.57 g/d) and YC (24.77 kg/d, 974.37 g/d and 851.66 g/d), while there was no significant difference between LC and NT, YC and C. Milk fat of C (3.99%) was greater than LC (3.83%) and YC (3.85%) ($P = 0.0147$), and NT (3.92%) was greater than LC; however, there was no significant difference between NT and C, NT and YC. Milk protein of C (3.52%) was greater than YC (3.46%) ($P = 0.0023$), furthermore NT (3.55%) was also greater than YC and LC (3.49%), there was no significant difference between LC and C, NT and C, YC and LC. Somatic cell counts (SCC) of C (105.14×10^4/mL), LC (96.60×10^4/ml), NT (96.88×10^4/mL) and YC (99.74×10^4/mL) had no significant difference, but SCC in cows with supplementation tended to decrease. The results indicated that the supplementation of lactic acid bacteria and *Bacillus subtilis* natto can improve milk performance of dairy cows in late lactation, but the supplementation of yeast did not have significant effect.

Key Words: dairy cow, milk performance, probiotic

TH74 Diversity of monensin-sensitive rumen proteolytic bacteria under different nitrogen sources in vitro. Y. F. Lu[1,2], J. Q. Wang*[1], S. G. Zhao[1], D. P. Bu[1], and G. Q. Zhao[2], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Sciences, Beijing, China, [2]College of Animal Science and Technology, Yangzhou University, Yangzhou, China.*

Monensin has been shown to inhibit amino acid-fermenting bacteria in rumen. Objective of this study was to compare the rates of ammonia production with added monensin and the diversity of monensin-sensitive proteolytic bacteria in rumen fluid in vitro under different nitrogen sources. Rumen fluid from the Holstein cows was inoculated media under anaerobic chamber with added different substrates, with or without 5 μ*M* monensin. The tubes were incubated in 3 triplicates at 21 h for 39°C and ammonia was evaluated at 0, 7, 14 and 21 h of incubation. Data were analyzed using SAS. Moreover, MOTHUR was used to assign 16S rDNA sequences to operational taxonomic units (OTUs) based on 97% sequence identity criterion and bacterial diversity. Both the NH_3 production of protein and amino acid were significant decreased ($P < 0.01$) by monensin (P-M, AA-M) after 14 h and 7 h, respectively. NH_3 was formed more than twice as rapidly from amino acid (AA) compared

with protein (P) at 21h. The rate of NH_3 production from protein was on average 56.65 nmol mg of protein^{-1} h^{-1} lower than amino acid ($P < 0.01$). Monensin had a greater effect on the rate of NH_3 production from protein (39.33834 nmol mg^{-1} h^{-1}) compared with amino acid (99.57078 nmol mg^{-1} h^{-1}) ($P < 0.01$). Furthermore, a total of 230 16S rDNA gene sequences were assigned to 67 OTUs which were from the phyla *Firmicutes*, *Bacteroidetes*, *Gammaproteobacteria*. Phylum *Gammaproteobacteria* was only to the AA-M (OTU22) and NN (OTU35). P had the most abundant OTU and had 5 more OTUs than P-M, but AA had 1 less OTU than AA-M. However Simpson and Chao 1 indices indicated P and AA had more diversity of proteolytic bacteria than that with added monensin P-M and AA-M respectively, especially P had the most abundant diversity than other treatments. These results suggest that monensin had a greater effect on the rate of NH_3 production from protein compared with amino acid and monensin can reduce the diversity of proteolytic bacteria, especially using protein as the nitrogen resource.

Key Words: monensin-sensitive, proteolytic bacteria, rumen

TH75 Effects of antibacterial agents on ruminal biohydrogenation of unsaturated fatty acid in vitro. Y. H. Jiang[1,2], J. Q. Wang*[1], H.J. Yang[1], D. P. Bu.[1], E. W. Jin[1], H. T. Shi[1], W. H. Bao[1], and P. Sun[1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]College of Animal Science and Technology, China Agricultural University, Beijing, China.*

The objective of this study was to evaluate the rumen biohydrogenation of unsaturated fatty acid by adding antibacterial agents (containing streptomycin sulfate, Penicillin G, potassium, and chloromycetin) (RA) in vitro. A dual-flow continuous culture system was used with a 2 × 4 factorial design: with unsaturated fatty acid (no fatty acid, 0%-CK; oleic acid, 3%-OL; linoleic acid, 3%-LA; linolenic acid, 3%-LNA on a DM basis) and antibacterial agents (0 mg/mL, RA0; 0.1 mg/mL, RA) and 40 g basic diet as the substrate. Mixed ruminal fluid from 3 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. Twenty-four fermenters were used with a volume of 1000 ± 10 mL, the dilution rate was set at 6%/h. The experiment last 8 d, and all the samples were taken during the last 3 d. Each treatment has 3 replications. Statistical analysis was carried out by ANOVA (GLM) using SAS. The products of biohydrogenation of C18 unsaturated fatty acid were lower in OL, LA, and LNA than CK with adding RA (0.27, 0.25, 0.37 vs. 0.61 g/100 g fatty acid methyl esters, $P < 0.01$). Adding antibacterial agents decreased the concentration of C18:0 and t9C18:1 (0.783 vs. 0.379, 43.1 vs. 11.3g/100 g fatty acid methyl esters, $P < 0.01$), and the proportion of c9C18:1, c9c12 C18:2, and C18:3 were higher in RA than in control ($P < 0.01$). The biohydrogenation rate of OL was sharply decreased by adding RA ($P < 0.01$), and followed by LA ($P < 0.01$) and LNA ($P < 0.05$). Overall, antibacterial agents decreased the extent of biohydrogenation of C18 unsaturated fatty acids in rumen.

Key Words: antibacterial agent, biohydrogenation, rumen simulation system

TH76 Effects of supplemental bupleurum extract on blood parameters, antioxidant status and immune function in heat-stressed dairy cows. X. Z. Sun[1,2], J. Q. Wang*[1], D. P. Bu[1], J. B. Cheng[1,2], L. Pan[1], and W. Liu[1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, China, [2]College of Animal Science and Technology, Anhui Agricultural University, Hefei, China.*

The objective of this study was to investigate effects of bupleurum extract (BE) on blood parameters, antioxidant status and immune function in heat-stressed dairy cows. Forty Holstein cows (75 ± 15 DIM, 37.5 ± 1.8 kg of milk/d) were individually fed and randomly assigned to 1 of 4 treatments (10 cows/group). Treatments consisted of 0 (control), 0.25, 0.5 or 1.0 g BE /kg DM . The experimental lasted 10 wks. Average temperature–humidity index (THI) was 78.20 ± 2.40, 79.72 ± 3.26 and 78.26 ± 3.37 at 6:00h, 14:00h and 22:00h, respectively. Blood samples were collected from all of animals via tail vein before the morning feeding at wk 1, 4, 7, and 10. Data were analyzed by GLM procedure of SAS 9.2. Compared with control, cows supplemented with 0.5 g/kg BE increased the counts of red blood cell (5.97 vs. 5.52 10^{12}/L, $P < 0.05$), hematocrit (27.83 vs. 25.33 10^9/L, $P < 0.05$), and hemoglobin (95.11 vs. 86.85 g/L, $P < 0.05$). Cows supplemented with BE increased ($P < 0.05$) the count of blood platelet, mean corpuscular hemoglobin, but had no effect on creatine kinase activities and alkaline phosphatase activities compared with the controls. Furthermore, the activity of nitric oxide synthase (NOS) in serum was increased for cows fed diets supplemented with BE than for control cows (29.84, 29.98, 28.51 vs. 25.57 U/mL, $P = 0.01$), and the activities of glutathione peroxidase (GSH-PX) were higher in cows fed 0.25 or 0.5 g/kg BE than that in control cows ($P > 0.05$). The superoxide dismutase (SOD) activities were not affected ($P > 0.05$) by supplementing BE. Cows supplemented with BE increased concentrations of interleukin-4 (65.40, 64.07, 70.42 vs. 55.45 pg/mL, $P < 0.05$) and interleukin-6 (140.62, 113.47, 104.26 vs. 94.12 pg/mL, $P < 0.01$) Compared with the controls, whereas concentrations of CD4+ and CD8+ were not influenced. Results indicate that BE supplementation improved health status, increased antioxidant status and immune function in heat-stressed cows.

Key Words: antioxidant status, bupleurum extract, immune function

TH77 Effect of *Saccharomyces cerevisiae* I-1077 feed additive on rumen bacterial diversity in calves. F. Chaucheyras-Durand[1,2], V. Demey[1], F. Ossa[3], and E. Chevaux*[1], *[1]Lallemand Animal Nutrition, Blagnac, France, [2]Institut National de la Recherche Agronomique (INRA), Saint-Genès Champanelle, France, [3]Lallemand Animal Nutrition, Montreal, QC, Canada.*

The effect of live yeast on establishment of rumen bacterial community was studied on 2 groups of 8 calves. A supplemented group (SC) received from the first wk 4 × 10^9 cfu/d of *S. cerevisiae* I-1077 mixed with fibrous concentrate. The Control group did not receive any supplement. For each animal 2 rumen samples were collected by stomach tubing: one at 2 wk of age when calves were fed mainly milk replacer (MR), the other at 8 to 10 wk of age, after they had started consuming solid feed (SF) for at least 6–8 wks. DNA was extracted from these samples and the V6-V8 region of the 16S rRNA gene was PCR-amplified using universal primers (L1401/U968-GC). PCR fragments were separated by temporal temperature gradient gel electrophoresis (TTGE). Scans were analyzed with Gel Compar II software. Whatever the diet, 2 major clusters were obtained: 66% of Control samples fell in one cluster, 71% of SC samples grouped together in the other. The mean number of TTGE bands and the Shannon diversity index (H') were higher in SC than in Control samples regardless of the diet, this being particularly pronounced with MR (Table 1). Only for Control samples number of TTGE bands and Shannon index were slightly increased from MR to SF. However, due to the low number of animals, statistical differences could not be found. Although preliminary, these data suggest that bacterial diversity increases with age and with solid feed distributed to Control calves. They also suggest that diet supplementation with live yeasts may

accelerate microbial diversity in the developing rumen, which could be of importance to achieving a functional rumen ecosystem at weaning.

Table 1. Effects of the nature of feed and of SC supplementation on bacterial diversity in the rumen of calves (n = 8 per group); means (SE) of each parameter are shown.

	MR		SF		Diet		Treatment	
	Control	SC	Control	SC	MR	SF	Control	SC
TTGE bands (no.)	7.9 (1.7)	9.9 (1.9)	8.1 (1.4)	9.4 (2.5)	8.8 (1.8)	8.8 (2.1)	8.0 (1.5)	9.6 (2.2)
Shannon index H'	0.77 (0.1)	0.8 (0.1)	0.81 (0.1)	0.84 (0.1)	0.81 (0.1)	0.82 (0.1)	0.79 (0.1)	0.85 (0.1)

Key Words: calf, live yeast, rumen microbiota

TH78 Effects of cellulase and xylanase levels on the kinetics of in vitro fermentation of corn stover. A. Z. M. Salem*[1], Y. Liu[1], H. Ammar[2], L. M. Camacho[3], M. M. Y. Elghandour[1], H. Gado[4], and Z. Tan[5], *[1]Facultad de Medicina Veterinaria y Zootecnia, Universidad Autonoma del Estado de Mexico, Mexico, [2]Ecole superieure d'agriculture de Mograne, Mograne, Zaghouan, Tunisia, [3]Facultad de Medicina Veterinaria y Zootecnia, Universidad Autonoma de Guerrero, Cd. Altamirano, Guerrero, Mexico, [4]Animal Production Department, Faculty of Agriculture, Ain Shams University, Qalubia, Egypt, [5]Key Laboratory of Agro-ecological Processes in Subtropical Region, Institute of Subtropical Agricultural, the Chinese Academy of Sciences, Hunan, Changsha, China.*

An in vitro gas production technique was used to investigate combination effects of *Salix babylonica* extract (SB) with the exogenous fibrolytic enzymes of cellulase (C) and xylanase (X), or their mixture (1:1, vol/vol) on in vitro fermentation characteristics of a total mixed ration as substrate (208 (CP) and 364 (NDF) g/kg DM). Four levels of extracts (i.e., 0, 0.6, 1.2 and 1.8 mL/g DM) and 4 fibrolytic enzymes (1 μL/g DM; Control, X, C and XC (1:1, vol/vol)) were used in 4 × 4 factorial arrangement. In vitro gas production (GP) was recorded at 2, 4, 6, 8, 10, 12, 24, 36, 48 and 72 h of incubation. After 72 h, the incubation was stopped and supernatant pH was determined and then filtered to determine dry matter degradability (DMD). Fermentation parameters, such as the 24-h gas yield (GY_{24}), in vitro organic matter digestibility (OMD), metabolizable energy (ME), short-chain fatty acid concentrations (SCFA), and microbial protein production (MP) were estimated. Results show that the extract of *S. babylonica* and different kind of enzymes (X and C or XC by 1.1, vol/vol) supplementation influenced ($P < 0.001$) in vitro gas production after 12 h of incubation. Extract × enzymes interaction ($P < 0.001$) occurred for gas production at all incubation times of measures. Addition of *S. babylonica* extract (i.e., SB) at the highest doses (i.e., 1.8 mL/g DM) with absence of any exogenous fibrolytic enzymes, increased ($P < 0.05$) volumes of gas produced (216 vs. 145 mL gas/g DM) after 24 h of incubation. In general and except for values recorded at 12 h of incubation, GP was lowest (184 vs. 116 mL gas/g DM, $P < 0.05$) when the highest SB was combined with C addition. Extract × enzymes interaction ($P < 0.001$) decreased ruminal pH (6.67 vs. 6.63), while at the highest SB doses (1.8 mL/g DM) with the presence of C or X, increased ($P < 0.05$) OMD (60 vs. 46 g/g DM), ME (8.8 vs. 6.7 MJ/kg DM), GY_{24} (242 vs. 161 mL gas/g DMD) and SCFA (4.5 vs. 2.8 mmol/g DM). Data suggested that SB extract, C, and X effectively improved in vitro rumen fermentation, and the combination of enzyme with SB extract at the level of 1.8 mL/g DM was more effective than the other treatments.

Key Words: cellulose, corn stover, in vitro fermentation

TH79 Effect of exogenous glucoamylase enzyme on in vitro fermentation of diet with 25% of maize or sorghum grains. A. Z. M. Salem*[1], H. Ammar[2], L. B. Ortiz[1], H. Gado[3], M. M. Y. Elghandour[1], and G. D. Mendoza[4], *[1]Facultad de Medicina Veterinaria, Universidad Autonoma del Estado de Mexico, Mexico, [2]Ecole superieure dagriculture de Mograne, Mograne, Zaghouan, Tunisia, [3]Department of Animal Production, Faculty of Agriculture, Ain Shams University, Qalubia, Egypt, [4]Universidad Autónoma Metropolitana, Unidad Xochimilco, México.*

The objective of this study was to evaluate the effects of glucoamylase enzyme in the in vitro ruminal fermentation of total mixed rations (TMR) with 25% of maize (M) and other of 25% of sorghum (S) grains. The 2 diets (i.e., M and S) were treated with 0, 1.5 and 3 g of enzyme protein (65% of protein) per kg of grain in diet. In vitro gas production of TMR of M and S grains was measured (quantity of substrate) at 2, 4, 6, 8, 10, 12, 24, 48 and 72 h of incubation in ruminal fluid diluted in buffer solution (1:4, v:v) flushed with CO_2 and maintained at 39°C. The incubation was stopped at 72 h and after measuring the pH and supernatant was filtered to determine pattern of degradation of in vitro organic matter, neutral detergent fiber (NDFD), and acid detergent fiber (ADFD). The results showed that addition of glucoamylase enzyme to maize diet had no significant effect on kinetics of gas production. However, when added to sorghum diet, a high dose of the enzyme (3 g/kg DM) was traduced by a significant increase ($P < 0.05$) of the rate of gas production (c) and the volume of gas produced at 2, 4 and 6 h of incubation, with no statistical differences between the control and the lowest dose enzyme (i.e., 1.5 g/kg DM). Likewise, effect of glucoamylase was no significant either on the in vitro degradation of DM and cell wall (NDFD and ADFD) or on pH values. Effect of the enzyme supply on sorghum diet was significant ($P < 0.05$) only on pH (5.70 vs. 5.64), and no significant differences between both doses were recorded. Irrespectively to enzyme supply, kinetics of gas production and pattern of degradation of maize were generally higher than those of sorghum. A significant effect ($P < 0.0001$) of the diet (maize or sorghum) and the interaction between diet and enzyme were recorded for the volume of gas produced at different incubation times. The use of high doses of glucoamylase enzyme should be tested on the pattern rumen fermentation

Key Words: glucoamylase, in vitro fermentation, maize

TH80 Effects of feeding *Bacillus subtilis* and *Bacillus licheniformis* on performance, health parameters, and a low quality roughage diet intake and digestibility by lambs. E. Martínez*, A. A. Rodríguez, and L. C. Solórzano, *University of Puerto Rico, Mayagüez, Puerto Rico*

The dietary addition of *Bacillus subtilis* and *Bacillus licheniformis* (BSL) during 49 d, phase 1 (P1), and possible residual effects thereof during phase 2 (P2) without the probiotic addition on lamb performance, health parameters, and intake and digestibility of a low quality roughage was evaluated. Ten crossbred lambs (11.2 kg) were randomly assigned to one of 2 dietary treatments, with (T2) or without (T1) daily addition of BSL in P1. The diet consisted of 50% mixed grass hay (71.5% NDF, 5.2% CP) and 50% *Hyparrhenia rufa* hay (77.2% NDF, 4.5% CP) at a daily hay offering level equivalent to 4% of body weight on a dry basis; water was available ad libitum. The bacterial strains were mixed with a calcium carbonate carrier, and included in the additive to provide 1.33×10^9 cfu/g supplying 1.33×10^8cfu/head/daily. The additive was mixed with 225 g of a commercial concentrate (16.3% CP) and fed daily to the lambs during d 49 (P1). Residual effects were measured from d 50 to d 84 (P2). In both phases, lambs were weighed weekly to monitor changes in body weight. Feces and blood sampling and FAMACHA index scoring were carried out every 21 d on individual animals to determine changes in fecal egg counts (FEC), packed cell volume (PCV)

and relative anemia level, respectively. Feed intake and digestibility were determined in the latter part of each phase. Statistical analysis of data within period was performed as a completely randomized design with 5 replicates per treatment. During P1, the addition of BSL improved ($P < 0.05$) feed intake (484 vs. 445 g/d) and NDF digestibility (62.5 vs.58.7%), but did not affect lamb total body weight gain or changes in health parameters such as FEC, PCV and anemia level. During P2 total body weight gain, changes in FEC, PCV, anemia, diet intake (T1 = 588 and T2 = 564 g/d) and digestibility (T1 = 58.5 and T2 = 57.6%) were not affected ($P > 0.05$) by previous treatments. The addition of BSL improved diet intake and cell-wall digestibility in growing lambs, but no beneficial residual effects of the microbial additive were observed.

Key Words: *Bacillus* spp., health, lamb performance

TH81 Use of organic acids and polyphenols to mitigate induced ruminal acidosis in dairy heifers. R. De Nardi*[1], S. Segato[1], J. C. Plaizier[2], S. Li[2], E. Khafipour[2], I. Andrighetto[1,3], and G. Marchesini[1], *[1]Department of Animal Medicine, Productions and Health, University of Padova, Legnaro (Padova), Italy, [2]Department of Animal Science, University of Manitoba, Winnipeg, Manitoba, Canada, [3]Istituto Zooprofilattico Sperimentale delle Venezie, Legnaro (Padova), Italy.*

The aim of this study was to determine the effects of supplementation of dairy heifers with organic acids or polyphenol-essential oil mixtures on their ability to cope with induced subacute ruminal acidosis (SARA). In each of 3 periods heifers were fed a low starch (LS) diet (NDF 39.8%, NSC 36.4%, starch 24.0% DM) for 2 wk followed by a high starch (HS) diet (NDF 33.6%, NSC 43.2%, starch 30.0% DM) for 8 d. To induce SARA top dressed barley meal was given (0.5–1.5 kg) in the last 5 d of the study. During the HS diet 6 Holstein heifers were randomly assigned to 1 of 3 dietary treatments in a 3 × 3 factorial design: no supplement (Ct), a daily dose of 60 g of fumarate and malate mixture (Fm) or 100 g of polyphenol and essential oil mixture (Pol). Reticular pH values were continuously measured using wireless sensors and compared with pH measurements obtained by rumenocentesis. Fecal pH was measured at 0800, 1400 and 2100 h. Fm led to a lower DMI due to its possible lower palatability. The correlation coefficient comparing the pH values obtained using the 2 methods was 0.83 ($P < 0.001$). Although the mean and maximum daily reticular pH were not affected by the treatment, the nadir pH resulted the lowest in Ct treatment, confirming the effectiveness of both the supplements in mitigating the pH drop. This result was confirmed also by the greatest mean time spent daily by the control-fed heifers below the 5.6 pH threshold compared with Fm and Pol. The fecal pH was not affected by treatment, and its values were 6.43, 6.69, and 6.74, at 0800, 1400, and 2100 h, respectively ($P < 0.001$). This study showed that both the addition of fumarate-malate and polyphenol-essential oil mixtures could help in the prevention of SARA in cattle.

Table 1. Effect of supplementation on DMI and pH

	Ct	Fm	Pol	SEM	*P*-value
DMI,[1] kg/d	14.4	13.6	14.7	0.58	0.079
Reticular nadir pH[1]	5.48[b]	5.66[a]	5.60[a]	0.040	0.027
Reticular mean pH[1]	6.07	6.09	6.08	0.020	0.653
Reticular maximum pH[1]	6.58	6.56	6.53	0.038	0.448
Time spent below 5.6 pH,[2] min	120	16	21	—	0.091

[a, b]Means with different superscripts within a row differ ($P < 0.05$).
[1]Linear mixed model.
[2]Nonparametric Kruskal-Wallis test;

Key Words: organic acid, polyphenol, subacute ruminal acidosis

TH82 Effects of exogenous enzymes on in vitro gas production kinetics and degradation of wheat dried distillers grains with solubles and barley silage. Z. X. He*[1,2], S. Ding[1], L. Xu[1,3], K. A. Beauchemin[1], and W. Z. Yang[1], *[1]Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [2]Key Laboratory of Agro-Ecological Processes in Subtropical Region, Institute of Subtropical Agriculture, the Chinese Academy of Sciences, Changsha, Hunan, China, [3]College of Food Science and Engineering, Inner Mongolia Agricultural University, Hohhot, Inner Mongolia, China.*

In vitro batch cultures were conducted to examine the effects of exogenous enzymes (EE) on gas production (GP) kinetics and ruminal fermentation of wheat dried distillers grains with solubles (DDGS) and barley silage. Seven EE were obtained from several manufacturers (E1, E2, E3, E4, E5, E6 and E7) that contained a range of xylanase, endoglucanase, exoglucanase and protease activities. Each was evaluated at 6 doses (0, 0.5, 1, 2, 4, 8 μL/g DM). The GP was recorded at 3, 6, 9, 12, 24, 36 and 48 h for DDGS, and until 72 h for barley silage. After 48 h (DDGS) or 72 h (barley silage) of incubation, degradability of DM (DMD) and NDF (NDFD) were determined. To estimate kinetic parameters of GP, results (mL/g DM) were fitted using the NLIN option of SAS using equation $A = b \times (1\text{-}e^{-c(t-L)})$. For DDGS, there was an interaction ($P < 0.01$) between EE and enzyme dosage (ED) on rate of GP and GP. Rate of GP (/h) linearly ($P < 0.05$) increased with increasing ED, except for E6, and quadratic effects were rarely observed. Additionally, GP linearly ($P < 0.05$) increased with increasing ED mostly at 6, 9 to 12 h, except for E5 and E6. For some EE, DMD and NDFD linearly ($P < 0.01$) increased with ED. Maximum improvements ($P < 0.05$) in DMD and NDFD were, respectively: E2 (51 to 53%; 40 to 44%), E3 (51 to 53%; 40 to 45%), E4 (51 to 52%; 40 to 42%), and E6 (51 to 55%; 40 to 47%). For barley silage, there was overall no interaction between EE and ED for rate of GP and GP. A linear increase ($P < 0.05$) in GP with increasing ED was only observed during early incubation times (3 to 9 h) for most of the EE tested. The DMD and NDFD were generally not affected by the EE although NDFD numerically ($P = 0.10$) increased for E2 (0 vs. 1 or 2 mL/g DM; 49 vs. 55%), E3 (0 vs. 0.5 mL/g DM; 49 vs. 56%), and E6 (0 vs. 1 mL/g DM; 49 vs. 54%). These results demonstrate the potential of EE to improve ruminal degradability of DDGS, but the improvements in degradability of barley silage using EE are less pronounced. Furthermore, extending the incubation time to 72 h could negate the beneficial effects of EE on degradability.

Key Words: exogenous enzyme, gas production, wheat DDGS

TH83 Selenium-enriched tall wheatgrass hay as a substitute for sodium selenite in diets of dairy cattle. G. S. Cun*[1,2], P. H. Robinson[2], and S. E. Benes[1], *[1]California State University, Fresno, Fresno, [2]University of California, Davis, Davis.*

California's San Joaquin Valley (SJV) is one of the most agriculturally productive areas in the United States. However, due to strict environmental restrictions, re-use of agricultural drainage and tail water to irrigate salt-tolerant forage crops is attractive. 'Jose' tall wheatgrass (TWG) is a Se-accumulating salt tolerant forage suitable for such cropping systems, and as a ruminant feed, which re-uses agricultural drainage and tail water as an irrigant. Utilization of TWG as a Se supplement for dairy cattle would reduce importation of 'new' Se into the SJV of California as sodium selenite (NaSe), a common dietary supplement of dairy cattle, in the eastern SJV where Se levels are low in soils and forages. Our study utilized Se-enriched (~5 mg/kg of DM) TWG hay as a Se source for lactating dairy cows and determined Se accumulation patterns in blood, urine and feces to determine its bioavailability. Three pens of ~310 cows each were fed a similar total mixed ration in a 3 × 3 Latin square design with 4-wk periods, except that the supplemental Se source differed (i.e., none; from TWG; from NaSe).

The chemical composition of the diets was the same, except for Se which was higher ($P < 0.01$) in the TWG and NaSe diets (0.53 and 0.65 mg/kg DM) versus 0.35 mg/kg DM in the control diet. Feeding Se-enriched TWG increased blood Se by 6.4% over control, whereas NaSe increased it 4.8%, suggesting slightly higher bioavailability for Se in TWG hay versus NaSe. In contrast, the amount of dietary Se that was apparently digested increased from 47 to 58% with NaSe, but with TWG supplementation there was no increase over the control, suggesting lower bioavailability for TWG compared with NaSe. As Se outputs in the urine did not differ ($P = 0.07$) among treatments, the metabolizability of Se for the NaSe diet was higher than that for the Control and TWG diets. Overall, the similar metabolizability of Se in the TWG diet to that in the base diet suggests that Se-enriched TWG hay can be a value-added Se feed for cattle producers in the eastern SJV who are currently challenged by environmental regulations to reduce use of 'new' (to the SJV) trace minerals in their cattle rations.

Key Words: fortified forage, ruminant

TH84 The effect of different sources of zinc on some blood mineral of finishing lambs. M. Mallaki*, M. A. Norouzian, and A. A. Khadem, *The University of Tehran, Tehran, Iran.*

The effect of different sources of zinc on serum blood concentration of zinc, copper, iron, calcium and phosphor were studied. Eighteen male Zandi lambs (21.28 ± 0.85 kg BW and 70 ± 5 d of age) were randomly allocated to 1 of 3 dietary treatments in a randomized design. Animals in group 1 were treated as control (no zinc supplementation), whereas animals in groups 2 and 3 were supplemented with 25 mg of zinc/kg DM from either zinc peptide (ZnP) or zinc sulfate monohydrate (ZnS), respectively. Lambs were blooded from jugular vein at began of study (d 0) and d 35 and 69 of experiment for determination of serum mineral. The Zn serum concentration for ZnP (155.2 μg/dL) and ZnS (149.7 μg/dl) groups were greater than the control (134.6 μg/dL) group ($P < 0.05$). Lambs fed diets containing ZnP had lower concentration of serum Cu and Fe (76.17, 92.08, 96.58 and 146.5, 157.4, 182.4 μg/dL for ZnP, ZnS and Control, respectively; $P < 0.05$). There was no significant difference between experimental groups for serum Ca and P (11.59, 11.16, 11.38 and 8.86, 9.21, 9.88 mg/dL for ZnP, ZnS and Control, respectively). These results indicate source of Zn supplementation in diets of finishing lambs affect mineral profile of blood and increase concentration of Zn.

Key Words: blood mineral, finishing lamb, Zinc

TH85 Effects of supplemental niacinamide on lactation performance and rumen fermentation of Holstein cows under heat stress. L. Pan[2], D. P. Bu[2], J. Q. Wang*[1,2], J. B. Cheng[2], X. Z. Sun[2], and W. Liu[2], *[1]Agronomy College of Heilongjiang August First Land Reclamation University, Heilongjiang, China, [2]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Niacinamide (NAM) has been used to reduce heat stress in dairy cows. However, effects of NAM on relieving heat stress are not consistent. This experiment was conducted to study effects of NAM on lactation performance and rumen fermentation of heat-stressed cows. Twenty Holstein cows (DIM = 78.8 ± 11.0; milk production = 37.7 ± 1.8 kg/d; parity = 1.7 ± 0.3) were divided randomly into 2 groups and were individually fed a basal diet (control) or the basal diet with 8 g/head/d NAM. The experiment lasted for 10 wk in hot summer. Ambient temperature and humidity were daily measured 3 times. Milk yields and feed intake were recorded twice a week, and milk samples were collected every 10 d. Respiration rates (RR) and rectal temperatures (RT) were measured for 2 consecutive days every week. Rumen fluid samples were collected at wk 6 and 10 of the trial. Data were analyzed by repeated measurements using Proc Mixed procedure of SAS. During the experiment, average ambient temperature and temperature-humidity index were respectively 27.52 ± 1.54°C, 29.77 ± 1.89°C and 28.13 ± 1.69°C, and 78.20 ± 2.74, 79.72 ± 3.26 and 78.26 ± 3.37 at 6:00h, 14:00h and 22:00h. RR was decreased (69.27 vs. 76.31 breaths/min, $P < 0.01$; 71.64 vs. 77.15 breaths/min, $P < 0.01$), while RT was not different (39.18 vs. 39.17°C, $P = 0.92$; 39.53 vs. 39.44°C, $P = 0.27$) at 06:00 and 14:00 compared with control. There was no significant difference in milk yield or dry matter intake between treatments. However, 4% fat-corrected milk yields (28.82 vs. 27.27 kg/d, $P < 0.01$) and energy-corrected milk yields (31.28 vs. 29.63 kg/d, $P < 0.01$) were increased. There was no treatment effect on milk protein concentration or milk fat concentration, while milk fat yield was increased in NAM group compared with control (1.08 vs. 1.00 kg/d, $P < 0.01$). Rumen pH, ammonia-N concentration and total volatile fatty acid concentration were not different between groups. In conclusion, while indicators of heat stress were ameliorating for cows fed NAM, this slight increase in cow comfort did not result in improving lactation performance or rumen fermentation significantly.

Key Words: cow, heat stress, niacinamide

TH86 Effect of Rumensin and Amaferm on performance of heifers fed in dry lot and on wheat pasture. H. Gray*[1], P. Beck[1], K. Glaubius[2], and B. Stewart[1], *[1]University of Arkansas, Hope, [2]BioZyme Incorporated, St. Joseph, MO.*

Previous studies have found adding Rumensin to diets will increase cattle performance by improving ruminal efficiency. Results have shown that by adding Amaferm to the diet, fungal activity in the rumen will increase, allowing more surface area for bacteria to attach to and maximize the digestion of high fiber forages. The objective of this research was designed to test the effects of adding Rumensin and Amaferm on performance of growing beef heifers fed high roughage mixed diets in dry lot and while grazing wheat pasture. Angus influenced cross-bred heifers (n = 72; BW = 220 ± 5.5 kg) were placed in 12 (7 × 3 m) dry lot pens located in Hope, AR. Calves were fed ad libitum a diet of corn stalk hay (50% as fed) and corn distiller's grains, and corn as the primary concentrate energy sources for 83-d beginning in early November. Heifers were then placed on 12, 0.8-ha cool-season annual pastures keeping heifers within their original feeding groups, feeding Amaferm and/or Rumensin in 0.9 kg soybean hulls/heifer daily. Data were analyzed as a complete randomized design with 2 × 2 factorial arrangement of treatments using mixed procedure of SAS. Pen (or pasture) treatment was the experimental unit and heifer the sampling unit. There was no Rumensin by Amaferm interaction in dry lot or pasture performance ($P \geq 0.72$). In dry lot, total BW gain, ADG, feed intake and feed efficiency were not affected by treatment ($P \geq 0.16$). On pasture there, however, was a tendency ($P = 0.10$) for Amaferm to increase BW gain by 7.9 kg and ADG by 0.10 kg/d. These results indicate Rumensin and Amaferm did not affect performance of heifers fed of these high roughage low energy diets but Amaferm inclusion provided improved performance on high-quality pasture.

Key Words: Amaferm, growing heifer, Rumensin

TH87 Effects of salinomycin and virginiamycin supplementation on ruminal fermentation and blood characteristics of Nellore steers fed a high concentrate diet. A. J. C. Nuñez*[1], V. V. Almeida[2], J. P. Schoonmaker[3], I. E. Borges[1], F. Pinese[1], F. T. Mercado[1], E. M. Ferreira[4], A. V. Pires[4], P. R. Leme[1], and J. C. M. Nogueira Filho[1], *[1]FZEA/USP, Pirassununga, SP, Brazil, [2]FCAV/UNESP, Jaboticabal, SP, Brazil, [3]Purdue University, West Lafayette, IN, [4]ESALQ/USP, Piracicaba, SP, Brazil.*

This experiment was conducted to evaluate the effects of the supplementation with salinomycin (SL), virginiamycin (VM), or their combination on ruminal fermentation and blood characteristics of Nellore steers receiving an 80% concentrate diet (DM basis). Eight ruminally cannulated Nellore steers (322 ± 26 kg of initial BW) were allotted to a 4 × 4 replicated Latin square design with 16-d periods. Treatments were arranged as a 2 × 2 factorial, with 2 SL levels (0 and 13 ppm) and 2 VM levels (0 and 15 ppm) in the diet DM. Animals were housed in individual pens and fed once daily at 0800 h. On d 13 of each period, ruminal fluid samples were collected at 0, 2, 4, and 8 h post-feeding to determine pH and concentrations of VFA and lactate. Blood samples were collected by jugular venipuncture at 2 h post-feeding on d 14 of each period to determine pH and concentrations of lactate and bicarbonate. Statistical analyses were conducted using the MIXED procedure of SAS. No interactions between SL and VM levels, nor between time of collection and SL or VM levels were observed. The inclusion of VM in the diets decreased ($P = 0.01$) ruminal concentrations of acetate (63.4 and 59.4 ± 1.1 m*M* for 0 and 15 ppm VM, respectively), butyrate (12.0 and 10.5 ± 0.3 m*M* for 0 and 15 ppm VM, respectively), and lactate (0.42 and 0.39 ± 0.01 m*M* for 0 and 15 ppm VM, respectively), and increased ($P = 0.01$) ruminal concentrations of propionate (21.5 and 23.6 ± 0.6 m*M* for 0 and 15 ppm VM, respectively). There was a tendency ($P = 0.08$) for increased ruminal pH (6.42 and 6.48 ± 0.03 for 0 and 15 ppm VM, respectively) in VM-treated steers. There were no effects of VM level on blood pH and bicarbonate concentrations, but lactate concentrations were higher (0.57 and 0.79 ± 0.06 m*M* for 0 and 15 ppm VM, respectively; $P = 0.05$) in the blood of steers receiving the antibiotic. No effects of SL were observed for any analyzed variable. The inclusion of VM in high concentrate diets for Nellore steers improves ruminal fermentation by increasing propionate and decreasing lactate production.

Key Words: antibiotics, beef cattle, ionophore

TH88 Concentrate level and combined use of ionophore and virginiamycin on ruminal fermentation and blood characteristics of Nellore steers fed high grain diets. A. J. C. Nuñez*[1], V. V. Almeida[2], J. P. Schoonmaker[3], F. Pinese[1], I. E. Borges[1], F. T. Mercado[1], E. M. Ferreira[4], A. V. Pires[4], P. R. Leme[1], and J. C. M. Nogueira Filho[1], *[1]FZEA/USP, Pirassununga, SP, Brazil, [2]FCAV/UNESP, Jaboticabal, SP, Brazil, [3]Purdue University, West Lafayette, IN, [4]ESALQ/USP, Piracicaba, SP, Brazil.*

Eight ruminally cannulated Nellore steers (434 ± 35 kg initial BW) were used in a 4 × 4 replicated Latin square design (21-d periods) to evaluate the effects of concentrate and virginiamycin (VM) levels in diets containing salinomycin (SL) on ruminal fermentation and blood characteristics of Zebu cattle. Treatments were arranged as a 2 × 2 factorial arrangement, with 2 concentrate levels (70C and 90C diets had 70 and 90% concentrate, respectively) and 2 VM levels (0 and 15 ppm) in the diet DM. Steers were fed once daily at 0800 h and all diets included the ionophore SL (13 ppm). On d 18 of each period, ruminal fluid samples were collected at 0, 2, 4, and 8 h post-feeding to determine pH and concentrations of VFA and lactate. Blood samples were collected by jugular venipuncture at 2 h post-feeding on d 19 of each period to determine pH and concentrations of lactate and bicarbonate. Statistical analyses were performed using the MIXED procedure of SAS. There were no interactions between time of collection and concentrate or VM levels for any analyzed variable. Ruminal concentrations of acetate were lower ($P = 0.01$) for the 90C treatment in comparison with the 70C group. Acetate concentrations were also lower ($P < 0.01$) for steers receiving VM and SL in comparison with those fed only SL. The inclusion of VM increased ($P < 0.01$) ruminal concentrations of propionate in steers from the 90C treatment, whereas VM decreased ruminal butyrate concentrations ($P < 0.01$) for animals fed the 90C diet. Ruminal pH and lactate concentrations were not affected by VM inclusion. Increasing dietary concentrate level increased ruminal concentrations of lactate ($P < 0.01$) and decreased ruminal pH ($P < 0.01$). Blood pH and bicarbonate concentrations were lower ($P < 0.01$) in steers from the 90C treatment, whereas blood lactate concentrations did not differ between concentrate levels. Blood characteristics were not affected by VM inclusion. These results indicate that the combined use of SL and VM has positive effects on ruminal fermentation, especially when dietary concentrate levels are greater.

Key Words: antibiotics, beef cattle, salinomycin

TH89 Effects of different amino acid patterns on the expression of four major milk protein genes in primary cultured bovine mammary epithelial cells. X. F. Zhang[1], C. J. Ao*[1], M. Gao[2], E. Khas[1], H. Zhang[1], and L. W. Song[1], *[1]Department of Animal Science, Inner Mongolia Agricultural University, Hohhot, Inner Mongolia, China, [2]Inner Mongolia Academy of Agricultural & Animal Husbandry Sciences, Hohhot, Inner Mongolia, China.*

The objective of this study was to determine whether different amino acid (AA) patterns could affect milk protein gene (α_{S1}-casein, α_{S2}-casein, β-casein, κ-casein) expression in bovine mammary epithelial cells. Mammary tissues were collected from a 3 years old lactating Chinese Holstein dairy cow (DIM 100-d), Primary mammary epithelial cells were isolated by modifications of the methods of Miranda et al., (2009). A completely random design was used with 4 AA patterns as treatments (Table 1), each treatment has 3 replicates, and all experiments were repeated 3 times. Data were analyzed by the ANOVA using the GLM procedure of SAS (9.0). The concentration of total AA in each medium was 534 mg/L. The results showed that different patterns of AA can induce the expression of αs1-casein, β-casein and κ-casein genes differently ($P < 0.05$), in contrast, the expression of αs2-casein gene was not significantly affected ($P = 0.26$). The milk pattern, casein pattern and combination pattern of AA increased the expression of αs1-casein and κ-casein genes significantly ($P < 0.05$) compared with blood AA pattern. The milk pattern, casein pattern and blood pattern of AA upregulate β-casein gene expression compared with combination AA pattern ($P < 0.05$). In conclusion, the milk pattern might increase major milk protein genes expression, perhaps, an appropriate AA pattern will play a very important role in milk protein synthesis.

Table 1. The percentage of amino acids in different patterns[1]

AA, %	Blood	Milk	Combination	Casein
Tyr	2.18	5.67	6.30	6.63
Ala	11.66	3.78	2.91	2.77
Gly	29.77	2.27	0.40	0.48
Glu	10.5	29.3	25.0	26.4
Ser	8.31	6.05	5.93	6.03
Cys	4.15	0.76	1.16	0.48
Phe	2.29	6.05	6.54	6.63
Leu	5.75	10.97	18.52	17.37
lle	3.94	5.30	6.17	6.27
His	1.28	3.78	2.32	2.41
Lys	2.72	10.21	7.46	7.24
Thr	6.76	5.67	5.60	5.55
Met	0.80	2.27	3.65	3.74
Try	1.65	1.89	1.80	1.57
Val	8.25	6.05	6.22	6.39
Tyr	2.18	5.67	6.30	6.63

[1]Blood pattern comes from Weekes et al. (2009). Milk pattern and Casein pattern come from Martin et al. (1944). Combination pattern (80% casein pattern plus 20% lactoalbumin pattern) also comes from Martin et al. (1944).

Key Words: amino acid, bovine mammary epithelial cell, gene expression

TH90 Effects of tributyrin supplementation in milk replacer on performance and gut development of Holstein calves. G. Araujo*[1], M. Terré[1], A. Mereu[2], I. Ipharraguerre[2], and A. Bach3,1, *[1]Department of Ruminant Production, IRTA, Caldes de Montbui, Spain, [2]Lucta S.A., Barcelona, Spain, [3]ICREA, Institut de Recerca i Estudis Avançats, Barcelona, Spain.*

Sodium butyrate (SB) is often used as an additive for milk replacers (MR) to improve calf performance. Tributyrin (TRB) is a triglyceride containing equivalent amount of butyrate than SB but in a more stable form. The aim of this study was to evaluate the effects of supplementing a MR with TRB on performance and development of the gastro-intestinal tract (GIT) of suckling calves. Thirty-six Holstein calves (46 ± 5.9 kg BW and 12 ± 3.0 d age) were fed 4 L/d of MR at 12.5% DM dilution and water and starter feed ad libitum. Calves were randomly distributed in 2 groups. Milk replacer was either unsupplemented (CTR) or supplemented with 3 g of TRB per kg of DM (TRB). Five calves per group were feed-restricted at 200 g/d of starter and killed on d 42 of study to measure rumen VFA, pH and GIT weights. Starter and MR intakes were recorded daily on an individual basis and calves were weighed every 14 d. Data for VFA, pH and GIT weights were analyzed using ANOVA and performance parameters were analyzed using ANOVA with time as a repeated measure. Milk replacer intake was greater ($P < 0.01$) in CTR than in TRB calves (591.7 vs. 585.4 ± 39.02 g of DM/d; respectively). The CTR calves tended ($P = 0.06$) to have a greater starter feed intake than TRB calves, and total DMI was greater ($P < 0.01$) in CTR than in TRB calves (358.2 vs. 260.8 ± 1.15 g of DM/d; respectively). Moreover, BW and ADG were greater ($P < 0.01$) for CTR calves (68.2 ± 0.94 kg and 0.53 ± 0.024 kg/d, respectively) compared with TRB (63.8 ± 0.94kg and 0.42 ± 0.024kg/d; respectively). Gain to feed ratio was also greater ($P < 0.05$) for CTR calves compared with TRB (0.57 vs. 0.48 ± 0.026; respectively). Rumen pH, VFA profile, and GIT weights were not affected by treatments. Nevertheless, CTR calves tended ($P = 0.07$) to have a heavier abomasum than TRB calves, whereas TRB calves tended ($P = 0.08$) to have a heavier duodenum than CTR calves. In conclusion, these results provide no evidence that butyrate addition to MR in the form of TRB at 3 g/kg of DM has positive effects on performance or GIT development of pre-weaned calves.

Key Words: calf, performance, tributyrin

TH91 Casein and whey protein as delivery methods for synthetic vitamin B12 to increase intestinal absorption in lactating dairy cows. V. M. Artegoitia*[1], M. J. de Veth[2,3], F. Harte[1], D. R. Ouellet[4], and C. L. Girard[4], *[1]Department of Food Science and Technology, University of Tennessee, Knoxville, [2]Department of Animal Science, University of Tennessee, Knoxville, [3]Balchem Corporation, New Hampton, NY, [4]Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada.*

Improving vitamin B12 absorption is important for optimal performance in dairy cows and for increasing vitamin B12 concentrations in milk for human consumption. However, 80% of a supplement of synthetic vitamin B12, cyanocobalamin (CN-CBL), is degraded in the rumen of dairy cows and only 25% of the amount escaping destruction in rumen disappears in the small intestine. The objective of this study was to evaluate the efficacy of casein and whey protein as delivery methods for CN-CBL to increase intestinal absorption of vitamin B12 in cows. Four multiparous lactating Holstein cows (237 ± 17 DIM) equipped with a rumen cannula and catheters in the portal vein and a mesenteric artery were used in a randomized crossover design. They were fed 12 equal meals/d to maintain steady-state. On experimental days, they received an abomasal bolus of: 1) CN-CBL alone (100 mg; CA), 2) CN-CBL (100 mg) + casein (10 g; CC) or 3) CN-CBL (100 mg) + whey proteins (10 g; CW). After the bolus, blood samples were taken simultaneously from the 2 catheters every 30 min during the first 4 h and then every 2 h until 24 h post-bolus. Milk yield, DMI, and vitamin B12 porto-arterial concentration differences (P-A) were analyzed using the MIXED procedure of SAS. Milk yield and DMI were not affected by treatments ($P > 0.8$). Overall, vitamin B12 P-A was positive during the first 90 min after the abomasal bolus but negative or not different from 0 until the end of the sampling period ($P = 0.007$). On average for the 24-h period after the abomasal bolus of CN-CBL, vitamin B12 P-A was negative for CA ($P = 0.008$) and CW ($P = 0.06$) but not different from 0 ($P = 0.7$) for CC. There was a trend for a treatment effect ($P = 0.08$) for P-A with CA being lower from CC ($P = 0.03$; −21.43 pg/mL, SEM = 5.8 vs. 2.28 pg/mL, SEM = 6.3) whereas CW (−12.76 pg/ml, SEM = 5.9) did not differ from the 2 others treatments. The present results suggest that CN-CBL given with casein increases vitamin B12 absorption as compared with CN-CBL given alone. For practical applications of our findings, development of a casein-based formulation may improve CN-CBL absorption in dairy cows.

Key Words: bioavailability, cyanocobalamin, vitamin

TH92 The effects of propyl-propylthiosulphonate and capsicum addition on ruminal fermentation and animal performance of lactating dairy cows. A. Foskolos*[1], A. Siurana[1], A. Ferret[1], L. Castillejos[1], D. Bravo[2], and S. Calsamiglia[1], *[1]Universitat Universitat Autònoma de Barcelona, Bellatera, Spain, [2]Pancosma, Geneva, Switzerland.*

The last decade the social concern on food safety stimulated research on plant extracts (PE) as alternatives to antibiotics. However, data from in vivo experiments is limited. We conducted an in vivo study to test the addition of propyl-propylthiosulphonate (PTSO), a stable compound of garlic, and capsicum (CAP), the active compound of hot peppers, on ruminal fermentation and animal performance of lactating dairy cows. Six Holstein dairy cows fitted with cannulas in the rumen were assigned randomly to one of 3 treatments in a duplicate 3x3 Latin Square design. Treatments were: control (CTR; no addition of PE), CAP (0.5 g/animal/day of capsicum oil; Pancosma), and PTSO (0.25 g/animal/day of PTSO; Garlicon, Pancosma). Each experimental period lasted 4 weeks, the first 3 for adaptation and the fourth for sampling. Cows were milked twice daily and milk samples were analyzed for their chemical composition and fatty acid (FA) profile. Ruminal samples were collected at 8 h intervals on 4 consecutive days with a 2 h shift between days, providing 12 samples, one from every even hour of the 24 h day. Rumen liquid was analyzed for pH, ammonia-N and volatile fatty acid concentrations. Significance of was declared at $P < 0.05$. The addition of PE compounds did not affect dry matter intake, milk production and ruminal fermentation profile. The addition of PTSO increased milk concentration of monosaturated (29.9 vs. 26.7 for PTSO and CTR, respectively) and unsaturated FA (38.2 vs. 34.7 for PTSO and CTR, respectively) in expense of saturated FA (61.8 vs. 65.3 for PTSO and CTR, respectively). Moreover, PTSO addition decreased the concentration of C13:0 and C15:0 and increased the concentration of C16:1, C17:1, C18:1 and C18:2. The addition of CAP increased milk protein (3.39 vs. 3.29% for CAP and CTR, respectively) and fat (3.88 vs. 3.62 for CAP and CTR, respectively) concentration and reduced somatic cell counts (215 vs. 621 × 10^3 cells/mL for CAP and CTR, respectively). Results indicate that supplementation of CAP improved milk quality and PTSO improved the fatty acid profile of milk fat.

Key Words: capsicum, dairy cow, propyl-propylthiosulphonate

TH93 The effect of feed additives on in vitro volatile fatty acid production. A. Duncan*, A. Woldeghebriel, and M. Worku, *North Carolina Agricultural and Technical State University, Greensboro.*

The study was conducted to determine the effects of feed additives on in vitro production of VFA. Ruminal fluid was collected from 2 fistulated dairy animals (a cow and a steer averaging 650 kg) that were fed 11.4 kg of TMR consisting of equal amounts of soybean meal, whole cottonseed, and ground corn once a day with free access to hay. Feed grab sample was oven-dried, coarsely pulverized in a regular kitchen blender for one minute, and separated into 3 particle-sizes (PS; 0.85, 1.00 and 1.40 mm). The feed additives used were nitrate, fumarate and combination at 1:4 feed ratios. The experimental design was a 3 × 4 factorial (3 PS and 4 feed additive combinations). The treatments used were (1) feed only, as control (CON); (2) CON + nitrate; (3) CON + fumarate; and (4) CON + a 50/50 nitrate-fumarate mix. A 4-g sample from each PS for each treatment was weighed in triplicates and transferred to 500-mL flask. Each flask received 400 mL of rumen fluid-buffer mixture according to the Tilley and Terry procedures and incubated at 37°C for 48 h. Volatile fatty acid concentration from the rumen fluid was measured by GC. Data collected were analyzed using the GraphPad Prism software and means were compared using the Student's *t*-test ($P < 0.05$). Results of the study shows that the most abundant VFA found in the CON were acetate ($C_{2;}$ 53.4%), propionate ($C_{3;}$ 20.5%), and butyrate ($C_{4;}$ 16.4%) in a 2.6:1.0 C_2:C_3 ratio. However, the addition of nitrate alone, or in combination with fumarate increased the ratio of the VFA (65.2, 23.4, and 5.3, and 54.1, 28.1, and 10.4%, respectively). Addition of fumarate on the other hand increased the concentration of propionate by as much as 29.1% resulting in 2:1 C_2:C_3 ratio compared with the CON. The lower acetate to propionate ratio with fumarate may indicate a fundamental shift in the microbial population as indicated by the shift in the VFA profile.

Key Words: feed additive, in vitro, VFA

TH94 Anionic diets with chromium or methionine for transition cows on hormone and metabolic profile. I. R. F. M. Veiga[1], B. N. de Faria[1], T. L. Resende[1], A. B. D. Pereira[2], and R. B. Reis*[1,3], *[1]Veterinary School, Federal University of Minas Gerais, Belo Horizonte, Minas Gerais, Brazil, [2]University of New Hampshire, Durham, [3]FAPEMIG, Minas Gerais, Brazil.*

Seventy-two multiparous Holstein dairy cows were housed 25 ± 8 d before calving and allocated in 6 treatments, Control (C): basal prepartum diet (DCAD = +16.38 mEq/100gDM); Chromium (CC): control plus 7.56mg of organic chromium MiCroPlex (Zinpro Corporation); Methionine plus Chromium (CCM): control plus 7.56mg of organic chromium and 13.24g of DL-methionine hydroxy analog MFP (Novus International Inc.; Anionic (A): (DCAD = −15.69mEq/100gDM); Anionic plus Chromium (AC): Anionic plus 7.56mg of organic chromium; Anionic plus Chromium and Methionine (ACM): anionic plus 7.56mg of organic chromium and 13.24g of DL-methionine hydroxy analog. The completely randomized design with split plot was used and analyses for orthogonal contrasts were performed. Plasma levels of insulin, cortisol, glucose, nonesterified fatty acids (NEFA) and serum albumin were determined on days −21, −14, −7, −1, 1, 7, 14 and 21 relative to calving. The NEFA levels increased as the parturition approached with a peak for all treatments at first day postpartum. The main difference among treatments occurred during postpartum when treatment A showed higher levels of NEFA ($P = 0.051$; 0.010; 0.052; respectively for 1, 7 and 14 d postpartum) compared with AC diet. The insulin levels decreased until the first week postpartum when the lower values were found (5.95µg/dl). The variation among treatments appeared on 7 and 14 d after calving when treatment A had higher values of insulin compared with AC diet ($P = 0.049$; 0.018, respectively). On the other hand, the addition of chromium to the control diet increased the insulin levels during the postpartum compared with the control diet. There was no effect of A diets or the association with chromium and methionine on glucose and cholesterol during the transition period. The use of chromium associated with anionic diets could possibly alter the mobilization of body reserves of high producing dairy cows, but more research is necessary to prove this.

Key Words: insulin, mobilization of body reserves, nonesterified fatty acids

TH95 The effecs of anionic diets with chromium or methionine for transition cows on blood mineral levels. I. R. F. M. Veiga[1], B. N. de Faria[1], T. L. Resende[1], A. B. D. Pereira[2], and R. B. Reis*[1,3], *[1]Veterinary School, Federal University of Minas Gerais, Belo Horizonte, Minas Gerais, Brazil, [2]University of New Hampshire, Durham, [3]FAPEMIG, Minas Gerais, Brazil.*

Seventy 2 multiparous Holstein dairy cows were housed 25 ± 8 d before calving and allocated in 6 treatments, Control (C): basal prepartum diet (DCAD = +16.38mEq/100gDM); Chromium (CC): control plus 7.56mg of organic chromium MiCroPlex (Zinpro Corporation); Methionine plus Chromium (CCM): control plus 7.56mg of organic chromium and 13.24g of DL-methionine hydroxy analog MFP (Novus International Inc.); Anionic (A): (DCAD = −15.69mEq/100gDM); Anionic plus Chromium (AC): Anionic plus 7.56mg of organic chromium; Anionic plus Chromium and Methionine (ACM): anionic plus 7.56mg of organic chromium and 13.24g of DL-methionine hydroxy analog. The completely randomized design with split plot was used and analyses for orthogonal contrasts were performed. Plasma concentrations of calcium (Ca), phosphorous (P), magnesium (Mg), potassium (K) and 25 OH Vitamin D were determined on days −21; −14, −7; −1; 1; 7; 14 and 21 relative to calving. The Ca concentrations remained stable until calving and decreased on day one postpartum reaching the lowest level (9.31 mg/dL). It returned to values similar to prepartum (10.47 mg/dL) on d 14, and didn't differ among treatments. At the first day after calving the Mg concentration was different ($P = 0.038$) between A and C diets (2.52 mg/dL and 2.22 mg/dL, respectively). The P concentrations were above normal for dairy cattle at the beginning of the experiment for all anionic diets and control and returned to normal levels (4.23 to 7.02 mg/dL), after parturition. The treatment A had higher values of P from the first through the third week after calving compared with treatment C (6.31 vs. 4.98 mg/dL, $P < 0.05$). The 25 OH vitamin D concentrations had different pattern of variation along the experimental period among treatments. Two weeks after calving the 25 OH vitamin D was higher for treatment A (94.98 ng/mL) compared with C (77.03 ng/mL; $P = 0.047$) and AC (75.12 ng/mL; $P = 0{,}028$). Anionic diets did not change the precalving Ca concentrations on high producing dairy cows; however, the P levels were higher compared with the control diet. This could suggest a different mineral mobilization which could not be proven.

Key Words: calcium, postpartum

TH96 *Shigella* isolation, phylogeny and identification, with potential for cellulose hidrolysis in the rumen. L. Luna-Rodríguez, D. Hernández-Sánchez, M. Cobos-Peralta, H. Silva-Rojas, C. Cortez-Romero, S. S. González-Muñoz*, and R. Pinto-Ruiz, *Colegio de Postgraduados, Montecillo, Estado de México, México.*

The objective of this experiment was to isolate and cultivate a ruminal cellulolytic bacterium under anaerobic conditions, to carry out its phy-

logenetic and biochemical identification. From a ruminal fluid sample, a strain of *Shigella* nov. sp. was isolated under anaerobic conditions (39°C and pH 6.8), and cultivated in a selective medium using cellulose as the carbon source. The isolated bacterium is a coccobacillus, gram-negative, showing cellulolytic activity when red Congo was used in 10-d growth colonies. The phylogenetic analysis indicates that it is located in the monophyletic group pertaining to the *Shigella*, with 98% similarity to other species of the taxa. Therefore, this microorganism is a non-recognized species. The utilization of sugars and alcohol by the isolated strain was determined using kit API 50 CH and software API WEB. In agreement with the results, fermentation substrates were glycerol, ribose, xylose, sucrose, galactose and glucose, suggesting a potential for cellulose hydrolysis in the rumen. The isolated bacterium was not identified using biochemical tests, which is related to not being listed in the database. Besides, this result is in agreement with the fact that it is a non-recognized species.

Key Words: cellulolysis, isolation and identification, *Shigella*

Ruminant Nutrition: Feeding, Ruminal Fermentation, and Efficiency of Production III

TH97 Effects of different feeding frequencies on feeding behavior of feedlot Nellore cattle. J. Silva[2,3], T. V. B. Carrara[1], M. C. S. Pereira[2], A. L. N. Rigueiro[2], D. H. M. Watanabe[2], D. D. Estevam[2], D. P. Silva[2], D. V. F. Vicari[2], I. C. Batista Junior[2], F. T. V. Pereira[2], D. J. C. Oliveira[4], G. P. Mateus[4], C. A. Oliveira[2], and D. D. Millen*[2], *[1]São Paulo State University (UNESP), Botucatu, São Paulo, Brazil, [2]São Paulo State University (UNESP), Dracena, São Paulo, Brazil, [3]Supported by FAPESP, São Paulo, São Paulo, Brazil, [4]APTA, Andradina, São Paulo, Brazil.*

This study, conducted at the São Paulo State University feedlot, Dracena Campus, Brazil, was designed to determine the effects of different feeding frequencies on feeding behavior of Nellore cattle. The experiment was designed as a completely randomized block, replicated 12 times, in which 48 18-mo-old yearling Nellore bulls (358.2 ± 19.4 kg) were fed in individual pens for 94-d according to the following treatments: (1) feeding one time daily (1×; 0800), (2) feeding 2 times daily (2×; 0800 and 1400), (3) feeding 3 times daily (3×; 0800, 1100 and 1400), and (4) feeding 4 times daily (4×; 0800, 1100, 1400 and 1700). The adaptation program consisted of ad libitum feeding of 2 adaptation diets over period of 14-d with concentrate level increasing from 60% to 86% of diet DM. The finishing diet contained: 67.0% cracked corn grain, 14.0% sugarcane bagasse, 9.0% soybean hulls, 5.5% soybean meal, 4.0% supplement containing 30% of urea, and 0.5% limestone (DM basis). Orthogonal contrasts were used to assess linear, quadratic, and cubic relationship between feeding frequency and the dependent variable. Visual appraisal was made on d 42 of the study, and then every 5 min 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. Also, DMI was measured on d-42 of the study. Feeding frequency did not affect ($P > 0.10$) EAT and MEA. However, as feeding frequency increased, RUM (1× = 427.08 min; 2× = 385.83 min; 3× = 455.83 min; 4× = 429.17 min) and RES (1× = 837.50 min; 2× = 877.08 min; 3× = 779.58 min; 4× = 831.25 min) were cubically affected ($P < 0.01$). Likewise, as feeding frequency increased, DMI was affected ($P = 0.02$) linearly (1× = 8.34 kg; 2× = 8.69 kg; 3× = 9.59 kg; 4× = 9.15 kg). Thus, based on the results of this study, increasing feeding frequency affected RUM, RES and DMI of feedlot Nellore cattle. In a practical way, feeding yearling Nellore bulls 3 times daily seems to be the most feasible option, because longer RUM lead to greater DMI and shorter RES.

Key Words: behavior, frequency, zebu

TH98 Effects of different feeding frequencies on rumen papillae of feedlot Nellore cattle. T. V. B. Carrara[2,3], J. Silva[2], M. C. S. Pereira[2], A. L. N. Rigueiro[2], D. H. M. Watanabe[2], D. D. Estevam[2], D. P. Silva[2], D. V. F. Vicari[2], C. A. Oliveira[2], I. C. Batista Junior[2], F. T. V. Pereira[2], R. V. G. Soutello[2], M. D. B. Arrigoni[1], and D. D. Millen*[2], *[1]São Paulo State University (UNESP), Botucatu, São Paulo, Brazil, [2]São Paulo State University (UNESP), Dracena, São Paulo, Brazil, [3]Supported by FAPESP, São Paulo, São Paulo, Brazil.*

This study was designed to determine the effects of different feeding frequencies on morphological parameters of rumen papillae of feedlot cattle. The experiment was designed as a completely randomized block, replicated 12 times, in which 48 18-mo-old yearling Nellore bulls (358.2 ± 19.4 kg) were fed in individual pens for 94-d according to the following treatments: (1) feeding one time daily (1×; 0800 h), (2) feeding 2 times daily (2×; 0800 and 1400 h), (3) feeding 3 times daily (3×; 0800, 1100 and 1400 h), and (4) feeding 4 times daily (4×; 0800, 1100, 1400 and 1700 h). The adaptation program consisted of ad libitum feeding of 2 adaptation diets over period of 14-d with concentrate level increasing from 60 to 86% of diet DM. The finishing diet contained: 67.0% cracked corn grain, 14.0% sugarcane bagasse, 9.0% soybean hulls, 5.5% soybean meal, 4.0% supplement containing 30% of urea, and 0.5% limestone (DM basis). At harvest, rumenitis incidence (RUM) was determined, on the entire washed rumen, using a scale of 0 (no lesions noted) to 10 (severe ulcerative RUM). Likewise, a 1-cm^2 fragment of each rumen was collected from cranial sac. Manually, the number of papillae per cm^2 of rumen wall (NOP) was determined and 12 papillae were randomly collected from each fragment, and scanned, and mean papillae area (MPA) was measured by software for image analysis. The rumen wall absorptive surface area (RASA) in cm^2 was calculated as follows: 1 + (NOP × MPA) – (NOP × 0.002). Orthogonal contrasts were used to assess linear, quadratic, and cubic relationship between feeding frequency and the dependent variable. Feeding frequency did not affect ($P > 0.10$) RUM (1× = 2.0; 2× = 1.8; 3× = 2.2; 4× = 2.3), NOP (1× = 44.6; 2× = 43.3; 3× = 39.5; 4× = 42.4), MPA (1× = 0.52 cm^2; 2× = 0.49 cm^2; 3× = 0.47 cm^2; 4× = 0.56 cm^2), and RASA (1× = 23.09 cm^2; 2× = 21.64 cm^2; 3× = 20.17 cm^2; 4× = 24.61 cm^2). Thus, based on the results of this study, increasing feeding frequency did not negatively affect morphological parameters of rumen papillae of Nellore cattle.

Key Words: frequency, rumenitis, Zebu

TH99 Manipulating wheat source and monensin level on growth performance, carcass characteristics, and fatty acid of feedlot cattle. L. Xu*[1,2], Y. Jin[1], M. L. He[2], and W. Z. Yang[2], *[1]College of Food Science and Engineering, Inner Mongolia Agricultural University, Hohhot, Inner Mongolia, China, [2]Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

A study was conducted to evaluate growth performance, carcass trait and composition of fatty acid in carcass of feedlot steers fed diets varying grain type and monensin (Mon) dosage. Two hundred crossbred steers (initial BW 488 kg) were blocked by BW, allotted to 20 pens, and then randomly assigned to 5 treatments (4 pens per treatment) with 2x2+1 factorial arrangement. Treatments were control (CON: 10% barley silage, 90% barley-based concentrate, and 28 ppm Mon), and diets substituting soft or hard wheat for barley combining with 28 or 44 ppm Mon. The CON is a standard feedlot diet in western Canada. DMI (averaged 11.3 kg/d) was not different between barley and wheat or between soft and hard wheat diets. However, increasing Mon reduced ($P < 0.01$) DMI by 6% (11.7 vs. 11.0 kg/d). Intakes (g/d) of unsaturated FA (USFA; 119 vs. 121) were not different between barley and wheat diets, whereas that of saturated (SFA) was greater ($P < 0.01$) for barley diet (41 vs. 35). Further, intakes of PUFA and total FA were lower ($P < 0.01$) with soft (90 and 149) than with hard wheat (97 and 164) diets. Final BW (728 kg), ADG (1.79 kg) and G:F (159 g/kg DM feed) were not different between treatments. Carcass characteristics were generally not affected by treatments except that dressing percentage was slightly greater ($P < 0.05$) for barley (60.4%) than for wheat (59.7%) diet. Additionally, steers fed soft wheat had less ($P = 0.05$) back fat (18.2 vs. 20.6 mm)

and greater ($P < 0.05$) meat yield (52 vs. 50%) compared with hard wheat diet. Substitution of wheat for barley grain did not affect the total MUFA and PUFA, but decreased ($P < 0.05$) vaccenic acid (VA; 0.72 vs. 0.50% of total FA) and α-linolenic acid (ALA; 0.26 vs. 0.23% of total FA). These results indicate that wheat can effectively replace barley grain in finishing ration without negatively influencing growth performance, carcass traits and FA composition in meat. Feeding higher Mon seemed to have limit benefits to production efficiency even though DMI was reduced.

Key Words: feedlot steer, monensin, wheat source

TH100 Transcriptome analysis of epithelial and connective tissue fractions of rumen papillae from lactating dairy cattle. M. A. Steele*[1], O. AlZahal[1], S. Greenwood[1], J. C. Matthews[2], and B. W. McBride[1], *[1]University of Guelph, Guelph, ON, Canada, [2]University of Kentucky, Lexington.*

Transcriptome analysis of bovine rumen papillae has provided insight into dietary regulation of the rumen epithelial function. However, previous studies examined expression of epithelial and connective tissues combined in whole papillae, and therefore did not account for tissue specific contributions to nutrient regulation. The objective of this study was to develop a technique to determine the differences in gene expression in epithelial and connective fractions of rumen papillae. Tissue was biopsied from lactating dairy cows, frozen in cryomolds, cut into sections, dehydrated, stained and epithelial and connective sections isolated by laser capture microdissection. The total RNA was isolated from epithelial and connective tissue and global gene expression from with the highest RNA integrity (n = 3) was assessed using Affymetrix GeneChip Bovine Gene 1.0 ST Array. Data pre-processing was conducted using RMA method and detection of significant genes was conducted using ANOVA. The model included the fixed effect of tissue and a Benjamini-Hochberg false discovery rate of 0.1 was applied. There were 366 genes differentially expressed between tissues ($P < 0.001$). Analysis of epithelial and connective tissue using Ingenuity Pathways Analysis showed that epithelial and connective tissue in rumen papillae had distinct molecular signatures. Epithelial signatures were enriched with tight junction genes (DSG1, DES1, DCN) and connective signatures were enriched with genes involved in cell structure and extracellular matrix composition (ACTA2, ACTG2, COL6A1, COL6A3, CL1A1, COL1A2, COL3A1, MYL9). The top ($P < 0.01$) networks between the 2 tissues from the Ingenuity Pathway Analysis included Connective Tissue Disorders, Dermatological Diseases, Gastrointestinal Diseases and Tissue Morphology. Molecular signatures uncovered from this study using laser capture microdissection highlight the importance of examining the roles of cell types within rumen papillae when targeting therapies and studying mechanisms that affect nutrient regulation.

Key Words: rumen papillae, epithelium, gene expression

TH101 Feeding behavior and lactational performance in response to reciprocal combinations of barley and corn grains in the diets of Holstein cows. S. Kargar*[1,3], G. R. Ghorbani[1], M. Khorvash[1], and D. J. Schingoethe[2], *[1]Department of Animal Sciences, College of Agriculture, Isfahan University of Technology, Isfahan, Iran, [2]Dairy Science Department, South Dakota State University, Brookings, [3]Department of Dairy Science, College of Agricultural and Life Sciences, University of Wisconsin-Madison, Madison.*

The effect of diets based on barley (BBD) or corn (CBD), or their equal blend (BCBD) on dry matter intake (DMI), feeding, chewing behavior, and performance of lactating dairy cows were evaluated. Nine multiparous Holstein cows (75 ± 10 d in milk) were used in a triplicated 3 × 3 Latin square design with 21-d periods. Forage to concentrate ratio (40:60) was similar among treatments. Dry matter intake was not influenced by treatment ($P = 0.66$) and averaged 25.6 kg/d. Milk yield was similar across treatments ($P = 0.51$) but was numerically greater for cows fed BCBD than those fed others (48.0, 49.3, and 48.6 kg/d for cows fed BBD, BCBD, and CBD, respectively). Milk protein concentration ($P = 0.75$) and yield ($P = 0.36$) did not change across treatments and were 2.83% and 1.37 kg/d, respectively, on average. Milk fat percentage also increased ($P < 0.03$) in cows fed CBD relative to cows fed BCBD but not BBD (2.31, 2.28, and 2.57%, for cows fed BBD, BCBD, and CBD, respectively). However, cows fed CBD tended ($P < 0.08$) to yield greater milk fat than those fed BBD. Feed efficiency (milk yield/DMI) remained unchanged at 1.92. Dietary treatment did not influence meal and rumination patterns including number of bouts per day, duration of each meal, and inter-meal interval as well as eating rate and meal size. Although not significant, barley- compared with corn-based diets increased rumination time and thereby total chewing time by 36 min (766 vs. 730 min). These results indicate that the substitution of barley with corn have minimal effect on feeding behavior and productive responses of dairy cows.

Key Words: dairy cow, feeding behavior, grain source

TH102 Rumination times in balanced dairy cow rations. S. Rengman*[1], B. Johansson[1], L. Karlsson[2], M. Murphy[1], A. Sterk[3], and E. Weurding[3], *[1]Lantmännen Lantbruk Feed Development, Malmö, Sweden, [2]Felleskjøpet Feed Development, Trondheim, Norway, [3]Agrifirm Innovation Center, Apeldoorn, Netherlands.*

Ruminating and eating times are seen as indicators of sufficient structural feed in dairy cow diets. Several feeding systems have recommendations for chewing time related to DMI or NDF intake. High producing cows consume 5–6 kg NDF from forages, which are assumed to be governing rumination activities. The object of this study was to examine the variation in rumination times on several diets, differing in structural value as well as in proportions of easily fermentable carbohydrates and slowly digestible carbohydrates. Trial 1 (change over trial, n = 24) examined forage NDF. Trial 2 (n = 48, continuous trial) compared similar NDF levels from concentrates or forages, in a TMR. Trial 3 (n = 48, continuous trial) compared diets differing in structural values. DMI, milk production, milk composition and rumination times were recorded in all trials. Rumen pH was measured continuously in trial 3. All trials were conducted between Mar and Nov 2012. Forages were different mixes of grass, whole crop barley and corn silages. Rumination times were in the range 425–575 min/day. Cow variation was large but there were no clear associations between rumination times and diet composition or nutrient intakes. In Trial 1 no effect was seen on rumination times between high dietary NDF (34%) or low dietary NDF (28%), nor in milk composition. In Trial 2, a higher DMI was observed with diets containing NDF mostly from concentrates compared with diets containing NDF mostly from forage. No differences in milk yield or rumination times were observed but high amounts of concentrate NDF gave higher milk fat contents ($P < 0.05$). Particle sizes, determined with the Penn State separator, were within the recommended intervals. In Trial 3, diets high in structural values (peNDF = 34) had only a slightly higher rumination time than diets with lower structural values (peNDF = 30) but no significant correlation between rumen pH and rumination times. With balanced diets with normal forage contents to dairy cows in production there does not appear to be a simple correlation between rumination times and intake of structural feeds. Disturbances might

be due to aspects of feeding systems and housing management rather than dietary factors.

Key Words: health, production, rumen

TH103 Water intake in crossbred dairy calves. A. L. Silva[1], M. I. Marcondes[1], F. S. Machado[2], F. C. Sousa[1], A. S. Trece[1], M. M. D. Castro[1], T. E. Silva[1], and J. P. P. Rodrigues*[1], *[1]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil, [2]EMBRAPA Gado de Leite, Juiz de Fora, Minas Gerais, Brazil.*

Water is one of the main important nutrients for animals. Water requirements can be attended by 3 sources: free water intake (WI), water contained in foods and water produced by body's metabolism nutrients. The objective was to determine free water intake (WI) for crossbred Holstein-Zebu calves aged between 0 and 60 d. The experiment was conducted at Department of Animal Science, at Universidade Federal de Viçosa, Brazil. Eighteen male calves, crossbreed Holstein-Zebu, with an initial body weight of 36 ± 5.5 kg, were used. The animals were distributed into 3 treatments with 6 replications, and these consisted of 3 different levels of milk intake, which were 2, 4 and 8 L per day. The animals had free access to water and concentrate (starter). The animals were fed twice a day at 0600 and 1500 h, and water intake were measured every day at 0600 h. One container was maintained without access for animals, for calculations water evaporation. Environmental variables were also considered: relative humidity (RH), temperature and humidity index (THI) and black globe temperature and humidity index (BGTHI). Environmental effects, milk and starter intake and age were used in a multiple regression model, considering both linear and quadratic effects, to estimate calves WI. The test was conducted using MIXED procedure, SAS, at the level of significance of 5%. It was verified significant effects of dry bulb temperature ($P < 0.0001$), age in days ($P < 0.0001$), and starter intake ($P = 0.0028$) on WI. We did not observe quadratic effects for any of the tested variables ($P > 0.05$) and the multiple linear regression to estimate WI in calves can be expressed by equation: $WI = -2.9648 + 0.187 \times T_{db} + 0.02756 \times Day + 0.7257 \times SI$, where WI = water intake (L/d), T_{db} = dry bulb temperature (°C), Day = age of animal (da), SI = starter intake (kg/d). It can be concluded that water intake can be estimated using parameters as dry bulb temperature, age of animals and starter intake. Supported by CNPq, CAPES, FAPEMIG and INCT-CA/Brazil.

Key Words: dry bulb temperature, milk, starter

TH104 Improving the preweaning performance of dairy calves through sensory stimulation. A. Mereu[1], R. Hernández[2], J. C. Macias[2], J. Vargas[1], M. Candelas[2], and I. R. Ipharraguerre*[1], *[1]Lucta SA, Barcelona, Spain, [2]Nuplen, Gomez Palacio, Dgo., México.*

Fostering newborn calves to consume solid feed before weaning can contribute to ensure proper rumen development, growth, and health during this critical phase. We hypothesized that conferring the starter feed sensorial properties (smell and taste) similar to the milk replacer (MR) may allow stimulating intake of solid feed before weaning. To test this hypothesis, 50 Holstein calves (37.1 ± 4.6 kg of BW; 2.6 ± 1.5 d of age) were housed individually, paired by BW, and allotted to a control (CON) or a treatment (TRT) group (n = 25). From d 3 after birth until weaning (d 57), calves were fed 2 L of MR (20% CP, 20% CF) twice daily and a multi-particle starter (22.5% CP, 3.5% CF) for ad libitum intake. From the onset of the experiment onwards, the starter was offered either plain (CON) or treated (TRT) with an additive (1 kg/ton; Luctarom SFS-R; Lucta S.A., Spain) developed to emulate the sensory properties of the MR. Calves had ad libitum access to water throughout the trial. Starter and MR consumption were recorded daily whereas BW and chest diameter (CD) were measured at birth and d 57. Data were analyzed as a mixed-effects model with repeated measures in time in which calf was treated as random effect and treatment, week, and their interaction were considered as fixed effects. Over the last 4 weeks of the study, TRT calves consumed progressively more starter than CON animals reaching significance ($P < 0.01$) the week before weaning (942 vs. 1183 g/d). As a result, mean starter consumption tended ($P < 0.18$) to be higher for TRT (28.4 kg/calf) than CON calves (24.4 kg/calf). Compared with CON, feeding TRT increased ($P < 0.05$) ADG (325 vs. 412 g/d) and CD (95.4 vs. 89.6 cm), and tended ($P = 0.14$) to improve FG by 25% (1.5 vs. 1.2). In conclusion, conferring the MR and starter feed similar sensory properties stimulated calves to consume more solid feed and thereby improved their rate growth until weaning.

Key Words: calf, weaning, palatability

TH105 Intake, digestibility, and ruminal parameters in heifers fed treated jatropha (*Jatropha curcas*) seed cake. L. D. Silva, O. G. Pereira*, S. C. Valadares Filho, K. G. Ribeiro, T. C. Silva, and R. Tamehiro, *Federal University of Viçosa, Department of Animal Science, Viçosa, Minas Gerais, Brazil.*

The residue from the extraction of jatropha seed oil has a high concentration of crude protein and toxicity, mainly caused by phorbol ester, requiring treatment for use in animal feed. The aim of this study was to evaluate the effect of replacing soybean meal (SBM) for jatropha seed cake, with the peel, treated with ethanol (TJC), in diet for heifers, on intake, total digestibility of nutrients, pH and ruminal ammonia concentrations and indicators of liver function. The treatment of jatropha cake was made in an equipment of the Soxhlet type in an extraction system by ethanol 98%. Four heifers fitted with ruminal and abomasal cannulas were used, with an average initial body weight of 379 ± 2.13 kg, distributed in a 4x4 Latin square. The animals received 4 complete diets, isonitrogenated, containing 65% corn silage and 35% concentrate, in DM basis. The treatments consisted of 4 levels of replacement of SBM by TJC + urea/ammonium sulfate in the diet: 0, 33, 67 and 100%, in DM basis. Data were subjected to variance analysis using SAS. The content of phorbol ester in TJC was 0.04 mg/g. The intake of DM, OM, CP, EE, NFC and TDN decreased linearly ($P < 0.05$) with the increasing addition of TJC in the concentrate of the diets. It was recorded values of 1.8, 1.6, 1.6 and 1.2% of body weight, for DM intake in diets with 0, 33, 67 and 100% of TJC, respectively. There was no effect ($P > 0.05$) of TJC levels on total tract digestibility of nutrients of the diets. The averages were 68.3, 70.5 and 60.9% for DM, OM and CP digestibilities, respectively. The highest levels of TJC in the diets resulted in higher values ($P < 0.05$) of ruminal pH, however, it did not affect ($P > 0.05$) ruminal ammonia concentration. The serum levels of enzymes AST and ALT, which are indicative of liver function, were not affected ($P > 0.05$) by the diets. Thus, it can be concluded that in spite of the reduction of phorbol esters, the jatropha cake treatment with ethanol was not sufficient to promote an adequate intake of nutrients by heifers. Supported by CNPq, INCT-CA and FAPEMIG.

Key Words: dry matter intake, phorbol ester, ruminal ammonia

TH106 In situ degradation kinetics of brown midrib corn silage hybrids harvested prior to or at maturity. M. S. Holt*[1], K. Neal[1], J.-S. Eun[1], J. E. Creech[2], A. J. Young[1], and X. Dai[3], *[1]Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan, [2]Department of Plant, Soils, and Climate, Utah State*

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The objective of this study was to assess in situ DM and NDF degradation kinetics for new pre-matured BMR (pmBMR) varieties that can be double-cropped compared with a sole crop mature BMR (mBMR; Mycogen F2F387; Mycogen Seeds, Indianapolis, IN) and conventional corn silage (CCS; Dekalb DKC61-72; Monsanto Co., St. Louis, MO) harvested at maturity. Double-crop pmBMR varieties were the MasterGraze MC-BMR (pmBMR1; Masters Choice Inc., Anna, IL) and the synthetic BMR84 (pmBMR2; Ray Brothers Seed Farms, Ironside, OR). Two nonlactating dry (DC) and 2 multiparous lactating Holstein dairy cows (LC) were used for in situ measurements for ruminal degradation kinetics of DM and NDF. Four dietary treatments were compared: CCS, mBMR, pmBMR1, and pmBMR2. All cows received the 4 treatments, and data were analyzed separately for DC and LC. Total units of degraded DM were greatest for BMR hybrids compared with CCS in both DC and LC ($P < 0.01$). Incubating pmBMR1 had the lowest undegradable fraction with the greatest potentially degradable fraction and total units of degraded DM followed by mBMR in DC and LC. Incubating CCS had the least units of degraded DM for both cows with the greatest undegradable fraction in DC. Total units of degraded NDF were greater for BMR hybrids compared with CCS in DC and LC ($P < 0.01$). The pmBMR1 had the greatest potentially degradable fraction of NDF and extent of degradation in DC, whereas incubating mBMR resulted in the greatest potentially degradable fraction of NDF in LC. In addition, the greatest extent of digestion in LC was achieved by pmBMR1, while pmBMR2 had the greatest undegradable NDF fraction in LC. Incubating CCS caused the least units of degraded NDF for both DC and LC, whereas pmBMR2 had the greatest undegradable fraction of NDF and the least potentially degradable fraction of NDF for both DC and LC. Taken as a whole, this study indicates that rumen degradability may have been influenced more by hybrid than stage of maturity, as pmBMR1 had the greatest degradability, and pmBMR2 was not as degradable as mBMR.

Key Words: conventional corn silage, brown midrib corn silage, in situ degradation kinetics

TH107 Tail arterial blood or tail venous blood: Could represent external pudic arterial blood? Y. D. Zhang, J. Q. Wang*, D. P. Bu, M. Zhao, X. Q. Zhou, P. Zhang, and Y. J. Xu, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Arterial blood and venous blood are essential for estimating uptakes of milk component precursors by the mammary gland using arteriovenous difference. This blood also should be representative of the artery supply and venous drainage of udder. Representative venous blood could be easily collected from subcutaneous abdominal veins in dairy cows. Whereas arterial blood is harder to collect as external pudic arterial vessels embedded in the depth of muscle than venous vessels. Therefore, 13 Chinese lactating Holstein dairy cows (milk yield = 27 ± 2 kg/d) in mid-lactation (days in milk = 110 ± 20 d) were used to validate the technique of tail arterial blood or tail venous blood represented external pudic arterial blood. Tail arterial blood and tail venous blood was collected separately using blood collecting needle in the tail median coccygeal artery and tail median coccygeal vein vessel, external pudic arterial blood was collected using puncture needle in the abdomen. The samples were analyzed for copper, zinc, calcium, manganese, ferrum, free animo acids, and fatty acids. Data were analyzed using the GLM procedure of SAS (SAS 8.2; SAS Institute Inc., Cary, NC).No differences were found in copper (19.55 vs. 18.21 vs. 20.62 μmol/L, $P > 0.05$), zinc (37.20 vs. 36.78 vs. 38.45 μmol/L, $P > 0.05$), calcium (2.13 vs. 2.09 vs. 2.13 mmol/L, $P > 0.05$), manganese (1.00 vs. 1.00 vs. 1.02 mmol/L, $P > 0.05$), ferrum (7.19 vs. 7.17 vs. 7.20 mmol/L, $P > 0.05$), total free amino acids (1716.79 vs. 1721.43 vs. 1765.29 nmol/mL, $P > 0.05$), essential amino acids (879.97 vs. 878.25 vs. 916.32 nmol/mL, $P > 0.05$), non-essential amino acids (836.82 vs. 843.18 vs. 848.97 nmol/mL, $P > 0.05$), and total fatty acids (2898.24 vs. 2959.00 vs. 2984.45 μg/mL, $P > 0.05$)content in tail arterial blood, tail venous blood and external pudic arterial blood. It suggested that tail arterial blood or tail venous blood may represent external pudic arterial blood for calculating arteriovenous difference of substrates of milk synthesis.

Key Words: tail arterial blood, tail venous blood, external pudic arterial blood

TH108 Milk production and ruminal fermentation characteristics of dairy cows grazing birdsfoot trefoil pasture on a commercial organic dairy farm. R. G. Christensen[1], J.-S. Eun*[1], A. J. Young[1], and J. W. MacAdam[2], *[1]Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan, [2]Department of Plants, Soils, and Climate, Utah State University, Logan.*

Grazing cows on tannin-containing legumes such as birdsfoot trefoil (BFT; *Lotus corniculatus* L.) has been reported to improve dietary N utilization efficiency and milk production. This experiment investigated milk production and ruminal fermentation of grazing dairy cows on BFT on a commercial organic dairy farm for 10 wk in a completely randomized design. Eighteen multiparous cows in mid-lactation were paired by previous milk production, parity, and DIM, and randomly assigned to 2 grazing treatments: cool-season grass pasture (GP) vs. BFT pasture (BFTP). Cows received 2.27 kg of concentrate (barley grain and vitamin and mineral supplement) twice per day following milking. Experiment lasted a total of 10 wk, with 2 wk for adjustment to pasture treatments and 8 wk for data and sample collection. Milk yield and components were measured every 2 wk, whereas ruminal fluid was obtained using a Geishauser probe 3 h after p.m. feeding at 3, 6, and 10 wk of study. Milk yield averaged 26.4 kg/d, and was similar between treatments. Cows grazed on the BFTP tended to increase ECM yield ($P = 0.09$) compared with those on the GP (28.7 vs. 25.8 kg/d). In addition, cows grazed on the BFTP produced 3.57 kg/d more of 3.5% FCM compared with those on the GP ($P = 0.03$). Grazing cows on the BFTP resulted in increased milk fat concentration compared with the GP (3.86 vs. 3.44%; $P = 0.02$). Milk fat (1.02 vs. 0.88 kg/d, $P = 0.01$) and protein yield (0.87 vs. 0.69 kg/d; $P < 0.01$) were higher for the BFTP compared with the GP. Concentrations of MUN and ruminal ammonia-N did not differ between treatments. Total VFA concentration increased for the BFTP compared with the GP ($P < 0.01$). In addition, proportion of propionate was higher for cows grazed on the BFTP compared with those on the GP ($P < 0.01$). Overall results in this study indicate that grazing dairy cows on the BFTP enhanced ruminal fermentation as evidenced by increase total VFA concentration, which supported increased ECM and 3.5% FCM yields.

Key Words: birdsfoot trefoil pasture, lactating dairy cow, milk production

TH109 Behavior and physiological changes of dairy calves in response to the level of intake and weaning method. M. P. C. Gallo[1,3], M. R. Paula[1,2], D. Lezier[1,2], M. C. Soares[1,3], G. B. Mourao[1,2], and C. M. M. Bittar*[1,2], *[1]ESALQ/USP, Piracicaba, Sao Paulo, Brazil, [2]CNPq, Brasilia, DF, Brazil, [3]Fapesp, Sao Paulo, Sao Paulo, Brazil, [4]Capes, Brasilia, DF, Brazil.*

The effect of concentrate intake level at wk 5 of age and weaning method on the behavior and physiological changes of dairy calves was studied. In a 2 × 2 factorial design, 36 dairy calves were classified as presenting high (HCI: > 350g/d) or low (LCI: < 350 g/d) concentrate intake at the 5th week of life, and weaned by 2 methods: abrupt or gradual. Animals were individually housed, had water and concentrate free-choice and were fed 4L of milk-replacer. The abrupt weaning was done at the 8th week of age. Animals gradually weaned received milk-replacer at the rate of 4 L/d until wk 6, 3 L/d from wk 6 to wk 7, 2 L/d from 7 to 2 d before weaning, and 1 L/d until weaning at wk 8 of age. On d −14, −7, −2, 0, 2, 7 relative to weaning, animal's behavior was monitored and rectal temperature (RT), heart beat (HB) and respiratory rate (RR) measured 3 times (6, 12 and 18 h). There was no significant interaction of intake level and weaning method for all variables ($P > 0.05$). Weaning method had no effect ($P > 0.05$) on HB (97/min), RR (43.6/min) or RT (38.8°C). Concentrate intake level affected ($P = 0.02$) heartbeat, being 9% higher for the HCI group (102; 93 beats/min). Concentrate intake level had no effect on respiratory rate (43.6/min; $P > 0.05$), but affected rectal temperature at 18 h, with higher value for animals at the LCI group (39.2; 39.0°C, $P = 0.019$). Concentrate intake level had no effect on animal behavior ($P > 0.05$). Animals gradually weaned spent 17.5 more minutes eating concentrate (86.9 vs. 69.5 min; $P < 0.002$). On d 2, animals abruptly weaned vocalized more than those gradually weaned (112; 36 vocalizations/15 h; $P < 0.05$). On average, animals change some of the behavior parameters from d 0 to 2 and 7 after weaning ($P < 0.05$): decreased time standing; and increased time lying down, eating concentrate, grazing and ruminating. Even though the level of intake has effects on animals' performance, it did not affect animals' behavior. Weaning method changed some important behavior parameters, suggesting the gradual weaning method as the most adequate for animals' well-being.

Key Words: milk feeding, vocalization, weaning stress

TH110 Effects of different dry period managements on rumen microbiota before and after calving. H. R. Khazanehei*, J. C. Plaizier, S. Li, and E. Khafipour, *University of Manitoba, Winnipeg, MB, Canada.*

The effects of 2 dry period managements on rumen microbiota pre and postpartum were determined in 24 multiparous Holstein cows. Treatments were a 60-d dry period (60-d trt) with a 39-d far-off and a 21-d close-up diets, and a 40-d dry period (40-d trt) during which only the close-up diet was fed. The close-up diet had higher NEL and lower NDF but similar CP compared with far-off (1.43 vs. 1.28 Mcal/kg, 50 vs. 38%, and 14.6 vs. 14.7% DM basis, respectively). A common diet was fed to all cows after calving (1.69 Mcal/kg, 17.6% of CP, and 31% of NDF). Rumen samples were taken at wk −2, 2 and 7 relative to calving. Relative quantifications of 14 classical rumen bacteria, methanogenic archaea and ciliate protozoa were performed using real-time PCR and reported as fold change compared with −2 wk of the 60-d trt. There was no difference in the populations of *Anaerovibrio lipolytica*, *Anaerovibrio lipolytica*, *Fibrobacter succinogenes*, *Megasphaera elsdenii*, *Ruminobacter amylophilus*, *Ruminococcus albus*, *Selenomonas ruminantium*, *Succinivibrio dextrinisolvens*, and *Treponema bryantii* between weeks in the 60-d and the 40-d trts. Ciliate protozoa ($P < 0.04$), and *Succinimonas amylolytica* ($P < 0.03$) decreased postpartum in the 40-d trt. The shift in ciliate protozoa is likely due to a longer exposure to a high-energy diet in the 40-d trt, which reduced rumen pH and possibly the retention time. Acetate is a growth stimulator of *S. amylolytica* and probably after calving the increased grain:forage ratio and consequently the reduced acetate resulted in lower numbers of this bacteria. Methanogenic archaea ($P < 0.05$) and *R. flavifaciens* ($P < 0.05$) increased postpartum in the 40-d trt. The higher methanogenic archaea are possibly due to the higher population of H2-producing bacteria and the formate production by *R. flavifaciens* in the 40-d trt. *P. albensis* ($P < 0.01$, $P < 0.02$) and *P. bryantii* ($P < 0.04$, $P < 0.02$) increased in the 40-d and the 60-d treatments after calving, respectively. In conclusion, rumen microbiome results didn't show a huge advantage of using one management rather than the other.

Key Words: dry period, rumen microbiota

TH111 Enteric methane emissions from dairy cows fed corn silage or barley silage based diets. C. Benchaar*[1], F. Hassanat[1], R. Gervais[2], P. Y. Chouinard[2], H. Petit[1], and D. Massé[1], *[1]Agriculture and Agri-Food Canada, Dairy and Swine Research and Development Centre, Sherbrooke, QC, Canada, [2]Département des Sciences Animales, Université Laval, Québec, QC, Canada.*

The objective of this study was to compare enteric CH_4 emissions from dairy cows fed corn silage (CS) or barley silage based diets. Nine lactating, multiparous Holstein cows (DIM = 114 ± 33; BW = 707 ± 49 kg; milk yield 46.9 ± 2.6 kg) used in a replicated 3 × 3 Latin square (32-d periods, 14-d adaptation) were fed (ad libitum) a TMR (60:40, forage:concentrate ratio) with the forage portion being either barley silage (0% CS), corn silage (100% CS) or a 50:50 mixture (50% CS). Diets were formulated to contain 16.2% CP and 1.63 Mcal/kg NE_L. Production of CH_4 was determined (3 consecutive days) using respiration chambers. Dry matter digestibility and milk performance were determined over 6 consecutive days. Linear and quadratic contrasts (MIXED Procedure; SAS) were used to determine the effects of increasing CS proportions on variables response. Significance was declared if $P \leq 0.05$ and tendencies if $0.05 < P \leq 0.10$. Dry matter (DM) intake (21.9, 24.9, and 26.2 kg/d for 0, 50 and 100% CS, respectively), and digestibility (63.2, 65.8 and 69.3% for 0, 50 and 100% CS, respectively) increased linearly as the proportion of CS in the diet increased. Yields of milk, fat-corrected milk (FCM) and energy-corrected milk (ECM) increased linearly ($P \leq 0.01$) as dietary CS inclusion rate increased. Methane production tended ($P = 0.07$) to respond quadratically (487, 540 and 523 g/d for 0, 50 and 100% CS, respectively) to increasing CS dietary proportion. Linear decreases were observed when CH_4 production was adjusted for DM (22.3, 21.8 and 19.1 g/kg for 0, 50 and 100% CS, respectively) or gross energy intake (6.60, 6.49, 5.67%, for 0, 50 and 100% CS, respectively). When expressed on FCM and ECM yield bases, CH_4 emissions were numerically lower when cows were fed 100% CS treatment (i.e., quadratic effect $0.12 \leq P \leq 0.15$). In conclusion, under the experimental conditions of the current study, cows fed corn silage based diets exhibited lower CH_4 energy losses (up to 14% less) than cows fed barley silage-based diets.

Key Words: corn silage, barley silage, methane

TH112 Midwestern US by-product feedstuffs vary in ruminal nutrient digestion. J. Goeser*[1], C. Heuer[1,2], and L. Meyer[1], *[1]Rock River Laboratory Inc., Watertown, WI, [2]University of Wisconsin, Madison, Madison.*

Feedstuff byproducts fed to commercial dairy and feedlots are offshoots of grain refinement processes and may vary in ruminal nutrient digestion. NRC (2001) published feed library values for nutrition balancing but in some cases cites less than 10 samples. Our objective was to evaluate byproduct feed nutrient and digestion variation and assess RUP relative to NRC (2001) values. Soybean meal (n = 13), expeller meal (n = 12), canola meal (n = 11), corn distillers grain (n = 17), corn

gluten feed (n = 28), and soy hull (n = 8) samples were incubated, intact if meal or ground (4mm) if whole, in situ (6g per bag for 16h) in each of 3 lactating dairy cows consuming a commercial diet with a standard in each run. Residue bags were rinsed until effluent was clear to remove microbial CP. Bags were dried and weighed to determine DM digestion. Sample and combined residues were analyzed for N by combustion technique. A subset of samples was analyzed for NDF by modified Mertens technique. Nutrient digestion was calculated as [sample nutrient (g) – residue nutrient (g)]/sample nutrient (g). Data were analyzed using a linear model with fixed effects of feed and week and sample ID as random using SAS JMPv10. Feedstuff 16h in situ means were compared by Tukey's test. Feedstuff RUP means then were regressed on NRC (2001) feed library RUP values for 4× maintenance DMI and 50% forage diet. Feeds differed ($P < 0.05$) in 16h DMD, RUP and NDFD (Table 1). NRC feed RUP relationship with mean 16-h in situ feed RUP was NRC RUP = −11.1+ 1.04 × 16-h in situ RUP, R^2 = 0.82. While slope differed from zero (1.04, $P < 0.05$), the R^2 = 0.82 suggests deviation from NRC library RUPs. These results may be used to supplement feed library values for modeling.

Table 1. Commercial feedstuff nutrient content, 16-h in situ rumen dry matter digestibility (DMD), undegradable CP (RUP) and NDF digestibility (NDFD).

	CP	NDF	DMD	SE	RUP	SE	NDFD	SE
Corn gluten feed	24.8	36.4	75.0^{a}	1.1	17.1^{c}	1.5	47.6^{a}	2.8
Corn distillers grains	35.2	37.4	60.9^{b}	1.4	49.6^{a}	1.9	40.1^{ab}	3.4
Soy hulls	12.7	58.5	52.6^{e}	2.0	35.6^{b}	2.7	30.0^{b}	4.7
Canola meal	43.6		68.6^{bc}	1.7	30.1^{b}	2.2		
Expeller meal	48.0		61.8^{cd}	1.6	55.9^{a}	2.1		
Soybean meal	52.2		82.0^{a}	1.7	24.4^{bc}	2.3		

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

Key Words: by-product, rumen, digestion

TH113 Milk fatty acid profiles in Holstein dairy cows fed a corn straw or mixed forage diet. Y. D. Zhang, X. W. Zhao, J. Q. Wang, D. P. Bu*, P. P. An, and X. W. Xu, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Forages play an important role in fatty acid composition of bovine milk fat. Corn straw is traditional forage source in diets for lactating cows in small farms in china and has been replaced partly by Chinese wildrye, alfalfa hay and corn silage in model dairy farms. Objectives of this study was to examine diets differing in forage source and concentration on milk fat content and milk fatty acid (FA) composition. Twenty 4 Chinese lactating Holstein dairy cows in mid-lactation (136 ± 37 d in milk) were randomly assigned to high forage diets(MF, C:*F* = 40:60)with Chinese wildrye, alfalfa hay and corn silage as the forage source or low forage diets (CS, C:*F* = 60:40)with corn straw as the forage source. Experiment lasted for 9 week with first 2 week as adaption period. Milk samples were collected weekly and analyzed for fat content and fatty acid profiles. Data were analyzed as repeated measurements using PROC MIXED of SAS. Milk fat content was not different between 2 groups. Compared with CS diets, feeding MF diets increased C18:0, C18:3 and C20:0 content ($P < 0.01$) in milk fat, tented to decrease C < 16 fatty acids content ($P < 0.05$), especially C8:0 ($P = 0.06$), C10:0 ($P = 0.08$), C12:0 ($P = 0.07$) and C14:1 ($P = 0.01$) content in milk fat. while stearoyl-coenzyme A desaturase activity of C14:1/C14:0 ($P = 0.06$), C16:1/C16:0 ($P = 0.08$) and cis9C18:1/C18:0 ($P = 0.01$) were lower for MF group than CS group. There were no significant effect on MUFA ($P = 0.23$), PUFA ($P = 0.17$) and SFA ($P = 0.23$) content in the 2 diets. These data suggest that different forage diets alter milk fatty acids profiles.

Key Words: milk fatty acid, corn straw, mixed forage

TH114 Effects of replacing alfalfa hay and corn silage with corn straw in diets on feeding behavior of dairy cows. Y. D. Zhang, D. P. Bu, J. Q. Wang*, P. Zhang, J. Guo, M. Zhao, and X. Q. Zhou, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

A study was conducted to determine the effects of replacing alfalfa hay and corn silage as the only forage source with corn straw on feeding behavior. Thirty-two primiparous Holstein cows (55 ± 15 d, days in milk) were divided into 2 groups fed ad libitum a TMR containing either 17.30% alfalfa hay and 18.77% corn silage (control group) or 36.07% corn straw (CS group). The experiment period was 105 d with 14 d adaptation. Cows were fed with auto feeding system and feeding behavior was recorded continuously using a computerized monitoring system (RIC system, Insentec B.V., Marknesse, the Netherlands). Data were analyzed using the MIXED procedure of SAS (SAS 8.2; SAS Institute Inc., Cary, NC). Total visiting time per day was similar in the experimental groups (51.06 vs. 56.97 times/day, $P = 0.21$). Compared with the control group, meals per day (5.63 vs. 8.57 meals/d, $P < 0.01$), dry matter intake (17.43 vs. 21.35 kg/d, $P < 0.01$), crude protein intake (2.90 vs. 3.84 kg/d, $P < 0.01$) and consumption rate (68.65 vs. 103.25 g DM/min, $P < 0.01$) were lower in the CS group, indicating more attractiveness to the cows for feeding alfalfa hay and corn silage than the cows for feeding the corn straw as the forage source. These results indicate that forage sources affected feeding behavior of dairy cows.

Key Words: mixed forage, corn straw, feeding behavior

TH115 Efficacy of a commercial colostrum replacer in delivering passive immunity to Holstein calves. D. L. Cook*[1], T. TerHune[2], M. T. Socha[3], D. Carlson[1], D. J. Tomlinson[3], and J. M. DeFrain[3], *[1]Milk Products, Chilton, WI, [2]HMS Veterinary Development, Tulare, CA, [3]Zinpro Corporation, Eden Prairie, MN.*

Twenty male Holstein calves (mean birth weight, 41.8 ± 0.9 kg) from singleton births were assigned to a study to determine efficacy of a commercial colostrum replacer. All calves were from one commercial dairy herd and obtained from cows using a clean catch procedure to minimize environmental contamination and eliminate possibility of the calf nursing the cow. Prior to feeding the calf a dose of the colostrum replacer, the calf was weighed and a blood sample was collected for determination of pre-feeding serum IgG concentration. Between 1.3 and 2.4 h post birth, calves were fed 375 g of a colostrum replacer using a nipple bottle. The 375 g of colostrum replacer provided 150 g IgG and was reconstituted with 1.3 L of hot water (mean temperature, 47 ± 1°C) for a final volume of 1.4 L. A second blood sample was collected 24 ± 1 h after the colostrum replacer feeding. Serum IgG concentrations were determined using a radial immunodiffusion test for quantification of bovine IgG (Triple J Farms Product #728411; Kent Laboratories, Bellingham, WA). Average serum IgG concentrations were 14.0 ± 0.5 mg/mL and exceeded 10 mg/mL ($P \leq 0.05$). Mean apparent efficiency of IgG absorption was 38.5 ± 1.8% and incidence of failure of passive

transfer (serum IgG <10 mg/mL) was 10% (2/20 calves). The colostrum replacer was efficacious in delivering passive immunity to calves.

Key Words: calf, colostrum replacer, passive immunity

TH116 Lactational performance and ruminal fermentation profiles of dairy cows fed diets containing birdsfoot trefoil hay. R. G. Christensen[1], J.-S. Eun*[1], A. J. Young[1], and J. W. MacAdam[2], *[1]Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan, [2]Department of Plants, Soils, and Climate, Utah State University, Logan.*

Feeding condensed tannin-containing forages such as birdsfoot trefoil (BFT; *Lotus corniculatus* L.) to dairy cows has been reported to increase lactational performance through improved dietary N utilization. The objective of this study was to determine the effects of feeding BFT hay (BFTH) diets compared with alfalfa hay (AH) diet on lactational performance and ruminal fermentation profiles of dairy cows. Nine Holstein dairy cows (131 ± 15 DIM) were fed 3 experimental diets in a replicated 3 × 3 Latin square design with periods of 14-d adaptation and 7-d data and sample collection. Within each square, cows were randomly assigned to sequential dietary treatments as follows: AH-based TMR (AHT), AH and BFTH-based TMR (AHBFTHT), and BFTH-based TMR (BFTHT). The diets contained 42.0% AH, BFTH, or their combination as sources of forage and were isonitrogenous (16.1% CP) and isocaloric (1.60 Mcal/kg DM). Feeding the BFTHT increased DMI compared with the AHT (26.4 vs. 25.6 kg/d; $P < 0.01$). Cows fed the BFTHT tended to increase ($P = 0.08$) milk yield compared with those fed the AHT (39.9 vs. 38.3 kg/d). Feeding BFTH-containing diets tended to increase milk protein concentration ($P = 0.09$), resulting in increased milk protein yield ($P = 0.03$). Feeding the AHBFTHT tended to decrease milk fat concentration compared with the AHT or the BFTHT ($P = 0.09$). Concentration of MUN did not differ across dietary treatments. Dairy efficiency (ECM yield/DMI) was highest due to feeding the BFTHT. While total VFA concentration tended to increase ($P = 0.10$) by feeding the BFTHT compared with the AHT or the AFBFTHT, feeding BFTH-containing diets decreased acetate-to-propionate ratio compared with the AHT. Concentration of ammonia-N was similar across diets. Contrary to our expectation, feeding BFTH in dairy diets did not influence ruminal N fermentation, whereas feeding BFTH at a relatively high dietary concentration increased feed intake and milk production of mid-lactation dairy cows. The positive effects may have resulted from enhanced ruminal fermentation as evidenced by increased VFA production.

Key Words: birdsfoot trefoil hay, lactating dairy cow, ruminal fermentation

TH117 Feed efficiency and carcass traits of Nellore and Angus young bulls fed whole corn grain diet. J. R. R. Carvalho[1], M. M. Ladeira*[1,2], M. L. Chizzotti[1], P. D. Teixeira[1], L. A. Silveira[1], and M. C. L. Alves[1], *[1]Universidade Federal de Lavras, Lavras, MG, Brazil, [2]Purdue University, West Lafayette, IN.*

The objective was to evaluate the feed efficiency and carcass traits of Nellore and Angus young bulls fed with a regular feedlot diet and a whole corn grain (WCG) diet without the use of forage. Thirty-six animals, with average BW of 381.2 ± 11.87 kg, were used in a completely randomized design using a 2 × 2 factorial arrangement (2 breeds and 2 diets). The usual diet contained 30% corn silage and 70% of concentrate. The WCG diet presented 85% of corn and 15% of a commercial pellet based on soybean meal and minerals. Both diets had 12.5% CP and 2.88 Mcal/kg of ME. The animals were fed in individual pens and the performance was evaluated after 16h of fasting. Two animals, one Nellore and one Angus did not adapt to the WCG diet. After 81 d the animals were slaughtered using cerebral concussion and slitting of the jugular vein. Data were analyzed using PROC GLM in SAS. Angus cattle had greater weight gain, dry matter intake and feed efficiency (Table 1). Similar results were observed for hot carcass weight, rib eye area and fat thickness. However, Angus showed tendency to smaller dressing percentage, which may be explained by a greater proportion of the gastrointestinal tract in the BW of this breed (4.25 vs. 3.81[a], $P < 0.01$). The whole corn grain died provided greater feed efficiency without influence on carcass traits.

Table 1. Dry matter intake (DMI), average daily gain (ADG), feed efficiency (G:F), hot carcass weight (HCW), longissimus dorsi muscle area (LMA), back-fat thickness (BF) and dressing percentage (DP) of young bulls fed high concentrate diets[1]

	Nellore		Angus			*P*-value		
Item	30:70	WCG	30:70	WCG	SEM	Breed	Diet	B × D
DMI (kg/d)	10.4	6.9	13.8	10.2	0.41	<0.01	<0.01	0.44
ADG (kg/d)	1.4	1.0	2.0	1.8	0.16	<0.01	0.21	0.60
G:F	0.128	0.152	0.147	0.202	0.0126	0.01	<0.01	0.12
HCW (kg)	280.9	259.0	315.0	315.4	10.85	<0.01	0.31	0.30
LMA (cm^2)	72.1	67.6	84.8	79.3	5.13	0.02	0.32	0.91
BF (mm)	4.5	3.5	6.9	6.6	0.15	<0.01	0.19	0.46
DP (%)	59.5	60.1	58.3	59.2	0.57	0.08	0.16	0.78

[1]30:70 = diet containing 30% forage and 70% concentrate; WCG = diet with 85% corn grain and 15% commercial pellet (WCG).

Key Words: breed, feedlot, high concentrate

TH118 The relationship between carcass and non carcass composition and visceral organ mass, and residual feed intake in finishing beef cattle. M. L. Nascimento*[1], G. E. Carstens[2], F. R. B. Ribeiro[2], W. K. Krueger[2], L. O. Tedeschi[2], M. E. Davis[3], and W. E. Pinchak[4], *[1]University of Sao Paulo, Piracicaba, SP, Brazil, [2]Texas A&M University, College Station, [3]Ohio State University, Columbus [4]Texas AgriLife Research,, Vernon.*

The objective of this study was to examine the relationships between residual feed intake (RFI) and carcass, non-carcass composition, and visceral organs in finishing beef cattle. Trials involving 56 Angus bulls and heifers divergently selected for serum insulin-like growth factor-I (IGF-I; Trial 1), and 36 crossbred steers fed diets with no tannin, condensed or hydrolysable tannin sources (Trial 2) were used for this study. DMI of high-grain diets (2.85 Mcal ME/kg) was measured for 56 d, and RFI computed by regression of DMI on mid-test $BW^{0.75}$ and ADG within gender. Thirty-two bulls and heifers with divergent RFI in trial 1, and all steers in trial 2 were harvested, and dissectible percentage of 9–11th rib lean and fat measured. Empty gastrointestinal tract (GIT), visceral organs, and dissectible fat depots surrounding GIT, visceral organs and KPH were weighed. IGF-I was significant for several traits in Trial 1, whereas, diet effects were not significant for any trait in Trial 2. Thus, appropriate traits in Trial 1 were adjusted before meta-analysis. Meta-regression was conducted using Proc Mixed (SAS) with RFI class and gender as fixed effects, and trial and harvest group as random. DMI and F:G of low-RFI animals was 18.7% and 16.2% lower ($P < 0.001$)

than in high RFI animals. High-RFI animals tended ($P = 0.07$) to have greater LM area and percentage dissectible lean, and lesser backfat depth ($P < 0.10$) and dissectible fat ($P = 0.15$) than high-RFI animals. Final BW, carcass and empty BW (EBW), rumen, small and large intestines, liver, heart, kidney, dissectible KPH and visceral organ fat (g/kg EBW) were similar ($P > 0.10$) between low- and high-RFI animals. Low-RFI animals had lesser ($P < 0.05$) empty GIT (10.4 vs. 11.0 ± 0.3 g/kg EBW) and dissectible GIT fat (5.82 vs. 6.36 ± 0.23 g/kg EBW), and tended ($P = 0.07$) to have lesser total dissectible internal fat (8.61 vs. 9.15 ± 0.29 g/kg EBW) compared with high-RFI animals. Differences in visceral organ mass did not contribute to variation in RFI. However, low-RFI animals tended to deposit less carcass fat and had 8% less dissectible GIT fat then high-RFI animals.

Key Words: feed efficiency, visceral organ

TH119 Use of a fescue seed model to study effects of ergot alkaloids on temperature regulation in steers. J. Eisemann*, G. Huntington, M. Poore, M. Hanna, and M. Williamson, *North Carolina State University, Raleigh.*

The objective was to measure changes in surface temperature (ST) of the left ribs, rectal temperature (RT), blood pressure (BP), heart rate (HR), respiration rate (RR), and serum prolactin (PRL) in steers fed diets containing either endophyte-free (E−) or toxic endophyte-infected (E+) fescue seed under conditions where the environmental temperature (ET) was within the thermoneutral zone (TNZ). Angus steers (n = 8) were housed indoors in individual pens and adapted to a basal diet of 40% concentrate mix:60% switchgrass hay. Seed replaced soyhulls in the basal diet for E− and E+ (2.0 mg/d ergovaline; 5.8 µg/kg BW). Design was a single reversal with 14-d periods (PD) and 21 d between PD. Baseline measurements were taken 2 d before the start of each PD. Measurements were taken at 0730, 1230 and 1530 on d 4, 8, and 14 of each PD. Digital infrared thermographic imaging was used to measure ST. Automated, digital BP equipment with the inflatable cuff on the tail was used for BP and HR. Data analysis included effects of treatment, day, time of day, and period, with d −2 data as a covariate. Mean (SD) daily ET min was 11.4°C (2.2) and max was 17.0°C (3.4). Steers' BW and DMI did not differ ($P < 0.82$) for E− and E+ and were 348 and 347 kg, and 6.91 and 6.92 kg/d, respectively. Similarly, RT (38.2 and 38.1°C), RR (24 and 24 breaths/min), and diastolic BP (56 and 58 mmHg) did not differ ($P < 0.31$) for E– and E+, respectively. Steers' HR (72 vs. 65 beats/min) and systolic-diastolic BP difference (55 vs. 50 mmHg) were greater ($P < 0.05$) with E− than E+. Compared with E+, systolic BP (114 vs. 106 mmHg, $P < 0.07$) and PRL (71 vs. 43 ng/mL, $P < 0.15$) tended to be greater and ST (31.0 vs. 31.5°C, $P < 0.18$) tended to be lesser for E−. Steers' RT, ST and RR increased ($P < 0.01$) with sampling time on a given day. Values at 0730, 1230, and 1530 were: RT (°C) 38.0, 38.2, and 38.4, respectively; ST (°C) 29.8, 31.7, and 32.2, respectively; and RR (breaths/min) 22, 24, and 24, respectively. Decreased HR and BP responses to E+ are similar to responses previously reported for steers where ET was above the TNZ.

Key Words: steer, tall fescue, environmental temperature

TH120 Soybean hull and enzyme inclusion effects on diet digestibility and growth performance in beef calves consuming corn-based diets. J. R. Russell*, W. J. Sexten, and M. S. Kerley, *University of Missouri, Columbia.*

A feedlot study was conducted to determine increasing soybean hull (SH) inclusion and enzyme addition effects on diet digestibility and animal performance. The hypothesis was SH inclusion and enzyme addition would increase fiber digestibility with no negative effect on animal performance. Eight treatments (TRT) were arranged in a 4 × 2 factorial using 4 diets (DIET) and 2 enzyme inclusion rates (ENZ). The diets contained whole shell corn (WSC) with 0, 7, 14 or 28% SH replacing WSC. The ENZ was a commercial proprietary mix of *B. subtilis*, *A. oryzae* and *T. viride* (Cattlemace, R&D Life Sciences, Menomonie, WI) included in diets at 0% (E0; S0, S7, S14, S28) or 0.045% (E45; S0e, S7e, S14e, S28e). Eighty steers (287 ± 31 kg BW) were stratified by weight and blocked into one heavy block and one light block per TRT (2 pen/TRT). Steers were fed for 70 d with titanium dioxide included in the final 14 d and fecal samples collected on d 70. Diets were balanced for post-ruminal AA and RDP based on available ME. Individual DMI was measured using a GrowSafe FI system. There was no difference ($P > 0.05$) in initial BW, final BW or ADG. The DMI was cubic ($P < 0.05$) due to DIET and was greatest for 7 and 28% SH. There was no difference ($P > 0.05$) in DMI due to ENZ or DIET × ENZ. There was a DIET × ENZ interaction ($P < 0.05$) for G:F in which S0, S0e, S14e and S28e were greatest ($P < 0.05$). The S14e and S28e were greater ($P < 0.05$) than S14 and S28, thus ENZ improved G:F in WSC diets with greater SH inclusion. There was no ENZ or DIET effect ($P > 0.05$) on any digestibilities except ADF in which E0 was greater ($P < 0.05$) than E45. The NDF digestibility tended to have a cubic response ($P = 0.1$) to DIET and was greatest for 7 and 28%. The only DIET × ENZ interaction for digestibilities was nitrogen ($P < 0.05$). Fiber digestibility in WSC diets did not improve with SH inclusion or ENZ addition. Steers fed WSC diets containing 14–28% SH and 0.045% ENZ converted feed at the same rate as steers fed 100% WSC with no difference in ADG.

Key Words: digestibility, fermentation, soybean hulls

TH121 Doses of monensin in combination with virginiamycin in the diet of Nellore beef cattle in feedlot. J. M. B. Benatti*[1], J. A. A. Neto[1], I. Sokoloski[2], M. H. Moretti[1], P. Terencio[3], F. D. Resende[4], and G. R. Siqueira[4], *[1]Universidade Estadual Paulista–FCAV, Jaboticabal, São Paulo, Brazil, [2]Universidade de São Paulo–Esalq, Piracicaba, São Paulo, Brazil, [3]Cargill, São Paulo, Brazil, [4]Agência Paulista de Tecnologia dos Agronegócios, Alta Mogiana, Colina, Saõ Paulo, Brazil.*

In Brazil the use of antibiotics is common in total diets, but the combination of 2 additives is recent practice and little studied. This study aims to determine the dose of monensin in combination with virginiamycin in the diet of Nellore beef cattle in feedlot. The treatments consisted of a control diet and different doses of monensin (0, 10, 20 and 30 mg / kg DM) associated with virginiamycin (25 mg / kg DM). For this, we used 280 Nellore beef cattle, with initial body weight of 348.2 ± 29.07 kg, distributed in 35 pens with 8 animals each. A randomized complete block design was used (block as initial body weight) and considered the pen as repetition, being 7 per treatment. Data was analyzed using PROC MIXED procedure of SAS (version 9.0) and means were compared by orthogonal contrasts (control vs. virginiamycin; effect linear, quadratic and cubic within the dose of monensin), it was considered as statistically significant $P < 0.10$ and was explored trends $P < 0.20$. The virginiamycin provided alone improved feed efficiency by 12.9% during the adaptation period ($P < 0.10$) and tended to increase body weight ($P = 0.154$) and reduce dry matter intake ($P = 0.12$). As for the total period of confinement, virginiamycin increased carcass weight ($P = 0.06$) and tended to increase the final BW ($P = 0.10$) and ADG ($P = 0.16$). Monensin in combination with virginiamycin during adaptation had an increasing linear effect trend for feed efficiency ($P = 0.12$) and decreasing linear effect on body weight ($P = 0.01$), weight daily gain

($P = 0.01$) and dry matter intake ($P < 0.01$). Already in the total period of confinement, monensin caused decreasing linear effect for dry matter intake ($P = 0.03$), no adjustment of behavior for gain ($P = 0.642$), with an average 1.375 kg/day and increase linear effect for feed efficiency ($P = 0.01$). Virginiamycin increases carcass weight compared to the control treatment. The inclusion of monensin doses up to 30 mg/kg DM associated virginiamycin reduces consumption, does not alter weight gain and improves feed efficiency in Nellore beef cattle

Key Words: adaptation, additive combination, antimicrobial

TH122 Using near-infrared spectroscopy (NIRS) to predict the relationship between fecal starch concentration and feed efficiency for feedlot cattle. L. J. Jancewicz*[1,2], M. L. Swift[1], G. B. Penner[2], J. J. McKinnon[2], K. A. Beauchemin[1], and T. A. McAllister[1], *[1]Agriculture and Agri-Food Canada, [2]University of Saskatchewan.*

This study evaluated the relationship between starch content of feces and feed efficiency (gain:feed; G:F) of feedlot cattle. A feedlot study was conducted using 160 crossbred beef steers (538 ± 35.6 kg) allocated to 1 of 4 finishing diets (4 pens/treatment, 10 steers per pen) in a 2 × 2 factorial treatment arrangement. Treatments differed in the type of cereal grain (barley vs. wheat) and processing index (PI) (75 vs. 85%). A lower PI indicates more extensive processing. Fecal samples were collected from the rectum of 5 steers from each pen every 28 d for 3 periods. Each period, the samples were pooled by pen, and dried and ground using a 1-mm sieve. A NIRS (Unity Spectrastar 2400 RTW) was used to predict fecal starch concentration using dried ground samples and using an equation developed from 144 fecal samples. Samples for the equation were sourced from previous studies that evaluated a wide range of dietary treatments and included total fecal collection from beef cattle. Barley processed to a PI of 85% resulted in 54.2% more starch in the feces than when processed to 75% ($P < 0.01$). For wheat, this increase was 63.7% ($P < 0.01$). Grain source had no effect on G:F, however, PI did have an effect on G:F ($P < 0.05$). There was no correlation between fecal starch concentration and G:F for the barley-based diets; however, for cattle fed wheat-based diets, a correlation was observed between starch and G:F ($r = -0.78$, $P < 0.05$). These data demonstrate the potential of using fecal material to predict G:F in feedlot cattle, but suggest the relationship is affected by the difference in response to processing between grain sources.

Key Words: NIR, feed efficiency, fecal starch

TH123 Annual energy requirements of Nellore cows, pregnant in different breeding seasons, in Brazilian savannah. A. L. B. Netto[1], J. C. Souza[1], H. J. Fernandes*[2,1], E. P. Rosa[2], B. D. D'Auria[2], A. Aguiar[3], L. O. Tedeschi[4], L. M. Surita[2], and L. M. Paiva[2], *[1]Federal University of Mato Grosso doSul, Campo Grande, MS, Brazil, [2]State University of Mato Grosso do Sul, Aquidauana, MS, Brazil, [3]University of Florida, Gainesville, [4]Texas A&M University, College Station.*

The objective of this research was to compare the energy requirements of beef primiparous cows (*Bos* sp.), that got pregnant in the spring of 2009 (November, at 13 mo age), or in the fall of 2010 (April, at 18 mo age). A total of 72 Nellore cows (36 in each group) were used. Cows were continuously grazing Xaraés grass (*Brachiaria brizantha* 'MG5') pastures in Brazilian savannah conditions. The animals were weighed without fasting in February, May, August and November of 2011, and in February of 2012. Energy requirements for maintenance were estimated using the weight of the animals. The birth date was used to estimate the date of pregnancy. The energy requirements for pregnancy were estimated using information of the dates of pregnancy and parturition, and the average birth weight of calves on the farm. Milk production and composition were analyzed using 8 cows from each group and lactation curves were adjusted to estimate the energy requirements for lactation. Energy requirements were performed using equations proposed by the National Research Council (NRC, 2000) for beef cattle. Calves from the cows of the spring season were weaned in May (fall of 2011) and calves from the cows of the fall season, in August (winter of 2011). Data were analyzed according to a completely randomized design using PROC GLM of the SAS (SAS Institute Inc.). When compared with cows pregnant in spring, cows pregnant in the fall had higher nutritional requirement for maintenance (4028 and 3668 Mcal/year, $P < 0.001$), lower nutritional requirements for pregnancy (225 and 807 Mcal/year, $P < 0.001$), and similar nutritional requirements for lactation (981 and 938 Mcal/year, $P = 0.150$). The total annual energy requirements were lower for cows pregnant in the fall (5126 and 5413, $P < 0.001$) compared with cows pregnant in the spring, mainly due to the lower requirements for pregnancy. Cows pregnant in the autumn season (in April) will weaned a calf in the winter of the following year (in August), and will get pregnant again in the following spring (November), producing one less calf during their productive life.

Key Words: grazing, nutritional requirement, tropical

TH124 Interaction of corn distillers grain and monensin on site and extent of digestion in feedlot heifers. L. Xu*[1,2], Y. Jin[1], M. L. He[2], and W. Z. Yang[2], *[1]College of Food Science and Engineering, Inner Mongolia Agricultural University, Hohhot, Inner Mongolia, China, [2]Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

A digestion study was conducted to evaluate the effects of increasing corn distillers grain (DG) and monensin (M) on site and extent of digestion in feedlot heifers. Five ruminally and duodenally cannulated beef heifers were used in a 5 × 5 Latin square with 2 × 2+1 factorial arrangement. Treatments were control (CON; 10% barley silage, 90% barley-based concentrate, and 28 ppm M), and diets substituting 20% or 40% corn DG for barley grain combining with 28 or 48 ppm M. The CON is a standard feedlot diet in western Canada. Yb and ^{15}N were used, respectively, as digesta and microbial marker. Contrasts were generated to compare CON vs. the average of DG; DG concentration (20 vs. 40%); and the M dosages (28 vs. 48 ppm). DMI (kg/d) tended ($P = 0.10$) to be greater with DG (8.8) than with CON (7.8) without difference between 20DG and 40DG, whereas it reduced ($P = 0.05$) by increasing M (9.4 vs. 8.2). Flow (kg/d) of OM to duodenum was less ($P < 0.01$) for CON (2.9) than for DG (4.0), and for 48M (3.5) than for 28M (4.5) with no difference between 20DG and 40DG (4.0). Ruminal OM digestibility was greater ($P < 0.01$) with CON (75%) than with DG diet (65%); greater ($P < 0.03$) with 20DG (68%) than with 40DG (62%); and greater ($P < 0.05$) with 48M (68%) than with 28M (63%). However, total digestibility (% of intake) of OM was not affected by treatments. Intake (g/d) of N was greater ($P < 0.01$) with DG (255) than with CON (148). Total N flow to duodenum (g/d) was higher ($P < 0.01$) with DG (215) than with CON (137), and reduced ($P < 0.05$) with increasing M (234 vs. 196). Microbial N production (averaged 100g/d) was not affected by treatments, whereas microbial efficiency was improved ($P < 0.04$) with 40DG versus 20DG (21 vs. 17 g/kg fermented OM). Rumen degradability of CP was greater ($P < 0.01$) with CON (72%) than with DG (58%), in contrast the total digestibility of CP was higher ($P < 0.01$) for DG (81%) than CON (72%). These results indicate that

manipulating the levels of corn DG in feedlot diets change DMI, site and extent of OM and CP digestibility. The effects of supplementing M above the industry recommendation on energy and protein supply to animal appear minimal.

Key Words: beef heifer, distillers grain, monensin

TH125 Carcass traits by male beef cattle finished in feedlot with sources of roughage and crude glycerin. A. F. Ribeiro*, J. F. Lage, A. J. Neto, R. A. Silva, L. G. Rossi, E. E. Dallantonia, L. M. Delevatti, G. M. Delamagna, M. B. Abra, M. O. Santana, and T. T. Berchielli, *São Paulo State University, Jaboticabal, SP, Brazil.*

The objective of this study was to evaluate the carcass traits of young bulls fed crude glycerin - 80% of glycerol. Ten percent of crude glycerin was used on concentrate in replacement of corn. Three sources of roughage: corn silage (T1), sugar cane (T2) and sugar cane bagass (T3) were used at the inclusion level on the diet dry matter of 28, 27 and 17%, respectively. Diets were adjusted to contain 15% of NDF from roughage. Thirty Nellore young bulls with 416Kg ± 24.68 initial BW, were randomly assigned to 3 treatments, with 10 replicates during 90 d. Animals were slaughtered at 550.5 kg BW. The carcasses were weighed for obtained the hot carcass weight (HCW) and dressing percentage (DP). The carcasses were refrigerated for 24 h at 0°C and then rib fat thickness (RFT) and ribeye area (REA) were measured in the region between 12th and 13th rib. Data were analyzed using the GLM procedure of SAS and the treatments effects were considered significant at $P < 0.05$. No difference were detected ($P > 0.05$) for SBW (541.7; 564.4; 558.4 Kg), HCW (297.5; 310.4; 303.5 Kg), DP (54.86; 54.97; 54.37%), RFT (5.9; 4.2; 4.87mm) and REA (75.9; 80.24; 79.18cm^2) among treatments T1, T2 and T3 respectively. The results suggested that animals fed with crude glycerin in diets with different roughages have similar carcass traits.

Key Words: corn silage, glycerol, Nellore

TH126 The response of prepubertal Holstein heifers to altering the ratio of dietary crude protein to metabolizable energy. H. R. Motalebei, K. Rezayazdi, M. Dehghan-Banadaky*, and H. Kohram, *Department of Animal Science, University of Tehran, Karaj, Tehran, Iran.*

Twenty 4 Holstein heifers with a mean age of 210 d and the average weight of 217 kg were used. Heifers were randomly assigned to 3 rations: (1) ration which includes 10% crude protein (CP) less than NRC (2001) (49.35 g of CP per Mcal ME); (2) control ration which crude protein based on NRC (2001) (54.93 g of CP per Mcal ME); 3) ration with includes 10% crude protein more than NRC (2001) (60.64 g of CP per Mcal ME). Metabolizable energy (ME) in all rations was based on NRC requirements (14 Mcal in day). All heifers were housed in individual pens. Experimental and adaptation periods were 140 and 14 d respectively. Blood samples were collected at the beginning and at the end of the experimental period, at every 28 d and in end experimental ruminal fluid samples were collected using an oro-ruminal probe and a suction pump for pH and N-NH_3 determination. Plasma urea nitrogen (PUN) and N-NH_3 was affected by rations ($P < 0.05$) and PUN and N-NH_3 were higher in ration 3 than rations 1 and 2, but no significant differences were observed in pH ruminal, glucose, total protein and albumin blood between rations. We concluded that 10% crude protein less than NRC (2001) was suitable for prepubertal heifer nutrition.

Table 1. Effects of different ratio of CP to ME on ruminal and blood parameters

	CP/ME (g/Mcal)				
Item	49.35	54.93	60.64	*P*-value	SEM
Glucose (mg/dL)	70.32	66.33	66.20	NS	2.611
Total protein (g/dL)	9.22	8.77	9.37	NS	0.336
Albumin (g/dL)	6.05	5.64	5.90	NS	0.242
PUN (mg/dL)	9.49^{c}	10.14^{b}	12.1^{a}	0.03	0.692
Rumen N-NH_3 (mg/dL)	7.09^{c}	9.53^{b}	11.94^{a}	0.001	0.804
Rumen pH	6.72	6.75	6.66	NS	0.064

Key Words: blood, protein-energy ratio, rumen

TH127 Effect of replacing soybean meal with whole soybean on digestibility of the diet of grazing heifers. A. G. Silva*[1], M. F. Paulino[1], I. F. Smith[1], E. E. L. Valente[2], L. S. Martins[1], D. M. Almeida[1], A. L. Braga Netto[3], and G. Mendes Filho[4], *[1]Federal University of Vicosa, Vicoa, Brazil, [2]Federal University of Lavras, Lavras, Brazil, [3]State University of Mato Grosso do Sul, Aquidauana, Brazil, [4]Federal University of Tocantins, Araguanina, Brazil.*

The aim of this work was to evaluate the effect of replacing soybean meal with whole soybean grain in supplements on nutritional characteristics of growing heifers grazing in the transition dry-rainy season. A total of 40 heifers with at least 50% of Nellore breed weighing 290 ± 6 kg were used. Animals were assigned to an area composed of 4 paddocks of 5 ha, uniformly covered with *Uruchloa decumbens* grass. The experimental design was a completely randomized with 4 treatments and 10 replicates. The supplements contained approximately 30% of crude protein (CP) and progressive replacement of soybean meal with whole soybean grain at 0, 50 and 100%. Supplement was offered at the amount of 1.0 kg/animal/day except the control, which received only mineral mixture ad libitum. For the evaluation of nutritional characteristics a 9-d trial was carried out after adaptation. The 3-marker method was used. A manual grazing simulation was conducted for qualitative assessment of pasture. Supplementation improved the digestibility of dry matter (DM) and of all constituents of the diet ($P < 0.10$), except of the neutral detergent fiber corrected for ash and protein (NDFap) ($P > 0.10$). There was also a linear increase effect ($P < 0.10$) of the replacement of soybean meal with whole soybean grain on the coefficients of apparent digestibility of DM, organic matter (OM), ether extract (EE), and non-fibrous carbohydrates (NFC). The improvement in the digestibility of DM and of the dietary constituents of the supplemented animals may be due to the presence of compounds more easily digested in the diet of animals that received concentrate supplementation. According to Lazzarini et al. (2009), 7% of CP in the forage is sufficient to promote the appropriate use of fiber of low quality forage. This probably explains the lack of significant effect on the digestibility of NDFap since the nitrogen compounds in the forage would be sufficient for the proper use of pasture fibrous compounds. We concluded that the digestibility is optimized with the replacement of soybean meal with whole soybean grain in concentrate supplements.

Key Words: digestibility, grazing heifer, soybean

TH128 Comparison of omasal and reticular digesta samples to estimate the ruminal digestibility in cattle fed diets containing sugar cane in natura or ensiled sugar cane and corn silage. L. D. S. Mariz*, S. de C. V. Filho, E. Detmann, S. A. Santos, F. A. C. Villadiego, L. F. Prados, D. Zanetti, F. Sales, A. N. Nunes, and L. C. Alves, *Universidade Federal de Vicosa, Vicosa, Minas Gerais, Brasil.*

The aim of this study was to evaluate the ruminal digestibility of dry matter and other constituents in the diet using samples obtained from the omasum and reticulum in cattle. Five rumen-fistulated crossbred cattle with an average initial live weight of 333 ± 17 kg were used in the experiment, distributed in a 5 × 5 Latin square design. A total of 5 diets containing 60% forage and 40% concentrate based on dry matter and containing different forages were tested: corn silage; sugar cane in natura; a sugar cane silage control; sugar cane silage supplemented with 0.4% calcium oxide and sugar cane silage supplemented with 0.8% calcium oxide, based on natural materials. The crude protein (CP) in all of the forages was corrected to 11% based on dry matter (DM), using a mixture of urea/ammonium sulfate (9:1). Six collections of reticular and omasal digesta were performed in each experimental at 12 h intervals. At the end of each experimental period, these samples were to generate 2 phases: the filtrate, which corresponded to the liquid phase and small particles, and the residue, which corresponded to the large particle phase. There was no interaction ($P > 0.05$) between sampling location and the treatments for any of the analyzed variables. The ruminal digestibility for DM, organic matter (OM), CP, neutral detergent fiber (NDF) and non-fiber carbohydrates (NFC) was similar ($P > 0.05$) for the digesta collected in the omasum and the reticulum. There was an effect of the sampling site ($P < 0.05$) detected for the ruminal digestibility of ether extract (EE), which was lower in the digesta collected in the omasum. The intestinal digestibility of CP and EE was found to be higher ($P < 0.05$) in the omasal digesta than in the reticular digesta. Considering all diet constituents, the omasum is the preferred sampling location. Due to the ease of collection, additional studies should be conducted with reticular digesta because numerous nutrients in ruminal digesta are similar to those in omasal digesta.

Key Words: omasal digesta, reticular digesta, ruminal digestibility

TH129 Effect of replacing soybean meal with rumen-protected soybean meal on production performance and milk composition in early lactation dairy cows. C. G. Zhang[1], L. M. Huang[1,2], G. L. Liu*[1,2], X. K. Zhang[1], and G. Yang[1], *[1]State Key Laboratory of Dairy Biotechnology, Shanghai Bright Holstan Co. Ltd., Shanghai, China, [2]Shanghai Dairy Breeding Center Co. Ltd., Shanghai, China.*

The objective of this study was to evaluate the effect of replacing soybean meal (SBM) with rumen-protected soybean meal (RPSBM) on production performance and milk composition in early lactation dairy cows. According to the parity (P), days in milk (DIM) and milk yield (MY), Eighty-one dairy cows were selected randomly as control group (CK, n = 42, $P = 2.7 \pm 0.5$, DIM = 46.4 ± 3.5 d, MY = 42.5 ± 7.3 kg/d) and test group (TK, n = 39, $P = 2.5 \pm 0.4$, DIM = 44.4 ± 2.2 d, MY = 43.3 ± 6.7 kg/d). The basal diet was the control diet, whereas the diet replacing 17% SBM in control diet with RPSBM was the test diet. The trial lasted 69 d with a 7 d adaptation. Daily feed intake of TK and CK were recorded and converted into average dry matter intake (DMI) per cow, individual MY were recorded every 5 d, individual milk samples were collected at a 4:3:3 mixtures of morning, noon, evening milk by volume for detecting milk fat percentage and milk protein percentage at d 0, 30, and 60. Data were analyzed using ANOVA model of SAS 9.0. The results indicated that DMI of TK at all recorded days has an increasing trend ($P > 0.05$) compared with CK, average DMI (kg/d per cow) of TK and CK were 23.1 ± 5.8 and 22.3 ± 4.9 during entire trial period. Average MY (kg/d) at d 33, 38, 64 of TK (45.0 ± 6.3, 43.9 ± 6.7, 41.9 ± 7.0) was significantly higher ($P < 0.05$) than CK (42.3 ± 8.6, 41.3 ± 7.8, 39.2 ± 7.7), whereas there were no significant changes ($P > 0.05$) between CK and TK at other recorded days. Average MY (kg/d per cow) of TK and CK at 69 d trial were 42.8 and 41.6, respectively. The milk protein percentage and milk fat percentage of TK were not significantly changed ($P > 0.05$) compared with CK. The treatment increased milk yield but had no effect on milk composition in early lactation dairy cows.

Key Words: dairy cow, production performance, rumen-protected soybean meal

TH130 Effects of Chinese herbal medicinal formula supplementation on production performance and immune profile in late-lactation dairy cows. Y. J. Su[1], G. L. Liu*[1,2], C. G. Zhang[1], G. Yang[1], and Z. Liu[1], *[1]State Key Laboratory of Dairy Biotechnology, Shanghai Bright Holstan Co. Ltd., Shanghai, China, [2]Shanghai Dairy Breeding Center Co. Ltd., Shanghai, China.*

Traditional Chinese Medicine (TCM) has shown beneficial effects on the performance and immune system of humans and animals. In this study, Chinese herbal medicinal formula (CHMF) was a proprietary TCM additive containing 5 kinds of herbal extracts. to evaluate the effects of CHMF on the production performance and immune profile of dairy cows, 40 Chinese Holstein cows (DIM = 240 ± 13.4d; BW = 532 ± 42.3kg) were employed and randomly distributed to 2 groups involving 30 d periods: 20 cows were assigned to a conventional diet (CON) that contained corn silage, alfalfa hay, Chinese leymus and commercial concentrate, and the other 20 cows were fed the same diet supplemented with 50g cow^{-1} d^{-1} of CHMF (CH).The results showed that there was no difference in average DMI for cows fed the 2 diets (16.52 versus 16.54 kg/d, $P = 0.867$), but the CH cows tended ($P = 0.10$) to have a higher milk yield than CON cows (18.73 versus 18.24 kg/d, respectively). Milk protein, fat, lactose and solids not fat (SNF) percentage were not affected by addition of CHMF. Fat and protein yield (kg/d) were also not affected by the experimental diets. The somatic cell count (SCC) was numerically lower in CH group than in CTR group (640,000 versus 900,000 cell/mL, $P = 0.12$). On the other hand, blood analysis revealed that the CH group had significantly ($P < 0.05$) higher neutrophil activity and IgG levels than the CON group. In conclusion, supplementation of CHMF in diets not only had positive effects on milk production and composition, but can be useful for prevention of subclinical intramammary infection in late-lactation dairy cows.

Key Words: Chinese herbal medicinal formula, immune profile, production performance

TH131 Effects of wheat source and monensin level on intake and rumen fermentation in feedlot heifers. W. Z. Yang*[1], L. Xu[1,2], C. Li[3], S. Ding[1,4], and T. A. McAllister[1], *[1]Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [2]College of Animal Science, Inner Mongolia Agricultural University, Hohhot, Inner Mongolia, China, [3]College of Animal Science and Technology, Inner Mongolia University for the Nationalities, Tongliao, Inner Mongolia, China, [4]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada.*

With adverse growing or harvesting conditions, abundant supplies of feed wheat become available in Canada. While many feedlot operators include wheat into the rations, few studies have documented the effects of wheat type on animal response. A study was conducted to examine rumen fermentation by substituting wheat grain (soft or hard) for barley and to determine whether increasing monensin (Mon) reduce incidence of rumen acidosis for feeding ruminal highly digestible wheat to feedlot heifers. Five ruminally cannulated beef heifers were used in a 5 × 5 Latin square with 2 × 2+1 factorial arrangement. Treatments were control (CON; 10% barley silage, 90% barley-based concentrate, and 28 ppm Mon), and diets substituting soft or hard wheat for barley combining with 28 or 44 ppm Mon. The CON is a standard feedlot diet in western Canada. DMI (kg/d) was greater ($P < 0.05$) for CON (8.4) than for wheat (averaged 7.7) diets. There was no difference in DMI between soft (7.6) and hard (7.8) wheat, whereas increased Mon reduced ($P < 0.05$) the DMI (8.1 vs. 7.3). Mean rumen pH was higher ($P < 0.05$) for CON (5.91) than for wheat diets (averaged 5.59). The duration of pH < 5.8 (9.9 vs. 16.2 h) and pH < 5.5 (4.3 vs. 11.5 h) was lower ($P < 0.01$) for CON than for wheat diets. However, rumen pH parameters were affected neither by wheat type nor by Mon level. Total VFA concentrations (mM) were lower ($P < 0.05$) for CON than for wheat diets (161 vs. 177). Molar proportion of propionate was higher ($P < 0.05$), thus ratio of acetate to propionate was lower ($P < 0.05$) with high Mon (1.39 vs. 1.11). These results indicate that substitution of wheat for barley grain in feedlot ration increased incidence of rumen acidosis regardless of soft or hard wheat. Increased Mon supplementation had no evident effect on alleviating rumen acidosis but may potentially alter rumen fermentation pattern with more propionate production.

Key Words: feedlot heifer, rumen fermentation, wheat source

TH132 Meat quality of Girolando steers fed spineless cactus. R. A. S. Pessoa*[1], J. R. C. Silva[1], A. S. C. Veras[1], M. A. Ferreira[1], I. Ferraz[2], and P. C. Vasconcelos[1], *[1]Universidade Federal Rural de Pernambuco, Recife, Pernambuco, Brazil, [2]Instituto Agronômico de Pernambuco, Recife, Pernambuco, Brazil.*

The objective of this study was to evaluate the effect of the substitution of cottonseed meal by urea on meat quality of Girolando steers (5/8

Holstein-Zebu). Eighteen animals, with average initial body weight of 320 kg and 24 mo of age were used, kept in feedlot system and assigned to a randomized block design, established in accordance with the weight of animals, being 3 treatments and 4 blocks. The experimental period lasted 84 d divided into 3 periods of 28 d. The treatments were 3 urea levels (0.0, 1.5 and 3.0%) in substitution of cottonseed meal (23.0, 11.5 and 0.0%) in diets based on spineless cactus with approximately 12.0% of crude protein and 65.0% of total digestible nutrients. The control diet was composed of 60.0% of spineless cactus, 15.0% of sorghum silage, 0.0% of urea:ammonium sulfate mixture (9:1), 23.0% of cottonseed meal and 2.0% of mineral mixture, in dry matter basis. After skinning and evisceration the carcasses were cut longitudinally into 2 halves and samples were taken from the longissimus dorsi muscle in the left half carcass of each animal. The samples was stored for later analysis. After defrosting, the measures of pH, color (L* a* b*), shear force, water-holding capacity (WHC) and cooking losses were performed. The data were submitted to ANOVA using the SAS. Color lightness, meat redness, yellowness, pH, shear force, water-holding capacity and cooking losses were not affected by the treatments ($P > 0.05$) (average of 35.67; 5.92; 4.93; 6.0; 3.99; 36.33 and 28.41, respectively). The replacement of cottonseed meal by urea did not alter the meat quality of Girolando steers feed diets based on spineless cactus. FACEPE process number: 2008/0979.

Key Words: *Opuntia ficus indica*, shear force, urea

TH133 Effects of replacing corn silage with alfalfa hay on blood metabolites of Holstein cows in early lactation. A. Akbari, A. Zali, M. Ganjkhanlou*, M. Dehghan-Banadaky, and A. Emami, *University of Tehran, Tehran, Iran.*

In present study, effects of replacing corn silage with alfalfa hay on blood metabolites of Holstein cows in early lactation were investigated. Fifteen Holstein cows (37 ± 10 DIM) were used in completely randomized design lasted for lasting 9 weeks. Three levels of hay and corn silage were used as treatment: (1) 10% alfalfa–30% silage corn, (2) 20% alfalfa–20% silage corn, and (3) 30% alfalfa–10% silage corn. The ratio of forage: concentrate was the same (40: 60) in all treatments. Cows were fed their feed as total mixed rations (TMR) twice daily. Dry matter intake of each cow was measured daily. To determine blood parameters, blood samples were collected all of the cows, at 3, 6 and 9 weeks experiment, 4 h after the morning feeding. Blood samples were taken from the tail vein and by vacuum tubes containing anti-coagulant (EDTA) was performed. Blood samples by centrifugation were centrifuged at 3000 rpm and 15 min and then obtained plasma was separated. Parameters such as glucose, total protein, NEFA, BHBA, and plasma urea nitrogen (BUN) were measured by using autoanalyzer system and test kits. Data were analyzed using the GLM model procedure (SAS Institute, 2003). Normality of distribution and homogeneity of variance for residuals were tested using PROC UNIVARIATE and adjust Tukey-Kramer (SAS Institute, 2003). Dry matter intake was higher ($P < 0.05$) when cows fed diet 2 (23.20 kg per day) compared with diet 1 (22.95 kg per day) and diet 3 (18.64 kg per day). Blood parameters were unaffected by treatment ($P > 0.05$), but then treatment effects on certain blood parameters were given. Although the amount of glucose in diet 1 (68.41 mg/dl) was higher than diet 2 (60.90 mg/dl) but a little difference had as diet 3 (65.55 mg/dl). Also in diets 1, BUN and total protein were less than the other 2 diets ($P > 0.05$). It is concluded that feeding alfalfa hay more than corn silage did not influence blood metabolites but, reduced dry matter intake.

Key Words: alfalfa hay, corn silage, milk production

TH134 Continuous measurement of methane production before and after feeding in continuous cultures fed bermudagrass. K. M. Young*, J. R. Burgess, C. T. McDonald, and T. C. Jenkins, *Clemson University, Clemson, SC.*

The objective of this study was to design a system that could detect gas concentrations continuously in ruminal continuous cultures to better assess changes in methane (CH_4) occurring before and after feeding. The custom-built system used CH_4 and CO_2 infrared sensors (Edinburgh Instruments, OEM Gas Sensors, UK) and an O_2 infrared sensor (KE Series, Figaro USA Inc., Arlington Heights, IL) calibrated with a zero and span gas to measure gas concentrations in 1 L of headspace. To evaluate the system, 30 g of Tifton 85 bermudagrass harvested at 35 d of maturity was fed daily in 2 equal amounts at 0800 and 1600 h for 3 7 d periods. Forage was harvested from plots at the University of Georgia, and freeze-dried and ground (2-mm sieve) before feeding. Gas readings were taken every minute throughout the day and captured on a spreadsheet. For statistical analysis, only hourly recordings were used between 0800 and 1600 h on d 5, 6 and 7. Data were analyzed by the Fit Model Procedure in JMP (SAS Institute) with time, day, and their interaction as main effects and period as random effect. Average CO_2 and O_2 concentrations before feeding were 77% and 0.5% respectively with fermenters kept under continuous flow of CO_2 at 20 mL/min. Methane production increased ($P < 0.01$) between 0800 and 1600 h (12.1, 12.6, 17.0, 21.9, 23.6, 26.4, 26.9, 27.1 and 28.1 mmol) when averaged across d 5–7. A decrease ($P < 0.01$) in methane production on d 7 (26.1, 23.7, 15.4 mmol/d for d 5–7) is thought to result from repeated opening of the culture vessel to obtain samples. Methane was estimated at 33.8 mmol/d using the Mills et al. (2003) equation adapted for use in continuous cultures using ADF, N, starch and DMI, which were comparable to values in the present system. The novel gas analysis system developed for continuous cultures in this study successfully measured changes in CH_4 concentration before and after feeding that were comparable to previously reported values.

Key Words: continuous culture, methane

TH135 In vitro screening of potential enzyme additives to enhance degradation of wheat dried distillers grains with solubles and barley silage. Z. X. He*[1,2], S. Ding[1], L. Xu[1,3], K. A. Beauchemin[1], and W. Z. Yang[1], *[1]Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [2]Key Laboratory of Agro-ecological Processes in Subtropical Region, Institute of Subtropical Agriculture, the Chinese Academy of Sciences, Changsha, Hunan, China, [3]College of Food Science and Engineering, Inner Mongolia Agricultural University, Hohhot, Inner Mongolia, China.*

The aim of this study was to identify potentially effective feed enzymes for wheat dried distillers grains with solubles (DDGS) and barley silage. In vitro batch cultures were used to examine the effects of exogenous enzymes (EE) on gas production (GP) and degradability of DM (DMD) and NDF (NDFD) after 6, 12, 24 and 48 h. Seven EE containing a range of xylanase, endogulcanase, exoglucanase and protease activities were used. Each was evaluated at 3 doses: 0 (control), 1 (low) and 2 (high) μL/g of DM. For DDGS, GP was higher ($P < 0.05$) during the first 12 h for E2 (143 mL/g OM), E4 (141 mL/g OM) and E6 (140 mL/g OM) compared with control (131 mL/g OM), whereas GP after 24 or 48 h was higher ($P < 0.05$) only for E2 at low dose. Degradability of DM was improved by 2 to 3 percentage units at 6 h and 3 to 4 percentage units at 24 h for most EE. However, at 48 h, only E2 (71%), E4 (72%) and E6 (72%) increased DMD compared with control (68%). There was a minimal effect on NDFD at 6 or 12 h, but at 24 h, the percentage unit increases compared with control (42%) were 7 (E4, low), 7 (E1

and E6, high), 5 (E2 and E3, low), and 5 (E5 and E7, high). At 48 h, the percentage unit increases compared with control (57%) for NDFD were 6 (E2, E4) and 5 (E5, E6) for high dose. For barley silage, GP was generally not affected by EE. Degradability of DM was greater ($P < 0.05$) for E2 (48%), E4 (49%) at low dose, and E6 (48%) at high dose compared with control (43%) at 24 h; it was greater ($P < 0.05$) for E2 (60%) at low or high dose, E4 (63%) at high dose, and E6 (59%) at high dose compared with control (54%) at 48 h. Similarly, NDFD tended ($P < 0.10$) to increase with E2 (26%), E4 (28%) and E6 (27%) compared with control (23%) at 24 h, and increased ($P < 0.05$) with E2 (41%), E4 (45%) and E6 (40%) compared with control (32%) at 48 h. The results indicate ruminal degradability of DDGS and barley silage can be improved using EE. However, the response to EE is often dose-dependent and differs with incubation time. The incubation at both 24 and 48 h are recommended to identify EE that consistently improve degradability.

Key Words: barley silage, exogenous enzyme, wheat DDGS

TH136 Replacing corn silage with chopped alfalfa hay on performance, apparent digestibility, and chewing activity of dairy cows. A. Akbari, A. Zali, M. Ganjkhanlou*, M. Dehghan-Banadaky, and A. Emami, *University of Tehran, Tehran, Iran.*

This study investigated replacing of long chopped alfalfa hay (AH) with corn silage digestive processes, chewing activity and performance of dairy cows in a long-term period (80 d). Fifteen Holstein dairy cows in the early lactation stages (37 ± 10 DIM) were designed in a completely randomized design. Treatment were diets with (1) 25% alfalfa hay plus 75% CS (CS75); (2) 50% alfalfa hay and 50% CS (CS50); and (3) 75% alfalfa hay plus 25% CS (CS25) on a forage-DM basis. Diets were fed ad libitum as TMR with a concentrate to forage ratio of 60:40. Cows were milked 3 times daily at 0200, 1000, and 1800 h by semi-automatic milking machines. Milk production was recorded at each milking during the experiment. Data were analyzed using the MIXED MODEL procedure and adjust Tukey-Kramer (SAS Institute, 2003). Partially replacing AH with CS resulted in increasing dry mater intake (DMI) fallowed with increasing intakes of net energy for lactation ($P < 0.05$), and peNDF without affecting apparent digestibility ($P > 0.05$). Total eating time and eating per kg intake of DM, NDF, peNDF > 1.18 and peNDF > 8 was quadraticlly affected by replacing AH with CS($P > 0.05$), resulting greater total chewingg time and total chewing time per kg DMI as well as actual milk production ($P < 0.05$). In contrast increasing AH level in the diet resulted in more milk protein percentage ($P < 0.05$). Surprisingly in our long-term consideration there were quadratic effect of replacing CS with AH was observed in rumination time per NDF intake as well as fat related (e.g., fat percentage and yield and FCM) ($P < 0.05$). On the other hand CS50 treatment in our study had a higher milk corrected fat production (29.51, 28.02 and 27.41 kg, for CS75, CS50 and CS25 respectively) due to saving energy at optimum point of chewing time. Therefore, according to our data and condition it may conclude that an equal ratio of CS and AH is resulted to best performance and health in dairy cow nutrition.

Key Words: chewing activity, forage, apparent digestibility

TH137 Impact of increased dietary grain inclusion on blood metabolites and rumen fermentation characteristics of prepubertal dairy heifers. T. S. Dennis*, J. E. Tower, H. Schmitz, A. Mosiman, and T. D. Nennich, *Purdue University, West Lafayette, IN.*

The objective of this study was to evaluate the effect of increasing dietary grain:forage ratio on blood metabolites and rumen fermentation characteristics of prepubertal dairy heifers. Seventy-eight Holstein heifers (133.1 ± 27.4 kg, 125 ± 22 d of age) were randomly allocated by body weight (BW) to 1 of 15 pens. Pens were randomly assigned to dietary treatments balanced for CP and ME containing grain:forage ratios of 80:20 (80%), 60:40 (60%), or 40:60 (40%) and fed for 56 d. Following the treatment period, all pens were switched to a common diet containing 40% grain and 60% forage and fed for an additional 56 d. Blood was collected from all heifers on d 0, 28, 56, 84, and 112. Rumen fluid was collected esophageally from 10 heifers per treatment (2 heifers/pen) to determine rumen pH, NH_3, volatile fatty acids (VFA), and in vitro cellulose disappearance. Data were analyzed as repeated measures using PROC MIXED of SAS with pen as the experimental unit. Heifers fed 80% had greater PUN and glucose than 60% and 40% during the treatment period ($P < 0.01$); however, PUN and glucose were similar between dietary treatments during the common period ($P > 0.10$). Rumen pH was least for 80% and greatest for 40% on d 56 ($P < 0.01$), but similar during the common period ($P > 0.10$). Rumen NH_3 was similar between treatments during the common period from d 56 to 112 ($P > 0.10$). During the treatment period, total VFA concentrations were greater for 80% and 60% than 40% on d 56, averaging 118.2, 108.1, and 74.2 m*M*, respectively ($P < 0.01$). Molar proportions of acetate and A:P ratio on d 56 of the treatment period were greatest for 40% ($P < 0.01$). Also, 40% had lower molar proportions of propionate and butyrate as compared with 80% during the treatment period on d 56 ($P < 0.01$). After being placed on a common diet, total VFA and molar proportions of VFA were similar between treatments ($P > 0.10$). Cellulose disappearance in vitro was similar between treatments overall ($P > 0.10$). As expected, blood and rumen metabolites were altered when heifers were fed diets with greater grain inclusion rates.

Key Words: dairy heifer, grain inclusion, rumen fermentation

TH138 Effects of energy source (starch or fat) on performance, eating pattern, and carcass quality of Holstein bulls fed high-concentrate rations during the finishing period. M. Devant*[1], B. Quintana[1], and A. Bach[2,1], *[1]Department of Ruminant Production-IRTA, Torre Marimon, Caldes de Montbui, Barcelona, Spain, [2]ICREA, Barcelona, Spain.*

This study evaluated the effects of energy source (starch or fat) on performance, eating pattern, and carcass quality of Holstein bulls fed high-concentrate diets during the finishing period. A total of 79 bulls (291 ± 2.1 kg BW and 216 ± 0.8 d age) were divided into 2 treatments: (1) 51% starch and 5.7% fat (HSLF) and (2) 41% starch and 7.2% fat (LSHF) in a completely randomized design. Concentrates were isonitrogenous and isoenergetic. Palm oil was increased (from 2.7 to 4.0%), while corn (from 25.5 to 18.6%) and barley (from 31.0 to 22.0%) decreased in HSLF and LSHF, respectively. Individual concentrate intake and eating pattern were recorded daily with a computerized concentrate feeder, and BW was recorded every 14 d. Animals were slaughtered after 97 d and HCW, and carcass quality were evaluated. Data were analyzed using a mixed-effects model with repeated measures. During the first 2 wk of study, LSHF showed less ($P < 0.05$) eating rate (105.5 ± 2.28 g/min) than HSLF (113.7 ± 2.28 g/min) bulls. However, total DMI did not differ between treatments (6.5 ± 0.17 kg/d) because meal duration (10.2 ± 0.22 min) and meal size (0.89 ± 0.030 kg) of LSHF were greater ($P < 0.01$) than in HSLF bulls (9.3 ± 0.22 min and 0.81 ± 0.030 kg, respectively). During the 3 to 6 wk differences between treatments in eating rate were maintained ($P < 0.01$); however meal size and meal duration were not affected by treatment. In consequence, DMI was less

($P < 0.05$) in LSHF (6.4 ± 0.17 kg/d) than in HSLF bulls (6.9 ± 0.17 kg/d). Thereafter, eating rate of LSHF increased to levels of HSLF bulls, and no differences among treatments were observed. Carcass weight and dressing percentage were greater ($P < 0.05$) in HSLF than in LSHF bulls (234 and 229 ± 1.6 kg, 53.1 and 52.4 ± 0.23%, for HSLF and LSHF, respectively). During the first weeks of the finishing period, eating pattern of the concentrate may be affected when substituting starch for fat. The increase in fat content of the finishing concentrate maintaining the energy density in bulls may decrease carcass weight and dressing percentage.

Key Words: beef, energy source, eating pattern

TH139 Effects of zinc sources on performance, hematology, and biochemistry of blood serum in finishing lambs. M. Mallaki*, M. A. Norouzian, and A. A. Khadem, *The University of Tehran, Tehran, Iran.*

The purpose of this study was to investigate the effects of organic and inorganic zinc sources on performance, hematological and biochemical parameters of blood serum in finishing lambs. Eighteen male Zandi lambs (21.28 ± 0.85 kg BW and 70 ± 5 d) were randomly allocated to one of 3 dietary treatments in a randomized design. Animals in group 1 were treated as control (no zinc supplementation), whereas animals in groups 2 and 3 were supplemented with 25 mg of zinc/kg DM from either zinc sulfate monohydrate (ZnS) or zinc peptide (ZnP), respectively. There was no difference among groups for numbers of red blood cells (14.95, 14.59 and 13.84; respectively), hemoglobin concentration (11.24, 11.14 and 11.20; respectively), packed cell volume (36.17, 35.52 and 37.20; respectively), and mean corpuscular hemoglobin concentration (7.6, 7.2 and 8.2; respectively). White blood cell count was lower in ZnP group (8.66 vs 11.07 and 11.86; ZnP, control and ZnS respectively) ($P = 0.08$). Activities of aspartat amino transferase and alanin amino transferase were similar between experimental groups. Dry matter intake and ADG in ZnP groups were greater ($P < 0.05$) than ZnS and control groups. There was no difference in feed conversion ratio between groups. These results demonstrated that zinc may be beneficial for the performance and health of finishing lambs.

Key Words: hematology, performance, zinc

TH140 Effects of supplemental bupleurum extract on lactation performance and rumen fermentation in Holstein cows subjected to heat stress. L. Pan[1], D. P. Bu*[1], J. Q. Wang[1], J. B. Cheng[1,2], X. Z. Sun[1,2], W. Liu[1,3], R. X. Hu[1,3], and C. Y. Ren[1,3], *[1]Chinese Academy of Agricultural Sciences, Beijing, China, [2]Anhui Agricultural University, Hefei, Anhui, China, [3]Gansu Agricultural University, Lanzhou, Gansu, China.*

Bupleurum extract (BE) has been shown to alleviate negative effects of high ambient temperature. This experiment was conducted to investigate effects of supplemental BE on lactation performance and rumen fermentation of cows under heat stress. Forty Holstein cows were assigned to one of 4 groups (n = 10) according to milk yield (37.5 ± 1.8 kg/d), day in milk (75 ± 15) and parity (1.7 ± 0.4) in a completely random block design. Four treatment diets consisted of supplemental BE at 0, 0.025, 0.05 or 0.1% of dry matter, which were randomly assigned to one of 4 groups. Cows were housed in a tie-stall barn and were individually fed the treatment diets. The experiment lasted for 10 wk in hot summer. Ambient temperature and humidity were measured 3 times a day. Milk yield, feed intake, respiration rates (RR) and rectal temperatures (RT) were measured twice a week, and milk samples were collected every 10 d. Rumen fluid samples were collected at wk 6 and 10 of the trial. Data were analyzed by repeated measures using Proc Mixed procedure of SAS. During the experiment, average temperature-humidity index were respectively 78.20 ± 2.74, 79.72 ± 3.26 and 78.26 ± 3.37 at 0600 h, 1400 h and 2200 h. Average RR (65.61^a, 60.32^b and 67.42^a vs. 71.40^a breaths/min, $P < 0.01$) and RT (39.10^b, 39.04^b and 39.07^b vs. 39.28^a °C, $P < 0.01$) were decreased for cows fed BE supplementation. Compared with control, cows supplemented with BE increased dry matter intake (22.79^a, 21.59^b and 22.07^b vs. 20.94^c kg/d, $P < 0.01$) and milk production (34.73^a, 33.38^b and 32.37^{bc} vs. 31.50^c kg/d, $P < 0.01$). There was no treatment effect on milk fat concentration or milk protein concentration, while milk fat yield (1.13^a, 1.12^a and 1.09^{ab} vs. 1.02^b kg/d, $P < 0.05$) and milk protein yield (0.97^a, 0.95^a and 0.92^a vs. 0.89^b kg/d, $P < 0.01$) were increased compared with control. Rumen pH, ammonia-N concentration and total volatile fatty acid concentration were not different among groups. Overall, supplemental BE at 0.025% or 0.05% could improve lactation performance without changing rumen fermentation in cows subjected to heat stress.

Key Words: bupleurum extract, cow, heat stress

TH141 Effect of ration on intake, digestibility, and rumen microbial yield in heifers under intensive fattening system. J. Mora, X. Cortes, H. J. Morazan, A. R. Seradj, D. V. Mata, and J. Balcells*, *Dept. Animal Production, University of Lleida, Lleida, Spain.*

Twelve crossbred heifers (BW: 362 ± 25 kg) were randomly distributed in 2 feeding groups and received, concentrate [CON; cereal grain 64 g/100 DM and protein meals 26 g/100 DM; CP: 15.5% CF: 10.8%] plus cereal straw and a total mixed ration [TMR; silages of sunflower 30 g/100 DM, ryegrass 28 g/100 DM and complete immature corn cob 42g/100 DM; CP: 14.0; CF: 15.4) and both rations were supplied ad libitum. Digestibility, intake and duodenal flow were determined using 2 flow marker system [Lignin sulfuric (Li-Sf), and Ytterbium acetate (Yb)]. Ten days before sacrifice (0 to 10d), Yb was supplied orally twice a day (0800 and 1800 h) at a dose (2 mg Yb/kgBW) using a drencher, the first 7 d (0 to 7 d) were for marker changeover and the rest (7 to 10 d) for collecting feces. Microbial nitrogen (MN) yield was quantified using 2 microbial markers, purine bases (BP) and ^{15}N (2 mg ^{15}N/g N ingested) that was supplied along with Yb (d 5 to 10). At harvest (d 10) animals were shipped by feeding group to the harvest plant at 0700, harvested at 1030 and rumen and abomasums digesta were sampled (1100–1130 h). Rumen content was filtered using a surgical gauze and rumen fluid sampled (4 mL) to determine ammonia-N (N-NH_3) and volatile fatty acids (VFA) concentration. The rest of rumen liquid was used to isolate the bacterial reference sample by differential centrifugation. The N-NH_3 levels in the rumen (95.6 and 124.1 for CON and TMR, respectively, $P = 0.23$) suggest an excess of degradable N and might explain the N-losses between intake and rumen out-flow. Type of ration did neither alter ammonia nor VFA concentrations but TMR induced a VFA profile with a greater acetate proportion. Heifers fed TMR in relation to those received concentrate plus straw (CON) showed a greater level ($P < 0.05$) of DM intake (4.5 vs. 5.5 kg; SEM = 0.32), apparent digestibility in the whole tract (0.87 vs. 0.91; SEM = 0.01), MN yield (21.8 vs. 38.4; SEM = 3.5) and efficiency (g of MN/kg DOMR, 19.3 vs. 24.4; SEM = 1.1 for CON and TMR, respectively). High quality TMR in growing heifer improves rumen fermentation condition and microbial-N yield efficiency.

Key Words: digestibility, ^{15}N, purine base

TH142 Effect of endophyte-infected tall fescue seed on ruminal metabolism and physiology in Angus steers. D. H. Kim*[1], J.

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This study was conducted to evaluate the effect of fescue toxicosis on changes in rumen physiology and metabolism. Eight ruminally cannulated Angus steers (BW = 548 ± 33 kg) were blocked in pairs based on BW and randomly allocated to 4 blocks. The steers were fed alfalfa cubes at 1.5 × NE_m and dosed (1 kg/d) with ground endophyte-infected tall fescue seed (E+; 4.45 mg ergovaline/kg DM) or endophyte-free tall fescue seed (E−) via rumen cannula once daily for 21 d. On d 14, rumen fluid was collected before feeding and every 2 h for a subsequent 8 h period. Rumen contents were removed before the morning feeding on d 16 for evaluation of ruminal fill, and then the rumen contents were returned to the rumen with a probe for continuous monitoring of ruminal pH, temperature and pressure. Dry matter intake was not different (P = 0.293) between treatments (82.20 ± 1.05 and 79.80 ± 1.38 g of DM/$BW^{0.75}$ for E− and E+, respectively), whereas rumen content DM was higher (P = 0.060) for E+ than E− (16.26 ± 2.26 and 12.97 ± 1.72 g of DM/kg of BW, respectively). Total VFA, acetate, propionate, and butyrate concentrations, and acetate:propionate ratio were higher for E+ than E− (Table 1). Likewise, ammonia concentration was higher (P = 0.058) for E+ dosing. Ruminal pH and temperature were not affected by treatment (P = 0.657 and 0.499, respectively), whereas ruminal pressure was lower (P < 0.001) for E+ dosing. Serum prolactin concentration was lower (P < 0.001) for E+ (0.40 ± 0.02 and 25.49 ± 2.61 ng/mL for E− and E+, respectively). Data in this study indicate that endophyte-infected tall fescue seed may contribute to depression of ruminal VFA absorptive function related to ruminal motility changes.

Table 1. Comparison of ruminal metabolism and physiology between endophyte-infected tall fescue seed (E+) and endophyte-free tall fescue seed (E−)

Item	Treatment		SEM	*P*-value
	E−	E+		
Total VFA, mM	104.56	131.36	13.03	0.002
A:P ratio	3.93	4.33	0.13	<0.001
Acetate	73.35	93.40	9.62	0.002
Propionate	19.01	21.76	2.10	0.052
Butyrate	8.25	11.01	1.02	<0.001
Ammonia, mM	7.37	9.06	1.34	0.058
pH	6.84	6.83	0.17	0.657
Temperature, °C	38.73	38.80	0.26	0.499
Pressure, mbar	1035.65	1020.83	9.32	<0.001

Key Words: ruminal physiology, steer, tall fescue

TH143 Feeding incremental levels of ground flaxseed linearly reduced milk yield and enteric methane emission in organic Jersey cows. T. L. Resende*[1], A. F. Brito[2], K. J. Soder[3], D. H. Woitschach[4], A. B. D. Pereira[2], and R. B. Reis[1], *[1]Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil, [2]University of New Hampshire, Durham, [3]USDA-ARS, University Park, PA, [4]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil.*

Twenty (8 primiparous and 12 multiparous) organic Jersey cows averaging 425 kg BW (SD ± 37) and 111 DIM (SD ± 62) in the beginning of the study were blocked by milk yield and parity and randomly assigned to treatments in 5 replicated 4 × 4 Latin squares to investigate the effects of incremental dietary levels of ground flaxseed (0, 5, 10, or 15% diet DM) on intake and yields of milk and milk components. Sixteen cows (4 squares) were used to measure enteric methane emissions using the SF_6 tracer technique; 12 cows (3 squares) were used to collect ruminal samples using an oral lavage tube. All cows were fed TMR containing (% diet DM): 55% alfalfa/grass baleage, 8% grass hay, and 37% concentrate; soybean meal (from 6 to 2% diet DM) and cornmeal (from 27 to 16% diet DM) were replaced with flaxseed (from 0 to 15% diet DM) to keep diets isonitrogenous while roasted soybean (2% diet DM) was maintained constant across treatments. Yields of milk and milk components were reduced linearly when cows were fed incremental levels of flaxseed. The linear reduction in DMI with increasing flaxseed explains the observed decreases in the yields of milk and milk components. Methane emissions expressed in g/d was reduced linearly with increasing flaxseed possibly as a result of decreased DMI and enhanced molar proportion of ruminal propionate. However, no significant differences were found when expressing enteric methane emissions on an efficiency basis, averaging 15.8 g/kg DMI and 10.6 g/kg ECM across treatments. Increasing flaxseed reduced milk yield but appears to be effective at mitigating methane emission.

Table 1. Effect of ground flaxseed on performance and ruminal metabolism

	Flaxseed (% diet DM)					*P*-value	
	0%	5%	10%	15%	SED	Linear	Quadratic
DMI, kg/d	16.9	16.8	15.7	16.1	0.29	<0.001	0.33
Milk, kg/d	21.2	21.0	20.6	19.9	0.35	<0.001	0.25
Milk fat, kg/d	0.98	0.99	0.94	0.93	0.03	0.05	0.69
Milk protein, kg/d	0.73	0.73	0.69	0.66	0.02	<0.001	0.33
Ruminal total VFA, mM	64.9	65.4	66.2	71.3	4.00	0.13	0.42
Ruminal acetate, % total VFA	72.8	72.3	72.2	71.8	0.29	<0.01	0.73
Ruminal propionate, % total VFA	14.4	14.7	15.4	16.4	0.25	<0.001	0.06
Methane, g/d	276	260	250	232	23	0.05	0.95

Key Words: flaxseed, methane, organic dairy cow

TH144 Effect of source of corn silage and level of dry matter intake on rumen nutrient pool sizes and turnover in dairy cows. F. Lopes*, D. E. Cook, R. W. Bender, and D. K. Combs, *Department of Dairy Science, University of Wisconsin, Madison.*

Our objective was to compare how digestibility and passage of fiber differ due to source of corn silage at 2 levels of dry matter intake. Eight rumen-cannulated dairy cows (110 ± 5 d in milk) were assigned to replicate 4 × 4 Latin squares with 21 d period to evaluate rumen nutrient pool sizes and turnover. Treatments were arranged as a 2 × 2 factorial with main effects of intake [restricted (3.1% of body weight) vs. ad libitum] and source of corn silage (conventional (NCS) vs. BMR). Treatments were (1) NCS-restricted (28.22% NDF); (2) NCS-ad libitum (25.40% NDF); (3) BMR-restricted (27.38% NDF); and (4) BMR-ad libitum (25.37% NDF). Intake and milk production were measured during d 14 to 21. Ruminal contents were evacuated manually 4h after and 2 h before feeding on d 20 and 21. Rumen content was analyzed for OM, NDF, iNDF (indigestible neutral detergent fiber) content. Data were analyzed with MIXED procedure of SAS with fixed effect of diet, period and intake, and cow within square was the random effect. Ruminal digesta volume and mass did not differ among treatments. Intake of DM and aNDF were not affected by source of corn silage. Milk yield was

not affected by intake but milk fat (%) was higher for treatments with restricted intake compared with ad libitum intake. Rumen pool size of DM and NDF did not differ among treatments but pool size of iNDF was higher for diets with NCS than BMR diets. Ruminal turnover rates of DM and NDF did not differ, ruminal turnover of iNDF tended ($P < 0.08$) to increase at higher intake.

Table 1.

	NCS		BMR		
Item	restricted	ad lib	restricted	ad lib	SEM
DM intake, kg/d	25.14[bc]	27.99[ab]	22.81[c]	28.18[a]	1.46
NDF intake, kg/d	7.10	7.13	6.21	7.17	0.42
Digesta wet mass, kg	76.26	85.51	77.64	80.88	4.65
Ruminal pool, kg					
DM	9.90	11.33	10.36	10.87	0.74
NDF	5.46	6.12	5.74	5.93	0.31
iNDF	3.18	3.70	2.57	2.56	0.25
Ruminal turnover rate, %/h					
DM	11.33	10.40	9.37	11.14	0.74
NDF	5.77	4.93	4.62	5.25	0.40
iNDF	2.26	2.90	2.55	3.43	0.56

[abc]$P < 0.05$.

Key Words: corn silage, fiber digestibility, turnover

TH146 Performance and intake of finishing Nellore young bulls on pasture in the rainy season supplemented with crude glycerin. E. San Vito*, J. F. Lage, R. A. Silva, P. Castignino, A. F. Ribeiro, L. R. Simonetti, L. M. Delevatti, M. Machado, E. E. Dallantonia, R. A. Reis, and T. T. Berchielli, *São Paulo State University, Jaboticabal, São Paulo, Brazil.*

The aim of this work was to evaluate the effect of crude glycerin (CG; 80% of glycerol) inclusion as a substitute to corn grain in the intake, average daily gain (ADG) and shrunk body weight final of finishing Nellore young bulls on pasture, supplemented in the rainy season. Fifty Nellore young bulls with initial shrunk body weight of 427 ± 15.76 kg were randomly assigned to 5 treatments, with 2 replicates. The animals were distributed in 10 paddocks, with 1.8 ha each (2 paddocks per treatment), of *Brachiaria brizantha* 'Xaraés' with a height of 30 cm. Treatments were constituted by 5 levels of CG inclusion in the supplement: (0, 70, 140, 210 and 280 g/kg dry matter (DM) of CG based on dry matter) as a substitute to the corn grain. The animals were supplemented daily in a proportion of 300g/100kg of body weight. The supplement was constituted of corn grain, soybean meal, urea, gluten meal and mineralized salt, containing 300 g/kg DM of crude protein based on dry matter. The experiment was conducted in 141 d, and the animals were weighed in the beginning and in the end of the experiment, after 14 h of solids and liquids shrunk to evaluate the average daily gain. Thirty animals were used for evaluation of intake and nutrient digestibility, estimated using 3 markers: isolated, purified and enriched lignin (LIPE), titanium dioxide (TiO_2) and indigestible neutral detergent fiber (iNDF), used for estimation of fecal excretion, supplement intake and forage intake, respectively. Data was analyzed using the GLM procedure of SAS program and the effects of treatments were considered significant at $P < 0.05$. There was no statistical significance ($P > 0.05$) among the treatments, for ADG and shrunk body weight final, dry matter intake and dry matter digestibility, with mean values of 0.869, 550.3, 10.8 and 58.2, respectively. The inclusion of crude glycerin until the level of 280 g/kg DM in the supplement did not affect the performance, dry matter intake and dry matter digestibility of finishing Nellore steers on tropical pasture in the rainy season.

Key Words: biodiesel, by-product, forage

TH147 Effects of increasing levels of whole raw soybean in the Nellore steer diets on ruminal fermentation and microbial protein synthesis. N. R. B. Cônsolo*, A. S. C. Pereira, R. Gardinal, J. E.Freitas Junior, J. R. Gandra, C. S. Takiya, F. P. Rennó, and G. D. Calomeni, *Universidade de São Paulo, Pirassununga, São Paulo, Brazil.*

Soybean is a significant and important source of protein for animal feeds and its production has grown over the years. Observing its importance a study was conducted to evaluate the ruminal fermentation and microbial protein synthesis of Nellore steers in feedlot conditions while fed increasing levels of whole raw soybean (WRS). Twelve steers, in individual pens, were assigned in a 4 × 4 Latin square design with 4 diets. The diets were T0 (0% of WRS), T8 (8% WRS), T16 (16% WRS), and T24 (24% WRS), in a dry matter basis. Each period had 14 d for adaptation and 4 d for data collection. On d 18, samples of ruminal liquid were collected through ruminal cannula at 0, 2, 4, 6, 8, 10, and 12 h after feeding for analysis of pH, VFA, and ammonia-N (NH_3-N). In addition, microbial protein synthesis was estimated by purine derivatives in spot urine samples. Statistical analyses were performed by Proc Mixed procedure of SAS software. Increasing levels of WRS increased ruminal pH ($P < 0.05$). In addition, WRS induced a linearly decreasing effect ($P < 0.05$) on the NH_3-N concentration. Regarding VFA, inclusion levels of WRS prompted a quadratic effect ($P < 0.05$) on total VFA concentration, while presented a linear effect ($P < 0.05$) in butyrate percentage and a quadratic effect in acetate molar concentration ($P < 0.05$) with the lower score in T8 (66.81 vs. 62.66 m*M* to control and T8 respectively). No difference ($P > 0.05$) was observed for the percentage of acetate or propionate and acetate to propionate ratio. Microbial protein synthesis was not altered by WRS treatment. Therefore, adding WRS in the diets tested in this trial did not affect microbial protein synthesis and had no negative effects on ruminal fermentation in beef cattle.

Key Words: protein source, volatile fatty acid, ruminant

TH148 Carcass traits of Nellore young bulls finished in pasture supplemented with crude glycerin. E. San Vito*, J. F. Lage, L. M. Delevatti, E. E. Dalantonia, M. Machado, L. R. Simonetti, R. A. Silva, P. Castagnino, R. A. Reis, and T. T. Berchielli, *São Paulo State University, Jaboticabal, São Paulo, Brasil.*

This trial aimed to evaluate the effects of feeding crude glycerin (CG) - 80% of glycerol - included as a substitute to corn grain in supplements of young bulls finished in pasture on rainy season on hot carcass weight (HCW), dressing percentage (DP), carcass shrink loss (CSL), rib fat thickness (RFT) and ribeye area (REA).Fifty Nellore young bulls with initial shrunk body weight of 427 ± 15.76 kg were randomly assigned to 5 treatments, with 2 replicates. The animals were distributed in 10 paddocks, with 1.8 ha each (2 paddocks per treatment), of *Brachiaria brizantha* 'Xaraés' with a height of 30 cm. Treatments were constituted by 5 levels of CG inclusion in the supplement: (0, 70, 140, 210 and 280 g/kg dry matter (DM) of CG based on dry matter) as a substitute to the corn grain. The animals were supplemented daily in a proportion of 300g/100kg of BW. The supplement control was constituted of corn grain, soybean meal, urea, gluten meal and mineralized salt, containing 300 g/kg DM of crude protein. The diets were isonitrogenous and formulated to meet the

requirements for maintenance and gain of the animals according to Brazilian recommendations. After 141 d on feed, the animals were slaughtered with 550.1 ± 32.6 BW. The carcasses were weighed for obtained the HCW and DP. The carcass were refrigerated for 24 h at 0°C and then rib fat thickness (RFT) and ribeye area (REA) were measured in the region between 12 and 13th rib. Data was analyzed using the GLM procedure of SAS program and the effects of treatments (linear and quadratic) were considered significant at $P < 0.05$. Glycerin level did not affect HCW ($P = 0.116$), DP ($P = 0.406$), CSL ($P = 0.169$), RFT ($P = 0.874$) and REA ($P = 0.215$) with mean values of 307.6, 55.6, 1.5, 2.9 and 84.3, respectively. Adding crude glycerin in supplement (28% of DM) does not affect the carcass traits of young bulls finished in pasture on rainy season.

Key Words: beef cattle, glycerol, rib fat thickness

TH149 Meat quality from Nellore young bulls finished on pasture supplemented with crude glycerin. E. San Vito*, J. F. Lage, R. A. Silva, L. M. Delevatti, E. E. Dalantonia, L. R. Simonetti, M. Machado, M. B. Abra, A. F. Ribeiro, and T. T. Berchielli, *São Paulo State University, Jaboticabal, São Paulo, Brazil.*

This trial aimed to evaluate the effect of crude glycerin (CG) inclusion as a substitute to corn grain on Warner-Bratzler shear force (WBSF), cooking losses (CKL), thawing loss (TL), total loss (TL) and intramuscular fat (IMF) of meat from young bulls. The CG used was derived from soybean biodiesel production (80% glycerol). Fifty Nellore young bulls with initial shrunk body weight of 427 ± 15.76 kg were randomly assigned to 5 treatments, with 2 replicates. The animals were distributed in 10 paddocks, with 1.8 ha each (2 paddocks per treatment), of *Brachiaria brizantha* 'Xaraés' with a height of 30 cm. Treatments were constituted by 5 levels of CG inclusion in the supplement: (0, 70, 140, 210 and 280 g/kg dry matter (DM) of CG based on dry matter) as a substitute to the corn grain. The animals were supplemented daily in a proportion of 300g/100kg of BW. The supplement was constituted of corn grain, soybean meal, urea, gluten meal and mineralized salt, containing 300 g/kg DM of crude protein. The diets were isonitrogenous and formulated to meet the requirements for maintenance and gain of the animals according to Brazilian recommendations. After 141 d on feed, the animals were slaughtered with 550.1 ± 32.6 BW. A boneless longissimus muscle (LM) section 10 cm thick was removed from the posterior end of the wholesale rib. LM samples were individually vacuum-packaged and held at −20°C for analysis. Data was analyzed using the GLM procedure of SAS program and the effects of treatments (linear and quadratic) were considered significant at $P < 0.05$. There was no statistical significance ($P > 0.05$) among the treatments, for WBSF ($P = 0.509$), CKL ($P = 0.826$), TL ($P = 0.491$), TL ($P = 0.810$) and ether extract ($P = 0.516$) with mean values of 3.6, 28.2, 2.9, 30.2 and 0.95, respectively. The inclusion of crude glycerin until the level of 280 g/kg DM in the supplement did not affect the meat quality of young bulls finished on tropical pasture in the rainy season.

Key Words: glycerol, intramuscular fat, shear force

TH150 Microbial protein synthesis in dairy cows fed with sources of unsaturated fatty acids. V. P. Bettero*[2,1], J. E. Freitas Junior[1], M. D. S. Oliveira[2], B. C. Venturelli[1], E. F. Jesus[2], R. Gardinal[1], G. D. Calomeni[1], K. A. Koyama[1], V. G. C. Lacuna[1], B. C. Benevento[1], R. V. Barletta[1], and F. P. Rennó[1], *[1]University of Sao Paulo, Pirassununga, Sao Paulo, Brazil, [2]State University Julio de Mesquita, Jaboticabal, Sao Paulo, Brazil.*

The aim of this study was to evaluate the microbial protein synthesis in dairy cows supplemented with sources of unsaturated fatty acids. Eight Holstein cows in the mid lactation (80 ± 20 d in milk; mean SD) cannulated in the rumen and abomasums (580 ± 20 kg of weight; mean ± SD) with milk yield of 25 kg/d were assigned randomly into two 4 × 4 Latin squares, fed the following diets: (1) control (C); (2) refined soybean oil (inclusion of 3% in the total dry matter; OS); (3) whole soybean raw (WS; inclusion of 16% in the total dry matter); and (4) calcium salts of unsaturated fatty acids (CSFA; inclusion of 3% in the total dry matter). Milk yield and the dry matter intake were measured daily throughout the experimental period. Milk samples were collected on d 16 of the experimental period. Urine aliquots (50 mL) were obtained 4 h after feeding, on d 16 of the experimental period. Urine was filtered and diluted in 0.036 *N* sulfuric acid to prevent bacterial destruction of purine derivatives and precipitation of uric acid. A sample of pure urine was collected for determination of total nitrogen, urea and creatinine. The microbial protein synthesis was estimated as a function of the purine derivatives absorption. Data were analyzed using PROC MIXED of SAS 9.1 according with the orthogonal contrasts (C vs. SO + WS + CSFA); (SO vs. WS + CSFA) and (WS vs. CSFA). There was no difference ($P > 0.05$) in daily excretion in mmol/L and mmol/day of allantoin in urine and milk, urine uric acid excretion in urine L/day, total purine, purine derivatives, purines absorbable in mmol/day, microbial nitrogen production, microbial crude protein, g/day and efficiency of microbial protein synthesis between the experimental diets, although on the 2 last parameters OS (1187.13 g/day and 118.73 microbial CP/kg TDN consumed, respectively) was numerically higher than C (1086.19g/day and 108.63 microbial CP/kg TDN consumed, respectively) in 8.5%. The inclusion of unsaturated fatty acids in the diet of dairy cows did not influence the microbial protein synthesis.

Key Words: allantoin, fat feeding, microbial nitrogen

TH151 Protein maintenance requirements of goats. A. K. Almeida*, D. C. Soares, S. P. Silva, M. H. M. R. Fernandes, I. A. M. A. Teixeira, and K. T. Resende, *UNESP Univ Estadual Paulista, Jaboticabal, São Paulo, Brazil.*

We have proposed to investigate the effect of gender in protein maintenance requirements and the extension of the difference for Saanen goats between 30 and 45 kg of body weight (BW). We used 24 intact males, 23 females and 24 castrated males with initial BW of 30.0 ± 1.09 kg and initial age of 258 ± 53 d. At 30.0 ± 1.09 kg of BW, 6 intact males, 6 females and 6 castrates were slaughtered to estimate the initial body composition, we found one equations for each gender ($P \leq 0.0001$) for initial crude protein content. The other animals were randomly allocated into 18 groups (blocks) of 3 animals of the same gender, subjected to 0, 25 or 50% of feed restriction. The restriction level was calculated for each group of 3 animals, based on the ad libitum animals intake, when these animals reached 45 kg of BW, they were slaughtered, dictating the number of days of the other 2 animals in the group. After that the body was grinded, freeze-dried and analyzed nitrogen (N) content. To estimate the retained N, we took the final body composition minus initial body composition. As expected, we did not find difference neither the apparent digestibility of CP ($P = 0.22$) nor gender ($P = 0.42$) for feed restriction level. We used the MIXED procedure SAS (SAS Inst. Inc., Cary, NC) to perform the regression of the retained N in the weight gain on N intake, we used the CONTRAST option to verify difference among genders, the ESTIMATE option gave us the overall intercept and slope. The net requirement of N for maintenance (MRNP) was assumed to be the intercept of the regression of the retained N in the daily gain (g of

N/kg$^{0.75}$ of EBW) on N intake (g of N/kg$^{0.75}$ of EBW), that represents the endogenous and metabolic losses of N multiplied by 6.25. Our study indicated the value of 419 ± 67 mg of N/kg$^{0.75}$ of EBW for minimal N losses, which corresponds to MRNP of 2.62 ± 0.5 g/kg$^{0.75}$ of EBW. The N intake required for maintenance, at retained nitrogen equal to zero, was 1.15 g of N/kg$^{0.75}$ of EBW, which corresponds to the intake of 7.16 g of CP/kg$^{0.75}$ of EBW. According to this study the feeding systems recommendations underestimates the protein requirements for goats. FAPESP process number: 2010/02482–4.

Key Words: gender, kid, nutrition plan

TH152 Encapsulated nitrate product replacing soybean meal on feedlot performance of finishing beef steers. M. L. R. Pereira[1], V. R. M. Couto[1], R. C. Araujo[1], F. A. Lino[1], A. M. Mobiglia[1], J. A. Silva[1], A. C. Carvalho[1], P. H.J. Cunha[1], and J. J. R. Fernandes*[1], *[1]Escola de Veterinaria e Zootecnia da UFG, Goiania, Goias, Brazil, [2]GRASP Ind. e Com. LTDA, Curitiba, Parana, Brazil.*

Nitrate salts can be used as NPN sources. Despite this, nitrate is not currently used due to the risk of methemoglobinemia. The objective of this experiment was to evaluate the effects of an encapsulated calcium nitrate product (16% total N and 65.1% NO_3 in DM basis) as a replacement of soybean meal during an 84-d finishing period of feedlot beef steers. One hundred 20 Nellore beef steers (339.5 kg of initial BW) were used in a randomized complete block design with 4 treatments and 5 replicates. Blocks were defined by initial BW and pens with 6 animals each were considered as replicates. Treatments were defined as follows: CTL = control diet using soybean meal without any further addition of NPN; ENP-1 = inclusion of 1% encapsulated nitrate product (ENP) in the dietary DM; ENP-2 = inclusion of 2% ENP; and ENP-3 = inclusion of 3% ENP. Diets were isonitrogenous and isoenergetic with a 90:10 concentrate:forage (sugarcane bagasse) ratio. Animals were stepwise adapted to treatments by feeding CTL for 4 d, ENP-1 for 4 d, ENP-2 for 5 d, and then ENP-3. During adaptation, blood methemoglobin (MetHb) in all animals were below 2% of total hemoglobin. A quadratic increase ($P < 0.05$) was observed on average MetHb throughout experimental period (0.62, 0.98, 1.54, and 1.45% for CTL, ENP-1, ENP-2, and ENP-3, respectively). The DMI decreased linearly ($P < 0.02$) with nitrate inclusion (9.6; 8.7; 8.8; 8.4 kg/d for CTL, ENP-1; ENP-2; ENP-3, respectively). Final BW and ADG were not affected ($P > 0.10$) by treatments. Feed efficiency, expressed in carcass weight basis, also did not differ ($P > 0.10$) among treatments, showing values of 0.121, 0.130, 0.128, and 0.127 according to the incremental dosages of ENP. No effects ($P > 0.10$) were observed on hot carcass weight, carcass yield, and fat thickness. In conclusion, encapsulated nitrate product is an effective NPN source, being able to replaced soybean meal resulting in similar animal performance. The observed basal levels of MetHb indicated that animals were not at risk for methemoglobinemia development.

Key Words: animal growth, beef cattle, methemoglobin

TH153 Production, composition and oxidative stability of milk enriched in polyunsaturated fatty acids from dairy cows fed alfalfa protein concentrate or supplemental vitamin E. M.-C. Fauteux*, Y. Lebeuf, R. Gervais, and P. Y. Chouinard, *Departement des Sciences Animales, Universite Laval, Quebec, QC, Canada.*

Alfalfa protein concentrate (APC; Extraluz, Desialis) produced by cold pressing of fresh forage followed by drying and pelleting of the extract is a source of protein (>50% CP) and carotenoids (>1000 µg/g of DM), the latter being known for their role as antioxidants. Effects of feeding APC or supplemental vitamin E on production, composition and oxidative stability of milk enriched in polyunsaturated fatty acids (PUFA) were evaluated using 6 lactating Holstein cows (DIM = 224; BW = 672 kg; milk yield = 20.9 kg) used in a replicated 3 × 3 Latin square (21-d periods, 14-d adaptation). Treatment diets were formulated to contain (% DM): CTL = 9% soybean meal (SBM); VitE = 9% SBM + 7000 IU vitamin E; and APC = 9% APC. All cows received continuous abomasal infusion of 450 g/d of linseed oil. As a result, milk fat content of c9c12 18:2 increased from 0.9% to 3.8%, while c9c12c15 18:3 increased from 0.3% to 12.5% during the experimental period compared with the pretrial period. There was no difference ($P > 0.68$) in milk fat (MF) content of these 2 fatty acids among treatments. Milk protein (3.60%), and fat content (4.30%) were similar among treatments ($P > 0.31$). Milk yield tended to be higher for APC (14.8 kg/d; b) compared with VitE (13.1 kg/d; a, $P = 0.08$) but was not different from CTL (13.4 kg/d; ab). Cows fed APC had a higher protein yield (521 g/d; b) compared with VitE (446 g/d; a) whereas CTL had an intermediary value (484 g/d; ab). Redox potential of fresh milk was reduced when cows were fed vitE (144 mV; a) and APC (152 mV; a) compared with CTL (189 mV; b). Dietary treatments had no effect on fresh milk contents of dissolved oxygen (8.1 mg/L; $P = 0.41$) and conjugated diene hydroperoxides (62.8 mmol/kg of MF; $P = 0.76$). Hexanal content of fresh milk was lower for cows fed VitE (0.03 mg/kg of milk; a) compared with CTL (0.07 mg/kg of milk; b) whereas APC had an intermediary value (0.05 mg/kg of milk; ab). In conclusion, feeding APC to dairy cows helped prevent oxidative degradation of milk enriched in PUFA.

Key Words: carotenoid, cow, oxidation

TH154 Effects of canola meal treatment with different levels of tannins extracted from pistachio hulls on the N fractions by the Cornell Net Carbohydrate and Protein System (CNCPS). M. Dehghan-Banadaky*, A. R. Jolazadeh, and N. Vahdani, *Department of Animal Science, University of Tehran, Karaj, Tehran, Iran.*

The objective of this study was to investigate the effects of different levels of extracted tannin from the pistachios hulls on protein fractioning of canola meal (CM) based on the Cornell net carbohydrate and protein system (CNCPS).The sun dried pistachio hulls was grounded through a 0.5 mm screen and soaked with ratio of 1:10 between pistachio and water. Filtered extract was concentrated by heating at 95 ℃. The CM was treated with pistachio concentrated extract (PCE) containing 11% Tannin in DM of extract, in different levels of 0, 5, 10, 15, 20 and 30 gr tannin in100 gr DM of canola meal . Protein fractioning of CM was determined according to procedures by Licitra et al. (1996). According to results, 5% level has shown the lowest soluble fraction (total of A, B1) among treatments. There was no significant difference among treatments in B2 fraction. All treatments were increased B3 fraction compared with control and 20% level has showed the highest B3 fraction. There was a reduction in C fraction when the level of PCE was increased. The lowest soluble fraction of CP followed by the highest escaped protein (B2+B3) elicited to recommend 5% level as the best treatment for CM, in lab scale.

Table 1. Mean and SE of proportion of the soluble and insoluble CP fractions expressed as percentages of total CP for CM based on the CNCPS

	Soluble fraction			Insoluble fraction			
Treatment	A	B1	A+B1	B2	B3	C	B2+B3+C
Control	3.3^{abc}±0.20	13.3^{f}±0.6	16.6^{e}±0.60	73.9^{a}±0.78	8.1^{b}±0.13	1.3^{a}±0.04	83.4^{a}±0.7
5%	3.8^{a}±0.10	16.3^{e}±0.6	20.1^{d}±0.64	69.4^{b}±0.76	9.4^{a}±0.09	1.1^{ab}±0.03	79.9^{b}±0.64
10%	3.7^{ab}±0.52	19.3^{d}±0.6	22.1^{c}±0.95	67.3^{c}±0.81	8.6^{b}±0.07	1.1^{ab}±0.09	77.3^{c}±0.95
15%	2.1^{bc}±0.17	22.3^{c}±0.6	25.2^{b}±0.68	65.3^{c}±0.62	8.3^{b}±0.18	1.1^{ab}±0.08	74.8^{d}±0.68
20%	2.7^{cd}±0.16	25.3^{b}±0.6	27.9^{a}±0.67	61.5^{d}±0.31	9.4^{a}±0.40	1.1^{b}±0.07	72.1^{e}±0.67
30%	2.1^{d}±0.12	27.88^{a}±0.3	29.8^{a}±0.25	60.1^{d}±0.34	9.3^{a}±0.15	0.7^{c}±0.10	70.2^{e}±0.20

Key Words: CNCPS, canola meal, tannin

TH155 Aflatoxin B1 binding by treated lactobacilli as a mycotoxin binder in ruminant gastrointestinal model. R. Motameny[2], M. Dehghan-Banadaky*[1], and S. Totonchi-Mashhour[2], *[1]Department of Animal science, University of Tehran, Karaj, Tehran, Iran, [2]Department of Animal Science, Faculty of Agriculture, Science and Research Branch, Islamic Azad University, Tehran, Iran.*

The present study investigated the ability of *Lactobacillus rhamnosus* PTCC 1637, *Lactobacillus plantarum* PTCC 1058, and *Lactobacillus acidophilus* PTCC 1643 in nonviable forms to bind high dosage of the AFB1 in simulated ruminant gastrointestinal model. Bacteria were grown in MRS broth (37°C, 24 h) and killed with heat or acid. The AFB1 naturally produced with *Aspergillus parasiticus* PTCC 5286 via fermentation of rice and extracted with chloroform. Differential analysis for aflatoxin B1, B2, G1, G2 was done by HPLC method. Result showed that from the total aflatoxins content, 84.64% was aflatoxin B1 and 15.36% was aflatoxin G1. Each sample contained 1×10^9 treated bacteria per 1.5 mL of buffer (18 µg/mL AFB1) that incubated continuously in pH 6.5 (16 h), 1.9 (1 h) and 7.8 (24 h) based on 3-step in vitro procedure that simulating rumen, abomasum and intestine situation of ruminants. At the end of incubation period bacteria were pelleted and the supernatant fluid containing unbound the AFB1 was collected and analyzed by microtiter plate ELISA method. Results shown 26.9, 21.4, 19.8% AFB1 binding percentage with *L. plantarum, L. rhamnosus* and *L. acidophilus*, respectively, with no significant differences among them ($P > 0.05$). Aflatoxin B1 binding percentage by heat and acid treatments were 21.9 and 23.8% respectively, with no significant differences. We concluded that, these strains and treatments had similar ability to reducing high dosage of impure aflatoxin B1 in ruminant model but more in vitro investigation are needed for selecting an appropriate mycotoxin binder based on lactobacilli.

Key Words: aflatoxin B1, ELISA, *Lactobacillus*

TH156 Ruminal fermentability of killed lactobacilli as mycotoxin binder. R. Motameny[2], M. Dehghan-Banadaky*[1], and AA Sadeghi[2], *[1]Department of Animal Science, University of Tehran, Karaj, Tehran, Iran, [2]Department of Animal Science, Faculty of Agriculture, Science and Research Branch, Islamic Azad University, Tehran, Iran.*

Heat and acid killed of *Lactobacillus rhamnosus* PTCC 1637, *Lactobacillus plantarum* PTCC 1058, and *Lactobacillus acidophilus* PTCC 1643 have ability to bind AFB1. Ruminal fermentability of these organic compounds is a key factor for assessing their usefulness as mycotoxin binders in addition to their aflatoxin binding properties. Objective of current study were to assess cumulative gas production of these treated bacteria as an indirect index for ruminal fermentation process. Briefly each strain were grown in MRS broth (37°C, 24 h), pelleted, washed, treated with heat or acid, washed, dried and finally 200 mg of each sample was weighed into a serum bottle (5 samples in total) before the injection of 30 mL rumen fluid based on Theodorou et al. (1994). Results showed that lowest ($P \leq 0.0001$) cumulative gas production (7.5 mL) obtained by *L. rhamnosus*, *L. plantarum*, and *L. acidophilus* with 14.4 and 14.3 mL gas production showed highest cumulative gas production during incubation time ($P \leq 0.0001$). Heat and acid treatments with 10.1 and 14.0 mL of cumulative gas production showed significant differences ($P \leq 0.0001$). Lowest gas production related to 2h of incubation period (3.9 mL), then gas production until 12 h was constant (5.1 to 6.4 mL) and from 24 to end of incubation period increased significantly ($P \leq 0.0001$) from time to another time (7.4 to 30.7 mL). Heat treated *L. rhamnosus* with lowest ruminal fermentability during 96 h of incubation period, showed appropriate property for selecting as mycotoxin binder in ruminant ration.

Key Words: gas production test, *Lactobacillus*, mycotoxin binder

TH157 Steam flaking barley grain decreases rumen pH when compared to grinding. M. Dehghan-Banadaky*, M. Eslamizad, and A. Lakki, *Department of Animal Science, University of Tehran, Karaj, Tehran, Iran.*

Results on the effect of steam flaking (SF) versus grinding (G) of barley grain on rumen pH have been inconsistent. In this study, 5 nonlactating, non-pregnant ruminally cannulated Holstein cow were used to compare the effect of G and SF barley grain on rumen pH. Treatments were applied to cows in a cross over design with five 10-d periods (7 d of adaptation and the last 3 d for sampling). Cows were fed a ration providing maintenance requirements based on NRC 2001. The experimental ration was similar between treatment except for the proportion of either SF or G barley .The total amount of barley fed was 4.2 kg daily with 100:0, 75:25, 50:50, 25:75 and 0:100 ratios of G to SF barley grain. Results indicated that SF barley grain significantly decreased rumen fluid pH when substituted for 75 and 100% of G barley grain in diet suggesting that SF increases rate and extent of starch digestion in the rumen.

Table 1. Rumen fluid pH in cows fed different ratios of ground to steam flaked barley grain

	Treatment						
	SF100: G0	SF75: G25	SF50: G50	SF25: G75	SF0: G100	SEM	*P*-value
Rumen pH	6.60^{a}	6.63^{ab}	6.69^{ab}	6.70^{b}	6.74^{b}	0.036	0.047

Key Words: barley, ground, steam flaking

TH158 Lactation performance and nitrogen balance in cows fed red clover or alfalfa based diets differing in rumen-degraded protein supply. M. Leduc*[1], R. Gervais[1], E. Baumann[1], Y. Lebeuf[1], GF Tremblay[2], and PY Chouinard[1], *[1]Universite Laval, Quebec, Quebec, Canada, [2]Agriculture and Agri-Food Canada, Quebec, Quebec, Canada.*

Polyphenol oxidase in red clover silage (RCS) is known to reduce proteolysis which can modify dietary N utilization in ruminants. Rumen metabolism of N could be further modified by applying heat treatments to dietary protein supplements. The objective of this trial was to compare the effects of RCS and alfalfa silage (AS) fed in diets differing in rumen-degraded protein (RDP) supply on milk yield and composition, and on N balance in dairy cows. Eight multiparous Holstein dairy cows (72 ± 17 DIM) were used in a replicated 4 × 4 Latin square design (21-d periods, 14-d adaptation). Four treatments were compared in a 2 × 2 factorial

arrangement with AS or RCS fed in diets providing 85 (RDP85) or 100% (RDP100) of calculated RDP requirements. Untreated and heat-treated (AminoPlus) soybean meals were used to adjust dietary RDP. Cows fed AS diets had a higher N intake (633 g/d; $P < 0.01$) than those fed RCS diets (540 g/d) as a result of higher dietary CP concentration (15.4 vs. 14.4%; $P < 0.01$) and DM intake (25.8 vs. 23.4 kg/d; $P < 0.01$). Milk yield was higher for cows fed AS (35.7 kg/d; $P < 0.01$) compared with RCS (34.3 kg/d). Cows fed RDP85 had a higher milk yield (35.4 kg/d; $P = 0.04$) compared with RDP100 (34.6 kg/d). Milk protein content and yield were higher for cows fed AS (3.29% and 1172 g/d, respectively; $P < 0.01$) compared with RCS (3.14% and 1075 g/d). Concentration of MUN was higher for cows fed AS (8.1 mg/dL; $P < 0.01$) compared with RCS (6.6 mg/dL). As a percentage of N intake, cows fed AS had a lower fecal N excretion (33.0% vs. 41.2%; $P = 0.01$) and a higher urinary N excretion (28.0% vs. 22.6%; $P < 0.01$) than cows fed RCS. As a result, total N excretion was similar among the 2 silages (62.4% of N intake; $P = 0.31$). Finally, efficiency of milk N secretion was lower when cows were fed AS (29.7%; $P = 0.02$) compared with RCS (32.1%). Varying RDP supply had no effect on N balance ($P > 0.16$). In conclusion, under the conditions of the current trial, feeding AS allowed a higher production of milk and milk protein but the efficiency of milk N secretion was lower as compared with RCS.

Key Words: polyphenol oxidase, red clover, rumen-degraded protein

TH159 Group size of veal calves does not affect production, physiological, or hematological indicators of welfare and has transient effects on health. E. M. Abdelfattah[2], M. M. Schutz[3], D. C. Lay Jr.[1], J. N. Marchant-Forde[1], and S. D. Eicher*[1], *[1]USDA-ARS, W. Lafayette, IN, [2]Banah University, Moshtohor, Qalyubia, Egypt, [3]Purdue University, W. Lafayette, IN.*

Holstein-Friesian bull calves (n = 168; 44 ± 3 d of age), were used to investigate the effect of group size on performance, health, hematology, and welfare of veal calves. Groups of calves were assigned to 1 of 3 group housing treatments with 2, 4, or 8 calves per pen (initial BW 65.3 ± 3.7, 66.5 ± 3.7, and 67.6 ± 3.7 kg, respectively). The pens within 2 barns were 3 × 1.20 m (2 calves/pen), 3 × 2.40 m (4 calves/pen), and 3 × 4.80 m (8 calves/pen), and provided the same space (1.8 m^2 per calf) during the 5-mo finishing period. All calves were fed milk replacer and solid feed twice daily at 12 h intervals. Body weights were measured at the beginning (Initial BW) and at the end of the experiment (Final BW). Hip height and heart girth were recorded monthly for 5 mo. Health was evaluated monthly using the University of Wisconsin calf health scoring chart. Data were analyzed as a RCB with repeated measures using PROC MIXED (SAS). No differences ($P \geq 0.5$) among treatments were found regarding BW or ADG for the entire 5-mo period. Group size resulted in similar hip height change ($P = 0.41$) and heart girth change ($P = 0.18$) over 5 mo. The incidence of diarrhea was similar among treatments ($P \geq 0.15$). An interaction of treatment and month was detected for both cough ($P = 0.03$) and nasal discharge ($P = 0.02$) scores. During mo 1, calves in groups of 8 or 4 coughed more compared with calves in groups of 2, whereas, in mo 2, calves in groups of 8 coughed more than calves in groups of 4 or 2. In mo 4, calves in groups of 8 had less nasal discharge than calves in groups of 2 or 4. Plasma cortisol ($P = 0.37$) and blood hemoglobin ($P \geq 0.13$) concentration were not affected by group size. In conclusion, the number of veal calves in a group, given the same space, has no detrimental effect on performance, and has transient effects on health of veal calves. Housing veal calves in group size of 2, 4, or 8 can be equally effective in terms of production and has no clear negative effect on welfare.

Key Words: group size, production, veal calf

TH160 Effect of meloxicam on gain and behavior of calves castrated by banding preweaning. J. A. Daniel*[1], P. D. Krawczel[2], and B. K. Whitlock[3], *[1]Department of Animal Science, Berry College, Mt. Berry, GA, [2]Department of Animal Science, The University of Tennessee, Knoxville, [3]Department of Large Animal Clinical Sciences, College of Veterinary Medicine, The University of Tennessee, Knoxville.*

The objective was to determine if oral meloxicam (M; a non-steroid anti-inflammatory) administered at castration of pre-weaning calves affected ADG or behavior. Prior to castration (14 d), Angus bulls were assigned to bull (BULL; n = 7; age 106 ± 6 d; BW = 174.2 ± 7.7 kg; scrotal circumference 17.7 ± 0.4 cm), castrated (BAN; n = 12; age = 105 ± 5 d; BW = 144.5 ± 7.6 kg; scrotal circumference = 16 ± 0.4 cm) or castrated with meloxicam (BAN+M; n = 13; age = 121 ± 6 d; BW = 145.8 ± 6 kg; scrotal circumference = 16.1 ± 0.3 cm) treatments with consideration of potential as a herd sire. On d 0, BAN and BAN+M had a rubber band applied tightly around the scrotum, and BAN+M also received oral M (2 mg per kg BW). On d 0, 14 and 28, animals were weighed and a 10-mL blood sample was collected via the tail vein for plasma concentrations of haptoglobin and fibrinogen. Dataloggers were affixed to the left rear leg to record behaviors [mean lying time (h/d), mean lying bouts (n/d), and steps (n/d)] at 1-min intervals, moved to the right rear leg on d 14 and removed on d 28. Behavior data were tested for effect of treatment, day, and treatment by day interaction and ADG data were tested for effect of treatment, period (pre, d 0–14, and d 14–28) and treatment by period interaction using JMP procedures for repeated measures. Day 0–14 ADG was greater for BULL than BAN or BAN+M ($P < 0.05$), but no other time periods or groups differed. Plasma concentrations of fibrinogen were greater for BULL than BAN or BAN+M on d 28 and BULL, BAN and BAN+M on d 0 ($P < 0.05$). Plasma concentrations of fibrinogen on d 14 for BAN+M were greater than BAN and BAN+M on d 28 ($P < 0.05$). In the first 14 d period, BULL spent more time lying on d 2, 3 and 13 and less on d 8 and 11, took more steps on d 7,8,10,11, and 12, had more lying bouts on d 4 and 13 than BAN and BAN+M ($P < 0.05$). BULL had more lying bouts than BAN on d 3 and 14 and more than BAN+M on d 5, 6 and 12 ($P < 0.05$). BAN took more steps on d 8, and had fewer lying bouts on d 3 than BAN+M ($P < 0.05$). Castration of pre-weaned calves decreased ADG and altered behavior. Fewer steps and more lying bouts for BAN+M suggest pain abatement.

Key Words: calf, castration, behavior

TH162 Panting score and respiratory rate in *Bos indicus* growing heifers. A. Camacho*[1], B. J. Cervantes[2], and R. Barajas[1], *[1]Facultad de Medicina Veterinaria y Zootecnia, Universidad Autonoma de Sinaloa, Culiacan, Sinaloa, Mexico, [2]Ganadera Los Migueles, S.A. de C.V., Culiacan, Sinaloa, Mexico.*

Panting score (PS) has been proposed as a practical method of estimate the thermal status of cattle exposed to high environmental heat loads. PS was developed using *Bos taurus* cattle, differences in heat tolerance and greater use of *Bos indicus* cattle in hotter areas of the world, generating interest in validating the use of PS in these kind of cattle. In this study, 50 *Bos* indicus heifers (195.8 ± 0.38 kg) were utilized to evaluate the relationship between panting score and respiratory rate in *Bos indicus* growing heifers. Heifer were weighed individually and randomly assigned to 1 of 2 types of allotment: (1) dirt-floor pens (6 × 12 m) without shade (No Shade); and (2) Pen as described plus shade (Shade). Shade was provided with ceiling of 6 × 4 m of metal sheeting positioned 3.7 m over soil level. During 30 d of experiment, each 2 d air temperature (t °C) and relative humidity (RH, %) were recorded at 1400 h inside of shaded and no shaded pens. panting score and respiratory rate (RR) were recorded at 1400 h in one heifer from each pen. PS was recorded using a 7-point score (0, 1, 2, 2.5, 3, 3.5, and 4), where PS = 0 indicates no elevation in RR (no thermal stress), and PS = 4 indicates severe thermal stress (open mouth, tong fully extended, head dropped, rapid labored breathing). RR was visually determined (±5 min). Each heifer-day was considered as experimental unit. Results were analyzed using linear regression procedures. Mean, maximum and minimum temperatures were 36.8, 44.2 and 25.4°C, respectively. Mean, maximum and minimum HR were 49.9, 89.4 and 33.2%, respectively. Significant relationships ($P < 0.00001$) were found between RR and PS in all cases. The equation obtained from heifers in Shade allotment was: RR (breaths/min) = 37.69 + 30.7957PS ($R^2 = 0.90$; n = 75). The equation from No Shade data was: RR (breaths/min) = 32.3416 + 35.6930PS ($R^2 = 0.84$; n = 75). And General relationship (polled Shade and No Shade data) was: RR (breaths/min) = 36.169 + 33.5561PS ($R^2 = 0.91$; n = 150). Results

suggest that panting score is a practical tool to assess the thermal status in *Bos indicus* cattle exposed to high temperatures.

Key Words: *Bos indicus*, hot weather, panting score

TH163 Effects of misting systems on physiological responses of dairy heifers in freestalls. G. A. Silva[1], S. V. Matarazzo*[2,1], I. Arcaro Junior[1], L. M. Toledo[1], and J. B. Demski[1], *[1]Instituto de Zootecnia, Nova Odessa, SP, Brazil, [2]Universidade Estadual de Santa Cruz, Ilheus, BA, Brazil.*

The thermal environment is a major factor that can negatively affect dairy. Cooling methods should be used to increase the cows' ability to lose heat and alleviated these adverse factors. To improve the thermal environment the objectives of this trial was to evaluate the influence of evaporative cooling on physiological responses of dairy heifers in freestall. Twelve heifers were allocated in 3 treatments (4 heifers/treatment) in a Latin rectangle design (Blouin et al., 2009). Treatments were applied from January to May, 2012. The trial was divided into 6 periods of 13 d (6-d for adaptation and 5-d for data collection). The treatments assigned were: Control (not cooled), Fan and misting on at any relative humidity (FM), Fan and misting on when the relative humidity ≤ to 70% (70% FM). The freestall was equipped with misting (36L/h) and fans (2.5 m/s) installed about 2.5 m above the feeding area. Air temperature and relative humidity inside and outside the facility were measured every 15 min over a period of 24 h using a data logger. Respiratory frequency (flank movement), rectal temperature (clinic thermometer) and rump surface temperature (infrared thermography) were taken each 3-h from 0800 to 1600 on all 30 d of data collection. The air temperature was decreased ($P < 0.05$) at 1600 and 1900 in FM (27.3°C) and 70% FM (27.5°C) treatment in relation to control (28.0°C). The relative humidity was higher than 70% at 0700 and 1900 in FM (96.5 and 81.1%) and 70% FM (87.5 and 75.2%) treatments. The temperature and humidity index (THI = 67) was in thermoneutral zone in all treatments. The respiratory rate showed positive results ($P < 0.05$) with lower values for treatments provided with fan and misting (49 vs. 55 movement/minute) when compared with control. Also, the rump surface temperature were lower ($P < 0.05$) in fan and misting treatments (34.1 vs. 35.0°C). Heifers showed similar ($P > 0.05$) rectal temperature (38.9°C). We conclude that treatments with misting systems were able to recover a thermal environment for the animals and it was reflected in physiological responses.

Key Words: misting, heifer

TH164 Estrus behavior in young Holstein heifers. B. F. Silper*[1], M. M. Reis[1], A. M. L. Madureira[1], T. A. Burnett[1], A. M. de Passillé[2], J. Rushen[2], and R. L. A. Cerri[1], *[1]University of British Columbia, Vancouver, BC, Canada, [2]Agriculture and Agri-Food Canada, Agassiz, BC, Canada.*

Estrus behavior of young Holstein heifers was described to improve knowledge of estrus detection. Behavior was evaluated for one estrus episode from each of 10 heifers (mean ± SD; 10.1 ± 0.5 mo old, 331.3 ± 33.7 kg of BW and 125.7 ± 4.1 cm in the withers) housed in a free stall barn in 2 groups of 11 and 12 heifers. Estrus behavior was recorded by video, activity monitored by data loggers attached to a rear leg, and behavioral changes were validated by comparison with ovarian ultrasonography. Thirty-one behaviors were evaluated during 15 h before and 15 h after the activity peak. Baseline behavior was monitored in a corresponding 30 h period one wk before estrus. Number of steps (NSTEP) and percentage of lying and standing times were obtained from the data loggers. Continuous data was analyzed by ANOVA using the proc GLM of SAS. NSTEP (mean ± SE) during estrus was 3 times higher than on baseline day (205.6 ± 12.8 and 77.8 ± 15.7 steps/h, respectively; $P < 0.0001$). The increase in NSTEP ranged from 130% to 523% among heifers. Percent time standing increased from 44 ± 4% to 64 ± 3% during estrus ($P < 0.01$). There was an increase in the occurrence of chin rest, acceptance of chin rest, attempt to mount, acceptance of mount, licking, being pushed and head butting ($P < 0.05$). Previously undescribed behaviors, such as following other heifers and crossing between front and back of the pen also increased (25-fold and 4-fold, respectively; $P < 0.01$). NSTEP was positively correlated with acceptance of chin rest ($R^2 = 0.80$), attempt to mount ($R^2 = 0.68$), and crossing ($R^2 = 0.62$). There was more than one heifer in estrus at the same time for 6 of the analyzed episodes. Chin rest, acceptance of chin rest, and front attempt to mount were reduced when more than one heifer was in estrus at the same time ($P < 0.05$), suggesting certain behaviors of estrus may be more difficult to detect when animals are synchronized. Estrus was apparent in behavioral changes but the difference between heifers in the degree of estrus expression was large. The increase in expression of many behaviors and the strong correlation with NSTEP reveals potential for improvement of on-farm estrus detection and heat detection based reproductive programs.

Key Words: estrus behavior, heat, mount

TH165 Effect of calving management on calf vitality, blood gas, behavior, and intake for 24 hours after birth. P. Ji[1], H. M. Gauthier*[1], S. Y. Morrison[1], S. E. Williams[1], K. M. Morrill[2], D. M. Haines[3], and H. M. Dann[1], *[1]William H. Miner Agricultural Research Institute, Chazy, NY, [2]Cornell Cooperative Extension, Canton, NY, [3]The University of Saskatchewan and The Saskatoon Colostrum Co. Ltd., Saskatoon, SK, Canada.*

Management of cows during calving may affect the well-being of the calf. Holstein heifers were housed in a bedded pack (21 ± 1 d) with a 4.6 × 4.0 m blinded area and were moved when calving was imminent to either an individual pen (IND; n = 24) or left in the pack (GRP; n = 23). Calves (n = 47) were evaluated. Labor duration and calving difficulty were recorded. Calf vitality was assessed and samples of caudal auricular arterial blood and jugular venous blood were collected at 0, 12, and 24 h. Behavior was monitored using visual observations, video review, and data loggers for 24 h. Calves were fed 675 g of colostrum replacer (184 g IgG; The Saskatoon Colostrum Co. Ltd.) at 1.5 h and were offered 1.89 L of milk replacer (MR) at 12 h. Data were analyzed as a completely randomized design using the MIXED procedure of SAS with repeated measures as appropriate. IND heifers were moved at 89 ± 11 min before calving. Mean birth weight was 37.9 ± 1.1 kg and 38.2 ± 0.8 kg for IND and GRP, respectively. Labor tended to be longer for IND than GRP (116 and 91, SE = 10 min, $P = 0.10$). There was no treatment effect ($P > 0.10$) for calving difficulty score (1.6 ± 0.1), or calf measures of temperature (39.0 ± 0.1°C), pulse (136 ± 3 bpm), or respiration (56 ± 2 bpm). Arterial blood showed increased acidosis at 0 h for IND over GRP based on differences ($P < 0.05$) in pH (7.18 and 7.29; SE = 0.01), HCO_3^- (21.7 and 27.2; SE = 0.9 mEq/L), anion gap (18.6 and 13.9; SE = 0.7 mmol/L), and base excess (−7.2 and −1.4; SE = 0.7 mmol/L). Feeding behavior at 0 or 12 h did not differ ($P > 0.10$), but IND consumed 0.32 L less MR than GRP ($P = 0.08$). At 24 h, no differences were found in serum total protein (5.5 ± 0.1 g/dL), IgG (19.2 ± 0.7 g/L), or apparent efficiency of absorption (34.4 ± 1.2%). From 1.5 to 24 h, standing (154 ± 13 min; 26 ± 2 bouts) did not differ ($P > 0.10$) between IND and GRP. Measures of calf vitality and behavior showed no effect of treatment. The stress of moving and isolation of

primigravid heifers in labor tended to increase labor duration with calves experiencing possibly more hypoxia and metabolic acidosis at 0 h and a decreased appetite at 12 h, regardless of eutocia.

Key Words: calving, acidosis, IgG

TH166 Herd-level reproductive performance and its relationship with lameness and leg injuries on freestall dairy farms. N. Chapinal*[1], M. A. G. von Keyserlingk[1], R. L. A. Cerri[2], K. Ito[3], S. J. LeBlanc[4], and D. M. Weary[1], *[1]Animal Welfare Program, University of British Columbia, Vancouver, BC, Canada, [2]Faculty of Land and Food Systems, University of British Columbia, Vancouver, BC, Canada, [3]Novus International Inc., St. Charles, MO, [4]Population Medicine, University of Guelph, Guelph, ON, Canada.*

Individual cows experiencing lameness are thought to have poorer reproductive performance. The objectives were to describe the variation in herd-level reproductive outcomes and to investigate the associations between these outcomes and the prevalence of lameness, hock injuries and knee injuries on 53 freestall dairy herds from the Northeastern US. Five reproductive outcomes were measured for a 12-month period for all multiparous cows in the herd using records from Dairy Comp 305: calving to conception interval (CCI), calving interval (CI), conception rate at the first insemination (CR1), pregnancy rate (PR), and insemination risk (IR). The prevalence of lameness (score ≥3 in a 5-point scale), hock injuries (score ≥2 in a 3-point scale) and knee injuries (scored as presence or absence) was assessed in one high producing pen. The mean ± SD for the 5 reproduction outcomes were: CCI = 127 ± 10 d, CI = 404 ± 10 d, CR1 = 37 ± 5%, IR = 60 ± 7%, PR = 20 ± 3%. The average prevalence of clinical lameness, hock injuries and knee injuries were 45 ± 19, 58 ± 31, and 31 ± 22%, respectively. Univariable associations between the reproductive outcomes and the predictors (prevalence of lameness and leg injuries) were tested and significant predictors were submitted to a model that included herd size as a covariate. Farms with higher prevalence of lameness had longer average CCI (estimate = 0.16 ± 0.07; R^2 = 0.09) and CI (estimate = 0.14 ± 0.07; R^2 = 0.07), and farms with higher prevalence of knee lesions had lower CR1 (estimate = −0.08 ± 0.03; R^2 = 0.13) and PR (estimate = - 0.05 ± 0.02; R^2 = 0.11). These results suggest that management to reduce rates of lameness and injuries may improve reproductive performance at the herd level. Further research is needed to investigate other factors that may contribute to or confound this relationship.

Key Words: conception rate, knee injury, pregnancy rate

TH167 Associations between herd-level factors and lying behavior of freestall-housed dairy cows. K. Ito*[1,2], N. Chapinal[1], D. M. Weary[1], and M. A. G. von Keyserlingk[1], *[1]Animal Welfare Program, University of British Columbia, Vancouver, BC, Canada, [2]Novus International Inc., St. Charles, MO.*

The objective of the current study was to investigate the associations between herd-level factors and lying behavior of high-producing dairy cows housed in freestall barns. Lying behavior of approximately 40 cows (38 ± 2) was monitored on each of 40 farms in the Northeastern United States (NE) and 39 farms in California (CA). All cows in the pen were gait scored using a 1-to-5 scale to calculate the prevalence of overall clinical lameness (score ≥3) and severe lameness (score ≥4). Facility and management measures such as stall design, bedding quality and flooring surface were collected. Herd-level factors associated with daily lying time, standard deviation (SD) of daily lying time, frequency of lying bouts, and lying bout duration at the univariate level were submitted to multivariable general linear models. In NE, daily lying time increased with the use of deep bedding (estimate = 0.80 ± 0.31 h/d) and as average DIM of the focal cows increased (estimate = 0.08 ± 0.04 h/d for a 10-d increase). The SD of daily lying time decreased as stall stocking density increased (estimate = −0.08 ± 0.03 h/d for a 10% increase), and increased with the presence of rubber flooring in the pen (estimate = 0.16 ± 0.08 h/d) and percentage of stalls with fecal contamination (estimate = 0.04 ± 0.01 h/d for a 10% increase). Frequency of lying bouts decreased (estimate = −1.90 ± 0.63 bouts/d) and average bout duration (estimate = 15.44 ± 3.02 min) increased with the use of deep bedding. In CA, daily lying time decreased as average DIM of the focal cows increased (estimate = 0.08 ± 0.03 h/d for a 10-d increase). The SD of daily lying time decreased when feed was delivered more than once per day (estimate = −0.24 ± 0.08 h/d). The percentage of lame cows was correlated with the percentage of stalls with fecal contamination (r = 0.45), which in turn was associated with fewer (estimate = −0.25 ± 0.06 bouts/d) and longer (estimate = 1.85 ± 0.39 min) lying bouts. These results suggest that lying behavior at the herd level but should be interpreted in context with lameness prevalence, production parameters, and facility management.

Key Words: deep bedding, lameness, management

TH168 Prevalence of knee and hock injuries and their association with stall base, bedding depth and bedding type on Canadian tie-stall dairy farms. C. Nash*[1], J. Zaffino[1], D. Kelton[1], D. Pellerin[2], T. DeVries[3], AM de Passillé[4], J. Rushen[4], E. Vasseur[5], and D. Haley[1], *[1]University of Guelph, Guelph, ON, Canada, [2]Université Laval, Québec, QC, Canada, [3]University of Guelph – Kemptville Campus, Kemptville, ON, Canada, [4]Agriculture and Agri-Food Canada, Agassiz, BC, Canada, [5]University of Guelph – Alfred Campus, Alfred, ON, Canada.*

Injuries to the knees and hocks of dairy cows are a common problem and are useful animal-based indicators of inadequate cow welfare, management, and housing design. The objective of this study was to examine the relationships between knee and hock injuries and stall base, bedding type, and bedding depth on 100 Canadian tie-stall dairy farms in Ontario (n = 40) and Quebec (n = 60). Forty Holstein cows per herd were assessed for knee and hock injuries on a 4-point scale (0 being no damage to 3 being severely swollen) by 13 trained observers and were considered injured if a score of 2 (lesions) or 3 (swelling greater than 2.5 cm) was given on one or more limbs. Inter- and intra-observer agreement for injury scoring met or exceeded a minimum Kw of 0.6. Stall base type and bedding type were recorded on each farm. Bedding depth was measured on a representative sample of 4 to 8 stalls for each of the 100 farms visited. Bedding depth was classified as deep (2 cm or greater) or little (under 2 cm). Pair-wise comparisons were made using a 2-sample *t*-test. The mean herd-level prevalence and range of knee injuries and hock injuries was 43% (0–89%) and 56% (6–94), respectively. Rubber mats (51% of herds) and mattresses (44% of herds) were the most common base type, while straw was the most common bedding type (85% of herds). Farms using other base types, such as cement, represented only 4% of our herds and so were excluded from further analysis. Farms using the combination of deep bedding on mattresses had 25% fewer knee injuries (30.88 ± 4.96 vs. 56.27 ± 4.54%; mean ± SE) and 24% fewer hock injuries (45.51 ± 4.62 vs. 69.42 ± 2.59%) than farms using little or no bedding on rubber mats ($P = 0.002$). Although the high level of injuries on some farms is concerning, it is promising that other farms have few to no knee or hock injuries. There was an association between stall base and bedding, and the prevalence of hock and knee injuries on tie-stall dairy farms, indicating that the

right stall base and bedding combination may help minimize hock and knee injuries on dairy cows.

Key Words: cow comfort, injury, stall base and bedding

TH169 Effect of cow comfort on longevity on tie-stall farms in Eastern Canada. F. Bécotte*[1], E. Vasseur[3], D. Lefebvre[2], A.-M. de Passillé[4], J. Rushen[4], D. B. Haley[3], and D. Pellerin[1], *[1]Laval University, Quebec, QC, Canada, [2]Valacta, Sainte-Anne-de-Bellevue, QC, Canada, [3]University of Guelph, Guelph, ON, Canada, [4]Agriculture and Agri-Food Canada Research Centre, Agassiz, BC, Canada.*

Increasing longevity in dairy herds is an economic plus for the producers. The public's concern for animal welfare is increasing particularly when tied dairy production is involved. In trying to merge both groups' interests, the objective of this study was to evaluate the link between comfort and longevity. One hundred tie-stall dairy farms located in eastern Canada (60 in Quebec and 40 in Ontario) were enrolled. On these farms, comfort data were collected through 2 on farm visits. Lying time was assessed using accelerometers (HOBO), lameness was determined in stalls using 4 behaviors (edge, weight shifting, rest and unevenness in displacement). Cleanliness and injuries were scored using predetermined charts. Production, reproduction and health data were obtained from DHI agencies (Valacta and Canwest DHI). Pearson correlation coefficients were determined for 17 different variables representing comfort, production, reproduction, and health in regard to longevity (percentage of cows in third lactation or more). The analysis was done for Quebec and Ontario herds separately, and together. Due to the primary exploratory nature of this analysis, the level of significance was set to $P = 0.10$. Variables most related to longevity were average milk fat (r = −0.20; $P = 0.047$) and protein yield (r = −0.20; $P = 0.045$), age at first calving (r = 0.17; $P = 0.086$), heifer/cow ratio (r = −0.27; $P = 0.008$), percentage of non-injured cows (r = −0.19; $P = 0.065$) and percentage of cows lying between 10 and 14 h/d (r = 0.21; $P = 0.036$). The results differ between provinces. For Quebec, milk fat (r = −0.34; $P = 0.009$) and protein (r = −0.35; $P = 0.007$) percentages, average calving interval (r = −0.25; $P = 0.062$) and the heifer/cow ratio (r = −0.38; $P = 0.003$) were most related. For Ontario these variables were milk protein yield (r = −0.32; $P = 0.048$), calving interval (r = 0.32; $P = 0.041$), milk yield (r = −0.27; $P = 0.088$) and percentage of non-injured cows (r = 0.26; $P = 0.10$). Although production and reproduction variables seem to have an important effect on longevity, results show that there is an association between comfort and longevity and that the factors associated to longevity vary between the 2 provinces we compared.

Key Words: cow, comfort, longevity

TH170 Practices associated with dairy cattle wellbeing on organic and similarly sized conventional dairy herds. M. Bergman*[1], R. Richert[1], K. Stiglbauer[2], K. Cicconi-Hogan[3], M. Gamroth[2], Y. Schuken[3], and P. Ruegg[1], *[1]University of Wisconsin Madison, Madison, [2]Oregon State University, Corvallis, [3]Cornell University, Ithaca, NY.*

The objective of this study was to assess management practices associated with dairy animal wellbeing among organic and similarly sized conventional dairy herds. Management information, animal health scores and culling information were collected by study personnel during a single farm visit and over a 120 d period from organic (ORG; n = 192); conventional grazing herds (CONGR; n = 36); and conventional non-grazing herds (CONNG; n = 64). Associations among farm types and (1) each categorical variable were tested with χ^2, and (2) each continuous variable were tested with Wilcoxon tests. Farm type was not associated with housing at least one calf in a unit that did not enable turning around ($P = 0.901$). Calf bedding was inadequate on 54% of farms, but was not associated with management type ($P = 0.965$). Organic farmers were more likely to feed preweaned calves starter and hay than conventional farmers ($P < 0.001$). Fewer CONNG herds (14%) used analgesics during dehorning than ORG (34%) and CONGR (28%) ($P = 0.009$). Calves were weaned at an older age on ORG as compared with conventional farms (11.6, 8.3, and 8.0 weeks for ORG, CONGR and CONNG, respectively; $P < 0.001$). Calves were dehorned at an older age on ORG as compared with conventional farms (10.2, 6.1, and 9.7 weeks for ORG, CONGR and CONNG, respectively; $P = 0.03$). At least one cow was scored as having hock lesions on 78%, 92%, and 98% for ORG, CONGR and CONNG, respectively ($P < 0.001$). At least one cow was scored as overconditioned on 70%, 81% and 92% for ORG, CONGR and CONNG farms, respectively ($P < 0.001$). Organic farmers were more likely to treat fewer than 50% of animals with retained placentas, metritis, adult pneumonia and calf pneumonia ($P < 0.003$) than conventional farmers. Culling rates across all farms were 7.4% of adult cows and 4.3% of weaned heifers and were not associated with farm type ($P > 0.089$). Mortality across all farms was 2.5% for adult cows and 2.4% for weaned heifers and was not associated with farm type ($P > 0.207$). In conclusion, several of the selected management practices that affect wellbeing differed among the 3 farm types.

Key Words: wellbeing, organic, conventional

TH171 Effect of meloxicam on gain and inflammatory response of calves castrated by banding post-weaning. B. Whitlock*[1], P. Krawczel[2], J. Carroll[3], N. Burdick Sanchez[3], J. Dailey[3], J. Daniel[4], and J. Coetzee[5], *[1]Department of Large Animal Clinical Sciences, College of Veterinary Medicine, The University of Tennessee, Knoxville, [2]Department of Animal Science, The University of University of Tennessee, Knoxville, TN 37996, Knoxville, [3]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [4]Department of Animal Science, Berry College, Mt. Berry, GA, [5]Veterinary Diagnostic and Production Animal Medicine, College of Veterinary Medicine, Iowa State University, Ames.*

Castration may detrimentally affect the health and performance of weaned calves, and painful procedures are increasingly becoming a public concern. The objective of this study was to determine the effects of castration (by banding) with or without administration of meloxicam, a non-steroid anti-inflammatory, on performance and inflammatory response in weaned beef calves. Forty-eight (weaned) beef calves [10.0 ± 0.2 mo old; 304 ± 6 kg BW] were blocked by age, BW, wither height, scrotal circumference, and source, then randomly assigned to 1 of 3 treatments (n = 16 calves per treatment: (1) intact bulls (BULL), (2) castration by banding (BAN), or (3) castration by banding with orally-administered meloxicam (3 mg per kg BW on d 0 and 14; BAN+M). Calves were assigned to 8 pens (2 calves per treatment within each pen) one wk before treatment administration for acclimation to group housing. Body weight and plasma haptoglobin and fibrinogen concentrations were assessed on 0, 3, 7, 14, and 28 d after treatment. Rectal temperature was recorded at 5-min intervals for 14 d by dataloggers fitted to the calves on d 0. Data were tested for effects of treatment, day, pen, and treatment by day interaction using procedures for repeated measures. BULL gained more (0.69 ± 0.12 kg/d; $P < 0.05$) than BAN (0.15 ± 0.11 kg/d) or BAN+M (0.14 ± 0.11 kg/d) over 28 d. There was no effect of treatment ($P = 0.36$) or treatment by day interaction ($P = 0.21$) on mean plasma haptoglobin concentration. There was no effect of treatment ($P = 0.84$) or treatment by day interaction ($P = 0.25$) on mean plasma fibrino-

gen concentration. There was an effect of treatment ($P < 0.001$) and a treatment by time interaction ($P < 0.001$) on mean rectal temperature during the 14 d after treatment administration. Over 14 d, BAN+M had the greatest mean rectal temperature (39.47°C ± 0.006°C), BAN had the second greatest temperature (39.42°C ± 0.006°C), and BULL had the lowest temperature (39.41°C ± 0.005°C). Decreased ADG indicates that castration was painful regardless of pain abatement. Benefits of meloxicam were not evident from changes in growth performance or inflammatory response.

Key Words: calf, castration, anti-inflammatory

TH172 Meloxicam mediates short-term behavioral changes of castrated calves. P. D. Krawczel*[1], J. A. Carroll[2], N. C. Burdick Sanchez[2], J. W. Dailey[2], J. A. Daniel[3], J. F. Coetzee[4], and B. K. Whitlock[5], *[1]Department of Animal Science, The University of Tennessee, Knoxville, [2]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX [3]Department of Animal Science, Berry College, Mt. Berry, GA, [4]Veterinary Diagnostic and Production Animal Medicine, College of Veterinary Medicine, Iowa State University, Ames, [5]Department of Large Animal Clinical Sciences, College of Veterinary Medicine, The University of Tennessee, Knoxville.*

Castration may detrimentally affect the health and performance of weaned calves and painful procedures are increasingly a public concern. Therefore, practical pain mitigation is critical. The objective was to determine the effects of castration (by banding) with or without administration of NSAID, meloxicam, on the behavior of weaned beef calves. Forty-eight (56 d post-weaning) beef calves [10.0 ± 0.2 (mean ± SE) mo old; 304 ± 6 kg BW] were blocked by multiple factors then randomly assigned to 3 treatments (n = 16 calves per treatment): (1) intact bulls (BULL), (2) castration by banding (BAN), or (3) castration by banding with orally-administered meloxicam (3 mg per kg BW on d 0 and 14; BAN+M). On d −7, calves were assigned to 8 pens (2 calves per treatment within each pen). Behaviors [mean lying time (h/d), mean lying bouts (n/d), and steps (n/d)] were recorded at 1-min intervals for 27 d by dataloggers fitted to the calves on d 0. Data were analyzed using a mixed model in SAS with repeated measures. Over 27 d, bull spent more time lying (13.9 ± 0.6 h/d) compared with BAN (11.9 ± 0.6 h/d; $P < 0.001$) or BAN+M (12.2 ± 0.6 h/d; $P = 0.004$), which did not differ from one another ($P = 0.85$). During the 3 d after each administration of meloxicam, treatment differences were evident among all treatments. BULL spent more time lying (12.9 ± 0.6 h/d) than BAN (9.7 ± 0.7 h/d; $P < 0.001$) and tended to spend more time lying than BAN+M (11.4 ± 0.6 h/d; $P = 0.07$). BAN+M spent more time lying than BAN ($P = 0.02$). Day and treatment by day interactions were evident for both periods ($P < 0.04$). Lying bouts were not affected by treatment over 27 d ($P = 0.23$) or the 3 d after meloxicam ($P = 0.32$). Steps per d tended to differ among treatments ($P = 0.09$); BULL took fewer steps (829 ± 75 n/d) than BAN (991 ± 76 n/d) or BAN+M (972 ± 75 n/d) over 27 d. BULL took fewer steps than BAN (886 ± 80 vs 1133 ± 81 n/d; $P < 0.001$), but did not differ from BAN+M (1035 ± 80 n/d; $P = 0.16$) over the 3 d after meloxicam. Decreased lying and increased steps suggest castration was painful regardless of pain abatement. The benefits of meloxicam were evident from decreased behavioral changes 3 d after administration.

Key Words: calf, castration, behavior

TH173 Lying behavior of indoor-housed dairy goats. G. Zobel*[1], K. Leslie[2], D. M. Weary[1], and M. A. G. von Keyserlingk[1], *[1]Animal Welfare Program, University of British Columbia, Vancouver, BC, Canada, [2]Population Medicine, University of Guelph, Guelph, ON, Canada.*

Lying behavior is often used to assess the suitability of indoor housing for dairy cattle, but to our knowledge no work has assessed lying behavior of lactating dairy goats housed indoors. The aim of this work was to describe the lying behavior of does on commercial dairy goat farms. Data loggers were applied to the rear legs of 60 Saanen Alpine × does (DIM: 293 ± 131 d) on 3 farms in southwestern Ontario. The 20 does assessed on each farm were all housed within a single pen, and were milked twice a day. The loggers recorded continuously for 12 d. Analyses were descriptive; results are presented as means ± SD. Overall, goats spent 12.2 ± 1.7 h/d lying down (farm range = 11.1 to 12.9 h/d, individual animal range = 8.2 to 15.7 h/d). This lying time occurred over the course of 24 ± 7 bouts/d (farm range = 22 to 27 bouts/d, individual animal range = 9 to 43 bouts/d). Lying bouts were categorized as short (≤30 min), medium (31 to 90 min) or long (>90 min). The majority (60%) of the lying bouts were short, averaging 12 ± 2 min/bout. Just 7% of bouts were long, averaging 124 ± 24 min/bout. The percentage of long bouts varied across goats, ranging from 1 to 38%. Total daily lying times were comparable to values reported for dairy cows, but this total is composed of more lying bouts of shorter duration. More work is needed to understanding the significance of variation in lying behavior of indoor-housed dairy goats within and among farms.

Key Words: goat, welfare, data logger

TH174 Effects of housing systems and farrowing crates on the performance of sows and piglets in Korea. J. Y. Lee*, J. H. Jeon, K. H. Park, S. H. Yang, Y. H. Yoo, and J. I. Song, *National Institute of Animal Science, Suwon, Korea.*

This study was conducted to evaluate the effect of different housing systems on the performances of sows and their piglets during gestation and lactation. A total of 54 sows (Landrace × Yorkshire) were randomly allocated into 4 treatments. Individual housing in stall and group housing during gestation and conventional and alternative farrowing crate during lactation were 2 × 2 factorially arranged to set 4 treatment groups. Individual sow was used as an experimental unit. During gestation, sows were housed either in stall individually or in group with electronic sow feeder. The sows were moved from gestation pen to farrowing pen with either conventional or alternative farrowing crates on d 105 of pregnancy. The alternative farrowing crate was designed to reduce crushed piglet and to meet the Korean guidelines for pig welfare certification which states free movement of sow during lactation. Performance measures were taken on sows and piglets. Back-fat thickness and body condition score of sows were not affected by difference of both farrowing crate types and housing systems for pregnant sows. However, the changes in back-fat thickness and body condition score during lactation period were significantly lower ($P < 0.05$) in alternative crate in compared with that of conventional farrowing crate. Feed intake of sows in the group housing was significantly higher ($P < 0.05$) than that of sows in stall during gestation. Although there was no difference of estrus interval of pregnant sows between housing systems, while that was remarkably ($P < 0.05$) decreased in alternative crate compared with in conventional crate. The birth weight of piglets from sows in group housing type was higher ($P < 0.05$) than that from sows in a stall type. Moreover, lower number of still-birth was also observed in alternative farrowing crate. This study showed that the housing systems and the farrowing crate types could affect sow and piglet performances. Moreover, the design of farrowing crate for sow and piglet welfare should be carefully considered through observation of piglet and sow behaviors and performance.

Key Words: sow welfare, group housing, farrowing crate

TH175 Behavior and welfare of intramuscular or subcutaneous injection in finishing pigs and piglets. K. A. Guay* and J. J. McGlone, *Texas Tech University, Lubbock.*

Physical castration (PC), typically performed at approximately 5 d of age, can stressful for pigs. One alternative to PC is to immunological castration (IC), but the stress of the handling associated with immunological castration (or other immunizations) has not been assessed. Our objectives were to determine if subcutaneous (SC) or intramuscular (IM) injections were more painful or stressful than PC for piglets as well as measure the pain and stress associated with receiving a SC or IM injection in finishing pigs. To do this, we ran 2 experiments in which litter served as blocks in this randomized complete block design. After farrowing, 3 to 5 d old male piglets were randomly assigned to nothing (NO), SHAM handling (SHAM), IM, SC or PC with no pain relief. Piglets were videotaped and behavior was sampled for 1 h prior and 1 h post treatment. Behavior monitored included standing, walking, lying, nursing, lying with sow contact and signs of pain (standing hunched over, shaking). Finishing pigs received SC, IM, SHAM or NO injection. Finishing pigs were also monitored for 1 h pre and post treatment, and monitored for eating, drinking, lying, standing, walking, vocalization, open mouth breathing, blotchy skin and signs of irritation (rubbing the injection site). Blood was collected from all pigs for cortisol analysis 60 min post treatments so that the handling of blood collection did not affect the pig behavior. Analysis was in SAS using General Linear Models procedure. PC piglets showed less ($P < 0.05$) lying in contact with sows and more ($P < 0.05$) pain-like behaviors than IM, NO, or SHAM treatments, but SC did not differ from PC. SHAM finishing pigs spent more time lying than the pigs in other treatment groups ($P < 0.05$). Cortisol did not differ among treatments for neither piglets nor finishing pigs. In conclusion, IM injections do not change piglet behaviors relative to no handling or sham handling. SC injections caused a small change in piglet and finishing pig behaviors. PC caused measureable pain-like behaviors and general behavioral dysregulation.

Key Words: castration, injection, pig

TH176 Models for facial recognition and body weight to more precisely provide individual pig care. J. J. McGlone*[1], B. L. Backus[1], K. Guay[1], J. Ao[2], Q. Wan[2], B. Nutter[2], R. Pal[2], and S. Mitra[2], *[1]Texas Tech University Animal and Food Sciences, Lubbock, [2]Texas Tech University Electrical and Computer Engineering, Lubbock.*

The US pig industry markets over 110 million pigs a year. An average worker spends only seconds per pig providing pig care. An automated solution that is able to transmit individual pig information to farm management would improve welfare and management at the individual pig level. Our objectives were (1) to develop software for individual pig recognition, and (2) estimate the body weight of pigs using facial dimensions. After weaning, 21 d old, littermate pigs were housed in 4 pens of 10 pigs. Weekly body weights and pictures were taken of each pig. Specific facial features were captured by image analysis. Among several systems tested, the Eigenface algorithm was used to estimate individual pig identity. Each face image in a training set represents a linear combination of the principal components of the distribution of faces. These principal components are called the eigenvectors (displayed as eigenfaces) which characterize the variation in faces from statistical computation of the covariance matrix of a set of the face images involved. The Eigenface sums the pixels in an image to generate a weighting vector that, with some variation, is unique for that individual. The Eigenface weight vector was calculated for each pig face image and tested to determine if it could reliably identify individuals. If the test image was correctly recognized as the most matched, we called it a 'direct hit'. Cross-validation reached a 72% level of accuracy for 'direct hits'. In the second objective, the mean distance in pixels between eyes for each pig was used to relate to body weight (pig faces grow in proportion to body weight). Over a range of body weights from birth through 100 kg, an exponential curve ($y = 71.97*x^{1/3}$) described the relationship between the weight of pigs and the distance between the eyes in pixels ($r^2 = 0.9874$); for the narrow weight range of 5 to 42 kg, a linear model ($y = 2.915*x+129.5$) described the relationship between distance between the eyes in pixels and body weight ($r^2 = 0.9925$). These early findings will be key components in an automated monitoring system that will have a significant effect on individual pig care.

Key Words: image analysis, pig, animal welfare

TH177 Gait analysis as an objective tool to measure painful and non-painful hoof lameness in multiparous sows. C. Mohling*[1], A. Johnson[1], K. Stalder[1], C. Abell[1], H. Coetzee[2], S. Millman[3], and L. Karriker[4], *[1]Animal Science, Iowa State University, Ames, [2]Cyclone Custom Analyte Detection Service, Iowa State University, Ames, [3]Veterinary Diagnostic and Animal Production Medicine, Iowa State University, Ames, [4]Swine Medicine Education Center, Iowa State University, Ames.*

Lameness diagnosis using subjective gait scoring may not be repeatable and reliable. Quantitative gait analysis is one tool that might provide objective measures to determine the severity of lameness. The objective of this study was to measure sow gait using quantitative gait analysis technology during painful transient lameness states. Twelve mixed parity sows weighing 228.51 ± 18.08kg (mean BW ± SD) were individually housed, and served as their own controls when sound before lameness induction. On d 0, lameness was induced in one randomized rear hoof using a chemical synovitis model. After completion of the first round, sows were given a 7d rest period and then the trial was repeated with lameness induced in the other rear hoof. Three treatment days were compared (1) sound (1 d before induction), (2) most lame (first day after induction of transient lameness) and (3) resolved (sixth day after induction). Sows walked freely in a continuous closed loop track (1 m wide) that transversed across a GAITFour mat (4.3 m with 13,824 sensors). Gait analysis measures collected were maximum pressure (greatest amount of weight placed on a single hoof), stride length (distance in cm between 2 sequential footfalls from the same hoof) and stride time (time in seconds between 2 successive footfalls by the same hoof). Data were analyzed using PROC MIXED, with sow as the experimental unit in a crossover design. Gait analysis measures were compared between the 3 treatment days. On the most lame day, sows exhibited less maximum pressure on the injected hoof ($P < 0.0003$), a shorter stride length ($P < 0.0002$) and a slower stride time ($P < 0.02$) compared with sound and resolved days. There were no differences for these measures between sound and resolved days ($P > 0.05$). There were no differences for maximum pressure, stride length or stride time regardless of round or hoof injected ($P > 0.05$). In conclusion, the GAITFour tool can be considered an objective tool for detecting lameness using differences in pressure, stride length and stride time on days when sows are sound and most lame.

Key Words: gait scoring, lameness, swine

TH178 Association of neonatal Fc receptor α-chain gene (FCGRT) promoter haplotypes with FcRn expression of dairy cows. X. L. Hu, J. Q. Wang*, S. G. Zhao, J. W. Zhao, and D. P. Bu, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Bovine colostrum contains a large amount of immunoglobulin G (IgG). Fc receptor (FcRn) plays an important role in either the secretion of IgG or the intake of IgG in the mammary gland. This study was conducted to analyze the association of neonatal Fc receptor α-chain gene (FCGRT) haplotypes with the activity of FCGRT promoter and the expression of mRNA and protein. Two SNPs were identified by sequencing the promoter region of FCGRT genomic DNA from mammary gland samples which were collected from 40 healthy Chinese Holstein dairy cows. The 2 SNPs (which were named C-1116T and C-756A) defined 3 different haplotypes which belonged to CC/CC, CA/CA and TA/TA genotypes respectively. The luciferase reporter gene vectors were constructed to identify the transcriptional activity of FCGRT gene promoter in 293 cells. Correlations of FcRn mRNA and protein expression with haplotypes of FCGRT in mammary gland were assessed by Real-time PCR and Western blotting. The results showed as follows: The expression vectors containing 3 different haplotypes of DNA (CC/CC, CA/CA, TA/TA) were successfully constructed. The activities of CC-PGL3-Basic was significant higher than those in CA-PGL3-Basic and TA-PGL3-Basic ($P < 0.05$), CA-PGL3-Basic was significant higher than that of TA-PGL3-Basic ($P < 0.05$). The expression of FcRn mRNA in haplotype C-C was associated with highest level in the mammary gland of Holstein cows ($P < 0.05$). And haplotype T-A was significantly higher than C-A ($P < 0.05$). The protein expression of FcRn in haplotype C-C was significantly higher than C-A and T-A ($P < 0.05$), but there were not significant differences between C-A and T-A. We concluded that the SNPs in the FCGRT promoter did produce an effect on transcriptional activity, mRNA level and protein expression of Fc receptor in mammary gland. The polymorphism of FCGRT promoter gene can modulate the FcRn expression in mammary gland, and make further effects on expression of FcRn and transportation of IgG.

Key Words: Fc receptor, FCGRT, Chinese Holstein cow

TH179 X marks the spot: Region of bovine chromosome X associated with heifer fertility traits in Brangus cattle. K. L. DeAtley[1], M. G. Thomas*[2], M. R. S. Fortes[3], J. F. Medrano[4], G. Rincon4,8, A. Islas-Trejo[4], M. L. Colgrave[5], R. L. Ashley[1], G. A. Silver[1], S. O. Peters1,7, A. Reverter[5], A. Canovas[4], and W. M. Snelling[6], *[1]New Mexico State University, Las Cruces, [2]Colorado State University, Fort Collins, [3]University of Queensland, Brisbane, QLD, Australia, [4]University of California, Davis, [5]CSIRO, Brisbane, QLD, Australia, [6]USDA-ARS-MARC, Clay Center, NE, [7]Berry College, Mount Berry, GA, [8]Zoetis, Kalamazoo, MI.*

Discovery of favorable reproductive genotypes could facilitate early-life selection in replacement female programs using *Bos indicus*-influenced heifers. In Brangus heifers, we identified a gene associated with heifer fertility traits on the X chromosome using complementary -omics technology (i.e., genomics, transcriptomics and peptidomics). Specifically, 802 Brangus heifers were genotyped with 53,692 SNP and evaluated for reproductive phenotypes (i.e., first service conception (FSC) and heifer pregnancy (HPG)). Yearling heifers were estrous synchronized, bred by AI, and exposed to natural service breeding for 70 d. Reproductive ultrasound and DNA-based parentage testing were used to determine if the heifer conceived by AI or natural service and to code for the traits of FSC and HPG. Success rates for FSC and HPG were 53.3 and 78.0 ± 0.01%, respectively. Genome-wide association studies revealed 2 QTL on the X chromosome spanning positions 90 to 110 Mb (UMD 3.1 assembly). The hypothalamus and anterior pituitary were harvested from pre- and post-pubertal heifers (n = 8) from this population and analyzed using quantitative transcriptome (RNA-sequencing) and peptidome (neuropeptides ≤10 kDa) techniques. In these tissues, the PCSK1N transcript was detected in the transcriptome. The locus (92.02 Mb) for this gene resides within the QTL observed on the X chromosome. Two peptide derivatives of this gene, PCSK1N[61–89 and 221–240] were detected in the peptidome of the tissues. Peptide quantification was performed using multiple-reaction monitoring mass spectrometry of peptide extracts. Post-pubertal heifers had ($P < 0.05$) higher pituitary peptide levels relative to pre-pubertal heifers (i.e., peak area estimates were 1,118,058 ± 91,847 > 65,504 ± 8,761 for PCSK1N [221–240] and 2,308,678 ± 71,117 > 490,032 ± 11,969 for PCSK1N[61–89], respectively). The gene ontology of PCSK1N and its peptide derivatives include peptide hormone processing and modulation of pro-hormone convertase activity. The PCSK1N gene should be considered a positional and functional candidate for study of the reproductive endocrine axis and heifer fertility.

Key Words: cattle, gene, neuropeptide

TH180 Association between IgE single nucleotide polymorphisms and parasite resistance in Senepol × Charolais crossbred heifers. M. Pagán, L. Emmanuelli, I. Rivera, E. Jiménez, D. Vélez, and G. Ortiz-Colón*, *University of Puerto Rico, Mayagüe, Puerto Rico.*

Bovine immunoglobulin E (IgE) was selected as a candidate gene to evaluate the association between single nucleotide polymorphisms (SNPs) and resistance to parasite infestation. Senepol × Charolais crossbred heifers (n = 46) weighing 250.85 ± 9.24 kg were used in the study. Upon weaning, all heifers were put on a rotational pasture system in a single group, and fecal samples were taken every 2 wk for a period of 16 wk. Parasite infestation levels were determined by McMaster's Fecal Egg Count Method (FEC). Animals whose FEC were ≥100 eggs/gram of feces were treated with commercial anthelmintics. During the study 14 heifers were never treated with anthelmintics. Single nucleotide polymorphisms were identified at intron #1 and exon #3 [both adenine (A)/guanine (G) transition] by means of a pool and sequencing strategy using primers designed to amplify coding and noncoding fragments of the heavy chain constant region of IgE (GenBank Accession # U63640). In non-treated animals nucleotide substitutions in intron #2 had the following genotypic frequencies: AA 0.31, AG 0.38, and GG 0.31 (A 0.5/G 0.5). Animals treated on one or more occasions during the study had the following frequencies: AA 0.83, AG 0.17, and GG 0.00 (A 0.92/G 0.08), which were different from the non-treated animals ($P = 0.0199$). In non-treated animals nucleotide substitutions in exon #3 showed the following frequencies: AA/0.14; GA/0.50; and GG/0.36 (A 0.39/G 0.61). Animals treated on one or more occasions during the study showed the following frequencies: AA/0.53; GA/0.00; and GG/0.47 (A 0.53/G 0.47), which were different from the non-treated animals ($P = 0.0015$). Because IgE polymorphisms has been implicated in resistance to gastrointestinal nematodes infection in ovines, the segregation pattern of IgE SNPs reported suggests a similar scenario in bovines.

Key Words: IgE, polymorphism, bovine

TH181 Characterization of milk composition in Charolais cows and its association to SNP's in candidate genes. V. I. Pacheco Contreras*, A. M. Sifuentes Rincón, G. M. Parra Bracamonte, and V. R. Moreno Medina, *Centro de Biotecnología Genómica, Instituto Politécnico Nacional, Reynosa, Tamaulipas, México.*

We evaluated the gene-trait association of 62 SNPs panel located in 26 candidate genes involved on milk yield and composition. The main milk components (MMC), i.e., lactose (L), protein (P) and fat (F); were evaluated in a population of Mexican Charolais cows (n = 67), in periods of 30 ± 10 d during 4 to 5 mo. P, F and L percentage were determined according to the infrared technique and the cows were genotyped using the Sequenom MassARRAY technique. Genotype effect on MMC was analyzed using a MIXED model which included lactation period, calving season, age of the dam at calving and the herd as fixed effects. Ten markers were significantly ($P \leq 0.05$) associated with P, F and L percentage. GHR F279Y, FASN 17924A>G, LEP *Mbo*IA>B and LEP1180 were significant for protein percentage. For fat percentage 2 SNPs (CCR2 414C>T and PPARGC1A c.1847C>T) were significant and 3 (LTF 28A>C, CCL2 1364A>C and PRL RsaIA>G) showed a trend. Six SNPs (PRL RsaI A>G, DGAT K232Aa, DGAT K232Ab, PPARG1A c.1847C>T, LEP 1180C>T and LEP 3100C>T) were significant for lactose percentage. In beef cattle, several studies had shown the effect of environmental factors on milk yield and composition; however, the association of these traits with genotypes is scarce. Here we show novel associations of SNP markers to MMC in a Charolais population, further studies in a higher population are required to confirm our results.

Key Words: milk component, candidate gene, Charolais cattle

TH182 A SNP in the DRD2 gene influences adjusted birth and 205-day weights of calves grazing endophyte-infected tall fescue. K. M. Ely*[1], C. J. Kojima[1], A. M. Saxton[1], and R. L. Kallenbach[2], *[1]University of Tennessee, Knoxville, [2]University of Missouri, Columbia.*

Tall fescue (*L. arundinaceum* Schreb.) is the most prevalent forage in the Southeastern United States due to the presence of the endophytic fungus *N. coenophialum*. The fungus enhances the persistence of tall fescue, but decreases the productivity of cow-calf herds grazing it. A SNP at the dopamine receptor D2 (DRD2) gene yields genotypes of AA, AG or GG. We evaluated the relationship between DRD2 genotype and adjusted birth weight (ABW) and adjusted 205-d weight (A205) in fall- and spring- calving beef herds (FC and SC respectively) grazing endophyte-infected tall fescue in Missouri. The herds were AI-bred and managed similarly. The ANOVA model included genotype, calving season, and their interaction (SAS 9.3, Cary, NC). Comparisons of least squares means are shown in Table 1. Both A205 and ABW were lower in FC compared with SC ($P < 0.0001$). Genotype influenced ABW such that calves of GG dams were lighter ($P = 0.0008$). An interaction was noted between calving season and genotype ($P = 0.0346$) due to FC calves of AA and GG cows having lower ABW. Genotype influenced A205 ($P = 0.002$) with calves of AG dams being heavier than their AA or GG counterparts within calving season. Genotype and allele frequencies in FC were AA = 0.23, AG = 0.43, GG = 0.34, A = 0.45 and G = 0.55; frequencies in SC were AA = 0.22, AG = 0.51, GG = 0.27, A = 0.475 and G = 0.525. These results suggest that the AG genotype is advantageous for calf growth in both fall- and spring- calving herds grazing endophyte-infected tall fescue. Selection for the advantageous genotype may already be occurring in managed spring-calving herds.

Table 1. Least squares means of phenotypes by genotype (AA, AG, and GG) and calving season (fall and spring)

	AA		AG		GG	
	Fall	Spring	Fall	Spring	Fall	Spring
ABW (kg)	34.95^{B}	36.96^{A}	36.96^{A}	37.22^{A}	35.21^{B}	36.73^{A}
A205 (kg)	231.08^{CD}	243.12^{B}	236.56^{C}	250.52^{A}	224.68^{D}	245.14^{AB}

Key Words: fescue toxicosis, DRD2, beef cattle

TH183 Effect of stearoyl-CoA desaturase gene polymorphism on milk production traits of Hungarian Holstein Friesian cows. T. G. Jaleta*[1] and L. Czeglédi[2], *[1]Max Planck Institute for Developmental Biology, Tuebingen, Baden Wurteenberg, Germany, [2]University of Debrecen, Center of Agricultural Sciences and Engineering, Institute of Animal Science, Debrecen, Hajdu Bihar, Hungary.*

The objectives of this study were to estimate the genotype and allele frequencies of SCD gene and to investigate the effect of SCD 878 C/T gene polymorphism on milk production traits in Hungarian Holstein Friesian cows. Hair root samples were collected from 277 Hungarian Holstein Friesian lactating dairy cows. Genotyping and amplification of SCD gene was done using TaqMan probe method. The alanine valine amino acid substitution of 878 C/T SNPs at A293V were considered according to Tanguichi et al. (2004). Descriptive statistics, Hardy-Weinberg equilibrium and ANOVA were used for the analysis TaqMan probe results and recorded 305-d milk yield, fat and protein yield, SCC, fat and protein content. The estimated genotype frequency of the SCD gene polymorphism of Hungarian Holstein Friesian population were CC (34%), CT (53%) and TT (13%) and the allele frequency was C (61%) and T (39%). Hardy-Weinberg equilibrium ($P = 0.046945$, $\chi^2 = 3.947$) was not maintained in the studied population. Analysis of variance result showed that no significant difference ($P > 0.05$) between the SCD genotypes and milk production traits under study. Even though the difference was not statistically significant, 305-d milk yield, fat and protein yield, fat and protein content were higher for cows with TT genotype and SCC was lower when compared with cows with CC genotype. Detailed studies have to be conducted on the effect of SCD gene on dairy production traits especially fat composition which has significant role in human health.

Key Words: SCD gene, genotype, polymorphism

TH184 Developmental gene expression patterns in the skeletal muscle transcriptomes of Yorkshire and Tongcheng pigs. Y. Zhao*[1,2], M. Lei[1], J. Li[1], J. P. Steibel[2], H. Liu[1], G. Liu[1], S. Xu[3], Y. Xiong[1], D. Xu[1], and C. W. Ernst[2], *[1]Huazhong Agricultural University, Wuhan, China, [2]Michigan State University, East Lansing, [3]Animal Husbandry Bureau of Tongcheng County, China.*

Pig skeletal muscle growth is a complex process initiated early in fetal development and involving coordinated gene expression, which ultimately affects the quantity and quality of meat produced. The aim of this study was to examine gene expression patterns at 11 developmental stages (30, 40, 55, 63, 70, 90 and 105 d postcoitum (dpc), birth, 1, 3 and 5 wks postnatal) in pigs from the Yorkshire (YK; lean-type Western breed) and Tongcheng (TC; meat-type native breed, Hubei Province, China) breeds. RNA from longissimus dorsi muscle of 5 pigs (different litters) per stage for each breed was evaluated by sequencing (Illumina Genome Analyzer IIx). Short read sequence tags

were assembled and aligned to the pig reference genome (v. 10.2). Within-breed differential expression was examined by comparison of consecutive stages (FDR <0.001). Differentially expressed (DE) genes were observed between all stages in both breeds with more DE genes in fetal stages. The largest numbers of DE genes were between 30 and 40 dpc (1536 and 436 increased expression, 2379 and 681 decreased expression in TC and YK, respectively). In late gestation, more TC genes were DE between 90 and 105 dpc with fewer DE genes between 105 dpc and birth, whereas for YK fewer genes were DE between 90 and 105 dpc with more genes DE between 105 dpc and birth. DE genes were classified by gene ontology (GO) and pathway analyses. As expected many DE genes fell under the biological process GO classification of muscle system. Evaluation of muscle genes revealed that while many genes exhibited similar expression patterns in the YK and TC breeds, some genes exhibited breed-specific expression patterns. GDF11 was more highly expressed in TC than YK pigs at 30 dpc ($P < 0.001$). MYOG and TNNC2 were more highly expressed in TC than YK at 90 dpc ($P < 0.001$). MYLPF and TNNC2 were more highly expressed in YK than TC at 5 wk of age ($P < 0.001$). This study provides a comprehensive transcriptome evaluation of 11 developmental stages from 30 dpc to 5 wk of age in 2 pig breeds. Results reveal both developmental and breed-specific gene expression patterns.

Key Words: pig, skeletal muscle, transcriptome sequencing

TH185 Abundance of total genomic 5-methylcytosine and 5-hydroxymethylcytosine in different pig tissues. B. A. Freking* and D. J. Nonneman, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Methylation of genomic DNA is essential in regulating gene expression in many biological processes including reproduction, development, and growth. Cytosine residues in mammalian genomes are enzymatically modified to 5-methylcytosine (5MC), which participates in transcriptional regulation of genes. The 5MC modified base can be further enzymatically altered to 5-hydroxymethylcytosine (5hMC) by the TET family of methylcytosine dioxygenases. The function of 5hMC in gene regulation is not clear. Because these 2 modifications are indistinguishable by traditional sequencing methods even when supplemented by bisulfite conversion, analysis of 5MC and 5hMC is confounded using that approach. Our objective was to quantify the abundance of both modified bases in several porcine tissues using a colorimetric immunoassay specific for each modification. The content of 5MC or 5hMC DNA was quantified using a commercially available kit according to the manufacturer's instructions. Eight mature pregnant females (4 multiparous Meishan, 4 primiparous white composite) were sampled for 11 different tissues at critical periods during gestation to contribute fetal tissues for a separate study. Tissues included brain, endometrium, heart, small intestine, kidney, muscle, liver, lung, ovary, pancreas, and uterus. Data were analyzed by mixed-model ANOVA procedures fitting breed and tissue as fixed effects and gilt as a random effect. Breed was not significant for any of the variables tested so data are presented by tissue across breeds as a percentage of total DNA. Values for 5MC ranged from 1.25 ± 0.26% for pancreas to 5.68 ± 0.26% for small intestine. Values for 5hMC ranged from 0.006 ± 0.014% for pancreas to 0.294 ± 0.014% for brain. These data indicated a higher abundance of 5hMC and a higher ratio of 5hMC to 5MC in brain tissue (1.7-fold) compared with all other tissues examined, perhaps indicating a greater role of this modified base in tissues of the central nervous system.

Key Words: methylation, pig

TH186 Genomic regions associated with resistance to necrotic enteritis in chicken lines. Y. H. Hong*[1], E. Kim[2], D. Hue[1], S. I. Jang[3], and H. S. Lillehoj[3], *[1]Chung-Ang University, Anseong, Gyeonggi-do, Republic of Korea, [2]Iowa State University, Ames, [3]USDA-ARS, Beltsville, MD.*

Necrotic enteritis (NE) is an infectious disease caused by toxins produced by *Clostridium perfringens*, affecting 40% of the commercial broilers. The chicken lines selected and inbred for resistance to Malek's disease were found to be subject to resistance to NE. Two highly inbred chicken lines of Fayoumi and Adol were applied to identify the regions responding to intensive artificial selection for resistance to NE in chickens. The genome of resistant line and susceptible line in each breed was scanned with the 60K SNP panels. A total of 155 regions completely fixed in resistant or susceptible lines were found across the genome of both breeds. The comparison of divergently fixed regions between breeds allowed reducing the number of candidate region affecting the resistance to NE. Consequently, common haplotype of 5 regions (>200 kb and 50 SNP) subject to the susceptibility to disease were detected in the resistant or susceptible lines of 2 different chicken breeds. Annotation of the regions spanning divergently fixed regions revealed a set of candidate genes such as IL12A and TLR4 participating in immune response. The comparative analysis of both breeds revealed the evidence of selection in the region of the 6.2–6.4 Mb on chromosome 18, which overlap a previously reported QTL on disease resistance in broiler. Besides, consensus haplotypes associated with resistance to NE were found in regions of possibly relevant genes including myostatin (MSTN) and myosin (MYH3) that play an important role in muscle development. The high-resolution genome scans of divergent selection within- and between-breed suggest the candidate genes influencing the resistance to necrosis enteritis for the future study. This project was supported by the NRF grant funded by the Korea government (MEST; No. 2010–0009360), Republic of Korea.

Key Words: chicken, SNP, necrotic enteritis

TH187 Associations of pituitary specific transcription factor-1 (*POU1F1*) gene polymorphisms with growth and carcass traits in sheep. A. Jalil-Sarghale[1], M. M. Shahrebabak[1], H. M. Shahrebabak*[1], M. Sadeghi[1], and M. C. Mura[2], *[1]University of Tehran, Karaj, Tehran, Iran, [2]University of Sassari, Sassari, Italy.*

POU1F1 (PIT-1 or GHF-1) as a member of the POU family of transcription factors, is mainly expressed in the pituitary and upregulate the growth hormone, prolactin, thyroid-stimulating hormone β, *POU1F1* itself and also growth hormone releasing hormone receptor genes. This gene is located on chromosome 1. The aim of this research was to study the polymorphism of the *POU1F1* gene and its relationships with growth and carcass traits in 3 Iranian sheep breeds: Zel (thin-tail), Lori-Bakhtiari (fat-tail) and Zel-Atabay (fat-tail) crossbred. Blood samples from 90 Lori-Bakhtiari (research station), 60 Lori-Bakhtiari (slaughterhouse) 90 Zel (research station) and 40 Zel-Atabay (slaughterhouse) crossbred sheep were collected to extract DNA and the desired fragment was amplified and digested with Aci1 endonuclease. Research station samples were analyzed with statistical model including: sex, age and genotype. Similar model were used for samples derived from slaughterhouse except animal weight before slaughtering was included in the model. The results showed that the genotypes frequency varied between breeds. In the Lori-Bakhtiari breed A allele and in the of Zel breed and Zel-Atabay crossbred G allele was most frequent. When *POU1F1* genotypes were tested, animals with AG genotype showed a smaller breast circumference than those with AA genotype in Lori-Bakhtiari breed and Zel-Atabay crossbred ($P < 0.05$). Also, animals with GG genotype have more blood

triglycerides compared with those with AG and GG genotypes in Zel breed ($P < 0.05$). In addition, genotypes had significant association with abdominal fat in Lori-Bakhtiari breed (slaughterhouse) and with body length, height, thigh environment in Zel and Zel-Atabay crossbred ($P < 0.05$). In conclusion, the results confirm the hints proposing that *POU1F1* is a preferential target for further investigation on mutations that influence growth and carcass traits variations.

Key Words: *POU1F1* gene, polymorphism, sheep

TH188 Molecular analysis of calpastatin gene in fat-tailed Lori-Bakhtiari sheep in Iran. A. H. F. Khaltabadi[1], H. M. Shahrbabak*[2], and M. A. Talebi[3], *[1]Department of Animal Science, faculty of agriculture, University of Arak, Arak, Iran, [2]Department of Animal Science, Academic of Agronomy and Animal Science, University College of Agriculture & Natural Resources, University of Tehran, Karaj, Iran, [3]Department of Animal Science, Agriculture and Natural Resources Research Center, Shahrekord, Iran.*

Calpastatin inhibits both the rate and extent of postmortem proteolysis and plays a role in muscle growth and meat quality. Lori-Bakhtiari sheep is gene pool reservation and suitable for meat and wool production that until now has not been studied using molecular markers, especially with the view of calpastatin gene. Therefore, the present study was conducted to determine the genetic diversity of calpastatin gene in Lori-Bakhtiari sheep station. The 622-bp fragment of this gene was amplified by polymerase chain reaction (PCR) from DNA samples of 100 Lori-Bakhtiari sheep. Polymerase chain reaction products were characterized by the restriction fragment length polymorphism (RFLP) technique using 2 restriction enzymes, *Msp*I, and *Nco*I, yielding all 3 genotypes, MM, MN and NN. The results of this experiment indicated that this population is highly polymorphic, furthermore in the most studied Iranian sheep breeds, all 3 genotypes of this gene have not been detected whereas we detected all 3 genotypes, and hence researchers must increase attention to meat quality and quantity in breeding programs of this breed. Because polymorphism in this breed is high and there are all 3 genotypes in their population, we can simply achieve effect of any genotype in increasing of meat quantity and quality with information recording and genotyping in next studies and select the best genotypes in breeding programs. The PCR products were electrophoresed on 1% agarose gel and stained by etidium bromide. Then, they were digested with restriction enzyme *Msp*I and then electrophoresed on 2.5% agarose gel with ethidium bromide and revealed 2 alleles, allele A and allele B. Data were analyzed using PopGene32 package. In this population, MM, MN, NN genotype have been identified with the 53, 40, 7% frequencies. M and N allele frequencies were 0.73, 0.27, respectively. The population was found to follow Hardy-Weinberg equilibrium

Key Words: calpastatin, Lori-Bakhtiari, sheep

TH189 Association between transferrin polymorphism and some blood parameters in Makoei fat-tailed sheep. A. H. F. Khaltabadi[1], H. M. Shahrbabak*[2], and H. Mohammadi[3], *[1]Department of Animal Science, Faculty of Agriculture, University of Arak, Arak, Iran, [2]1Department of Animal Science, Faculty of Agricultural Sciences and Engineering, University College of Agriculture and Natural Resources, University of Tehran, Karaj, Alborz, Iran, [3]Department of Animal Science, Faculty of Agriculture, Tabriz, Iran.*

Transferrin (TF) is a serum glycoprotein that binds free iron ions. The objective of the present research was to determine transferrin polymorphism and to find association between transferrin polymorphism and some blood parameters of blood in the population of Makoei sheep lambs. Blood samples were collected from a total 576 sheep of both sexes in Iranian fat-tailed breed Makoei sheep from the jugular vein in tubes containing EDTA and centrifuged at 4°C. Separate aliquots of plasma and erythrocytes were stored at −20°C until they were analyzed. Transferrin (TF) typing was performed using PAGE, as described by Tucker and Clarke (1980). The levels of triglyceride blood, total protein blood, glucose blood and cholesterol blood have been measured. Significant differences in Transferrin genotypes group for 3 parameters were considered, those results as below: level of triglyceride ($P < 0.001$) and total protein ($P < 0.0001$) were statistically significant; while level for cholesterol blood ($P < 0.066$) not significant but it approximately significant. The AA genotype resulted in a significant increase in triglyceride (29.91 mg/dL), total protein (9.961 mg/dL) and AQ genotype significant decrease in triglyceride (18.45 mg/dL), total protein (7.075 mg/dL). No significant difference was observed between the genotypes in and glucose blood ($P < 0.633$) . These results indicate that new marker associated with blood parameters can be used in marker-assisted selection in fat-tailed sheep.

Key Words: blood parameter, transferrin, polymorphism

TH190 Association of polymorphisms in the transferrin with carcass traits in Makoei fat-tailed sheep. A. H. F. Khaltabadi[1], H. M. Shahrbabak*[2], and H. Mohammadi[3], *[1]Department of Animal Science, Faculty of Agriculture, University of Arak, Arak, Iran, [2]Department of Animal Science, Academic of Agronomy and Animal Science, University College of Agriculture & Natural Resources, University of Tehran, Karaj, Alborz, Iran, [3]Department of Animal Science, Faculty of Agriculture, University of Tabriz, Tabriz, Iran.*

Transferrin is a glycoprotein responsible for the transport of iron from sites of absorption and heme degradation to those of storage and utilization by binding 2 Fe^{3+} ions in association with the binding of an anion, usually carbonate. It is expressed by the liver and secreted into plasma. The objective of this study was to evaluate the association transferring genotypes with carcass quantity traits in Makoei sheep. Blood samples were collected from a total 576 sheep of both sexes in Iranian fat-tailed breed, Makoei sheep, from the jugular vein in tubes containing EDTA, kept refrigerated during the transport and centrifuged at 4°C. Separate aliquots of plasma and erythrocytes were stored at −20°C until they were analyzed. Transferrin (TF) typing was performed using the polyacrylamide gel electrophoresis (PAGE) as described by Tucker and Clarke (1980). The relationship was studied between selected carcass quantity traits and the transferrin (TF) genotype. In the Makoei sheep, the transferring genotypes are associated with an increase in slaughter weight ($P < 0.001$), total carcass weight ($P < 0.0001$) and carcass weight without fat-tail ($P < 0.0001$). Animals of BC genotype showed a significantly heavier slaughter weight than those of genotype BB (25.939 vs. 25.212 kg). The carcass weights of animals with the BE genotype to be higher than those of the TT genotype (11.968 vs. 11.0008 kg). The carcass weight of animals with the AQ genotype was heavier than those of the CK genotype (10.994 vs. 10.279 kg). In conclusion, considering above result was shown, protein Tf^{B} might be associated with carcass characteristic.

Key Words: carcass trait, transferrin, Makoei

TH191 Expression of acetyl-CoA carboxylase alpha (ACC-α) in thin and fat tail sheep breeds associated with lipogenesis pathway. H. O. Mousapour*, A. Nejati-Javaremi, M. Moradi-Shahrbabak,

H. Moradi-Shahrbabak, and M. J. Najafpanah, *University Of Tehran, Karaj, Tehran, Iran.*

The objective of the current study was to evaluate the acetyl-coenzyme A carboxylase α (ACC-α) gene expression as a most important enzymes in the regulation of lipogenesis. In this research 2 independent resources have been investigated in thin and fat tail Iranian sheep breeds. Thus, Zel and Lori Bakhtiari sheep breeds were studied that are thin and fat tail kind of breeds, respectively. Eight lambs from both breed in 2 sex were selected for sampling. Selected sheep's have the same age and characteristics of racial purity that was managed in same condition and fed until the age of 6 mo. Samples from lipogenic tissues (fat tail / tail, visceral fat and liver) and also longissimus muscle tissue were taken when the breeds has 6 mo of age. Total RNA from tissue samples were extracted by using an isolation reagent kit (Tripure, Roch Applied Science). Extracted RNA was treated by DNase I enzyme for removing genomic DNA residues (Fermentas, Thermo Fisher Scientific). Rocket Script Reverse Transcriptase enzyme (Bioneer) was used to full length cDNA synthesis. Expression of the ACC-α gene was measured by using the Real-Time PCR. Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) was used as internal standard. Results showed a significance difference of ACC-α expression levels between both breed ($P < 0.05$), also it was shown that sex of breeds has no effect on expression of ACC-α in studied tissues ($P > 0.05$). The minimum amount of gene expression levels was observed in longissimus muscle that is argued with regard to ACC-α gene function. The results of current trail confirmed that there is significance difference between relative gene expressions of ACC-α in thin and fat tail sheep breeds at liver tissue, which is a substantial result due to role of the liver tissue at lipogenesis process. With regard to the issue that So far no research has been done in this area, evaluating the expression of lipogenic genes can be introduces new insights in lipogenesis process at fat tail and thin sheep breeds that can to be effective in adjustment the mechanisms of fatty acids synthesis in sheep breeds.

Key Words: ACC-α, lipogenesis, gene expression

TH192 Constraints for nutritional grouping in Wisconsin dairy farms. F. E. Contreras-Govea*, V. E. Cabrera, L. E. Armentano, R. D. Shaver, and P. M. Crump, *University of Wisconsin-Madison, Department of Dairy Science, Madison.*

The objective of this survey was to quantify the percentage of dairy farmers that feed a single ration and identify existing constraints to grouping and precision feeding of lactating cow groups. A 2-page questionnaire was mailed to all Wisconsin dairy farms with 200 or more lactating milking cows (n = 800). After one reminder, the response rate was 25% (196). The survey consisted of 12 questions that covered general description of the farm and specific about grouping and feeding. Average lactating dairy cows per herd was 604 (range 200 to 3,200) and rolling herd average was 11,657 kg milk/cow per yr (range 7,031 to 14,968). Data were analyzed using the non-parametric Wilcoxon-Rank scores, which compared the responses among 5 herd size categories: 200–250, 251–380, 381–525, 526–802, and > 802 lactating cows. Questions were asked about what farmers are currently doing regarding to grouping, how they perceive grouping and feeding groups, and constraints to feeding more than one ration to lactating cows. Responses ranked from 1, strongly disagree, to 5, strongly agree. A difference among herd size was found for criteria for grouping lactating cows. Herds with more than 250 cows gave more importance to the need for keeping pens full (3.65) ($P < 0.025$) and having a fresh cow group ($P < 0.001$), with the latter as the most important (4.62) for all farm sizes. Criteria for feeding more than one ration were not different among herd size categories. Higher ranking were given to fresh vs. all other cows (3.77) and stage of lactation for non-fresh cows (2.96). A quarter of respondents (25%) reported feeding the same ration to all lactating herd. Within this 25%, 63% (31 farms) were in the range of 200 to 380 lactating cows. The main constraints for feeding more than one ration were given to keep it simple (48%) and the perception that milk drops when cows are moved to a different group (52%). We concluded that 75% of dairy farms in Wisconsin feed more than one ration and 91% perform some grouping in lactating cows, but there are farms with herd size between 200 and 802 (81%) that could increase feed efficiency by enhancing some management tools of grouping and nutritional feeding.

Key Words: grouping, nutritional feeding

TH193 A survey of starch digestibility on Wisconsin dairy farms. A. Huibregtse[1], C. Heuer[2,3], R. Shaver*[2], and P. Hoffman[2], *[1]Oconto County Extension, Oconto, WI, [2]Dairy Science Department, University of Wisconsin, Madison, [3]Rock River Laboratory, Watertown, WI.*

University of Wisconsin-Extension county-based agricultural agents conducted a field study to evaluate changes in starch digestibility over the winter months on 30 commercial Wisconsin dairy farms. Study farms milked 223 ± 206 cows with bulk tank milk yields of 32.7 ± 5.5 kg/d per cow. Corn silage (WPCS), high moisture corn (HMC), and dry corn samples were collected from each farm, and analyzed for DM and starch contents, particle size, and 7-h ruminal in vitro starch digestibility (IVSD; % of starch). Composite manure samples, collected from each farm by combining rectal grab fecal samples from 10 cows within the herd between 45 and 120 DIM, were analyzed for starch content to estimate total-tract dietary starch digestibility (TTSD). Feed and manure samples were collected from each of the study farms during November 2011 and then again during April 2012. The WPCS DM (35.0% ± 4.5 vs. 36.2% ± 5.1) and starch (34.7% ± 5.4 vs. 34.1% ± 4.8; DM basis) concentrations and kernel processing score (KPS; % starch passing 4.75 mm sieve; 37.0% ± 11.1 vs. 61.1% ± 12.4) were similar for fall and spring sampling periods, respectively. The IVSD for WPCS was 6.6%-units greater in spring than fall (90.3% ± 3.7 vs. 83.7% ± 7.5). The range for IVSD of WPCS samples was 35.8%-units in fall compared with 13.7%-units in spring. Across all farms and both sampling periods for WPCS samples, > 20% contained ≥ 40% DM and > 25% were under-processed (KPS <50%). The HMC DM content (72.0% ± 7.2 vs. 74.8% ± 5.9), mean particle size (MPS; 1725 μ ± 562 vs. 1548 μ ± 626), and IVSD concentrations (75.7% ± 8.2 vs. 74.5% ± 7.2) were similar for fall and spring sampling periods, respectively. Across all farms and both sampling periods for HMC samples, 44% contained > 75% DM and 32% were under-processed (MPS >2000 μ). Fecal starch content (3.3% ± 3.0 vs. 4.1% ± 4.0) and estimated TTSD (95.9% ± 3.7 vs. 94.9% ± 5.0) were similar for fall and spring sampling periods, respectively. Fecal starch content was <5% of DM for 75% of samples. Results indicate that improved control of WPCS and HMC harvest and processing practices and longer WPCS ensiling times would enhance starch digestibility for some dairy farms.

Key Words: corn silage, starch, digestibility

TH194 Determining forage dry matter by microwave, Koster Moisture Tester, and Q-Dry methods. F. H. Pino* and A. J. Heinrichs, *The Pennsylvania State University, University Park.*

This study examined dry matter (DM) determination of feeds by 4 different methods to evaluate the relationship between each one and traditional forced air oven (FAO). Samples (n = 60; 35 corn silage, 15 grass silage, and 10 TMR) were analyzed by microwave (MW), Koster Moisture Tester (KMT), Q-Dry, and FAO. According to manufacturer specifications 50, 50, 40, and 200 g of sample were used for MW, KMT, Q-Dry, and FAO, respectively. Using MW, DM was determined by heating the sample sequentially for 1.5 min, 45 s, 30 s, and 20 s repeatedly until sample weight did not change. For KMT, DM was measured by initially heating for 30 min, recording sample weight, then heating each sample repeatedly for 10 min until the weight did not change. For Q-Dry samples were deposited on a plate and DM was determined automatically. Determination of DM in FAO was calculated by weighing samples before and after placing in the oven at 65°C for 48 h. Data were analyzed by simple linear regression (Minitab, Inc.) utilizing FAO as control. Results are shown as slope of the equation (b) and coefficient of determination (R^2). A linear relationship ($P < 0.001$) was observed for corn silage between FAO and MW (b = 0.942, $R^2 = 0.971$), KMT (b = 0.719, $R^2 = 0.813$), and Q-Dry (b = 0.869, $R^2 = 0.941$). In addition, grass silage showed a linear relationship ($P < 0.001$) between FAO and MW (b = 0.967, $R^2 = 0.98$), KMT (b = 0.944, $R^2 = 0.968$), and Q-Dry (b = 0.97, $R^2 = 0.951$). For TMR samples a linear relationship ($P < 0.001$) also was observed between FAO and MW (b = 0.923, $R^2 = 0.963$), KMT (b = 0.674, $R^2 = 0.939$), and Q-Dry (b = 0.0.978, $R^2 = 0.975$). All the samples together gave corresponding high correlations: MW, KMT, Q-Dry vs. FAO, b = 0.931 $R^2 = 0.978$; b = 0.721, $R^2 = 0.875$ and b = 0.920, $R^2 = 0.965$ respectively ($P < 0.001$). All methods resulted in similar DM determination, exhibiting a strong, linear relationship with FAO; however, MW showed the best fit followed by Q-Dry, and then KMT. Based on these data we suggest MW or Q-Dry the best alternative to traditional oven-drying on farms.

Key Words: dry matter, corn silage, grass silage

TH195 Proposal for a universally applicable method of evaluating feed cost and shadow pricing for dairy cattle based on locally available feeds. D. Barber[1] and R. A. Patton*[2], *[1]Agri-Science Queensland, Department of Agriculture, Fisheries and Forestry, Lawes, QLD, Australia, [2]Nittany Dairy Nutrition Inc., Mifflinburg, PA.*

A challenge of dairy nutrition extension is teaching a method of feed pricing that is fair and easily grasped by farmers and nutritionists. Traditional methods have involved apportioning monetary values to crude protein and energy using corn grain and soybean meal as references. Drawbacks are that local products may vary nutritionally from those found in US derived databases, in many local markets corn and soybean meal are not available, quoted prices of these 2 ingredients do not reflect local market conditions, and use of corn-soy indexes often lead to an over valuation of protein, which in pasture situations may not be a limiting nutrient. The method involves the computation of the values of protein and energy using tTDN as described in NRC 2001. The nutrient value of feeds is apportioned to protein and energy by subtracting tCP from tTDN. The % of CP and % of energy are multiplied by the market price to arrive at a cost for CP and energy. Break-even cost can be computed by selecting the feed with the lowest CP cost and the feed with the lowest energy cost available in the market to be the reference feeds. The CP and energy content of other feeds available are then multiplied by the reference values to obtain the break-even price. The CP content of the feed selected as the protein reference must have over 30% CP with an NDF content greater than 10%, and the feed selected as the energy reference feed must have a starch content over 40%. Advantages of this system are (1) stakeholders can quickly understand the system; (2) the system is relevant to stakeholder understanding of the market; (3) tTDN values are generally available in popular ration balancing programs; and (4) the system can be easily adapted to spreadsheet applications. The disadvantage is that the values necessary for accurate calculation of tTDN are not always available. Work with Queensland dairy producers suggests a high understanding and acceptance of this method. We conclude that this method can reduce feed costs and encourage dairymen to be more nutritionally aware.

Key Words: CP cost, energy cost, break-even price

TH196 Variation in alfalfa silage, corn silage and high-moisture dry matter content within and among silo bags. L. F. Ferraretto* and R. D. Shaver, *University of Wisconsin-Madison, Madison.*

The objectives of the study was to determine the variation in DM content within and among silo bags of alfalfa silage (AS), corn silage (CS) and high moisture corn (HMC). A data set comprised of 57 AS, 42 CS and 11 HMC silo bags, fed between 2003 and 2010, was obtained from the University of Wisconsin Emmons Blaine Dairy Research Center. Dry matter content was measured weekly or biweekly either in a forced-air oven at 60°C for 48 h or via portable near infrared spectroscopy (Dinamica Generale, Mantova, Italy). Average and standard deviation (SD) were measured for individual bags. Descriptive statistics of average of individual bags were used as an indicator of variation among bags. Descriptive statistics of SD of individual bags were used as an indicator of variation within bags, with values multiplied by 2 to demonstrate difference between minimum to maximum DM values within bags. The DM content of AS ranged from 31.6 to 50.4% among the 57 bags with an average of 40.8%. Furthermore, the variation within AS bags ranged from 1.8 to 28.4%-units of DM, with an average of 9.0%-units of difference. Likewise, CS presented high variation among bags, with a range of 31.1 to 54.7% DM and average of 37.9%. Variation within bags followed the same pattern with a range of difference of 1.2 to 8.8%-units of DM (average of 4.2%-units). Although the variation among bags observed for HMC was lower than AS and CS (averaged 72.1% DM, with a range of 69.9 to 73.9%), variation within bags was relatively high (ranged 2.6 to 8.0%-units with an average of 4.6%-units difference). These data suggest that variation within bags is as high as among bags and thus, frequent sampling within bags for as fed to DM corrections is an important feed management practice to maintain uniform TMR in dairy farms.

Key Words: silo bag, dry matter content, silage

TH197 Evaluation of on-farm feed nutrient composition determined by near infrared spectroscopy. M. S. Akins*[1], L. F. Ferraretto[2], C. Weigel[1], J. Dewell[1], M. Dobberstein[3], and R. D. Shaver[2], *[1]University of Wisconsin-Platteville, Platteville, [2]University of Wisconsin-Madison, Madison, [3]Dinamica Generale US Inc., DeKalb, IL.*

This study's objective was to evaluate the use of near infrared spectroscopy (NIRS; Dinamica Generale, Mantova, Italy) for on-farm feed DM, CP, NDF, ADF, starch, fat, and ash content. To calibrate the NIRS to feeds at the University of Wisconsin-Madison and University of Wisconsin-Platteville, 5 samples of corn silage(CS), alfalfa silage(AS), and high-moisture corn(HMC) from each location were analyzed using NIRS to obtain a spectral analysis, then sent to Dairyland Laboratories, Inc.(Arcadia, WI) for analysis. Spectral and analysis data were used to update calibration equations. Samples of CS (n = 88), AS (n = 39), and HMC (n = 47) were obtained approximately twice weekly for 12 wk from both locations and stored at −20°C until analyzed by NIRS on the same day. Undried, unground samples were used for on-farm NIRS analysis. The sample scanned by on-farm NIRS was sent to Dairyland Laboratories, Inc. for analysis. Samples were microwave dried to 92–96% DM, ground to pass a 1 mm screen (Udy cyclone mill; Fort Collins, CO), and analyzed using a Foss 5000 NIRS (Hillrød, Denmard). Bias was calculated as the difference between lab and portable NIRS analysis. On-farm NIRS was comparable to lab NIRS for DM, CP, ADF, and NDF content in CS. Starch content for CS varied (bias of 2.6 ± 6.3% units) between on-farm and lab NIRS. For AS and HMC, on-farm measurement of DM was similar to lab NIRS with variability between on-farm and lab NIRS for other nutrients. Overall, on-farm NIRS had lower ranges of nutrient values compared with lab NIRS and a more diverse sample set is likely needed to predict nutrient composition of feeds from different lots and locations.

Table 1. Nutrient analysis (DM basis, ±SD) from a commercial lab and on-farm NIRS

	Corn silage		Alfalfa silage		High-moisture corn	
Item	Lab	On-farm	Lab	On-farm	Lab	On-farm
DM	34.6±3.5	33.7±2.6	47.3±6.2	49.9±7.0	73.9±1.6	72.1±1.7
CP	7.9±0.5	8.2±0.4	20.8±0.9	20.4±1.0	9.0±0.7	9.6±0.2
Starch	29.2±10.6	26.6±4.9	—	—	69.0±1.5	68.2±0.9
ADF	23.6±4.0	24.4±2.4	31.2±1.6	29.5±1.4	1.8±0.5	2.2±0.4
NDF	39.5±5.5	40.6±3.7	38.1±2.3	37.1±2.4	5.2±0.9	6.8±0.7
Fat	2.8±0.4	3.2±0.2	2.9±0.2	3.0±0.1	2.9±0.3	3.0±0.1
Ash	3.9±1.0	4.7±0.5	12.1±1.3	12.2±0.4	1.4±0.1	1.5±0.1

Key Words: feed nutrient analysis, NIRS

TH198 An update on the Repro Money Program: A farmer-directed team-based extension program to improve reproductive

performance in Wisconsin dairy herds. M. C. Cordoba*, P. M. Fricke, P. L. Ruegg, R. D. Shaver, K. A. Weigel, and V. E. Cabrera, *University of Wisconsin-Madison, Madison.*

Repro Money is an extension program offered to Wisconsin dairy farmers who want to improve reproductive performance of their dairy herd. This farmer-directed team-based approach consists of 4 meetings during a 6- to 8-mo period. The goal is to help dairy farmers best utilize their personnel and advisers in a coordinated way to improve reproductive performance and profitability. Data from all farms that enrolled and completed the program (n = 13) between fall 2010 and summer 2012 were included in this analysis. These farms averaged 385 cows (range = 67 to 850) with a rolling herd average of 12,524 kg/cow per year (range = 21,350 to 32,000 kg). Financial and management data were obtained with the aid of a guided situation assessment, action plan, and goal setting tool. Data were analyzed before and after participating in the program to evaluate the program's effect on enhancing reproductive performance and herd profitability. After finishing the program, number of days in milk decreased 6 d (0 to 43), insemination risk increased 3% (53 to 56%), conception risk increased 3% (38 to 41%), and the 21-day pregnancy rate increased 3% (19 to 22%) among these herds. These improvements were estimated to yield an average economic gain of $55/cow per year with a total economic gain of $177,185/yr for the participating farms. This amount is expected to increase due to future additional improvements and management changes to be implemented using the program principles because 70% of participating farms decided to continue with regular meetings after finishing the program. All 13 farms that finished the program were highly satisfied with the outcomes with 85% of farms achieving the goals set, which included increasing the 21 d pregnancy rate, increase conception risk, and decreasing days to first AI. The 3 most important management changes that resulted from participating in the Repro Money Program were to perform better recordkeeping, focus on transition cow management, and improve synchronized breeding protocols. Supported by AFRI Competitive Grant no. 2010-85122-20612.

Key Words: reproduction, management, team-based

TH199 Changes in lying behavior and milk yield associated with changing freestall dimensions and bases. B. A. Wadsworth*, A. E. Sterrett, J. D. Clark, D. L. Ray, and J. M. Bewley, *University of Kentucky, Lexington.*

Two freestall barns at the University of Kentucky Coldstream Dairy were renovated in November 2011. The objective of the study was to characterize changes in lying time (LT) and milk yield (MY) associated with changing freestall dimensions and bases. The brisket locator was transitioned from a wooden board to a 7.6 cm schedule 40 PVC pipe. The length of the stall, from brisket locator to curb side of the alley was increased from 1.7 m to 1.8 m. The neck rail height was increased from 1.0 m to 1.2 m (top of stall base to bottom of rail). Mean stall width was 1.2 m. Dual Chamber Cow Waterbeds (Advanced Comfort Technology, Reedsburg, WI) (DCCW) replaced old rubber-filled mattresses in 50 stalls in barn A. New rubber-filled mattresses (MAT) replaced old rubber-filled mattresses in 50 stalls in barn B. IceRobotics (Edinburgh, UK) IceQube sensors recorded LT. Milkline milking systems (Italy) recorded MY. All variables were classified for Holsteins (n = 34), relative to renovation time (RENTIME) with pre-renovation (40 d) data collected from September 28 to November 6, 2011, and post renovation (40 d) data collected from December 18, 2011, to January 29, 2012. The GLM procedure of SAS (Cary, NC) was used to test for the fixed effects of barn, parity, RENTIME, and milk yield and all 2-way interactions on LT and the fixed effects of barn, parity, DIM and RENTIME, and all 2-way interactions on MY. All main effects were kept in each model regardless of significance level. Stepwise backward elimination was used to remove non-significant interactions ($P \geq 0.05$). Daily LT was not significantly ($P = 0.59$) different before and after renovations. Daily LT was also not significantly ($P = 0.56$) different between DCCW and MAT. Milk yield was a significant ($P < 0.01$) predictor of LT. As MY increased, LT decreased. Daily MY was not significantly ($P = 0.06$) different before and after renovations. Daily MY was also not significantly ($P = 0.12$) different between DCCW and MAT.

Key Words: lying time, freestall, waterbed

TH200 A decision support tool for compost bedded pack barn bedding cost analysis. E. Eckelkamp*, J. Taraba, and J. Bewley, *University of Kentucky, Lexington.*

The objective of this project was to create a user-friendly dashboard decision support tool for compost bedded pack barn bedding cost analysis. User inputs included: month, barn orientation, distance to closest building, fan presence and speed, milk yield, herd size, total barn area (square meters), target pack moisture, alternative bedding costs, wood source, bedding load volume (cubic meters), and bedding moisture percentage (MC). Drying rates were calculated using 30-year Kentucky historical weather data. Mean temperature, wind speed, fan speed, and the drying driving force determined drying rate and days between bedding addition. Kiln dried and green bedding were evaluated separately along with 3 bedding mixtures: coarse shavings, coarse shavings and fine dust mixture, and fine dust. Analysis outputs included daily bedding cost (CD), number of yearly bedding loads (LY), bedding costs per year (CY), days between bedding addition (TD), and least expensive bedding option. To compare alternative beddings in Scenario 1 and 2 with all model assumptions held equal except bedding MC, kiln-dried bedding (KD) was set at 6.00% and green bedding (GR) at 35.00%. In Scenario 1, the following inputs were used: May, no fans, orientation parallel with an open ridge, 46 m between buildings, coarse shavings and fine dust mixture, $780 per bedding load, and bedding volume of 198 m^3. The CD, LY, CY, and TD for GR and KD were $70.91, 33, $25,881.82, and 11 and $41.05, 19, $14,984.21, and 19 respectively. The best option for Scenario 1 was KD mixture. In Scenario 2, natural ventilation was changed to fans on high speed (9.7 km/h). The CD, LY, CY, and TD for GR and KD were $27.86, 28, $10,167.86, and 13 and $16.60, 8, $6,057.45, and 47 respectively. In Scenario 3, costs were changed to $780.00 for KD and $400.00 for GR using fans on high speed. The best option for Scenario 2 was also KD mixture. The CD, LY, CY, and TD were $14.29, 28, $5,214.29, and 13 and $16.60, 8, $6,057.45, and 47 for GR and KD, respectively. The best option for Scenario 3 was GR mixture.

Key Words: economic dashboard, compost bedded pack barn

TH201 Tools for teams: Improving the success of dairy farm teams. L. Holden*[1], R. White[1], V. Ishler[1], R. Goodling[1], K. Baase[2], and T. Kitsos[3], *[1]The Pennsylvania State University, University Park, [2]Cornell Cooperative Extension, Morrisville, NY, [3]University of Vermont, St. Albans.*

Use of dairy advisory teams has become a common management practice for dairy farm businesses. While the use of teams has been shown to create some improvements at the farm level, many teams struggle to have lasting positive impact. The program objective was to develop an extension education program – "Tools for Teams" – to allow team members to learn about what tools were available, use those tools with

their own teams, and participate in follow up sessions to refine the tool use and improve the overall success of the teams. In phase 1 of the program, workshops were conducted with follow-up webinars to allow program participants to actively learn how to use the tools and to help with implementation of use, rather than simply providing a one-way flow of information. Participants were introduced to the tools in an interactive workshop format using a case study to demonstrate a variety of web-based tools useful for teams. Several of the tools demonstrated included: PA Dairy Tool, Monthly Monitor, and Dairy Analysis Tools as well as general team tools with formats for setting agendas, developing action plans and gaining feedback in member evaluations. Following the workshops, participants were encouraged to use the tools with their teams and provide feedback to instructors through a series of specially designed webinars. Each webinar focused on the use of one tool and instructors answered questions, received feedback and provided follow up for more effective use. Initial evaluations showed positive impact with increases in both knowledge gained - from non-existent or minimal before the program to moderate or considerable knowledge with all tools after the workshops. Participants indicated that level of use of these tools was likely to be increased as a result of attending this program. In phase 2 of the project, long-term effect at the farm level will be evaluated. This 2-phase format for extension education was useful for demonstrating complex team tools and allowed for more experiential learning and better implementation of tools with dairy advisory teams.

Key Words: dairy advisory team, management tool

TH202 Look who's talking when setting goals and protocols for calf care. W. M. Sischo[1], D. A. Moore*[1], M. Davis[1], K. Heaton[1], D. Kinder[1], S. Kurtz[1], J. Siler[2], R. Pereira[2], and L. Warnick[2], *[1]Washington State University, Pullman, [2]Cornell University, Ithaca, NY.*

As the structure of the dairy industry changes so does management. Owner-operator farms are giving way to farms with specialized personnel for management and tasks. As consequences, management structures are more complex, more critical decisions are made by middle management and workers, and communication between owners and workers is complex and indirect. The study objectives were to assess current communication practices on US dairies and describe the actual and perceived communication between management and workers regarding goal setting and daily task for calf feeding and health. Semi-structured Qualitative Research Interviews of at least 4 people on each farm; owner, calf manager, calf care personnel, and herd veterinarian were conducted in Spanish or English using organizational communication flowcharts and a survey of attitudes and practices. Fifty-three farms from 5 states were enrolled. Interviews were conducted with owners (55), veterinarians (51), feeders (37), calf managers (30), herd managers (18), herdsmen (10), treaters (17), and others (7). Lines of communication were perceived differently depending on job titles. From owners' perspectives, when establishing feeding goals, s/he talked to the veterinarian on 67% of farms, calf manager (50%), and feeder (17%). In contrast, from the veterinarian's perspective, on 79% of farms they communicated with owners when setting feeding goals, herd managers on 41% and calf managers on 35% of farms. Calf managers communicated with herd managers on 75% and owners on 50% of farms. Feeders were rarely noted by others to be involved in setting goals, except from their perspective where 71% reported talking to calf managers while only a third of calf managers reported them involved. When setting calf health goals, most owners and veterinarians saw communication occurring between them (72–85%). That communication was not perceived by calf managers or treaters. More than half of treaters reported communication between them and the calf manager when setting health goals. This study shows the complexity of communication on dairies with layers of employees and that different perspectives on who's talking exist.

Key Words: communication, organization, education

TH203 Educational farm tours improve public understanding, impressions, and trust in modern dairy production systems. T. A. Ferris*[1], N. D. Thelen[2], and M. A. Dunckel[3], *[1]Department of Animal Science, Michigan State University, East Lansing, [2]Michigan State University Extension, Ann Arbor, [3]Michigan State University Extension, Alpena.*

Breakfast on the Farm (BOTF) events in Michigan involve public farm tours with educational stations providing consumers a first-hand look at modern food production. Ten of 12 tours in 2010 and 2011 coordinated by Michigan State University Extension involved dairy operations with 16,270 participants. Exit surveys from 1,567 of these participants indicated that 44% had not visited a dairy farm in the past 20 years (first-time visitors) and 21% had made only 1 or 2 prior dairy farm visits. On a 5-point scale from Strongly Disagree to Strongly Agree, 79% of first-time visitors Strongly Agree and 94% either Agree or Strongly Agree to the statement "I have a better understanding of modern dairy production." Of those with 1 or 2 prior visits, 70% Strongly Agree and 96% either Agree or Strongly Agree to this statement. Results are similar for level of agreement with the statement "My general impression about modern dairy farming has improved as a result of my visit today." Respondents rated their "General Impression" about 4 topics "Before" and "After" their BOTF visit: "How farmers care for the environment," "How farmers treat food-producing animals," "Steps taken to safe guard milk," and "Housing provided for dairy animals." For "Housing provided for dairy animals" the percentage with Very Positive impressions "Before" and "After" shifted from 26 to 76%, respectively, for first-time visitors, and from 27 to 71%, respectively, for those with 1 or 2 prior visits. Those with Very Negative (n = 32) or Negative impressions (n = 87), dropped to 2 and 8 people, respectively. Similar results occurred for the 3 other topics. Two questions attempted to gauge the increase in trust: "As a result of today's tour, my trust in milk as a safe food has increased" and "As a result of today's tour, my trust in dairy farmers as a source of information about food production has increased." On the 5-point scale, 68% of those making their first visit to a modern dairy farm Strongly Agree and 86% either Agree or Strongly Agree to the first statement and 73% Strongly Agree and 91% either Agree or Strongly Agree to the second statement.

Key Words: educational farm tour, modern dairy production, consumer trust

TH204 Developing a regional extension dairy programs through the use of DHI production data in Northern New York. K. M. Morrill*[1], S. Morrison[2], H. M. Dann[2], and H. M. Gauthier[2], *[1]Cornell Cooperative Extension, Canton, NY, [2]William H. Miner Agricultural Research Institute, Chazy, NY.*

The objective of this retrospective study was to evaluate 2012 milk quality and production on Northern New York (NNY) dairy farms and identify opportunities to develop extension programs. Data were provided by DRMS (Raleigh, NC) for NY state dairy herds (n = 1620 herds, 295,786 cows) on DHI test. Data were analyzed on a state and regional (n = 252 herds) basis to determine overall means and influence of herdsize (<100 cows, 100 to 499 or >499 cows), breed (Holstein, Jersey, other), and management scheme (organic or conventional) on production parameters. Overall means were similar on a statewide and

regional basis. Average daily milk production/lactating cow ranged from 10.7 to 47.5 kg/day, with a mean of 28.9 kg/day (SD = 5.7). Percent fat in NNY ranged from 3.0 to 5.0%, the overall mean was 3.8% (SD = 0.3). Percent protein in NNY ranged from 2.8 to 3.8%, the overall mean was 3.1% (SD = 0.2). The percentage of cows/herd that had a SCC score <4 ranged from 27 to 92% with a mean of 69.5% (SD = 10.9). The percentage of cows/herd that had a SCC score of 4 ranged from 4 to 27% with a mean of 12.5% (SD = 4.2%). The percentage of cows/herd with a SCC score of 5 ranged from 2 to 24% with a mean of 8.0% (SD = 3.3). The percentage of cows/herd with an SCC score of 6 ranged from 1 to 17% with a mean of 5.0% (SD = 2.4). The percentage of cows/herd with an SCC score >6 ranged from 1 to 19% with a mean of 5.2% (SD = 2.8). Management scheme did not influence any production parameters; however there was a breed effect ($P < 0.05$) on %fat, %protein and milk/cow (Holstein = 32.5, Jersey = 23.8, other = 28.1 kg/day, respectively). There was a herdsize effect ($P < 0.05$) on all SCC scores, with herds >500 cows have a greater ($P < 0.05$) percentage of cows with a SCC score ≤5 as compared with farms with <500 cows. There was also a herdsize effect on average daily milk/cow (small = 24.0, medium = 27.1 and large = 33.1 kg/cow/day, respectively). This data suggests that NNY extension dairy programs should be developed to improve milk quality on dairies with <500 lactating cows.

Key Words: quality milk, DHI, extension

TH205 Advising and technical support for dairy goat farmers: An Antonio Narro University service and extension experience in northern Mexico. P. A. Robles-Trillo*[1], F. G. Veliz[1], R. Rodriguez-Martinez[1], M. A. De Santiago-Miramontes[1], G. Arellano-Rodriguez[1], C. A. Meza-Herrera[2], and E. Martínez-Aranda[1], *[1]Universidad Autonoma Agraria Antonio Narro, Torreon, Coah. Mexico, [2]Unidad Regional Universitaria de Zonas Aridas, Universidad Autonoma de Chapingo, Bermejillo, Durango, Mexico.*

The Lagunera region, located in northern Mexico, at 25°N, 103°W, 1243 m asl, and annual averages of 24°C temperature and 270 mL rainfall, has almost 500,000 dairy goat heads producing more than 78,829,000 L per year, mainly raised under extensive and marginal conditions. This complex production system requires technical support. Therefore, our University carries-out a service project to achieve a link with the goat productive sector. The aim of this extension project is to provide advice and technical support for dairy goat producers, involving in such technical support and technical training to students which participate as practitioners and extension agents. Technical support and training involves visits to local farmers to perform different activities such as a) formulation and evaluation of rations, b) evaluation of the reproductive and productive state of livestock, c) determination of milk chemical composition, d) management and care of young, juvenile and adult goats, e) routine hygienic milking, f) recording of different management practices as well as g) monitoring of the herd health conditions. The project covers approximately 12,000 animals producing a peak production close to 18,000 L of milk per day, distributed in 40 dairy goats farms in some areas of the states of Coahuila and Durango which conform the Region Lagunera. A total of 18 students have been participating as social service providers, while 100 students have been involved as dairy goat practitioners, generating a total of 200 technical visits while small scale basic research studies. The Region Lagunera is one of the most important dairy goat producing areas in Mexico. Therefore both technical and academic activities through this kind of projects, should help to increase goat production throughout environmental-responsible while sustainable actions. The last should promote not only an escalation in the efficiency of goat milk production for human consumption and transformation but also an increase in the quality of life of marginal producers devoted to goat production under semiarid environments.

Key Words: extension, dairy goat, farmer

TH206 Relationships among performance parameters and beef bull sale price. J. L. Gleason, M. A. McCann, and S. P. Greiner*, *Virginia Polytechnic Institute and State University, Blacksburg.*

Data from state central bull test program sales in Virginia was utilized to evaluate the relationship between sale price and various measures of performance. A total of 1,869 bulls sold between 2002 and 2011at 2 locations were included in the analysis. Bulls at both locations were developed in test groups for either 112 or 133 d. Breeds included Angus (AN, n = 1645), Simmental (SM, n = 140), and Simmental × Angus (SA, n = 84). Sale price differential (PD) was calculated as the deviation in individual sale price from contemporary group mean (by location, breed, test group, year). Partial correlations adjusted for effects of year, location, and test group revealed positive associations between PD and final BW, ADG, and yearling wt (YW) for all breeds (r = 0.22 to 0.50). Only AN exhibited a relationship between PD and birth weight (BW; r = −0.14). Expected progeny differences (EPD) for calving ease direct (CED), BW, weaning wt, YW, and milk (MM) were similar in magnitude for their relationship with PD in AN bulls (r = 0.29, −0.29, 0.21, 0.29, and 0.22 respectively). In contrast, YW was the single growth EPD related to PD for SM (r = 0.19), while MM EPD had a strong association with PD in SA (r = 0.39). Relationships between carcass measures and PD were generally smaller in magnitude compared with growth traits. Best fit multiple regression equations to predict PD included different variables between breeds with the majority of the variation in PD for AN accounted for by YW, CED EPD, ADG and YW EPD (R^2 = 0.53), while YW, ADG and BW were most relevant for SM (R^2 = 0.29). Comparison of prediction models derived from AN bulls sold in 2010 and 2011 revealed selection index EPDs of beef value and weaned calf value to be of more importance in explaining variation in PD compared with models utilizing the same variables in earlier years. These results substantiate the importance of performance criteria in bull selection decisions, and indicate a time lag exists between the introduction of new selection technology and adoption by the commercial cattle industry.

Key Words: performance, price, beef

TH207 Factors affecting sale price of bulls sold in the Florida Bull Test. V. R. G. Mercadante*, D. D. Henry, F. M. Ciriaco, N. DiLorenzo, and G. C. Lamb, *North Florida Research and Education Center, University of Florida, Marianna.*

The annual Florida Bull Test (FBT) was initiated in 2000 to provide producers with a source of bulls that have been thoroughly evaluated at the same location. It provides an opportunity for seed stock producers to advertise their breeding programs and marketing bulls promoting awareness and understanding of the latest animal breeding concepts while showcasing superior genetics in the southeast United States. Since 2010 changes were made to the test to obtain individual feed efficiency (FE) data in addition to performance data. Daily feed intake was monitored using the GrowSafe system at the North Florida Research and Education Center Feed Efficiency Facility (FEF). Bulls received free choice access to a corn gluten and soy hull based supplement, grass hay, and water targeting a 1.6 kg ADG. After a 3-wk adaptation period, mean of 2 unshrunk weights were obtained on d 0, 28, 56, 84, and 112. On d 56 bulls were moved from the FEF onto pastures where they remained, consuming a similar diet, until completion of the test. The procedure

CORR of SAS was used to asses traits associated with increased sale prices for each of 3 years. The number of bulls offered for sale was 30, 45, and 58 for 2010, 2011, and 2012, respectively. Mean sale price was $2,247, $2,851, and $3,221 for 2010, 2011, and 2012, respectively. In 2010, sale prices were positively correlated ($P < 0.05$) with DMI during the first 56 d on test (DMI), bull age at the sale (AGE), BW on d 112 (BW), ADG, weight per day of age (WDA), final index (INDEX; sum of ADG and WDA) and frame score (FS), GF tended ($P = 0.08$) to be negatively correlated with sale price, whereas RFI was not correlated ($P > 0.10$) with sale prices. In 2011, sale prices were positively correlated ($P < 0.05$) with DMI, GF, BW, ADG, WDA, INDEX, whereas FS, RFI, and AGE were not correlated ($P > 0.10$) with sale prices. In 2012, sale prices were positively correlated ($P < 0.05$) with DMI, BW, ADG, WDA, INDEX, whereas FS, RFI, GF, and AGE were not correlated ($P > 0.10$) with sale prices. We conclude that performance traits such as DMI, ADG, and WDA had greater effects on sale price of bulls than FE and age of bulls sold in the FBT.

Key Words: Florida Bull Test, residual feed intake, performance

TH208 Moos, Ewes and More: A public education event. E. L. Berg*, S. M. Ostby, K. A. Vonnahme, S. Wagner, S. E. Anderson, J. D. Hayden, L. A. Christianson, C. Stoltenow, and K. B. Koch, *North Dakota State University, Fargo.*

According to USDA estimates, only 0.3% of the US population claims farming as their primary occupation. In ND, 5% of the population identifies themselves exclusively as farmers, but in Fargo, the state's largest city and the location of North Dakota State University, the estimate falls to 0.4%. Consequently, there is a diminishing awareness among the general population about the origins of food and fiber. In an effort to educate an interested public about the influence of animals in their daily lives, the NDSU Department of Animal Sciences developed Moos, Ewes and More in 2010. This annual open house event is designed to reconnect the public with animal agriculture through interactive demonstrations, product sampling, and education. Structured demonstrations of sheep shearing, cow milking, and farrier work alternate every 30 min, while on-going demonstrations include wool spinning and ultrasonography of pregnant ewes. Food samples consist of ice cream and a variety of meat products. Interactive activities include bottle feeding calves, collection and microscopic viewing of rumen contents from fistulated cattle, performing mock surgeries on stuffed animals, roping plastic steers, and educational scavenger hunts. Faculty, staff, and students answer questions and educate attendees at stations displaying livestock and their products. There is a booth explaining animal welfare vs. animal rights and the NDSU Institutional Animal Care and Use Committee compliance officer is present to answer questions about the use of animals in research. The importance of animals in the development of life saving medical advances and the training of physicians in emergency support procedures are presented by experts from a local hospital. Animal Sciences faculty and staff participation throughout the past 3 years has ranged from 78 to 88%, and approximately 45 undergraduate and graduate students participate each year. The number of attendees has increased from 497 in 2010 to 989 in 2012. Providing an open forum for dialog and education between animal scientists and the public is essential in order for those without farm experience to understand the benefits of animal agriculture and research.

Key Words: education, public, welfare

TH209 Survey of central North Carolina horse owners regarding parasite anthelmintic resistance. N. C. Whitley*[1], B. Chase[2], and S. B. Routh[1], *[1]North Carolina A&T State University, Greensboro, [2]Guilford and Rockingham County Extension Service, Greensboro and Reidsville, NC.*

Gastrointestinal nematode anthelmintic resistance is a growing issue in the horse industry. One cause of resistance is thought to be overuse of anthelmintics such as in routine, rotational deworming such as that recommended in the past. To determine the current knowledge of horse owners in central North Carolina regarding anthelmintic resistance and deworming, a survey was conducted through an email list belonging to an agent with the North Carolina Cooperative Extension Service. The survey was part of one issue of the agent's monthly equine email newsletter and was sent out to over 400 horse owners primarily in the central region of North Carolina. The survey consisted of open-ended questions about parasite resistance and fecal egg counting. Seventy-eight surveys were returned; however, 2 respondents did not fully complete the survey and 3 were duplicates, resulting in 73 valid surveys. Of those responding, 52% were concerned or very concerned about anthelmintic parasite resistance occurring on their farm, 15% were somewhat concerned and 33% were not concerned. Participants (65%) indicated they made changes on their farm to slow resistance though only 5% had parasite resistance and 45% did not know if they had parasite resistance on their farm; the remaining 50% did not feel they had parasite resistance on their farm. Fecal egg counting had been conducted on 65% of the farms at some point in time; for 17% it had been 3 mo or less, for 17% 4 to 6 mo, for 37% 7 to 9 mo, for 28% 10 to 12 mo and for 21% it had been over 12 mo since the last fecal egg count was conducted. When asked about deworming, for the 70% who indicated they routinely dewormed and rotated anthelmintics, 40% did so based on veterinarian recommendations, 15% did so using charts or calendars and 16% used fecal egg counts to decide about deworming. According to this informal preliminary survey of horse owners in central North Carolina, more training of horse owners and perhaps veterinarians is needed to have more widespread incorporation of best management practices for sustainable horse parasite management.

Key Words: horse, parasite, resistance

TH210 Occurrence of aflatoxin in dairy cow feed and raw milk in China. N. Zheng[1,2], J. Q. Wang*[1,2], Y. P. Zhen[1,2], X. M. Xu[1,2], R. W. Han[1,2], S. L. Li[1,2], and X. Y. Qu[1,2], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences,, Beijing, China, [2]Ministry of Agriculture - Milk and Dairy Product Inspection Center (Beijing), Beijing, China.*

Aflatoxin (AF) M1 is carcinogenic and exists in milk due to dairy cows consuming AFB1 contaminated feeds. The legal limit of AFM1 in milk is set as 50 ng/L by European Union (EU) et al. and 500 ng/L by China, US, Japan et al. Meanwhile, the legal limit of AFB1 in dairy cow feeds also is established to control the level of AFM1 in milk. A limit of 10 μg/kg is set by China, Japan et al. and 5 μg/kg is set by EU et al. Furthermore, countries such as US and Canada set the legal limit of total AF (AFB1+AFB2+AFG1+AFG2) in dairy cow feed as 20 μg/kg. In the present study, the occurrence of AFs in dairy cow feed and raw milk in China was investigated. Two hundred dairy cows feed samples and 2 hundred raw milk samples were collected from 10 of the main milk-producing provinces in China. AFB1, B2, G1 and G2 in the feed samples were analyzed using the HPLC method. AFM1 in the raw milk samples was determined using the ELISA method. The data was statistically analyzed using the SPSS version 11.5 (SPSS, Inc., Chicago, IL). AFB1 and AFB2 were found in the feed samples, but not AFG1 and AFG2. In the feeds, 17.5% of feed samples contained only AFB1, 11.5% of samples contained only AFB2, and 24.5% of samples contained both AFB1 and AFB2. Totally 42% of the samples contained AFB1 within the range of 0.05–3.53 μg/kg, and 36% of the samples were positive for AFB2, with the content ranging from 0.03 μg/kg to 0.84 μg/kg. The content of AFB1 was significantly ($P < 0.05$) higher than that of AFB2 in the feeds. The AFB1 content in the positive feed samples was below the legal limit in China of 10 μg/kg and even below the EU legal limit of 5 μg/kg. The total content of AFs was below the U.S legal limit of 20 μg/kg. For the raw milk samples, 32.5% were positive for AFM1, containing 5.2–59.6 ng/L, a level far below the legal limit in China and the US of 500 ng/L, though 3 samples contained AFM1 exceeding the EU legal limit of 50 ng/L. It suggested that the AFM1 in raw milk in China is in the safe level due to the low concentration of AFB1 in dairy cow feeds.

Key Words: aflatoxin, feed, raw milk

TH211 Survey of 38 veterinary drug residues in raw milk in China. R. W. Han[1,3], N. Zheng[1,2], J. Q. Wang*[1,2], Z. N. Yu[3], X. M. Xu[1,2], Y. P. Zhen[1,2], X. Y. Qu[1,2], and L. C. Huang[1,2], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Ministry of Agriculture - Milk and Dairy Product Inspection Center (Beijing), Beijing, China, [3]College of Food Science and Engineering, Qingdao Agricultural University, Qingdao, Shandong, China.*

The aim of the study was to investigate the occurrence of veterinary drug residues in raw milk of China. A total of 178 raw milk samples were collected from 8 provinces of China in July, 2012. Thirty 8 veterinary drugs including 14 β-lactams, 8 quinolones, 8 sulfonamides, 5 tetracyclines and 3 macrolides were determined with a developed multiclass method by ultra-high-performance liquid chromatography-tandem mass spectrometry (UPLC-MS/MS). The limit range of quantification was 0.03–10 ng/mL and the recovery range was 67.9–117.7%. The data was statistically analyzed using the SPSS version 11.5 (SPSS Inc., Chicago, IL). A total of 21 veterinary drugs including 5 β-lactams, 6 quinolones, 6 sulfonamides, 2 tetracyclines and 2 macrolides were detected and the detection percentage were in the range of 1.7–37.1% for β-lactams, 0.6–47.8% for quinolones, 1.7–24.7% for sulfonamides, 3.4–14.6% for tetracyclines and 1.7–34.8% for macrolides. The maximum concentrations for detected veterinary drug residues were 7.68 ng/mL for β-lactams (cefoperazone), 11.2 ng/mL for quinolones (ciprofloxacin), 1.93 ng/mL for sulfonamides (trimethoprim), 5.78 ng/mL for tetracyclines (doxycycline) and 76.25 ng/mL for macrolides (lincomycin). The percentage of 5.1% samples was found no veterinary drug residues, while 94.9% samples contained veterinary drug residues with the maximum type of 7. Chi-squared statistics analysis showed there were no differences ($P > 0.05$) on the veterinary drugs' detection percentages among 8 provinces. No samples exceeded the maximum residue levels of the veterinary drugs regulated by China, European Union and Codex Alimentarius Commission. It showed the veterinary drug level in raw milk was safe for consumption in China.

Key Words: veterinary drug, raw milk, China

TH212 Occurrence of organochlorine pesticide residues in raw milk in China by gas chromatography triple-quadrupole mass spectrometry. X. M. Xu[1,2], N. Zheng[1,2], J. Q. Wang*[1,2], R. W. Han[1,2], and S. L. Li[1,2], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Ministry of Agriculture - Milk and Dairy Product Inspection Center (Beijing), Beijing, China.*

Most of the countries and international organizations have issued standards and regulations to limit pesticide residues in milk. China government set maximum residue limits (MRLs) of 18 organochlorine pesticides in milk. In the present study, a total of 178 raw milk samples from 8 primary milk producing provinces of China, including Inner Mongolia, Heilongjiang, Sichuan, Shandong et al., were determined for 18 organochlorine pesticides using Gas chromatography triple-quadrupole mass spectrometry (GC-MS/MS; 7000B, Agilent, USA) to assess the contamination of pesticide residues in raw milk in China. The limits of quantification (LOQ) were from 0.5 $\mu g.kg^{-1}$ to 6 $\mu g.kg^{-1}$ for 18 organochlorine pesticides respectively. Pesticides in milk samples were extracted by a solid phase system with acetone. An extract aliquot of acetone was injected into the GC-MS/MS. Recoveries of pesticides spiked in raw milk samples were 78–122%. Among 18 organochlorine pesticides, 10 pesticides of Aldrin, Endosulfan I, Endosulfan sulfate, DDT-p,p', Dieldrin,BHC-α, DDD-p,p', BHC-β, Lindane, DDE-p,p', were found in milk samples. The frequency of total samples containing detectable levels of 18 organochlorine pesticides residues was 1.2%, 1.2%, 1.2%, 2.4%, 2.4%, 2.9%, 4.1%, 14.1%, 14.7%, 22.4% in total milk respectively. There were no differences ($P > 0.05$) on the pesticides' detection among 8 provinces after Chi-squared statistics analysis. The maximum concentrations were 5.27 $\mu g\ kg^{-1}$ for Aldrin, 4.56 $\mu g\ kg^{-1}$ for Endosulfan I (α isomer), 4.33 $\mu g\ kg^{-1}$ for Endosulfan sulfate, 4.42 $\mu g\ kg^{-1}$ for DDT-p,p', 5.47 $\mu g\ kg^{-1}$ for Dieldrin, 4.64 $\mu g\ kg^{-1}$ for BHC-α, 4.80 $\mu g\ kg^{-1}$ for DDD-p,p', 4.56 $\mu g\ kg^{-1}$ for BHC-β, 4.56 $\mu g\ kg^{-1}$ for Lindane, 5.33 $\mu g\ kg^{-1}$ for DDE-p,p'. For all positive samples, only one sample contained Endosulfan (4.56 $\mu g\ kg^{-1}$) exceeded the legal limit of Japan (4 $\mu g\ kg^{-1}$), while the others were within the legal limit set by China, European Commission, New Zealand. This survey show the level of pesticides in milk in China is safe to consume.

Key Words: occurrence, pesticide residue, raw milk

TH213 Occurrence of heavy metals in raw milk in China. X. Y. Qu[1,2], N. Zheng[1,2], J. Q. Wang*[1,2], X. M. Xu[1,2], R. W. Han[1,2], Y. P. Zhen[1,2], and S. L. Li[1,2], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Ministry of Agriculture - Milk and Dairy Product Inspection Center (Beijing), Beijing, China.*

The levels of heavy metals are an important component to assess the quality of milk. The nations set the legal limit to control the levels of heavy metals in milk. China government set legal limit of 4 heavy metals, including lead of 0.05 mg/kg, chromium of 0.3 mg/kg, mercury of 0.01 mg/kg and arsenic of 0.05 mg/kg. The object of this study was to assess the levels of aluminum, lead, chromium, nickel, cadmium, mercury and arsenic residues in raw milk in China. One hundred and 70 8 raw milk samples were collected from China's 8 of the main milk-producing provinces. The heavy metals were determined using a validation simultaneous analysis method of inductively coupled plasma-mass spectrometry (ICP-MS). The limits of detection (LOD) of aluminum, lead, chromium, nickel, cadmium, mercury and arsenic were 0.01 mg/kg, 0.002 mg/kg, 0.01 mg/kg, 0.003 mg/kg, 0.001 mg/kg, 0.001 mg/kg and 0.001 mg/kg, respectively. The data was statistically analyzed using the SPSS version 11.5 (SPSS, Inc., Chicago, IL). A total of 48.9% of the milk samples contained aluminum, and 12.9% samples contained chromium, 23.6% samples contained nickel, 9.0% samples contained arsenic, 27.5% samples contained mercury, 28.1% samples contained lead, and no sample was positive to cadmium. For the positive samples, the maximums and means were 1.52 mg/kg and 0.28mg/kg of aluminum, 0.08 mg/kg and 0.04mg/kg of chromium, 0.005 mg/kg and 0.002mg/kg of mercury, 0.106 mg/kg and 0.011 of nickel, 0.033 mg/kg and 0.008mg/kg of lead and 0.002 mg/kg and 0.001 of arsenic. Aluminum, chromium and mercury were existed in all provinces, and the levels of these 3 heavy metals had no significant ($P > 0.05$) difference in 8 provinces. Nickel, lead and arsenic were not found in Tianjin and Inner Mongolia. The concentrations of lead, chromium, mercury and arsenic in all positive samples were below China's national legal limits. It showed that the heavy metals in milk in China were in the safe level.

Key Words: heavy metal, raw milk, China

TH214 Occurrence of four mycotoxin residues in raw milk in China. L. C. Huang[1,3], N. Zheng[1,2], J. Q. Wang*[1,2], J. B. Cheng[1,3], R. W. Han[1,2], X. M. Xu[1,2], and S. L. Li[1,2], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Ministry of Agriculture - Milk and Dairy Product Inspection Center (Beijing), Beijing, China, [3]College of Animal Science and Technology, Anhui Agricultural University, Hefei, China.*

A study was conducted to investigate the occurrence of mycotoxins in raw milk in China. A total of 178 raw milk samples from 8 primary milk producing provinces of China, including Inner Mongolia, Heilongjiang, Sichuan, Shandong, et al., were examined for aflatoxin M_1 (AFM_1), ochratoxin A (OTA), α-zearalenol (α-ZEL) and zearalenone (ZON). Mycotoxins were simultaneously determined by UPLC-MS/MS (TQ-S, Waters, USA), with the limits of quantification (LOQ) of 3, 12, 9 and 3 $ng \cdot kg^{-1}$ for AFM_1, OTA, α-ZEL and ZON, respectively. LOQs were sensitive enough to meet the requirement of the maximum residue limits (MRLs) regulated by European Union, Codex Alimentarius Commission and China. The data was statistically analyzed using the SPSS version 11.5 (SPSS, Inc., Chicago, IL). 84% of the raw milk samples were contaminated with AFM_1, 38% with OTA, 74% with α-ZEL and 87% with ZON. The average concentration of AFM_1, OTA, α-ZEL and ZON in positive samples were 14.7, 20.4, 115.2 and 22.1 $ng \cdot kg^{-1}$, respectively. The samples contained AFM_1, OTA, α-ZEL and ZON were found in all provinces. The lowest detection rates for 4 mytcotonxins were 60% of AFM_1 and 35% of ZON in Inner Mongolia, 50% of OTA in Shandong, 23.8% of α-ZEL in Hubei, while the highest detection rates for 4 mytcotonxins were 100% of AFM1 in Shandong and Tianjin, 96.3% of OTA in Anhui, 100% of α-ZEL in Shandong, 100% of ZON in Shandong, Shanxi and Tianjin. The maximums of AFM_1, OTA, α-ZEL and ZON were 95.5 $ng \cdot kg^{-1}$ (Inner Mongolia), 198.9 $ng \cdot kg^{-1}$ (Inner Mongolia), 648.3 $ng \cdot kg^{-1}$ (Anhui) and 111.9 $ng \cdot kg^{-1}$ (Inner Mongolia), respectively. Among the 4 mycotoxins, only AFM_1 is set MRL in milk all over the world, and 50 $ng \cdot kg^{-1}$ represented by European Union and 500 $ng \cdot kg^{-1}$ represented by US and China are 2 peak limits. In the present study, the AFM_1 concentrations of 4 samples were between 50 $ng \cdot kg^{-1}$ and 500 $ng \cdot kg^{-1}$. However, high percentages of positive samples for OTA, α-ZEL and ZON were found in milk in China. So the contaminant of mycotoxins in raw milk in China should be considered, and the effective measure should be applied to decrease the contaminant of mycotoxins.

Key Words: mycotoxin, raw milk, China

TH215 Effect of prophylactic use of antibiotics in intravaginal sponges on the response of inhibitor screening tests in goats milk. T. Romero[1], J. Balado[2], R. L. Althaus[3], M. C. Beltrán[1], and M. P. Molina*[1], *[1]Instituto de Ciencia y TecnologAnimal. Universitat Politecnica de Valencia, Valencia, Spain, [2]Diputacion Provincial de Castellón, Ares del Maestrat, Castellón, Spain, [3]Cátedra de Biofisica, Facultad de Ciencias Veterinarias, Universidad Nacional del Litoral, Esperanza, Argentina.*

The objective was to determine whether the prophylactic use of antibiotics in the placement of intravaginal sponges in estrus synchronization treatments in caprines may be the cause of the presence of inhibitors in milk and, therefore of positive results in screening tests. Ninety-eight Murciano-Granadina goats were used, divided into groups of 14 animals each. Intravaginal sponges were placed in 6 groups using commercial antibiotics: Terramycin Oral (oxytetracycline), Hipradoxi (doxycycline), and Framicas (sulfathiazole 96% and framycetin 4%) with 2 different concentrations of each. In a control group goat sponges were placed without any antibiotic. Milk samples were collected daily along the 7-d-post-treatment period. SCC and pH were determined in all samples and analyzed by means of 3 microbiological screening methods (BRT MLR, Delvotest MCS and Eclipse 100). Moreover, milk of the first 3 d as well as the positive samples in microbiological tests were analyzed with receptor binding protein methods specific for tetracyclines and sulfonomides. When sponges were removed, the degree of cleanliness was visually assessed to evaluate antibiotic efficacy. The detection limits of the methods were calculated using logistic regression, and the χ^2-test was used to evaluate the degree of cleanliness of the sponges. Microbiological methods presented positive results, the BRT MLR method showed the highest number of them for all antibiotics, even in the control group, indicating a lower selectivity of the method for goat milk. By contrast, positive results were lower in Delvotest MCS and Eclipse 100 for all treatments. Antibiotic sponges presented superior odor, color and minor adhesions than the control group; treatments with tetracyclines (oxytetracycline and doxycycline) having a higher degree of cleanliness with the higher dose. It can be concluded that the prophylactic use of oxytetracycline, doxycycline and sulfathiazole in intravaginal sponges used in estrus synchronization treatments in goats does not seem to constitute a risk of antibiotic residues in milk.

Key Words: goat milk, intravaginal sponge, antibiotic screening method

TH216 Validation of new SNAP Beta-Lactam antibiotic residue test kit for goat milk screening. S. S. Zeng*, K. Tesfai, E. Vasquez, I. Portugal, and C. Watson III, *Langston University, Langston, OK.*

Experiments were conducted to validate the SNAP Beta-Lactam Test Kit (SNAP NBL) for screening antibiotic residues in goat milk for human consumption. Raw goat milk collection, preparation of drug-fortified goat milk samples, drug-incurred study, sample testing, data collection and analysis, and result interpretation were performed according to the FDA-DVM validation protocol (i.e., SNAP-Beta Lactam Test Form, FDA 2400n). Results indicate that the SNAP NBL Test Kit did not show any positive readings (i.e., 100% specificity) in unfortified and uncontaminated fresh or frozen goat milk. This test kit had 100% sensitivity in detecting antibiotic residues in fortified goat milk with ampicillin, amoxicillin, cephapirin and penicillin G at their respective tolerance and/or safe levels set forth by FDA for cow milk. It must be noted that this test might be more sensitive for goat milk than for cow milk with detection below the tolerance and/or safe levels of the drugs, leading to possible sub-violative positive results. The SNAP NBL Test Kit was also effective in screening for antibiotic resides in milk throughout lactation after goats were treated with antibiotic drugs. The clearance time of antibiotic residues from the mammary glands to tolerance levels and detection levels of the SNAP test depended on the drugs used and the amounts applied. In conclusion, the SNAP NBL Test Kit was effective in screening antibiotic residues in goat milk and is recommended for use in dairy goats

Key Words: goat milk, antibiotics, SNAP test

TH217 Antimicrobial residues in pasteurized milk assessed by the inhibition test of microbial growth and HPLC-DAD. A. P. A. Magnavita[1], S. A. A. Fernandes[1], S. P. B. Ferrão[1], S. A. Gualberto[1], and S. V. Matarazzo*[2], *[1]Universidade Estadual do Sudoeste da Bahia, Itapetinga, Bahia, Brasil, [2]Universidade Estadual de Santa Cruz, Ilheus, Bahia, Brasil.*

The objective of this study was to qualitatively evaluate the occurrence of antibiotic residues in pasteurized milk, under State Inspection, marketed in the state of Bahia, Brazil. Milk samples were collected monthly between November/2010 and October/2011 from commercial establishments. The Delvotest SP-NT was applied to 252 pasteurized milk samples, in duplicate, of 21 different brands. In the positive and/or suspect samples both oxytetracycline (OTC) and tetracycline (TC) were quantified by HPLC-DAD. Of all the samples, it was observed that 207 were negative (82.0%), 19 positive (7.6%) and 24 suspect (9.6%). The positive and/or suspect samples were concentrated in the first semester of the year (January to July). Of the 19 positive samples in the screening test, OTC was detected in all and TC in 6. In the 24 suspected samples, in only one was the presence of OTC not detected and in 8 no TC was found. Of the milk brands evaluated, the presence of antibiotic residues was not detected in 4; in the other brands both positive and suspect samples were verified in some period of the year. The screening test used was effective for identifying the presence of antibiotic residues (OTC and TC), confirmed by liquid chromatography. Results indicate the presence of antibiotic residues above legal limits, however, in low proportion. In 10 of the 16 dairy facilities with antibiotic residues in milk, the EDI was less than the maximum recommended by the European Union. In general, pasteurized milk sold in cities of Bahia presented low occurrence of antibiotic residues, of which OTC was predominant. This requires that the presence of antibiotic residues is controlled in milk from Bahia.

Key Words: pasteurization, antibiotic, Delvotest SP-NT

TH218 Regulatory processes for substances used in animal food. M. G. Alewynse* and S. A. Benz, *Center for Veterinary Medicine, Food and Drug Administration, Rockville, MD.*

There is increasing interest in the marketing of novel substances for use in animal food. Animal food includes both livestock feed and companion animal food. These substances may be intended to be a source of nutrients or, like enzymes, may affect the characteristics of the food itself. Food falls under the regulatory authority of the US Food and Drug Administration (FDA). Within FDA, the Center for Veterinary Medicine (CVM) regulates both food and drugs intended for animals. The Division of Animal Feeds is responsible for regulating substances used in, or as, animal food. Substances added to a food must be safe and achieve their intended purpose. Two regulatory pathways are available for new substances. The food additive petition process is described in regulation 571 in Title 21 of the Code of Federal Regulations (21 CFR 571). The safety of the substance at the intended use rate must be addressed for both the animal and the environment. For food producing species, the safety of human food obtained from the animals must also be addressed. When FDA approves a food additive petition, a regulation in 21 CFR 573 is established addressing the proposed use of the substance in animal food. The second pathway is for qualified experts to determine that a particular use of a substance in animal food is exempt from the premarket requirements of the Federal Food, Drug, and Cosmetic Act because this use is generally recognized as safe (GRAS). A GRAS determination generally demands the same quantity and quality of data/ information needed for a food additive approval with the added requirement that this information be in the public domain. Sponsors can notify CVM about a GRAS determination through the animal food GRAS notification program. CVM maintains an internet list of animal food GRAS notices and CVM's conclusions about each notice. More information about these processes is available at http://www.fda.gov/AnimalVeterinary/Products/default.htm. Another pathway for substances that raise no safety concerns is provided by the Association of American Feed Control Officials to establish an ingredient definition in its Official Publication.

Key Words: animal food regulation, food additive/GRAS, ingredient definition

TH219 Detection of antimicrobial and anthelmintic residues in bulk tank milk from Minas Gerais State, Brazil. F. N. Souza[1], A. F. Cunha[1], L. C. A. Picinin[2], M. O. Leite[1], C. F. A. Penna[1], M. R. Souza[1], L. M. Fonseca[1], and M. M. O. P. Cerqueira*[1], *[1]Department of Food Technology and Inspection, Belo Horizonte, Minas Gerais, Brazil, [2]Department of Food Science and Technology, Florianopolis, Santa Catarina, Brazil.*

The present study aimed to detect residues of drugs in bulk tank milk samples from Minas Gerais State, Brazil. A total of 70 and 83 milk samples were submitted to antimicrobial and anthelmintic screening tests, respectively. The antimicrobial residues detection included quinolones, ceftiofur, thiamphenicol, streptomycin, tylosin and tetracyclines; while antithelmintics detection included benzimidazoles, amino benzimidazoles, levamisole, avermectins, thiabendazole, moxidectin and triclabendazole. The preparation of the milk samples and the detection of the antimicrobials (Anti Microbial Array II, cat no. EV3524A; Randox Laboratories Ltd., UK) and of the anthelmintics (Anthelmintics Array, cat no. EV3770; Randox Laboratories Ltd., UK) residues were performed by biochip array platform, using competitive antibody-capture immunoassay as recommended by the manufacturer's protocol. Here, 2.86%, 2.86% and 11.3% of the bulk tank milk samples were positive for the antimicrobials quinolones, streptomycin and tetracyclines

residues, respectively. Regarding the anthelmintics, 55.42%, 53.57%, 60.24%, 67.47%, 73.49%, 45.78% and 6.02% were positive for amino benzimidazoles, levamisole, avermectins, thiabendazole, moxidectin, triclabendazole and benzimidazoles residues, respectively. No milk sample had value above the Brazilian maximum residue levels (BMRLs) for antimicrobials, although 6.02% (n = 5) of the milk samples showed values above the BMRLs for avermectins (≥10 μg/L). The findings of the present report indicate the need of a stricter monitoring of the veterinary drugs residues in milk produced in Minas Gerais State. To reach this objective, continuous monitoring programs should be applied to offer a safer product to consumers.

Key Words: veterinary drug, milk, dairy cattle

TH220 Development of phage-based technologies to reduce *E. coli* O157:H7 contamination of beef products and produce. Y. Pan*, Y. Hong, J. Zhang, and P. D. Ebner, *Purdue University, Department of Animal Sciences, West Lafayette, IN.*

E. coli O157:H7 has developed into a ubiquitous pathogen with infections associated with products ranging from ground beef to produce to processed foods. We had previously demonstrated that phage-based technologies could reduce foodborne pathogen transmission and colonization in live animals. Here we examined whether a phage cocktail consisting of 3 phages could reduce *E. coli* O157:H7 in experimentally contaminated ground beef and produce. The 3 phages were isolated from human wastewater samples and belonged to the Myoviridae and Siphoviridae families. The phages were chosen from a growing library based on their rapid growth (40 to 50 min life cycle) and in vitro killing efficiencies. Phages were added to ground beef (20g) contaminated with *E. coli* O157:H7 (10^7 cfu) at an MOI = 1.0. Phage treatment significantly reduced ($P < 0.05$) the concentration of viable *E. coli* O157:H7 in contaminated ground beef by 2.0 $\log_{10}$ compared with untreated samples when stored at room temperature for 24h and 0.5 $\log_{10}$ when stored at refrigerated condition (4C). Likewise, the phage cocktail reduced *E. coli* O157:H7 by 0.5 $\log_{10}$ in undercooked ground beef (internal temperature of 46C; $P < 0.05$) compared with untreated samples. Similarly, spinach samples (3 pooled leaves) were inoculated with *E. coli* O157:H7 (10^7 cfu) and treated with the phage cocktail at an MOI = 1.0. Concentrations of *E. coli* O157:H7 in phage treated spinach samples were reduced 3.3 $\log_{10}$, 2.9 $\log_{10}$ and 2.8 $\log_{10}$ at 24, 48, 72 h, respectively, compared with untreated samples when stored at room temperature. Similar experiments were conducted with Swiss cheese, but no significant differences were found. Taken together, these results provide additional support for the development of phage-based approaches to control *E. coli* O157:H7 contamination in food products.

Key Words: *E. coli* O157:H7, phage, ground beef

TH221 Detection of ceftiofur residues in milk of cows treated for mastitis using the BetaStar Plus assay. K. Grooms*[1], D. Grooms[1], E. Jagodzinski[1], B. Norby[1], R. Erskine[1], L. Halbert[1], and J. Rice[2], *[1]Michigan State University, College of Veterinary Medicine, East Lansing, [2]Neogen Corporation, Lansing, MI.*

Development of a cow-side assay to detect antibiotic residues in milk would be advantageous to reduce risks of violative residues in marketed milk. The objective of this project was to evaluate the effectiveness of a rapid immunomigration assay (BetaStar Plus, Neogen Corporation, Lansing, MI) in detecting cephalosporin residues in milk from individual cows treated for mastitis. This assay is currently FDA approved for detecting β-lactam and cephalosporin residues in commingled milk. 38 dairy cows with clinical mastitis from 4 dairy farms were enrolled and treated with intramammary ceftiofur hydrochloride (Spectramast-LC, Pfizer Animal Health) according to the manufacturers label recommendation. Composite milk samples were collected a) before first antibiotic treatment, b) before the last antibiotic treatment, c) the last milking of the product-labeled milk withhold, d) the first milking after the product-labeled milk withhold had been met, and e) 72 h after the product-labeled milk withhold had been met. Samples were tested using the BetaStar Plus assay within 48 h of collection. Parallel samples were submitted to the Iowa State University Cyclone Analyte Detection Service for liquid chromatography mass spectrometry (LC MS). There were 2.6%, 57.9%, 42.1%, 15.8%, and 0.0% BetaStar Plus assay positive samples at each of the respective time points. The assay had a sensitivity and specificity of 93.3% and 78.3% respectively when compared with LC MS analysis using FDA published residue tolerance levels for ceftiofur (or ceftiofur metabolites) as a threshold. If the detection of any ceftiofur residue (or ceftiofur metabolites) by LC MS was considered as "positive," the sensitivity and specificity of the BetaStar Plus assay was 87.0% and 94.4% respectively. The BetaStar Plus assay could be useful to detect ceftiofur residues in milk from individual cows treated for mastitis before being sold for human consumption.

Key Words: antibiotic, residue, mastitis

TH222 Macrocyclic lactones residues in milk from family farming properties in the state of Rio Grande do Sul, Brazil. U. A. Souza[1], J. Reck[2], J. R. Martins[2], A. Webster[1], G. Klafke[2], G. Rubesam[3], F. Barreto[3], and L. Kindlein*[1], *[1]Federal University of Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil, [2]Institute of veterinary research Desidério Finamor, Eldorado do Sul, Rio Grande do Sul, Brazil, [3]Agriculture Ministry, Livestock and Supply, National Agricultural Laboratory, Porto Alegre, Rio Grande do Sul, Brazil.*

The objective of this study was to determine the presence of macrocyclic lactones (LM) residues in milk on cattle and Northwest or southern regions of the state of Rio Grande do Sul, Brazil. The control of chemical residues in animal products in Brazil is regulated by regulatory agencies through programs such as the National Residue Control (PNCR) and the Program for Residue Analysis of Veterinary Drugs (PAMVet), aimed at ensuring food security the consumer. The practices adopted in agricultural production, however, involve the use of drugs to control infectious and parasitic diseases in farm animals. The LM veterinary drugs are effective in controlling endo and ectoparasites, being widely used in dairy cattle. For this experiment, we collected 72 samples of milk cooling tanks properties smallholder farming regions Northwestern (55) and South (17) of the state of Rio Grande do Sul. The residue of LM were extracted from bovine milk by addition of acetonitrile and purified by freezing of the matrix co-extracts with a temperature of about −20°C. The purified extract was analyzed by LC-MS/MS. Among the 72 samples, 18 (25%) had LM residues whose active ingredients identified were: ivermectin (n = 15), moxidectin and ivermectin (n = 1), moxidectin (n = 1) and abamectin (n = 1). The southern region of the state showed higher occurrence of LM residues in milk (35.3%, 6/17) compared with the Northwest (21.8%, 12/55). The residues found in milk samples were below the limit set by Codex Alimentarius (<10 $\mu g.mL^{-1}$), but these drugs cannot be used in lactating animals whose milk is intended for human consumption. The results indicate the improper use of antiparasitic drugs in dairy herds studied. It is concluded that milk from dairy farms of the Northwest and Southern regions of the state of Rio Grande do Sul have LM residues.

Key Words: antiparasitic drug, food security, residue

TH223 Inhibitory effects of mint oils alone or combining with tannin extract against foodborne pathogens. B. J. Min[1], B. R. Min*[2], and J. H. Lee[3], *[1]Tuskegee University, Department of Food and Nutritional Sciences, Tuskegee, AL, [2]Tuskegee University, Department of Agricultural and Environmental Sciences, Tuskegee, AL, [3]Fort Valley State University, Department of Agricultural Sciences, Fort Valley, GA.*

Antimicrobial study was carried out to investigate inhibition effect of mint oil alone or combining with tannin extracts against foodborne pathogenic bacteria using agar diffusion assay. Commercial chestnut tannins (CNT; containing 80% hydrolysable tannins) and 2 mint oils; 2% peppermint (PP) and 2% spearmint (SP) were tested. Experimental solutions (n = 3/treatment) were prepared with 70% ethanol (EtOH) only (control), T1 (PP+EtOH), T2 (SP+EtOH), T3 (CNT+PP+EtOH), T4 (CNT+SP+EtOH) or T5 (CNT+PP+SP+EtOH) were investigated. To determine concentration of CNT extract before using in combination with mint oils, CNT was diluted with 70% ethanol solution at different ratio (1:10, 1:100, 1:500, 1:1000 dilutions) and tested inhibition activities against foodborne pathogens. A brain heart infusion broth (BHIB) soft agar was used for inoculation of *L. monocytogenes* and TSB soft agar was used for *E. coli* O157:H7 and bacteria was grown to 6 to 7 Log cfu/mL. Each 50 µL of solutions from the prepared solutions was dispensed into hole in the plate to measure the inhibition effect. After incubation, the diameter of inhibition zones was measured at least 3 cross-section points, and mean value was used for inhibition zone. From the screening test, CNT ethanol solution with 1:100 dilutions was selected for further study. All data were analyzed as a completely randomized design. Antilisterial effect of T1 (12 mm) was higher ($P < 0.05$) than effect of T2 (11.3 mm). For the combined treatment of T3 and T4 exhibited larger ($P < 0.05$) inhibition zone against *L. monocytogenes* compared with inhibition zone of T1 and T2. However, there was no significant effect of T5 to increase ($P > 0.05$) inhibition activity compared with T3 and T4. Among the prepared solutions, inhibition zone of T3 against both pathogenic bacteria was significantly larger ($P < 0.05$) than inhibition zone of other prepared solutions. The results indicate that the incorporation of mint oil with tannins might be applicable to the livestock feeding system for improving the quality of feeding to livestock and of their products.

Key Words: mint oil, tannin extract, food safety

TH224 A genotyping tool for *Enterobacter sakazakii* isolates from powdered infant formula and environment. Y. Chai[2], Y. Lu[1], C. Man[1], Y. Guo[2], X. Dong[2], Y. Lang[2], M. Guo*[3], and Y. Jiang1,2, *[1]National Dairy Engineering and Technology Research Center, Northeast Agricultural University, Harbin, Heilongjiang, China, [2]Department of Food Science, Northeast Agricultural University, Harbin, Heilongjiang, China, [3]Department of Nutrition and Food Sciences, The University of Vermont, Burlington.*

Enterobacter sakazakii is a foodborne pathogen. It has emerged as a cause of neonatal meningitis, septicemia, enterocolitis and associated with neonatal high mortality rate. In many cases, powdered infant formula (PIF) has been identified as the source of infection. The objective of this study is to discriminate 70 *E. sakazakii* isolates, separated from PIF in different areas and from processing environment, with pulsed-field gel electrophoresis (PFGE) to find the relation between sample and environment. All isolates were identified as *E. sakazakii* by biochemical profiles based on API 20E method and esculin test. In addition, PFGE was carried out with *Xba*I restriction enzyme. To obtain the best reaction conditions of PFGE, the bacteria liquid concentration was optimized. The OD value of bacteria liquid exhibited between 1.0 and 2.0 at 610 nm. The 70 isolates and 5 *E. sakazakii* type strains from ATCC or other laboratory displayed different banding patterns with PFGE analysis. There were 45 distinct pulsotypes among the 75 *E. sakazakii* strains. The result indicated that PFGE subtyping technique had very strong discriminatory power. Combining information on sample origin and pulse type, the No. 41 and the No. 44 isolated from PIF in the same region showed the same pattern. It demonstrated that both of them were from the same contamination source. Similarly, the No. 51 and the No. 53 isolates from PIF in the same area showed the same PFGE pattern. Furthermore, there were 3 strains, the No. 60 was from processing environment but the No. 71 and the No. 72 were from PIF, showed the same PFGE pattern. This revealed that the contamination of PIF was caused by processing environment. The results of this study showed that PFGE could be applied as an effective and reliable tool for distinction and tracing of *E. sakazakii* from PIF and environment. This work was supported by National Science and Technology Project (2013BAD18B11, 2012BAK17B04 and 2012BAD28B02).

Key Words: *Enterobacter sakazakii*, pulsed-field gel electrophoresis, powdered infant formula

TH225 The effectiveness of hurdle strategies consisting of pulsed light treatment and antimicrobials on the inactivation of pathogenic bacteria on cheese. L. Hsu*, B. M. Miller, and C. I. Moraru, *Cornell University, Ithaca, NY.*

Cheese products have been involved in outbreaks or recalls involving contamination with *Listeria monocytogenes* or *Escherichia coli* O157:H7. As one possible source of pathogens is post-process contamination, inclusion of a terminal decontamination step will help ensure cheese safety. Pulsed light (PL) treatment, consisting of short, high-energy light pulses, can effectively inactivate microorganisms on surfaces. This study examined the effectiveness of PL on inactivation of *E. coli* ATCC 25922 and *L. innocua* FSL C2–008 on cheese. PL was used alone or in combination with the antimicrobials nisin and natamycin, and applied directly on the cheese or through clear packaging. White Cheddar and Kraft singles were cut into 2.5 cm × 5 cm slices. *E. coli* and *L. innocua* were grown to stationary phase in tryptic soy broth and brain heart infusion at 37°C, respectively. Ten droplets of 10 µL were spot inoculated on each cheese slice, to yield initial inoculums of 5 or 7 log cfu/cm^2. Inoculated samples were dried overnight at 4°C. For treatments through packaging, low density polyethylene or commercial packaging was placed on top of the cheese sample before PL. For the combination treatments, cheese slices were dipped into 2.5% Nisaplin or 50 ppm natamycin for 2 min, air-dried for 2 min, spot-inoculated, and air-dried for 15 min. Cheese samples were exposed to PL doses of 1.1–13.2 J/cm^2. Treated samples were stomached for 2 min in Butterfield phosphate buffer, plated on selective media, and survivors enumerated by standard plate counting. Experiments were triplicated and data statistically analyzed. PL achieved 2.5–2.8 log reductions of *L. innocua* on Kraft singles and Cheddar, respectively, and 2.0–3.0 log reductions of *E. coli* on cheddar, after 3.3 and 6.6 J/cm^2. Packaging did not reduce PL effectiveness. Nisin enhanced inactivation compared with just PL. Natamycin reduced PL effectiveness by up to 1 log and thus should not be used with PL. This data suggests that PL, applied directly or through packaging, could be a realistic approach for decontamination of cheese surfaces and that nisin may further enhance its effectiveness.

Key Words: pulsed light, cheese, pathogen

TH226 Microbial assay and proximate composition of suya meat (an intermediate moisture meat) in Osun State, Southwest Nigeria. A. O. Akinwumi*, A. A. Odunsi, G. O. Adebayo, and T. O. Akande, *Ladoke Akintola University of Technology, Ogbomoso, Oyo, Nigeria.*

In an attempt to assess the influence of environment on meat quality, 72 ready-to-eat suya (a popular intermediate moisture meat) samples were collected at various major suya selling points within the 6 agricultural zones of Osun State, southwest Nigeria for microbial assay and proximate analysis. The agricultural zones are Ede, Ife, Ilesha, Iwo, Osogbo and Ikirun. Twelve samples each were collected at 2 selected local governments in each zone. The swabs were taken to the laboratory and serial dilution, inoculation of diluents into a sterile nutrient agar for incubation and catalase test, and Gram staining for characterization and identification were conducted. Findings identified the following isolates and their frequencies of occurrence as, *Staphylococcus aureus* (22.2%), *Staphylococcus saprophyticus* (11.1%), *Bacillus subtilis* (22.2%), *Klebsiella oxytoca* (5.6%), *Escherichia coli* (16.7%), *Salmonella* species (11.1%), and *Citrobacter freundi* (11.1%). *Bacillus subtilis* and *Staphylococcus aureus* were observed in all the zones of the state. The proximate composition of suya samples with the presence of the isolates compared with the control (without the presence of the microbes) showed a significant higher ($P < 0.05$) protein content (23.78 – 27.27%) and fat (34.23 – 42.79%). This has shown that there is need to improve on the hygienic processing and handling of suya to ensure safety of the consumers.

Key Words: suya, intermediate moisture meat (IMM), microbial assay

TH227 Effect of exposure to copper sulfate or zinc oxide on bacterial antibiotic susceptibility profile. A. F. Amaral[2], G. Schaefer[2], L. J. Lara[2], G. M. Preis[2], A. D. B. Melo[2], L. V. C. Girao[2], and M. H. Rostagno*[1], *[1]USDA-ARS, West Lafayette, IN, [2]Purdue University, West Lafayette, IN.*

Copper sulfate and zinc oxide have been extensively used as alternatives to antibiotics for health and growth promotion in animal production. However, there are emerging questions regarding potential cross-resistance between these compounds and antibiotics in gastrointestinal microbial populations. Therefore, an in vitro study was conducted to determine if exposure to high or low concentrations of copper sulfate (CuSO4) or zinc oxide (ZnO) affects bacterial susceptibility to antibiotics. Strains of *Salmonella* Typhimurium, *Salmonella* Enteritidis, *Escherichia coli*, *Staphylococcus aureus* and *Enterococcus faecalis* were exposed to 500, 10 and 0 ppm of CuSO4 or 2000, 10 and 0 ppm of ZnO in Mueller Hinton broth for approximately 24 h. A total of 3 independent repetitions of the study were conducted. After exposure, the minimum inhibitory concentration (MIC) for each strain was determined against a panel of antibiotics using a commercially available microdilution assay (Sensititer, Trek Diagnostic Systems). No effect on the MICs was observed when the strains were exposed to different concentrations of ZnO. However, when exposed to 500 ppm of CuSO4, the MICs for *Staphylococcus aureus* and *Enterococcus faecalis* (gram-positive bacteria) increased ($P < 0.05$), whereas when exposed to 10 ppm, the MICs did not change. Curiously, the opposite was observed with *Salmonella* Typhimurium, which had its MICs decreased ($P < 0.05$) after exposure to 500 ppm of CuSO4, whereas the MICs did not change after exposure to 10 ppm. In the case of *Salmonella* Enteritidis and *Escherichia coli*, no changes in MICs were observed after exposure to CuSO4. In conclusion, this study demonstrates that exposure to ZnO does not affect the antibiotic susceptibility profile of the strains tested, whereas exposure to $CuSO_4$ causes qualitative changes (i.e., bacterial response to antibiotics). However, it was shown that these changes are variable, not only according to the concentration of $CuSO_4$, but also according to the strain tested. Further studies are ongoing using intestinal microbial mixed populations to determine potential quantitative effects.

Key Words: copper sulfate, zinc oxide, antibiotic susceptibility

TH228 Variable antimicrobial effect of essential oils against different bacterial strains. A. D. B. Melo[2], A. F. Amaral[2], G. Schaefer[2], G. M. Preis[2], L. J. Lara[2], L. V. C. Girao[2], and M. H. Rostagno*[1], *[1]USDA-ARS, West Lafayette, IN, [2]Purdue University, West Lafayette, IN.*

Essential oils are increasingly being used as feed additives to promote health and growth in swine and poultry production. The antimicrobial activity of essential oils is widely accepted, but scarcely understood. Moreover, very little attention has been given to their use in bacterial sub-lethal concentrations. Therefore, a study was conducted to investigate the antimicrobial activity and to determine the minimum inhibitory concentration (MIC) of essential oils from *Origanum vulgare* (oregano), *Melaleuca alternifolia* (tea tree), *Cinnamomum cassia* (cassia) and *Thymus vulgaris* (white thyme) against *Salmonella* Typhimurium, *Salmonella* Enteritidis, *Escherichia coli*, *Staphylococcus aureus*, and *Enterococcus faecalis*. The MIC of the essential oils studied was determined by disk diffusion and broth dilution methods (3 independent replicates for each strain, oil and method). All essential oils tested showed antimicrobial effect against all bacterial strains, suggesting a broad spectrum against gram-positive and gram-negative bacteria. However, MICs for gram-negative bacteria were the same, or in most of the cases, lower in comparison to MICs for gram-positive bacteria, suggesting increased sensitivity to the oils tested. Overall, the white thyme oil had the strongest antimicrobial effect (0.015 - 0.06%), followed by the oregano (0.03 – 0.06%), cassia (0.03 – 0.25%) and tea tree (0.12 – 0.25%) oils. The MICs determined by broth dilution were lower than MICs determined by disk diffusion ($P < 0.05$). This study demonstrates the powerful antimicrobial effect of essential oils. However, it also shows that results need to be cautiously interpreted, taking in consideration the antimicrobial susceptibility methods applied. Even though essential oils are assumed to be safe additives, further studies are needed to better understand their effects on microbial populations. Therefore, studies on the potential development of resistance to essential oils, as well as cross-resistance to antibiotics through exposure to sub-lethal concentrations (i.e., sub-MIC) are currently in progress.

Key Words: essential oil, antimicrobial, feed additive

TH229 Clenbuterol hydrochloride residues in beef and beef liver tissues from different retailers points in Texcoco, Mexico. E. Olaya-Fernandez[1], G. Aranda-Osorio*[1], E. Maldonado-Siman[1], J. A. Cadena-Meneses[1], M. Huerta-Bravo[1], and O. Hernandez-Mendo[2], *[1]Universidad Autonoma Chapingo, Texcoco, Mexico, [2]Colegio de Postgraduados, Montecillo, Mexico.*

The objective of this study was to evaluate the risk likelihood of acquiring beef and bovine liver with concentrations above 2 µg/kg of clenbuterol (limit level from NOM-004-ZOO-1994) from different meat retailers points (i.e., street markets, butcher shops and supermarkets). There were sampled 6 commercial retailers' points for each category (36 in total). Samples were taken in November–December and April, high and low beef production seasons, respectively, and analyzed under 2 ELISA test kits (Neogen and Ridascreen). Edible tissues with concentrations above 2 µg/kg of clenbuterol (Neogen) were confirmed

by Ridascreen. The concentrations of clenbuterol were evaluated by the GLM procedure of SAS (2004) for sampling, distribution center and tissue type effects. Means were compared using the Tukey test ($\alpha = 0.05$). To determine the risk of probability, the CATMOD procedure was utilized. The evaluation of the kits was carried out with Student's *t*-test. There were differences ($P < 0.05$) due to sampling season, retailers points and tissue type. In average, the concentrations of clenbuterol in tissues collected during the high season were 1.40 µg/kg of clenbuterol, while for those collected during the low one were only 0.75 µg. Edible tissues from street markets and butcher shops had concentrations of 1.81 and 1.71 µg/kg of clenbuterol, respectively, whereas tissues from supermarkets had only 0.05 µg. Beef liver showed concentrations of 1.79 µg/kg of clenbuterol, while muscle presented only 0.58 µg. In general, the risk likelihood of obtained edible tissues with high concentrations of clenbuterol per kg of product was higher during the high than for the low beef production season, for street markets and butcher shops than for supermarkets (concentrations considered negligible), and for beef liver than for beef. The Neogen kit appears to be an economic and practical alternative to analyze clenbuterol concentrations in beef edible tissues.

Key Words: clenbuterol residue, edible tissue, risk likelihood

TH230 In vitro NDF digestion parameters differ when using a forage fiber bag. J. Goeser*[1], C. Heuer[1,2], and L. Meyer[1], [1]*Rock River Laboratory, Inc., Watertown, WI,* [2]*University of Wisconsin, Madison, Madison.*

In vitro NDF digestibility (NDFD) parameters are useful in predicting TDN, microbial protein production and energy available for milk production. Ration models use either single time point measures or digestion rates; however in vitro techniques affect digestion parameter results. Prior work found no effect of rumen fluid standardization (add primer and allow fluid to produce gas before inoculation) on digestion kinetic parameters however did not evaluate sample handling techniques (TEC). Our objective was to determine if 2 different rumen in vitro TEC yield comparable results. Sorghum (n = 1), corn silage (n = 3), legume (n = 2), and grass (n = 3) samples (dried, 1mm grind) were weighed (0.5g) either into a 125-mL flask (NO) or into an Ankom F57 forage fiber bag (BAG) for in vitro digestion. Rumen fluid was collected and standardized before inoculation. Samples were analyzed in duplicate and digested for 24, 30, 48 and 120h using each TEC. NDF was analyzed by either an Ankom^{200} forage fiber analyzer or refluxing technique. NDFD (% of NDF) was calculated as $100 \times [(NDF_{0h} - NDF_{residue})/(NDF_{0h})]$. The data were analyzed using both linear and non-linear approaches. The linear model included fixed effects of time, feed type, TEC and interactions. Rate (K_d, %/h), extent (%NDF), and lag (h) were fit with a single pool non-linear model, Extent × (1-Exp × (-k_d × (Time-Lag))), using SAS JMPv10 for each feed type. The model was fit with and without a 0h time point to assess lag differences. Parameters for NO and BAG were compared using 95% confidence intervals. Following the linear analyses, NO yielded greater NDFD estimates than BAG (46.4% vs. 40.0%, $P < 0.01$) with an interaction between TEC and feed type ($P < 0.01$). Corn silage was the greatest feed type differing by TEC (53.7% NO vs. 36.7% BAG, $P < 0.05$). The K_d did not differ by TEC when 0h was not included in the analyses (3.0%/h NO vs. 3.4%/h BAG, NS) however lag differed (−8.8h NO vs. 9.5h BAG, $P < 0.05$). When including 0h (as is the case with routine analyses), K_d differed by TEC (3.8%/h BAG vs. 2.2%/h NO, $P < 0.05$). Results suggest the forage fiber bag slows in vitro digestion when incubated in a 125ml flask and TEC interacts with feed type.

Key Words: NDF, digestion, technique

TH231 Relationship between one-seed juniper terpene concentration and herbivory by small ruminants. R. E. Estell*[1], S. A. Utsumi[2], A. F. Cibils[3], and D. M. Anderson[1], [1]*USDA ARS Jornada Experimental Range, Las Cruces, NM,* [2]*Michigan State University, Kellogg Biological Station, Hickory Corners,* [3]*New Mexico State University, Las Cruces.*

Plant secondary metabolites affect the amount of use by herbivores for several woody species. We examined the relationship between terpenoid concentrations and *Juniperus monosperma* herbivory by small ruminants. The study was part of a larger effort in which goats (n = 10) or mixed species (5 goats and 4 sheep) were allotted to 16 plots (20 × 30 m) containing one-seed juniper for 6 d during 2 seasons at 2 stocking rates. Juniper leaves were sampled from 311 saplings on the same day they were browsed. Saplings were categorized by size (small [<0.5 m], medium [0.5–1.0 m] or tall [>1.0 m]) and browsing intensity (low [<33%], moderate [33–66%] or heavy [>66%] herbivory). Juniper bark was also collected from 12 saplings during spring. Leaves and bark were analyzed for terpenoids with gas chromatography-mass spectrometry. Terpene data were pooled across species and stocking rate and ANOVA was conducted for season, sapling size, and herbivory level. The volatile profile of one-seed juniper leaves and bark consisted of 65 and 55 compounds, respectively. Total estimated terpenoid concentrations in leaves and bark were 18.3 ± 0.3 and 8.9 ± 0.8 mg/g, respectively, and the dominant terpene in both tissues was α-pinene (11.1 ± 0.2 and 7.6 ± 0.7 mg/g, respectively). Total terpenoid concentration was greater ($P < 0.001$) in spring than summer (20.6 ± 0.5 vs. 16.7 ± 0.3 mg/g, respectively) and lower ($P < 0.001$) in small saplings than medium or tall saplings (16.5 ± 0.6 vs. 19.8 ± 0.4 and 19.5 ± 0.4 mg/g, respectively). Total concentration also differed ($P < 0.001$) among all 3 browsing categories (16.1 ± 0.4, 18.7 ± 0.5, and 21.2 ± 0.6 mg/g for heavy, moderate, and light herbivory, respectively). Approximately 42% of the variation in browsing intensity could be explained ($P < 0.001$) by 12 compounds ([E]-β-farnesene, cis-sabinene hydrate, bornyl acetate, γ-eudesmol, germacrene A, γ-cadinene, α-pinene, [Z]-β-ocimene, terpin-4-ol, cis-piperitol, cis-p-menth-2-en-1-ol, and camphene hydrate). Our results indicate that the terpene profile of one-seed juniper is related to sapling size, season, and degree of use by sheep and goats.

Key Words: goat, sheep, terpene

TH232 In situ dry matter disappearance of bermudagrass and sudangrass hays harvested at different time of the day. G. Scaglia*[1] and H. T. Boland[2], [1]*LSU Agricultural Center, Iberia Research Station, Jeanerette,* [2]*Mississippi State University, Prairie Unit, Prairie.*

Rates of in situ DM degradation of forages were estimated from samples taken on d 75 of the experimental period at 7 AM and 4 PM. Forage samples from 'Hayking' and 'Piper' sudangrass and common bermudagrass were incubated in the rumen of 4 ruminally cannulated beef heifers (BW = 460 ± 12 kg) for 0, 2, 4, 8, 12, 24, 36, 48, 72, and 96 h. Heifers grazed on 'Alicia' bermudagrass for 15 d prior and during the experimental period. Forage samples were ground through a 2 mm screen and 5 g placed in Dacron bags in duplicate at each time. Bags were placed in mesh bags, incubated in the rumen, taken out of it at the specified time, and frozen. All bags were then thawed and placed in a washing machine (zero-h bags too). Bags were then placed in an oven at 50°C for 48 h and weighed for DM disappearance. Degradation data for DM were fitted to the nonlinear regression model: $P = A+B(1-e^{-Ct})$ using the NLIN procedure, where P = proportion (%) of DM degraded at time t, A = readily digested fraction, B = slowly digested fraction, A+B = total potentially digestible fraction, C = rate of digestion for the slowly digested fraction, and *t* = time of incubation. Effective degradability was estimated as: $a+[(b*c)/(c+k)]e^{(-k*L)}$ assuming a passage rate of 0.03. Data were analyzed using PROC GLM and means separated using Tukey's. Fraction A was different ($P = 0.02$) between 'Hayking' (7.85%) harvested in the PM and bermudagrass harvested AM (4.48%). Regardless of time of day at harvest bermudagrass presented the greatest ($P < 0.05$) fraction B (63.1%), its degradability (7.7%/h), and effective degradability (ED of 48.5% at constant Kd) whereas for the other grasses these parameters were similar (B = 52.7 and 45.8%, C = 5.3 and 6.17%/h, ED = 38.3 and 35.7%, for 'Hayking' and 'Piper', respectively). The A fractions in 'Hayking' sudan and bermudagrass were greater ($P < 0.05$) in hay cut in the PM (7.8 and 6.4%, respectively) compared to the AM cutting (5.6 and 4.5%, respectively) but not ($P = 0.32$) for 'Piper' sudan (6.8 and 6.7% for AM and PM, respectively). No differences ($P > 0.05$) in B were detected across forages. In this study,

bermudagrass had better kinetics parameters for the slowly digested fraction than sudangrass varieties

Key Words: bermudagrass, in situ, sudangrass

TH233 Tillering dynamics in Marandu grass pasture submitted to different grazing intensities under continuous stocking. S. S. Santana*[1], L. F. Brito[1], P. M. de Franca[1], U. Bragiato[1], M. E. R. Santos[2], A. C. Ruggieri[1], and R. A. Reis[1], *[1]Faculdade de Ciencias Agrarias e Veterinarias/UNESP, Jaboticabal, SP, Brazil, [2]Universidade Federal de Uberlandia, Uberlandia, MG, Brazil.*

The effect of grazing intensities on tillering dynamics in *Brachiaria brizantha* 'Marandu' pasture was evaluated at FCAV/UNESP, Jaboticabal City, São Paulo State, Brazil, from December 2010 to May 2011. Three grazing intensities, defined by sward heights of 15, 25 and 35 cm, were evaluated in early (ES) and late summer (LS). The heights were maintained by young Nellore bulls grazing under continuous stocking. The treatments were distributed in a completely randomized design with 4 repetitions (paddocks). Three areas (0.0625 m^2 each) were delimited in each experimental unit, representing the average initial condition of the pasture. At the beginning of the evaluation, all tillers within the frames were counted and marked with colored plastic coated wire. Every 30 d, all tillers were counted again and the new tillers were marked with wire of different color. These data allowed calculating the tiller appearance rate (TAR) and tiller death rate (TDR). The model for TAR and TDR included the effects pasture height and period of summer, compared using Tukey's test. Mean values for TAR and TDR were 50.3% and 16.4% in ES and 32.4% and 5.7% in LS, respectively. These results characterized higher tiller renovation in marandu pasture in the beginning of the summer ($P = 0.0220$ for TAR and $P = 0.0001$ for TDR). Grazing intensities did not affect TAR ($P = 0.3010$, mean value of 42%) since this characteristic is controlled by leaf appearance rate, insensible to defoliation. Higher stocking rates (sward of 15 cm) resulted in higher TDR ($P = 0.0213$), especially in ES. In LS, TDR in shorter sward height was higher than in the 35 cm height ($P = 0.0993$), solely. Grazing intensities affect the dynamics of the tillering with higher tiller renovation in smaller sward height.

Key Words: management, tiller appearance rate, death appearance rate

TH234 Effect of harvesting date on chemical composition and in vitro digestion of buffelgrass (*Cenchrus ciliaris* L.) during autumn in Northeastern Mexico. N. C. Vásquez Aguilar*[1], H. Bernal Barragán[1,3], R. G. Ramírez Lozano[1], M. A. Cerrillo Soto[2,3], M. V. Gómez Meza[1], E. Gutiérrez Ornelas[1,3], and M. Guerrero Cervantes[2,3], *[1]Universidad Autónoma de Nuevo León, San Nicolás de los Garza, Nuevo León, México, [2]Universidad Juárez del Estado de Durango, Durango, México, [3]Red Internacional de Nutrición y Alimentación en Rumiantes, México.*

The aim of this study was to evaluate the nutritive value of buffelgrass grown in the semiarid region of Northern Mexico. Twenty one samples were randomly collected emulating the feeding behavior of cattle, from September through December 2012, from several undisturbed grazing sites at Marin, Mexico, a county with dry climate, an annual avg. temperature of 23°C and 530 mm rainfall. Contents of crude protein (CP) and carbon (LECO), hemicellulose, cellulose, lignin, and ether extract (EE) were determined. The in vitro dry matter digestibility (IVDMD; Daisy^{II}, ANKOM), and in vitro gas production (GP, glass syringes) were measured. Metabolizable energy (ME) was calculated from GP, CP, and EE. Data were analyzed in a completely randomized design with ANOVA. Nutritional value varied ($P < 0.05$) among samples, with extreme CP values measured in late September and November (12.9 and 3.4% DM; $P < 0.05$). Carbon content decreased ($P < 0.05$) from September to October (46.7 to 43.8% DM) and from November to December (47.0 to 45.0% DM). No differences ($P > 0.05$) were found in EE (avg. 2.1% DM). Hemicellulose decreased ($P < 0.05$) from September to December (29.2 to 23.4% DM). Cellulose was higher ($P < 0.05$) in September than October (31.4 vs. 23.8% DM) and in November than December (33.0 to 26.1% DM). Lignin was highest ($P < 0.05$) in September than thereafter (9.8 vs. avg. 6.6% DM). Values for IVDMD (mean 66.7%), in vitro gas production at 24 h incubation (mean 30.6 mL/200 mg DM), and ME (avg. 6.9 MJ/kg DM) were lowest ($P < 0.05$) in September (54.9%, 24.6 mL/200 mg DM, and 5.9 MJ/kg DM, respectively) and highest ($P < 0.05$) in December (72.6%, 36.7 mL/200 mg DM, and 7.7 MJ/kg DM, respectively). Cellulose ($r = -0.775$), C:N ratio ($r = -0.713$), and Hemicellulose ($r = -0.615$) correlated negatively ($P < 0.05$) with IVDMD. Cellulose ($r = 0.793$) and NDF ($r = 0.593$) correlated positively ($P < 0.01$) with C:N ratio. In conclusion, buffelgrass collected in December had the highest nutritional value, in terms of CP, IVDMD and ME, for grazing ruminants.

Key Words: buffelgrass, chemical analysis, in vitro digestibility

TH235 Production of *Panicum maximum* Jacq. cultivars under two defoliation strategies. V. L.N. Brandao*, D.M. Fonseca, M. Williame, and C. G. Vitor, *Universidade Federal de Vicosa, Viçosa, MG, Brazil.*

Colonião and Sempre-Verde are forages that used to be widely used in Brazil, while Mombaça and Tanzânia are results of intense genetic breeding. Thus, the objective was to evaluate the production of 4 *Panicum maximum* cultivars submitted to different defoliation strategies. The experiment was conducted at Universidade Federal de Viçosa, Brazil, and it lasted 12 mo. The treatments consisted in 4 *Panicum maximum* cultivars (Mombaça, Tanzânia, Colonião and Sempre-Verde) evaluated by a pre-graze of 95% light interception (LI) by the canopy, or calendar days (28 d). The experiment was conducted as a split-plot design, in randomized blocks, with 3 replications. The forage mass was sampled on condition of pre-defoliation in representative locations of the experimental unit. For the treatments managed with 95% LI, the post-grazing residue was 50% of the canopy's height, and for the treatments based on calendar days the grazing residues were 40, 45, 35 and 30 cm for Mombaça, Colonião, Sempre–Verde and Tanzânia, respectively. The samples were manually separated into leaf, stem and dead material. Each sample was weighed and oven-dried at 55°C. Data were grouped into rainy or dry season. During the rainy season, it was observed that Colonião had the greater total dry mater (TDM) production ($P = 0.026$), and the management had influence on it, while Sempre-Verde had the greater TDM production during dry season ($P = 0.001$). Mombaça and Colonião had the greater leaf dry matter production ($P = 0.038$), especially when using 95% LI management as pre-grazing. Mombaça had the lowest stem dry matter production (SDM) during both seasons ($P < 0.05$). The dead material dry matter production was greater for Colonião ($P < 0.05$). Sempre-Verde had 80% of production during the rainy sea son and others had 90%. Therefore, while Sempre-Verde had the worst productivity, it had the lowest seasonality, which gives it an opportunity to be used during the dry season. In conclusion, it is suggested to use Colonião and Mombaça during rainy season, managed using 95% LI by the canopy as pre-grazing criteria, as this management had better results for every desirable feature.

Key Words: light interception, *Panicum maximum*

TH236 Tiller weight and tiller and branches density in tropical pastures of *Brachiaria brizantha* 'Marandu' mixed with *Arachis pintoi* 'Belmonte'. O. A. A. Lopes de Sa, G. S. Sant'ana, L. G. Freitas, A. D. Rosa, D. R. Casagrande, M. A. S. Lara, A. R. Evangelista, and T. F. Bernardes*, *University of Lavras, Lavras, Minas Gerais, Brazil.*

To improve the efficiency of forage production in mixed pastures it is necessary understand the interrelationships among grass tillers and legume branches in the sward. Variations in canopy structure caused by different sward height reflect in changes on dynamics of growth. The aim of this study was to evaluate the variation in tiller weight (TW) and tiller density of grass (TD) and branches of legume (BD) in sward of *Brachiaria brizantha* 'Marandu' mixed with *Arachis pintoi* 'Belmonte', mechanically harvested to 10, 20, 30 and 40 cm height, during 2012 fall, winter and spring. The experimental area was located at University of Lavras (21° 14′S; 45° 00′W), Brazil. The experimental units (10 m^2 plots) were arranged in a randomized complete block design with 4 replications. For TW, the plants were clipped at ground level. For counting of tillers, they were divided in basal tillers (emitted from the soil), aerial (vegetative tillers formed from axillary bud), and reproductive. The PROC MIXED of SAS was used to analyze the data. The TW, TD basal, aerial and reproductive varied as a function of interaction between sward heights and season ($P < 0.05$). In fall and winter seasons the TD reproductive increased linearly with increase in canopy height. This response was similar for winter and spring in the variables TW and TD aerial, being that TW varied of 1297 mg in winter for 891 mg in spring for canopies of 40 cm height, indicating that the inflorescences increased the TW in winter. In spring, the data were adjusted in a linear equation for TD basal. The TD basal decreased with increasing sward height, indicating that pastures of palissadegrass have a compensation mechanism TW/TD where highest densities are associated with small tillers and vice versa. For the variable BD, there was effect of sward height, and the BD set up a quadratic equation, with lower values for height of 40 cm, being that while 10 cm sward had 47 branches/m^2, 40 cm sward had 10 branches/m^2. Pastures with smaller height enable better conditions for development of *Arachis pintoi* in mixed systems.

Key Words: mixed sward, tropical grass, tropical legume

TH237 Yield and nutritional quality of deferred sorghum hybrids. S. P. Lagrange[1], H. M. Arelovich*[2,3], J. P. Vasicek[2], R. D. Bravo[2,3], and M.F. Martinez[2], *[1]INTA EEA Bordenave, Bordenave, Buenos Aires, Argentina, [2]Departamento de Agronomia, Universidad Nacional del Sur, Bahia Blanca, Buenos Aires, Argentina, [3]Comision de Investigaciones Cientificas (CIC), Bahia Blanca, Buenos Aires, Argentina, [4]CERZOS-CONICET, Bahia Blanca, Buenos Aires, Argentina.*

Forage deferral should improve winter food availability and quality for cow-calf grazing systems of semiarid Argentina. The objective was to determine morphometric characteristics, biomass yield and nutritional quality of forage harvested from sorghum hybrids (SH) as affected by deferral period through winter. SH and seed companies were: VDH 205 (grain), VDH 422 (silage), Sugargraze (forage-silage), VDH 701 (forage-photosensitive), all from Advanta; Lucero BMR (forage) from La Tijereta; and Pegual (Sudan-forage) from Génesis. SH were planted in 1.6 × 15 m-plots in a complete randomized block design. Plant density was 20, 25 and 35 plants/m^2 for grain, silage and forage SH respectively. Winter clipping intervals were 194-d (C1), 229-d (C2) and 246-d (C3) after planting on December 4. Forage was cut at 5 cm, and crude protein (CP), in vitro dry matter digestibility (IVDMD), and neutral detergent fiber (NDF) were determined. Pegual developed 44 tillers/m^2 followed by VDH 701 with 37 ($P < 0.05$). VDH701 and Sugargraze were the tallest with surpassing 270 cm in C1 and C2, staying taller VDH701 in C3 ($P < 0.05$), with the largest DM yield. Overall, a 32 % reduction in DM yield was found in C3. For VDH 205 and 422 prevailed heads (C1 and C2) increasing sheath fraction in C3. For VDH 701 and Sugargraze prevailed sheaths, as well as for Lucero and Pegual, with more heads compared to the other forage-SH. Sugargraze and VDH 701 exhibited the lowest DM content across cutting dates: 32 to 33% versus 50-60% for the other SH ($P < 0.05$). IVDMD decreased by cutting date: 60.7, 56.2 and 49.0 for C1, C2 and C3 respectively, being greater for VDH205, Sugargraze and VDH422. Sugargraze, VDH422 and VDH205 had the lowest NDF content which increased with cutting date. VDH205 had the highest average CP content (6.7%) followed by VDH422 (5.3 %) both steady across time; CP content only decreased in C3. Overall VDH422 had the best performance. SH can contribute with higher DM yield and better quality than other deferred forages to improve calf crop and land use efficiency

Key Words: sorghum, deferred forage, nutritional quality.

TH238 Influence of bacteriocinogenic lactic acid bacteria on the fermentation profile of elephant grass silage. M. P. Silva, T. C. Silva, L. D. Rufino, M. C. Agarussi, O. G. Pereira*, and H. C. Mantovani, *Federal University of Vicosa, Vicosa, Minas Gerais, Brazil.*

Lactic acid bacteria (LAB) involved in silage fermentation can produce lactic acid and compounds with proven antimicrobial activity, such as bacteriocins. In this study, bacteriocinogenic lactic acid bacteria isolated from silages of *Stylosanthes* 'Campo Grande', a tropical legume, were evaluated as potential inoculants for silages of elephant grass 'Cameroon'. The forage was ensiled in plastic bags measuring 25 × 35 cm and sealed with vacuum sealer machine. The inoculants assessed were (1) control (without inoculation); (2) commercial inoculant: Sil All (Altech, Brazil), consisting of *Lactobacillus plantarum*, *L. salivarius*, *Pediococcus pentosaceus* and *P. acidilactici*; (3) isolate *P. pentosaceus* 6.16; (4) isolate *P. acidilactici* 10.4; (5) isolate *P. acidilactici* 10.6; and (6) pool of the isolates 10.6, 6.16, and 4.10. A factorial 5 × 6 (5 inoculants × 6 fermentation periods) was used in a completely randomized design with 3 replications. The fermentation periods were: 1, 3, 7, 14, 28 and 56 d. For each fermentation period, the LAB population, silage pH and the concentration of organic acids were determined. Because the LAB population in the forage was 6.77 log cfu/g before ensiling, the rate of inoculation was 10^8 cfu/g fresh matter (FM) for all inoculants. The largest LAB population was recorded on the first day of fermentation for the silages produced with bacteriocinogenic isolates 6.10 (9.14 log cfu/g) and 6.16 (9.22. log cfu/g). An effect of the interaction inoculant × fermentation period ($P < 0.05$) was observed for silage pH. On the last day of fermentation, a higher ($P < 0.05$) pH value (4.19) was recorded in the silage inoculated with the isolate *P. acidilactici* 10.4. It was also observed an effect of the interaction inoculant × fermentation period on lactic acid concentration. In the last day of fermentation, it was recorded a higher concentration ($P < 0.05$) of lactic acid in the silage inoculated with *P. acidilactici* 10.6. These results indicate that bacteriocinogenic LAB can favor the fermentation profile of elephant grass silages, particularly the isolate *P. acidilactici* 10.6.

Key Words: antimicrobial activity, lactic acid, microbial inoculant

TH239 Using near-infrared reflectance spectroscopy as a predictor of in vitro true digestibility of bahiagrass (*Paspalum notatum*). N. L. Bell*[1], T. A. Wickersham[2], and J. L. Young[1], *[1]Stephen F. Austin State University, Nacogdoches, TX, [2]Texas A&M University, College Station.*

Our objective was to create a near-infrared reflectance spectroscopy (NIRS) calibration capable of performing predictions of in vitro true digestibility (IVTD) for bahiagrass (*Paspalum notatum*). Additionally, the calibration was developed to include predictions of moisture, NDF, ADF, and CP. Bahiagrass samples (n = 275) were collected from various locations across East Texas. Three ruminally cannulated Angus cattle provided a source of rumen fluid. Samples were run in duplicate in a Daisy^{II} incubator across a minimum of 2 rumen fluid batches to obtain an average IVTD for each sample. Samples with CV >0.05 within or among fluids (n = 12) were removed from the study to eliminate variability associated with animal differences. Values for moisture ranged from 2.6 to 9.8% with a mean of 6.6% and 1.44% SD. Values for NDF ranged from 63.6 to 80.4% with a mean of 70.9% and 3.33% SD. Values for ADF ranged from 29.5 to 48.4% with a mean of 36.7% and 3.40% SD. Values for CP ranged from 3.9 to 17.5% with a mean of 9.3% and 2.42% SD. Values for IVTD ranged from 47.8 to 87.7% with a mean of 67.7% and 5.49% SD in a Gaussian distribution. A Unity SpectraStar RTW system spectrophotometer and UCal software, developed by Unity Scientific, were utilized to develop a calibration by merging laboratory data for n = 152 samples with their respective spectral scans. Regression analysis of the calibration generated R^2 values of 0.844, 0.845, 0.907, 0.967, and 0.887 for moisture, NDF, ADF, CP, and IVTD respectively. Samples not included in the calibration set (n = 111) were scanned using the developed calibration and prediction values were compared with laboratory values to validate the calibration. The validation set yielded R^2 values of 0.144, 0.660, 0.495, 0.918, and 0.561 respectively for the same variables. Results indicated NIRS is effective in predicting CP and less effective in predicting moisture, NDF, ADF, and IVTD of bahiagrass. Calibration may be improved by collecting samples for the lower and higher IVTD value ranges to provide an equal distribution of sample data and create a more accurate prediction equation.

Key Words: bahiagrass, digestibility, near-infrared

TH240 A survey of the expected concentrations of lactic acid bacteria, pH, elapsed time in the tank, and temperature of the inoculant-water mixes used to treat silages. M. Windle*[1], C. Wacek-Driver[2], R. Kuber[3], and L. Kung Jr.[1], *[1]University of Delaware, Newark, [2]Vita Plus, Madison, WI, [3]Connor Marketing Inc.., Clovis, CA.*

A previous laboratory study showed that numbers of viable lactic acid bacteria (LAB) declined rapidly when water temperature equaled or exceeded 39–40°C. The objective of this study was to determine relationships between numbers of expected LAB and pH, ambient temperature, elapsed time in the tank, and temperature of the water that they were in during application. Inoculant-water mixes from applicator tanks (n = 53) in WI, MN, SD, and CA were sampled on–farm and immediately plated on de Man, Rogosa, Sharpe agar to enumerate LAB. Plates were incubated for 5 d at room temperature (24 - 27°C). Expected numbers of LAB were calculated from mixing rates and the minimum label guarantees. The difference between determined and expected (DD-E) numbers of LAB (log cfu/mL) was calculated and expressed in log scale. There was no relationship between pH of the inoculant-water mixture and DD-E ($P > 0.05$). Most (83%) inoculants had been mixed with water in the tank for <10 h. For these samples, there was a negative linear correlation ($P < 0.01$, $R^2 = 0.36$) between time that the inoculant-water mix was in the tank and DD-E. This suggests that numbers of LAB may be declining rapidly in tanks with time but this speculation was not directly tested. There was no correlation ($P > 0.05$) between ambient temperature at the time of sampling and DD-E. However, the temperatures of the inoculant-water mixtures were negatively correlated with DD-E ($P < 0.05$, $R^2 = 0.39$). If the DD-E for a sample was −0.3 log, this would equate to a final application rate that would be 50% less than the theoretical suggested dose. More than 30% of the samples fell into this category. Based on the current data set, a value of −0.3 log DD-E occurred when water temperatures were 33.3°C. Seven of 10 samples whose water temperature was above 33.3°C had DD-E even more negative than −0.3 log. These data support our previous findings and suggests that high temperatures of inoculant-water mixes have the potential to negatively affect the final application rate of a silage inoculant.

Key Words: forage, inoculant, silage

TH241 Biomass yield and quality of barley forage prior to ensiling as affected by fertilizer rate and harvest date. S. P. Lagrange[1], H. M. Arelovich*[2,3], F. X. Frache[2], R. D. Bravo[2,3], M.F. Martinez[2], and M. I. Amela[2], *[1]INTA EEA Bordenave, Bordenave, Buenos Aires, Argentina, [2]Departamento de Agronomia-CERZOS. Universidad Nacional del Sur, Bahia Blanca. Buenos Aires, Argentina, [3]Comision de Investigaciones Cientificas (CIC)., Bahia Blanca, Buenos Aires, Argentina.*

Planting barley (*Hordeum vulgare* L.) for the malt industry is growing in semiarid Argentina. However, barley grazing, hay production and more recently silage making is also practiced. A reduction in quality is expected after ensiling process, which could be attenuated by harvesting material of higher nutritional value. The objective was to evaluate forage yield and nutritional quality of barley ('Josefina INTA', bred for malt attributes) as affected by N fertilizer rates (NFR) at 2 grain maturity stages milky (M1) and dough (M2). Urea was applied at tillering at the rates of 0, 50, 100 kg N/ha upon 1.4 by 5 m plots allotted to a complete randomized block design. Furrows were 20 cm apart with a plant density 220 /m^2. Annual precipitation was 711.4 mm with 314.6 mm falling within the crop development period. Dry matter (DM) yield and forage content, crude protein (CP), neutral and acid detergent fiber (NDF, ADF), lignin (ADL) soluble non-structural carbohydrates (SNEC), in vitro DM digestibility (IVDMD) and metabolizable energy (ME) were determined. No interaction NFR by maturity stage was found for any variables. For DM yield no differences were found between NFR. Fertilized vs. non-fertilized crops produced 900 and 2000 kg DM/ha more for M1 and M2 respectively ($P < 0.01$). Overall quality parameters were higher for M1 harvest; however, within M2, NFR100 substantially increased CP ($P < 0.01$) with a nonsignificant trend observed for increased IVDMD. A larger DM volume with acceptable quality at NFR100 could be obtained at M2; however, the best ensiling conditions (lower DM content) and nutritive value were found harvesting at M1.

Table 1. Biomass yield and quality of barley forage with 3 rates of N fertilizer (0, 50, 100 kg ofN/ha) harvested at milky (M1) and dough (M2) stage prior to ensiling

	M1			M2		
	0	50	100	0	50	100
DM yield, kg/ha	6106^{a}	6989^{b}	6929^{b}	7324^{a}	9223^{b}	9562^{b}
DM,%	32.7^{b}	30.1^{a}	29.4^{a}	52.2	51.3	48.0
CP,%	8.8^{a}	10.4^{b}	12.3^{c}	4.8^{a}	6.8^{b}	8.9^{c}
NDF,%	51.8	52.9	54.0	61.9	60.3	59.7
ADF,%	25.9	26.7	26.4	33.5	27.6	29.7
ADL,%	3.0^{a}	3.3^{b}	4.1^{b}	5.1	5.5	5.8
SNEC,%	30.2^{b}	24.9^{a}	23.8^{a}	9.3	9.0	7.7
IVDMD,%	64.8	64.1	62.9	48.2	48.8	53.6
ME, Mcal/kg DM	2.3	2.3	2.3	1.7	1.8	1.9

^{abc}Differences within maturity stage ($P < 0.05$).

Key Words: barley, forage yield, forage quality

TH242 Protein precipitating phenolics change with herbivory and seed dispersal. C. E. Cooper*[1], H. D. Naumann[2], B. D. Lambert[4,3], and J. P. Muir[3], *[1]Tarleton State University, Department of Environmental and Agricultural Management, Stephenville, TX, [2]Texas A&M University, Department of Soil and Crop Sciences, College Station [3]Texas A&M AgriLife Research, Stephenville, [4]Tarleton State University, Department of Animal Science and Wildlife Management, Stephenville, TX.*

Protein precipitating phenolic compounds (PPP), such as condensed tannins, are hypothesized to be plant defense against herbivory. This experiment determined how PPP concentration of leaves of 2 warm-season perennial herbaceous legumes was affected by simulated herbivory. *Desmodium paniculatum* (panicled tick-clover; PTC) and *Lespedeza cuneata* (sericea lespedeza; SL) were reared in a greenhouse and subjected to one of 4 treatments: defoliation of previously undefoliated plants or successive defoliation of the upper 50, 75, and 100% of herbage regrowth of plants during vegetative stage, flowering, and seed set. The 2 species responded differently across defoliation events. Concentration of PPP remained stable or increased in PTC from vegetative stage to flowering with the exception of plants subjected to 100% defoliation in which PPP decreased ($P \leq 0.05$) compared with when they were first defoliated at vegetative stage. These plants also differed from all other treatments at flowering. All PTC treatment groups experienced a decrease ($P \leq 0.05$) in PPP between flowering and seeding. For PTC plants that had 100% of leaves removed, PPP decreased continuously and had the lowest ($P \leq 0.05$) concentration of all treatments at the third defoliation, suggesting that PTC plants defoliated at 100% might have lacked the resources to produce well-defended leaves. Concentration of PPP in SL increased ($P \leq 0.05$) in both non-defoliated control and 50% defoliated plants at flowering and remained elevated ($P \leq 0.05$) at seed set. The PPP in plants subjected to either 75 or 100% defoliation were unchanged across defoliation events. Results might correspond with seed dispersal strategies of the 2 species. Seed dispersal strategy in PTC depends primarily on epizoochory by adhering to herbivore hair, whereas SL depends on a combination of barochory and anemochory through simple seed drop. Decreasing PPP in leaves, and hence attracting herbivory, at seed maturity would be beneficial for PTC but not for SL. Results from this experiment indicate that seed dispersal strategy and stress from herbivory may play distinct roles in determining leaf PPP concentration.

Key Words: protein precipitating phenolics, herbivory, legume

TH243 Fermentation quality of maralfalfa grass (*Pennisetum* sp.) and tropical shrub foliage ensiled alone and in mixtures as feed supplements for cattle in Cundinamarca, Colombia. L. Bernal*, *Universidad de La Salle, Bogota, Colombia.*

The aim of this study was to determine the nutritional value and fermentation parameters of silages of maralfalfa (M) grass (*Pennisetum* sp) and of 3 tropical legumes *Gliricidia sepium*, *Leucaena leucocephala*, *Cratylia argentea* (G, L, C) and a non-legume shrub (T) *Tithonia diversifolia* alone and in mixtures. Nine treatments were evaluated: the 5 forages were ensiled pure (100%), and maralfalfa (40%) was mixed with shrub leaves (60%) to improve protein concentrations. Forages were harvested at the San Miguel Farm, Municipality of Paratebueno, Cundinamarca, Eastern Plains of Colombia. Treatments were stored at ambient temperature in small plastic bags of about 1 kg fresh matter in quadruplicates for a period of 42 d. At the end of the fermentation period, samples were taken for analysis of nutritional value (dry matter (DM) and crude protein (CP)) and fermentation parameters (pH, ammonia N, and relation with total N). The completely randomized trial included 9 treatments and 4 replicates of each treatment. Variables were analyzed by the procedure GLM by SAS. Nutritional quality difference ($P < 0.001$) existed among types of forage. Concentrations of DM were higher for mixtures than for pure species. *Tithonia diversifolia* and maralfalfa grass had the lowest DM (27%). Levels of CP were higher for legumes (G, L, C) 15.06 ± 0.39% and for mixtures including legumes (GM, LM, CM) 9.57 ± 0.48% in silage compared with grass or shrub alone (M, T) 4.97 ± 0.91%. Lowest pH values were achieved with *Tithonia diversifolia* and maralfalfa grass (pH 3.9 vs. 3.7), whereas *Cratylia* and *Leucanea* silages had highest pH (5.2 vs. 4.5). Mixtures had intermediate values. The legumes *Cratylia* and *Gliricidia* had highest the relationship between ammonia N/total N, and the lowest value was *Tithonia* and maralfalfa grass and their mixtures. Inclusion of tropical shrub legumes (at 60%) with maralfalfa is a good option for improving crude protein content of silages as important alternative feedstuffs to potentially enhance productivity in dual-purpose cows.

Key Words: tropical forage, nitrogen, silage

TH244 Volatile fatty acids and gas production of diets for growing calves with added yeast inoculants and fermented apple pomace. P. F. Mancillas-Flores[1], C. Rodriguez-Muela*[1], D. Diaz-Plascencia[1], G. Corral-Flores[1], Y. Castillo-Castillo[2], J. A. Grado-Ahuir[1], A. Flores-Mariñelarena[1], and A. C. Arzola-Alvarez[1], *[1]Universidad Autonoma de Chihuahua, Chihuahua, Chih. Mexico, [2]Universidad Autonoma de Ciudad Juárez, Juárez, Chih. México.*

The objective was to evaluate the effect on in vitro fermentation of diets added with yeast inoculants (YI) and fermented apple pomace (AP) for growing calves. Treatments used were T1: 1.2 kg of oat hay, 1.7 kg of corn silage and 1.2 kg calf concentrate per day as fed basis; T2: 1.2 kg of oat hay, 1.7 kg of corn silage and 1.2 kg of concentrate + 12% of fermented apple pomace; T3: 1.2 kg of oat hay, 1.7 kg of corn silage and 1.2 kg of concentrate + 2% of yeast inoculants. The concentrate was formulated with common ingredients for growing calves with 28.8% CP and 1.26 Mcal/kg of NEg. Glass bottles with sample, rumen liquid and artificial saliva were placed in a Shaker I2400 incubator to 39º C with constant shaking (67 rpm), protecting from the light during 96 h of testing period. Evaluated variables were gas production volume; VFA, ammoniac nitrogen ($N\text{-}NH_3$), and lactic acid concentration and pH. Sampling times were: 3, 6, 12, 24, 48, 72, and 96 h. VFA, $N\text{-}NH_3$, lactic acid concentration and pH were analyzed with a model including treatment and time as fixed effects. Highest gas production volume ($P < 0.05$) was in T3. VFA concentration was higher ($P < 0.05$) in T2 and T3 than in T1 (Table 1). $N\text{-}NH_3$ concentration increased, lactic acid concentration decreased and pH increased ($P < 0.05$) in T2 and T3 during sampling period. We conclude that adding YI and AP to growing calves diets increased VFA and $N\text{-}NH_3$ concentration and decreased lactic acid content.

Table 1. Volatile fatty acids concentration of growing calves diets with yeast inoculants and fermented apple pomace

	Treatment			
Variable	T1	T2	T3	SE
Acetic acid (mmol/L)	12.06[b]	16.0[a]	17.19[a]	0.90
Propionic acid (mmol/L)	3.52[b]	6.54[a]	6.13[a]	0.75
Butyric acid (mmol/L)	1.21[b]	2.63[a]	2.67[a]	0.41
Gas volume at 24 h (mL/0.2 g of DM)	1.97[b]	3.40[a]	4.20[a]	0.22
$N\text{-}NH_3$ (mmol/mL)	0.18[b]	0.21[a]	0.22[a]	0.01
Lactic acid (mmol/mL)	2.30[a]	1.46[b]	1.37[b]	0.20
pH	6.19[c]	6.56[b]	6.74[a]	0.06

Key Words: volatile fatty acid, yeast inoculant, fermented apple pomace

TH245 Grape pomace silage characteristics and in vitro digestibility with or without recycled poultry bedding. M. Basalan*[1] and F. N. Owens[2], *[1]Kirikkale University, Faculty of Veterinary Medicine, Department of Animal Nutrition, Kirikkale, Turkey, [2]Pioneer Hi-Bred International, Johnston, IA.*

To evaluate silage quality of grape pomace ensiled with recycled poultry bedding and waste (RPB) and its degradation in vitro, grape pomace samples obtained from local wineries were ensiled without or with 10, 20 or 40% RPB obtained from local broiler producers that had been processed and deep stacked. Materials were ensiled in 1 L mini-glass-silos and fermented for 45 d at room temperature. Silage characteristics measured included dry matter disappearance during ensiling, pH, acetic and butyric acid levels, and total bacteria and yeast concentrations. Additionally in vitro dry matter and neutral detergent fiber disappearance were determined with silages produced. Dry matter (DM) content of silages increased linearly ($P < 0.05$) with addition of recycled poultry bedding to grape pomace. The pH was elevated with linear effect by addition of poultry bedding and ranged from 3.97 to 4.75 with 0% to 40% RPB ($P < 0.05$) In contrast, DM loss during ensiling decreased ($P < 0.05$) with the addition of RPB. Acetic acid and butyric acid levels that reflect negatively on silage quality increased linearly ($P < 0.05$) with the addition of RPB. Total numbers of bacteria and yeast were not affected by the addition of RPB. In vitro dry matter and neutral detergent fiber disappearance were not affected ($P > 0.05$) by the addition of poultry waste. In conclusion, grape pomace ensiled with 10% to 20% recycled poultry waste should reduce acceptability problems with RPB though palatability and safety issues need further research attention.

Key Words: grape pomace, silage, recycled poultry bedding

TH246 Improvement of tall wheatgrass biomass yield and quality by intercropping with two legumes. M. Menghini[1], H. M. Arelovich*[1,2], S. P. Lagrange[3], M. Quintana[2], and A. Galassi[2], *[1]Comision de Investigaciones Cientificas, Bahia Blanca, Buenos Aires, Argentina, [2]Departamento de Agronomia-CERZOS, Universidad Nacional del Sur, Bahia Blanca, Buenos Aires, Argentina, [3]INTA EEA Bordenave, Bordenave, Buenos Aires, Argentina.*

Tall wheatgrass (*Thinopyrum ponticum*, Pdop.) is a drought resistant perennial grass seeded in Argentina on saline soils for cattle grazing. Intake and nutritional quality are the main constraints to animal performance. The objective was to evaluate the effect of intercropping legumes in a stand of tall wheatgrass on dry matter (DM) availability (DMA) and yield (DMY), as well as quality of the grass. Treatments were: CON (control); HV, intercropping hairy vetch (*Vicia villosa*) or WS, white sweetclover (*Melilotus albus*). On March 27, 2012 a chisel plow plus a land roller were run on plots marked on the tall wheatgrass paddock. Two days later HV and MA were seeded at 13 and 7 kg/ha in 3 replicates per treatment. Two cuts were performed in spring upon all treatments at fixed dates: 176 (C1) and 219 (C2) d after seeding. Neutral and acid detergent fiber (NDF and ADF), acid detergent lignin (ADL) and in vitro DM digestibility (IVDMD) were measured by random samples of 1 m^2 cut at 3 cm height on each plot. The disk method was used to estimate DMA at beginning of internodes elongation. All data was analyzed by ANOVA and means were separated by LSD ($\alpha = 0.05$), except for DMA which was subjected to regression analysis. In C2, DMY increased ($P = 0.02$; SE = 145) for VH (1354 kg/ha) compared with CON (597 kg/ha). Overall DMY were: 1521, 1792 and 2583 kg/ha for CON, SW and VH respectively ($P = 0.09$; SE = 296). A higher DM content was observed for CON = 47.6% compared with 32.6 and 33.7% for SW and HV, respectively ($P = 0.04$; SE = 3.6). Nonsignificant trends for NDF and IVDMD ($P = 0.07$ and 0.13, respectively) indicated a reduction in cell wall content of tall wheatgrass and improvement of IVDMD because of legume intercropping. No differences were observed for ADF and ADL. DMA = 129.51x – 453.92; 106.1x + 346.94 and 108.3x – 231.62, with $R^2 = 0.91$, 0.63 and 0.60 ($P < 0.01$) for CON, VH and SW, respectivel, were the calculated regression equations and respective correlation coefficients. These results suggest that overall DMY and quality of tall wheatgrass can be improved by legume intercropping. DMA seems more precisely estimated in pure stands of tall wheatgrass.

Key Words: tall wheatgrass, intercropping, legume

TH247 Agronomic performance and nutritional assessment of three varieties of *Brachiaria* and *Panicum*. M. Medina-Villacis*[1], I. Espinoza-Guerra[2], M. Samaniego-Armijos[1], J. Mackencie-Alvarez[1], L. Rizzo-Zamora[1], G. Suárez-Fernández[1], and A. Haro-Chong[1], *[1]Unidad de Estudios a Distancia, Quevedo, Los Rios, Ecuador, [2]Facultad de Ciencias Pecuarias, Quevedo, Los Rios, Ecuador.*

The objective of the research was to evaluate the agronomic performance and nutritional assessment of 3 varieties of *Panicum* and *Brachiaria* in different stages of maturity. A factorial arrangement 6 × 4 with 4 replications within a randomized complete blocks design (RCBD) was applied. The analyzed factors were: (A) 6 forage varieties (common forage, Tanzania, Tobiata, B. brizantha, B. decumbens and B. mulatto) and (B) 4 cutting ages in days (21, 42, 63, and 81 d).The evaluated variables were biomass feedstocks (BF) (kg DM/ha), weight of leaves (g), weight of stems (g), leaf length and width (cm), leaf:stem ratio, and chemical composition. The greater weight of leaves was shown by common forage with 159 g at 21 d, by Tobiata forage at 42 and 63 d with 1264 and 1527 g, respectively, and by common forage at 84 d with 1494 g ($P \leq 0.05$). The greater weight of stems was for Tobiata forage at 21, 42, and 63 d with 282, 1527, and 1867 g, respectively, whereas at 84 d the best results were obtained in the Tanzania forage with 2218.5 g ($P \leq 0.05$). The highest leaf:stem ratio was shown by the B. Decumbens forage at 42 d with 1.6 followed by *B. brizantha* forage at 21 d with 1.0, B. Mulatto forage at 63 d with 0.92, and Tobiata forage at 84 d with 0.99. The longer length of leaf ($P \leq 0.05$) was for Tobiata forage with 72.5, 89.1, 95.3, and 89.6 cm, at the 4 stages of maturity analyzed. The leaf width that stood out was for Tobiata forage at 21, 42, 63, and 84 d with 3.5, 3.0, 3.5, 3.5 cm, respectively. The *B. brizantha* forage presented, at 3 cutting ages, the highest number of leaves with 281 at 21 d, 489 at 42 d and 742 at 84 d whereas B. Mulatto had the highest results at 63 d ($P \leq 0.05$) with 667 leaves. The greatest level of protein was achieved by Tobiata forage (15.1%) at 21 d and by common forage at 42, 63, and 84 d ($P \leq 0.05$) with 13.5, 9.2, and 7.5%, respectively. Each of the forages examined differed in composition with advancing maturity and the relative ranking of the various forage species changed at the differing ages at harvest.

Key Words: biomass, *Panicum*, *Brachiaria*.

TH248 In situ ruminal energy degradability of three genera of tropical grasses at four regrowth ages during the rainy season in Veracruz, Mexico. H. Bernal-Barragán*[1], E. Castillo-Gallegos[2], N. C. Vásquez-Aguilar[1], C. A. Hernández-Martínez[1], J. Jarillo-Rodríguez[2], B. Valles de la Mora[2], and E. Ocaña-Zavaleta[2], *[1]Universidad Autónoma de Nuevo León, Fac. de Agronomía, General Escobedo, Nuevo León,México, [2]Universidad Nacional Autónoma de México,*

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The effect of regrowth age of tropical grasses on in situ ruminal degradability of energy was determined during the rainy season in a humid tropic area of Veracruz, Mexico. Samples of 4 grasses of genus *Brachiaria* spp. (Mulato, Chontalpo, Insurgente, and Chetumal), 3 *Pennisetum* spp. ("Cuban" king grass, Taiwan, and "Purple" king grass), and 3 *Panicum maximum* grasses (Privilegio, Tanzania, and Mombaza), cultivated in 10 m^2 plots with 0.5 m distance between plants, were cut at 10 (*Brachiaria* spp.) or 20 cm height (*Pennisetum* spp. and *Panicum* sp.) from 1 m^2 subplots at 3, 6, 9, and 12 weeks of regrowth from August to October 2008. Five gram of dried (65°C) and ground (1 mm screen) samples were weighed in triplicate into nylon bags (10 × 20 cm, 50 µm pore size) and incubated for 48 h in the ventral rumen of 3 ruminally fistulated cows. Gross energy (GE) content of the samples was measured using an adiabatic bomb calorimeter (Parr). Ruminally degraded energy was calculated considering the GE content before and after the incubation, as well as the DM-degradability of the samples. Data were analyzed as a complete randomized design with 3 × 4 factorial arrangement, (3 genera of grasses and 4 regrowth ages), utilizing SPSS. Before incubation GE of *Brachiaria* was higher ($P < 0.01$) than *Panicum* and *Pennisetum* (3900 vs. avg 3634 kcal/kg DM); GE was also highest ($P < 0.01$) at 3 and lowest at 6 and 9 weeks of regrowth (3895 vs. 3737 kcal/kg DM). There was a genus × age interaction ($P < 0.01$) for ruminal energy degradability, with values of *Panicum* decreasing from 67.4% at wk 3 to 59.0% at wk 9, and those of *Pennisetum* and *Brachiaria* remaining around ($P > 0.05$) 67.5% until wk 9, and decreasing ($P < 0.05$) thereafter to values of 58.4 and 53.6%, respectively. In situ ruminal degradability of energy (64.0%) correlated (r = 0.988; $P < 0.01$) with degradability of DM (64.9%). In conclusion, during rainy season in a hot-humid region, ruminal degradability of energy was lower for *Panicum* than for *Pennisetum* and *Brachiaria*.

Key Words: tropical grass, in situ ruminal fermentation, energy degradability

TH249 Nutritive value and fermentation quality of the silage of three kenaf (*Hibiscus cannabinas* L.) cultivars at three different growth stages. B. W. Kim*, K. I. Sung, J. G. Nejad, and J. S. Shin, *College of Animal Science, Kangwon National University, Chuncheon, Kangwon, South Korea.*

This study was conducted to evaluate the nutritive value and the quality of ensiled kenaf after fermentation with 3 cultivars at 3 different times of harvesting. Experimental plots were allocated with 3 harvest date (early; 8/3, medium; 8/15 and late; 8/28) and 3 cultivars (Tainung-a, Everglade, and Whitten). The DM yield increased with maturity in all 3 cultivars, especially in Whitten which showed the highest yield at each harvest time. The DM content in Whitten at late harvesting time was higher than other treatments (Tainung-a; 21.2 ± 1.3% DM, Everglade; 21.1 ± 1.3% DM, and Whitten; 23.1 ± 1.5% DM). The CP contents of the kenaf silage of all 3 cultivars ranged from 151 ± 9.8 to 164 ± 10.2 g kg^{-1} DM. Highest content of NDF was observed in Everglade at medium harvesting date, but the ADF content was highest in Everglade at early harvesting date ($P < 0.05$). All treatments produced a silage pH less than 4.0, which is sufficient for stable storage. However, the pH of Tainung-a was higher (3.95 ± 0.13) than other cultivars at all harvesting times ($P < 0.05$); other cultivars ranged from 3.50 ± 0.11 to 3.75 ± 0.16. Whitten had higher content of lactic acid (25.8 ± 2.25 g kg^{-1} DM) at early harvesting date than other cultivars; other cultivars ranged from 19.5 ± 2.07 to 22.5 ± 2.16 g kg^{-1} DM, whereas the acetic acid content (21.1 ± 1.98 g kg^{-1} DM) was higher in Tainung-a at medium harvesting date ($P < 0.05$); other cultivars ranged from 16.8 ± 2.01 to 18.8 ± 1.91g kg^{-1} DM. No significant difference was observed in ammonia-N and butyric acid concentrations among all treatments. These results indicate that a kenaf silage could be used as a fodder for ruminants. Especially, the Whitten harvested at late growing stage showed promise as a forage silage crop considering the higher yield and lower fiber contents under Korean environments.

Key Words: kenaf, silage

TH250 Effect of supplementing exogenous fibrolytic enzymes with cofactors on the preingestive hydrolysis of bermudagrass. J. J. Romero*[1], Z. X. Ma[1], A. A. Pech[1], C. R. Staples[1], C. F. Gonzalez[2], and A. T. Adesogan[1], *[1]Department of Animal Sciences, IFAS, University of Florida, Gainesville, [2]Department of Microbiology and Cell Science, IFAS, University of Florida, Gainesville.*

The objective was to determine the effects of adding cofactors to 5 exogenous fibrolytic enzymes (E; 1A, 2A, 11C, 13D, 15D) from *Trichoderma longibrachiatum* on preingestive hydrolysis of a 4–wk regrowth of Tifton 85 bermudagrass haylage (BH). Ground BH (1 mm; 0.5 g; 67.8, 33.9, 3.7 and 18.7% NDF, ADF, ADL, and CP, respectively) was treated in quadruplicate with nanopure water alone, each E alone or with Mn^{2+}, Co^{2+}, Fe^{2+}, Ca^{2+} and Mg^{2+}. Cofactors (C, 1mM) and 2 mL of each E solution (with 0.02% w/v sodium azide) were added to BH in culture tubes at dose rates of 4.5, 4.5, 10, 7.5 and 7.5 g /kg substrate for 1A, 2A, 11C, 13D and 15D, respectively and incubated for 24 h at 25°C. Data were analyzed as a completely randomized design with a 6 × 6 factorial treatment arrangement. The model included effects of E, C, and E × C. Water-soluble carbohydrate concentration was increased ($P < 0.05$) by adding all enzymes except 13D and further increased (E × C, $P < 0.01$) by adding Mn^{2+}, Co^{2+}, Fe^{2+}, Ca^{2+} and $Mg^{2+}$to 2A (5, 6, 10, 3, and 3%, respectively) or 11C (38, 23, 24, 15 and 13%, respectively), by adding Co^{2+} and Fe^{2+} to 15D (8, and 14%, respectively), and by adding Fe^{2+} to 1A (5%). Adding Mn^{2+}, Co^{2+}, and Fe^{2} to 13D increased WSC by 14, 15 and 23%, respectively. Adding 1A, 2A and 11C alone decreased ($P < 0.05$) NDF and ADF (%) but cofactor addition had no effect. Adding each E alone except 13D increased ($P < 0.05$) free ferulic acid (µg/g) and the response was further increased (E × C, $P < 0.01$) by adding Co^{2+} and Ca^{2+} to 2A (7 and 13%, respectively) and Mn^{2+} to 1A (8%). In contrast, free ferulic acid was reduced by adding all cofactors to 15D (7, 19, 15, 8, and 27%, respectively); by adding Mn^{2+}, Fe^{2+}, and Mg^{2+} to 2A (8, 17, 26, respectively); by adding Mn^{2+} and Fe^{2+} to 11C (3 and 9%, respectively) and by adding Mg^{2+} to 1A (10%). Cofactor addition to the enzymes increased WSC release but did not affect NDF or ADF concentrations and had variable effects on ferulic acid concentration.

Key Words: forage, enzyme, cofactor

TH251 Content of tannins and effect of polyethylene glycol on in vitro fermentation kinetics and digestibility of *Quercus hintonii* and *Quercus glaucoides* acorns and leaves. F. A. Nova*[1], J. G. F. Estrada[2], O. A. C. Ortega[3], A. R. Otero[1], and B. A. Portillo[1], *[1]Centro Universitario Temascaltepec Universidad Autónoma del Estado de México (UAEM), Barrio de Santiago, Temascaltepec, Estado de México, México, [2]Instituto de Ciencias Agropecuarias y Rurales (ICAR) (UAEM), El Cerrillo, Piedras Blancas, Toluca, Estado de México, México, [3]Facultad de Medicina Veterinaria y Zootecnia*

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This study was conducted to evaluate the content of tannins and effect of polyethylene glycol on in vitro ruminal fermentation kinetics and digestibility of leaves and acorns from the *Quercus hintonii* and *Quercus glaucoides*. The amount of total phenols (TP) was calculated as a tannic acid equivalent using the calibration curve, and total tannins (TT) were determined using polyvinyl-polypyrrolidone (PVPP), both through the Folin-Ciocalteu method. The content of condensed tannins (TC) and fiber-bound condensed tannins (FBT) was determined using the butanol/HCl/Fe^{3+} test. Fermentation kinetics, the digestibility of organic matter (IVDOM) and digestibility of neutral detergent fiber (IVDNDF) were evaluated using the in vitro gas production technique with and without the addition of polyethylene glycol (PEG 6000). A totally random design was used with a 2 × 2 factorial arrangement. With the addition of PEG, a positive effect was observed in IVDOM, IVDNDF and ME in leaves ($P < 0.001$). An increase of 60 g/kg DM in the IVDOM was noted in *Q. glaucoides* leaves. And an increase of 42g/kg DM was noted in *Q. hintonii* leaves. The IVDNDF of *Q. glaucoides* leaves increased by 89 g/kg DM ($P < 0.001$), and in *Q. hintonii* leaves, by 38 g/kg DM ($P < 0.01$). An increase of 91 g/kg DM was observed in the IVDOM of *Q. glaucoides* acorns, and an increase of 21 g/kg DM in *Q. hintonii* acorn ($P < 0.001$). The fermentation parameters of *Q. hintonii* and *Q. glaucoides* leaves improved with the addition of PEG. The *Q. glaucoides* species demonstrated greater gas production in the soluble fraction *a* (24.5 mL) and the *Q. hintonii* species demonstrated greater gas production in fraction *b* (45.4). *Q. hintonii* acorns had greater ($P < 0.01$) content of TP (289 g/kg DM), TT (284.7 g/kg DM), and CT (16.2 g/kg DM) and *Q. glaucoides* acorns had greater ($P < 0.01$) content of NPT (5.6 g/kg DM) and FBT (7.1 g/kg DM). A positive effect was observed on the leaves and acorns of the *Q. glaucoides* and *Q. hintonii* species with the addition of PEG, improving the IVDOM, IVDDF and the fermentation parameters.

Key Words: fermentation, acorn, tannin

TH252 Tropical pasture grazing management effects on in vitro rumen degradation kinetics evaluated with a semi-automated technique of gas production. M. R. Lovaglio*, J. R. R. Dorea, M. G. M. F. Santos, L. R. D. Agostinho Neto, D. F. A. Costa, and F. A. P. Santos, *University of Sao Paulo, Piracicaba, Sao Paulo, Brazil.*

The objective of this trial was to evaluate the rumen degradation kinetics and indigestible neutral detergent fiber (NDFi) in 2 different managements of Brachiaria brizantha pasture. The treatments were 2 pre-grazing heights (25 and 35 cm) corresponding to approximately 95% and 100% of light interception, respectively, and a target stubble height of 15 cm. The experimental design was in completely randomized blocks, with 4 blocks, 2 treatments and 2 replicates per treatment, constituting 16 paddocks of 0.1 ha each. Forage samples were collected on grazing horizon (15 to 25 cm and 15 to 35 cm). The NDFi in the samples was determined after 240 h of rumen incubation, and subsequent NDF analysis. The parameters of rumen degradation kinetics were estimated using the semi-automated method of cumulative gas production. The substrate (1 g) was incubated with rumen inoculum (10 mL) and bath culture (90 mL). The pressure was measured at 1, 2, 3, 4, 6, 8, 10, 12, 14, 17, 20, 24, 28, 36, 48, 72, 96 and 120 h after incubation. The rumen degradation parameters were estimated using bicompartimental logistic model and analyzed using SAS system. The final volumes of fibrous carbohydrate (121.4 mL and 119.3 mL ± 2.7 for 25 and 35 cm respectively), non-fibrous carbohydrate (107.3 mL and 100.8 mL ± 3.4 for 25 and 35 cm, respectively) and rate degradation of nonfibrous (0.0718 and 0.0735%/h ± 0.004 for 25 and 35 cm, respectively) carbohydrate (kdNFC) were not affected by grazing management. However, the degradation rate of FC decreased ($P < 0.05$) when pasture was managed with 35 cm (0.0200 and 0.0182%/h ± 0.001 for 25 and 35 cm, respectively). This result is according to NDFi values that increased ($P < 0.05$) with 35 cm management (18.8 and 21.2% ± 1.0 for 25 and 35 cm, respectively). The lag time was greater ($P < 0.05$) with 35 cm height than with 25 cm, probably from a more difficult microbial access to feed particles (5.4 and 6.0 h ± 0.2 for 25 and 35 cm, respectively). The pre-grazing height of 25 cm resulted in pastures of greater quality, and probably better quality of fibrous fraction.

Key Words: degradation kinetic, tropical pasture

TH253 Fatty acids differentially regulate expression of deiodinases in differentiated pig adipocytes. H. Yan*, W. Hanxiao, H. Lu, O. Adeola, and K. M. Ajuwon, *Purdue University, West Lafayette, IN.*

Deiodinases regulate several aspects of thyroid hormone metabolism. Deiodinase 2 (DIO2), a selenoprotein, activates thyroid hormone by converting the prohormone thyroxine (T4) by outer ring deiodination (ORD) to bioactive 3,3′,5-triiodothyronine (T3). Three deiodinases, DIO1, DIO2 and DIO3 are expressed in pig adipose tissue. However, only DIO2 is believed to be involved in thyroid hormone activation, whereas DIO3 inactivates thyroid hormone by inner ring deiodination of T3 and T4 to inactive metabolites, 3,3′,5′-triiodothyronine (RT3) and 3,3′-diiodothyronine (T2), respectively. DIO2 results in activation of oxidative genes such as acyl CoA oxidase (ACO) and peroxisome proliferator-activated receptor gamma co-activator 1-α (PGC1α) and promotes muscle differentiation. DIO3 is an imprinted gene and a candidate gene for litter size in pigs. Because of these important functions, we investigated the expression of these genes in adipose tissue of neonatal piglets and in differentiated adipocytes. Expression of DIO2 is several fold higher than that of DIO1 and DIO3. DIO2 expression was higher (2 fold, $P < 0.05$) in the adipose tissue of piglets with normal average birth weight vs. light weight littermates. Expression of DIO2, but not DIO1 and DIO3, increased during adipocyte differentiation and expression was maximal (3 fold) in fully differentiated adipocytes (D9 of differentiation) relative to preadipocytes. Differentiation of adipocytes in the presence of palmitate, oleic acid and docosahexaenoic acid (DHA) resulted in a higher (8 fold) expression of DIO2 with DHA treatment ($P < 0.05$), but not palmitate nor oleic acid. The increase in DIO2 by DHA was accompanied by a higher expression of uncoupling protein 3 (UCP3). These results show that DHA can be used to regulate thyroid hormone activation to alter the direction of metabolism and growth in pigs.

Key Words: T3, deiodinase, lipids

TH254 Comparison of growth performance and muscle fiber characteristics in different Japanese quail lines. Y. M. Choi*, S. Shin, M. P. Wick, and K. Lee, *The Ohio State University, Columbus.*

The objective of this study was to compare the growth performance and fiber characteristics of the pectoralis major muscle between the random bred control (RBC) and heavy weight (HW) Japanese quail lines to better understand the mechanisms leading to increased muscle mass. The hatch weights of the HW line were approximately 1.3 fold higher than that of the RBC line (8.15 vs. 6.43 g, $P < 0.001$). After 15 d post-hatch, the body weight (BW) and pectoralis major muscle weight (PMW) exhibited remarkable differences between the 2 quail lines. At 42 d post-hatch, the HW line was about 2.3 fold greater in the BW (232.0 vs. 100.2 g, $P < 0.001$), and had a higher percentage of the PMW compared with the RBC line (16.21 vs. 12.48%, $P < 0.001$). Color differences were observed between the superficial and deep regions of the pectoralis major muscle, the deep region showed redder and darker surface than the superficial region in both quail lines. Smaller type IIA fibers were grouped in the central area of the muscle bundle and were surrounded by larger type IIB fibers in both lines. No significant differences were observed in the total fiber numbers of the pectoralis major muscle or the numbers of superficial and deep regions between the 2 quail lines. Moreover, there were no significant differences in the cross-sectional area (CSA) of type IIB fiber between the RBC and HW lines. The HW line exhibited a greater CSA of type IIA fiber (superficial region: 239.5 vs. 122.9 μm^2, $P < 0.001$; deep region: 247.9 vs. 140.9 μm^2, $P < 0.001$) and a higher area percentage of type IIB fiber (superficial region: 75.10 vs. 46.99%, $P < 0.001$; deep region: 45.37 vs. 21.32%, $P < 0.001$) in both regions compared with the RBC line. Therefore, greater body and muscle weights of the HW quail line are result of differences in muscle fiber characteristics, especially the proportion of type IIB fiber and the CSA of type IIA fibers, compared with the RBC line. The results of this study suggest that muscle fiber hypertrophy has more of an effect on body and muscle weights of the different quail lines than muscle fiber hyperplasia.

Key Words: growth performance, muscle fiber characteristic, Japanese quail

TH255 Sequence identification of bovine microRNA in adipose tissue and their differential expression due to diet. S. K. Duckett*, M. D. Owens, and S. L. Pratt, *Clemson University, Clemson, SC.*

MicroRNA (miRNA) are small non-coding RNA which regulate adipocyte function via translational repression or RNA interference of targeted messenger RNA. The objectives of this study were to determine: 1) the identity of miRNA present in bovine adipose tissue using Illumina high-throughput sequencing technology, and 2) determine relative expression of specific miRNA by utilizing microarray procedures. Angus steers (18 mo of age and average BW of 289 kg) were finished on pasture only (PA; n = 3) or on a high-concentrate diet (C; 85% concentrate/15% roughage; n = 3). Subcutaneous fat samples (s.c.; 5 g per sample) were removed from the tail head area of each carcass at slaughter, rinsed with sterile saline, frozen in liquid nitrogen and stored at −80°C. Total cellular RNA was extracted using the mirVana miRNA Isolation Kit (Ambion, Austin, TX), with equal mass from each animal pooled and subjected to high-throughput sequencing procedures (LC Sciences, Houston, TX). MicroRNA sequences obtained from the sequencing data were used to generate custom uParaflo microfluidic arrays (LC Sciences, Houston, TX). Total cellular RNA from individual PA and C samples was used in a 3 × 3 microarray to determine differences in expression levels of specific miRNA. RNA sequencing yielded 12,143,031 mappable reads of which 8,459,286 (69.7%) mapped to the bovine genome and were identified as known miRNA (n = 606). Another 123,340 (1.0%) reads mapped to the bovine genome and are predicted to form a hairpin indicating them to be previously unidentified miRNA (n = 814). Overall, sequencing identified 1,389 miRNA of which 42 are unique to cattle. The microarray contained 1,374 unique miRNA identified from RNA sequencing. Fifty-five miRNA were differentially expressed due to diet ($P \leq 0.05$). Twenty-four and 31 miRNAs expression were decreased or increased, respectively, in the C group compared with the PA group. Therefore, multiple miRNA are expressed in bovine subcutaneous tissue and expression of specific miRNA can be altered due to diet further indicating a role for miRNA in lipid metabolism.

Key Words: microRNA, RNA sequencing, microarray

TH256 Differential expression of multiple transcripts of Agouti-related peptide in avian species and its association with nutritional status. C. Zhang*, Y. M. Choi, Y. Suh, and K. Lee, *The Ohio State University, Columbus.*

Agouti-related peptide (AgRP) is an endogenous antagonist of melancortin action. It is secreted by AgRP neuron in the arcuate nucleus, a major area of the brain to regulate food intake and energy homeostasis. Our bioinformat-

ics analysis demonstrated that there are 2 major isoforms–a- and b- isoform–in the chicken, turkey and quail. To confirm the multiple transcripts of AgRP in the avian species, we cloned the AgRP gene and localized the expression of the AgRP gene in various tissues of the chicken, turkey and quail. Both AgRP a- and b-isoform contain 3 exons in the coding sequence, but a-isoform has a unique exon in 5′ UTR. RT-PCR analysis detected the AgRP mRNA in all tissues examined: the hypothalamus, heart, liver, kidney, skeletal muscle and adipose tissues. We detected that in quails the AgRP a-isoform showed the highest expression in the hypothalamus and the adipose tissue, with an undetectable expression in the other tissues examined, but the b-isoform was not expressed in all the tissues examined. Based on our RT-PCR analysis in the quail and the sequence alignment with chicken and turkey AgRP genomic DNA sequences, there is a deletion of about 500bp on AgRP sequences in the quail, resulting in the absence of a b-isoform expression. In the turkeys, both the AgRP a- and b-isoform was variously expressed in all the tissues examined except in the liver. In addition, the fast and re-feeding experiment was applied to determine how food intake regulates the expression level of AgRP mRNA in the avian species. Interestingly, the AgRP a- and b-isoform demonstrated a differential expression pattern in the peripheral tissues and the hypothalamus, and their expression pattern changed along the different nutritional status. These results imply that the varied expression pattern of AgRP a- and b-isoform is correlated with the different promoter structures of these isoforms in the 5′ UTR, and might give us some hint to understand varied biological functions of both isoforms.

Key Words: agouti-related peptide, food intake, avian species

TH257 Regulation of bovine G_0/G_1 switch gene 2 (G0S2) and comparative gene identification-58 (CGI-58) genes. J. Ahn*[1], X. Li[1], Y. Suh[1], S. S. Hwang[2], and K. Lee[1], *[1]The Ohio State University, Columbus, [2]Rural Development Administration, Suwon, Republic of Korea.*

Adipose triglyceride lipase (ATGL) regulates the initial step of the breakdown of stored lipid by hydrolyzing triacylglycerol (TAG). ATGL has been recently shown to be inhibited by the G_0/G_1 switch gene 2 (G0S2) and co-activated by comparative gene identification-58 (CGI-58). Although regulation of ATGL-mediated lipolysis by G0S2 and CGI-58 may affect fat accretion and meat quality, G0S2 and CGI-58 have not been studied in cattle. The objectives of this study are to clone G0S2 and CGI-58 genes for cattle breeds, and to examine levels of G0S2 and CGI-58 expression in various tissues in relation to the regulation of ATGL. This study reports the cDNA and amino acid (AA) sequences of G0S2 and CGI-58 in 4 popular breeds of cattle (Angus, Holstein, Jersey, and Hanwoo; n = 2–3). The expressions of full-length and isoforms of G0S2 and CGI-58 were detected by agarose gel electrophoresis. Total gene expressions in various tissues were quantified by real-time PCR. One-way ANOVA followed by Tukey's test was used to analyze differences in G0S2 gene expression. The results revealed that full-length bovine G0S2 is 294 base pairs (bp) coding for 98 AA (substitution of Ser in Hanwoo at residue 37 and Thr in Angus at residue 64) and bovine CGI-58 is 1,047 bp coding for 348 AA (substitution of Arg in Angus at residue 56 and Val in Hanwoo at residue 120). A more significant homology (~90%) of CGI-58 cDNA and AA sequences were found between cattle and the human and mouse than in G0S2 (~60%). Two unique alternatively spliced variants were identified in CGI-58. Because both CGI-58 isoforms lack lipid droplet (LD) binding domains, both variants may not enhance the activity of ATGL via association with LD. G0S2 was highly expressed in adipose tissue and liver, and total CGI-58 was predominantly expressed in adipose tissue and muscle ($P < 0.05$). In conclusion, only full-length G0S2 and CGI-58 may be responsible for the regulation of ATGL. Considering the tissue-specific expressions, both G0S2 and CGI-58 may play important roles in adipose tissue, but CGI-58 may be more involved in the regulation of intramuscular fat in muscle than G0S2.

Key Words: cattle, lipolysis, gene regulation

TH258 Age-related changes in the expression of myogenesis-associated genes in the pig muscle. D. Loesel*[1], A. Tuchscherer[2], and C. Kalbe[1], *[1]Leibniz Institute for Farm Animal Biology (FBN), Institute for Muscle Biology and Growth, Dummerstorf, Germany, [2]Leibniz Institute for Farm Animal Biology (FBN), Institute for Genetics and Biometry, Dummerstorf, Germany.*

The number and size of skeletal muscle fibers are important aspects of postnatal growth, carcass and meat quality. Myofiber formation and hypertrophic growth depend on the proliferative activity of myogenic cells. The objective of this study was to monitor the ontogenetic expression of transcription factors associated with myogenesis. Gene expression was investigated in Semitendinosus muscle of German Landrace pigs at d 64 and 93 of gestation (dg), and at d 1, 7, 21, 28, 83, 145, 188, and 250 of age (n = 5 per age) using qPCR and immunohistochemistry (assessed over an area of 0.7–1.4 mm^2 in the cross section). Data were analyzed using the MIXED procedure of SAS with the fixed factor age taking variance inhomogeneity at the age levels into account. Expression of satellite cell marker PAX7 decreased ($P < 0.01$) from dg 64 until birth at mRNA (−82%) and protein level (−60%; given as number of positive nuclei per mm^2). MYOD declined by 50% from dg 93 until birth ($P < 0.05$) at the mRNA level and by 43% from dg 64 until birth ($P < 0.05$) at the protein level. MYOG protein decreased ($P < 0.05$), whereas mRNA expression was unchanged. From birth until d 28 PAX7 mRNA (−46%; $P = 0.09$) and protein (−60%; $P < 0.05$) were reduced. Both MYOD and MYOG mRNA were unchanged during this period, whereas MYOD (299 ± 17 vs. 62 ± 6; $P < 0.01$) and MYOG protein (321 ± 34 vs. 45 ± 11; $P < 0.05$) were reduced. Subsequently, the PAX7 and MYOD protein was lower at any age compared with d 28 ($P < 0.05$) whereas the MYOG protein was not altered. The mRNA expression of PAX7 remained unchanged until d 250, whereas MYOD mRNA ($P = 0.05$) and MYOG mRNA ($P < 0.01$) were lowered at d 188 or d 145, respectively. The reduction of PAX7 and MYOD expression from the fetal stages until birth reflects the end of the 2 waves of prenatal myogenesis in pigs. In the early postnatal period the decreasing expression of PAX7 could indicate the involvement of satellite cells in the appearance of tertiary myofibers and the subsequent increase in total fiber number. After weaning muscle growth mainly results from myofiber hypertrophy. However, decreased MYOD and MYOG mRNA expression may indicate that fiber hypertrophy has stopped around d 145 of age.

Key Words: pig, gene expression

TH259 Establishing lean and obese Mangalica pigs as a translational model for juvenile obesity and metabolic syndrome. C. F. Garrett*, R. H. Amin, C. L. Bratcher, E. P. Cambier, J. L. Bartosh, and T. D. Brandebourg, *Auburn University, Auburn, AL.*

Alabama is at the epicenter of an obesity epidemic precipitating increased incidences of type 2 diabetes and heart failure. However, no effective strategies exist for intervention or long-term prevention of obesity. To study the underlying mechanisms linking obesity and diabetes, the Mangalica pig was imported to Auburn University as a model of juvenile obesity given its extreme, early onset, morbidly obese phenotype. Obese or lean groups were created by either allowing ad libitum access to feed or restricting energy intake to 65% of ad libitum levels. Obese pigs exhibited 2.5-fold greater subcutaneous (SC) adipose tissue mass ($P < 0.001$) but no differ-

ences in muscle mass ($P < 0.39$) compared with their lean counterparts. Preliminary gene expression studies indicate leptin and TNFα mRNA expression levels were 2.1- and 2.54-fold higher in SC of obese versus lean pigs suggesting the development of inflamed adipose tissue ($P < 0.01$). Obese pigs exhibited severe fasting hypoglycemia (29 mg/dl in obese vs 67 mg/dl in lean pigs, $P < 0.01$), and altered liver enzyme levels consistent with development of hepatic dysfunction. Obese pigs also displayed impaired glucose tolerance following oral glucose challenge with 2 h glucose levels 3.2-fold higher in obese vs lean pigs ($P < 0.01$), suggesting development of obesity-induced insulin resistance. Conditions have been established to image left ventricle thickness and ongoing studies are being conducted at the Auburn University MRI Research Center to characterize the effect that emerging obesity has upon ventricular wall thickening, systolic and diastolic ejection volumes and vessel wall thickness to assess obesity-induced cardiovascular phenotypes. The melanocortin-4 receptor (MC4R) gene has been cloned from Mangalica pigs and allelic variation has been analyzed across 19 unrelated pigs to date. These data provide evidence that obese Mangalica pigs indeed have a metabolic phenotype that mimics juvenile obesity-like characteristics, as evidenced by impaired glucose homeostasis and a proinflammatory shift in gene expression that is consistent with the development of frank diabetes.

Key Words: obesity, pig, Mangalica

TH260 Selenium treatment promotes adipogenesis in chicken embryonic fibroblasts in vitro. A. Lee*, Y. Suh, and K. Lee, *The Ohio State University, Columbus.*

Poultry meat consumption has been increasing steadily worldwide due to increasing consumer demand and is of great economic value. Discovering nutritional methods to increase feed conversion to lean muscle may have great effect on the poultry industry by decreasing the cost of production. Selenium, which is a metalloid element that is necessary for proper body function, has been added to the adipogenic differentiation media to maximize the differentiation of primary pig, rat, and mouse preadipocytes into adipocytes. While it is known that selenium plays a role in preventing oxidative stress and protects against cancer, it is unknown what role selenium plays in adipogenesis. Embryonic chicken fibroblasts were cultured, grown to 80% confluence, and subsequently differentiated using an adipogenic cocktail and selenium supplementation at 0 μg/L, 37.5 μg/L, 75 μg/L, 150 μg/L, 225 μg/L, and 300 μg/L. Oil Red O staining demonstrated that selenium supplementation increases lipid droplet accumulation in a dose dependent manner. Quantitative Real-Time PCR analysis showed a dose dependent decrease in Pref-1 expression, and a dose dependent increase in PPARγ expression ($P < 0.05$), indicating increasing adipogenesis with increasing selenium supplementation. Subsequent cell number counts showed that proliferation was inhibited by selenium in a dose dependent manner. These results indicate that selenium may play a role in cell cycle regulation by inhibiting proliferation and promoting differentiation of fibroblasts to adipocytes. Microarray analysis of 2 samples from the 0μg/l and the 225μg/l selenium treatments was conducted and the results analyzed. The expression levels of many genes involved in cell cycle regulation, adipogenesis, fatty acid metabolism, and oxidative stress were significantly altered ($P < 0.05$). These results indicate that selenium plays a significant role in several mechanisms that lead to increased adipogenesis.

Key Words: selenium, adipogenesis, chicken embryonic fibroblast

TH261 Potential role of the epidermal growth factor receptor in estradiol-induced alterations in proliferation, protein synthesis, and protein degradation in bovine satellite cell cultures. B. C. Reiter*, E. Kamanga-Sollo, M. E. White, and W. R. Dayton, *University of Minnesota, St. Paul.*

Estradiol (E2) enhances muscle growth in several species; however, the mechanism by which E2 enhances muscle growth is not known. Treatment with 10 n*M* E2 stimulates proliferation and protein synthesis and inhibits protein degradation in cultured bovine satellite cells (BSC). This is particularly significant because satellite cells are the source of nuclei needed to support postnatal muscle fiber hypertrophy and are thus crucial in determining the rate and extent of muscle growth; however the mechanism(s) responsible for these E2-induced effects is not clear. Studies in other tissues have suggested that E2 may stimulate proliferation by activating the G protein-coupled estrogen receptor (GPER-1; formerly known as G protein-coupled receptor 30). Activation of GPER-1 results in activation of matrix metalloproteinases which release heparin-binding epidermal growth factor (hbEGF) from the cell membrane and released hbEGF interacts with the epidermal growth factor receptor (EGFR) resulting in increased proliferation. As an initial step in determining if this mechanism is involved in the effects of E2 on bovine satellite cell cultures, we have examined the effect of the specific EGFR tyrosine kinase inhibitor, AG1478, on the ability of E2 to affect proliferation, protein synthesis and protein degradation in BSC cultures. Treatment of BSC cultures with 10 μM AG1478 suppresses E2-stimulated proliferation ($P < 0.05$). Similarly, AG1478 treatment suppresses E2-stimulated increases in protein synthesis rate in fused BSC cultures ($P < 0.05$). In contrast, AG1478 treatment does not affect the ability of E2 to decrease protein degradation rate in fused BSC cultures. These data strongly suggest that E2-stimulated transactivation of EGFR is at least partially responsible for E2-induced increases in proliferation and protein synthesis rates in BSC cultures but is not involved in the E2-induced decrease in protein degradation.

Key Words: estradiol, satellite cell, EGF receptor

TH262 Interactive effects of zinc and ractopamine hydrochloride on β-adrenergic receptor. T. L. Harris*[1], A. D. Hosford[1], M. J. Anderson[1], C. K. Larson[2], and B. J. Johnson[1], *[1]Department of Animal and Food Sciences, Texas Tech University, Lubbock, [2]Zinpro Corporation, Eden Prairie, MN.*

β-Adrenergic receptor (βAR) agonists are commonly used in the beef cattle industry to improve growth rate, feed efficiency and carcass characteristics. A commonly used growth promoter, ractopamine hydrochloride (RH), has been shown to increase muscle hypertrophy by binding to the βAR. When activated, the intracellular βAR signal causes an increase in cAMP levels, however, many factors affect the responsiveness of the βAR. Zinc has been shown to increase βAR affinity for agonists by allosterically binding to the βAR. The objective of this study was to determine if zinc (Zn), when added in combination with RH, would stabilize the interaction of RH with the βAR, indicated by altered cAMP concentration, mRNA quantity, or protein abundance. Cultured bovine muscle satellite cells were established and treated at 120 h for 6, 24, and 96 h. Treatments were applied in a 2 × 2 factorial arrangement with 2 Zn levels (0 or 1 μ*M*) and 2 RH levels (0 or 10 μ*M*) in differentiation media. The cAMP levels were measured at 6, 24, and 96 h, while mRNA and protein were measured at 24 and 96 h. At 6 h, no differences ($P > 0.05$) were detected in cAMP levels between the treatments. However, at 24 h the 10 μ*M* RH +1 μ*M* Zn treatment had a greater concentration of cAMP ($P < 0.05$) compared with all other treatments. At 96 h the 10 μ*M* RH + 0 μ*M* Zn treatment had a lower concentration of cAMP ($P = 0.05$) compared with the control, but did not differ from other treatments. Using RT-QPCR analysis, no differences were detected in mRNA (β1 adrenergic receptor, β2 adrenergic receptor, AMPKα, myosin heavy chain I, myosin heavy chain IIA, and myosin heavy chain IIX) abundance between treatments for the genes evaluated. Protein abundance

was determined via Western blotting procedures to assess the quantity of β1 and β2 adrenergic receptors; however, no differences were detected in protein abundance between treatments. These results indicate that Zn in combination with a β-agonist, may help to sustain the response during prolonged exposure. These changes in cAMP response may prolong the biological response in skeletal muscle to β-adrenergic agonists, and appears to be independent of βAR protein abundance.

Key Words: β-agonist, cAMP, zinc

TH263 Effect of castration methods on performance of beef cattle. A. D. Moreira[1], F. D. Resende[2], G. R. Siqueira[2], J. F. Lage*[1], M. H. Moretti[1], J. M. B. Benatti[1], J. A. Alves Neto[1], R. C. Silva[1], and R. F. Marciel[1], *[1]Universidade Estadual Paulista, Jaboticabal, Sao Paulo, Brazil, [2]Agencia Paulista de Tecnologia dos Agronegocios, Colina, Sao Paulo, Brazil.*

This objective of this study was to evaluate the effect of castration methods (surgical or immunological) on performance and body weight (BW) of beef cattle fed on pasture. Thirty animals 1/2 Angus × 1/2 Nellore with 233.0 ± 38.2 kg of initial BW and 8 mo of age were fed in pasture of *Brachiaria brizantha* 'Marandu' receiving 3 g/kg BW/day of proteic-energetic supplement (25% crude protein and 60% of total digestible nutrients). Animals were supplemented for 356 d (20 d for adaptation and 336 d of experimental period), during the dry season (07/21/2011 - 11/03/2011) and the rainy season (11/04/2011 - 07/11/2012). The treatments comprised 10 replicates: non-castrated animals; surgical castrated and immunocastrated. The surgical castration was realized on last day of adaptation and the immunocastration was realized with Bopriva (anti-GnRH) being applied on the first day, 84 and 237 d after beginning of the experiment. Animals were weighted on each 42 d (maintained in collective pens and housed together in each treatment for 16 h in shrunk) to obtain the shrunk BW and average daily gain (ADG). Data were analyzed (randomly design) by the MIXED procedure of SAS and the Fisher test used considering 10% probability. Animals NC has greater ADG (0.798 kg; $P = 0.016$) than those submitted to SC (0.694 kg) and IC (0.721 kg). After 168 d of experimental period, the animals NC showed greater BW and this difference were observed until the end of experiment (522.8 kg; $P = < 0.001$) than those animals submitted to SC (490.6 kg) or IC (482.1 kg). Expectedly, the surgical or immunocastration method has a negative effect on performance of beef cattle.

Key Words: anti-GnRH, beef cattle, immunocastration

TH264 Effect of castration methods on tissue deposition of Angus × Nellore. A. D. Moreira[1], J. F. Lage*[1], F. D. Resende[2], G. R. Siqueira[2], J. M. B. Benatti[1], M. H. Moretti[1], J. A. Alves Neto[1], G. F. Berti[3], P. H. Goncalves[3], and M. A. P. Alves[3], *[1]Universidade Estadual Paulista, Jaboticabal, Sao Paulo, Brazil, [2]Agencia Paulista de Tecnologia dos Agronegocios, Colina, Sao Paulo, Brazil, [3]Centro Universitario de Barretos, Barretos, Sao Paulo, Brazil.*

This objective of this study was to evaluate the effect of castration methods (surgical or immunological) on deposition of muscular and subcutaneous fat (SF) tissues of beef cattle fed on pasture. Thirty animals 1/2 Angus × 1/2 Nellore with 233.0 ± 38.2 kg of initial BW and 8 mo of age were fed in pasture of *Brachiaria brizantha* 'Marandu' receiving 3 g/kg BW/day of proteic-energetic supplement (25% crude protein and 60% of total digestible nutrients). Animals were supplemented for 356 d (20 d for adaptation and 336 d of experimental period) during the dry season (07/21/2011 - 11/03/2011) and the rainy season (11/04/2011 - 07/11/2012). The treatments comprised 10 replicates: non-castrated animals (NC); surgical castrated (SC) and immunocastrated (IC). The surgical castration was realized on last day of adaptation and the immunocastration was realized with Bopriva (anti-GnRH) being applied on the first day, 84 and 237 d after beginning of the experiment. Animals were evaluated on beginning of experimental period and each 42 d, through the use of ultrasound. Images of ribeye area (REA) and SF were obtained and measured between the 12 and 13th ribs. Another image of SF were obtained in the intersection of the muscles gluteus medius and biceps femoris (P8FT) using the ultrasound ALOKA 500 V. Data were analyzed (randomly design) by the MIXED procedure of SAS and the Fisher test used considering 10% probability. Similar values of REA ($P = 0.519$) were observed for animals NC (70.91 cm^2), SC (66.36 cm^2) and IC (70.72 cm^2) and the daily deposition of REA ($P = 0.110$). Animals SC has greater SF (7.72 mm; $P < 0.001$) than those animals IC (5.93 mm) and animals NC (3.36 mm). Animals NC has lower P8FT (4.03 mm; $P = 0.004$) than those animals IC (7.27 mm) and animals SC (8.81 mm). Animals SC showed greater daily deposition of RFT ($P < 0.001$) and daily deposition of P8FT ($P < 0.001$) than those animals NC and IC. The castration methods do not affect the deposition of muscle tissue, but increase the deposition of SF. The surgical method is most efficient for deposition of SF in beef cattle fed in pasture

Key Words: anti-GnRH, subcutaneous fat, ultrasound

TH265 Effect of α-lipoic acid on in vitro differentiation of broiler chicks' myoblasts and adipoblasts. S. Sigler-Galván*[1], L. González-Dávalos[2], A. Shimada[2], E. Piña-Garza[3], and O. Mora[2], *[1]Programa de Posgrado en Ciencias de la Producción y de la Salud Animal, Universidad Nacional Autónoma de México (UNAM)), México City, DF, México, [2]Laboratorio de Rumiología y Metabolismo Nutricional (RuMeN), Facultad de Estudios Superiores Cuautitlán (FES Cuautitlán), UNAM, Querétaro, Querétaro, México, [3]Departamento de Bioquímica, Facultad de Medicina, Universidad Nacional Autónoma de México, México City, DF, México.*

α-Lipoic acid, a potent antioxidant, is an 8-carbon fatty acid. It is involved in mitochondrial biogenesis and in glucose uptake. In meat producing animals it has been reported to improve weight gain and carcass leanness, but it is not known whether the gain is through hyperplasia or hypertrophy of muscle and/or adipose tissue. The objective of this study was to evaluate the effect of α lipoic acid in chicken myoblast and adipoblast differentiation in vitro, by measuring the expression of myogenin, and PPARγ, respectively. Seventy one-day-old broilers (Ross × Ross strain) were slaughtered to obtain fibroblasts from muscle and adipose tissues, to start cell cultures, and differentiate them into the corresponding tissues. Cells were maintained in a proliferation medium for 4 d, until they reached a pre-confluent state (d 0). On the fifth day, the medium was changed to a differential medium (DM), and the experimental treatments were applied. One concentration (100 μ*M*) of lipoic acid was used in myoblasts; and 125 μ*M*, 250 μ*M* and 500 μ*M* into adipoblasts. At the end of differentiation, cells were harvested and total RNA was extracted from them. Single-strand cDNA was synthesized according to the manufacturer's instructions. RT was carried out using oligo (dT)12–18 primer and SuperScript II. Myogenin and PPARγ abundance measured by qPCR were used as an indicator of muscular or adipose differentiation, respectively. To normalize for the amount of cDNA, GAPDH and β-actin were amplified as the housekeeping genes, respectively. All data were analyzed using a completely randomized design. No significant differences were found ($P > 0.1$) in myogenin and PPARγ expression. The results indicate that the doses of α-lipoic acid used in this experiment did not induce myoblast or adipoblast differentiation in vitro, therefore it is suggested that the weight gain effect of lipoic acid observed in vivo was not necessarily related to cell differentiation.

Key Words: α-lipoic acid, myoblast, adipoblast

TH266 Effects of melatonin on stallion sperm motility and viability in vitro. A. Trabold[1], J. M. Reddish[1], K. Barnhart[1], M. A. Coutinho da Silva[2], and K. Cole*[1], *[1]Department of Animal Sciences, The Ohio State University, Columbus, [2]Department of Veterinary Clinical Sciences, The Ohio State University, Columbus.*

Recent research has shown that melatonin has positive effects on sperm viability during cryopreservation. Therefore, melatonin could potentially be included in commercial stallion semen extender to aid in the survival and function of fresh cooled spermatozoa. The objective of this study was to determine effects of melatonin on stallion sperm motility and viability during 48 h of storage at 5°C. In 4 separate trials, ejaculates from 3 stallions were collected and diluted to a final concentration of 500 million sperm/ejaculate with a skim milk-based extender, without antibiotics, supplemented with 0, 0.1, 1.0 or 10.0 m*M* of melatonin and stored at 5°C for 48 h. Total motility (TM), progressive motility (PM), track velocity (VCL), straight line velocity (VSL) and smoothed path velocity (VAP) were evaluated by Computer-Assisted Semen Analysis (CASA) at 0, 24 and 48 h of storage. An eosin-nigrosin stain was used to subjectively evaluate the live/dead ratio of spermatozoa at 0, 24 and 48 h of storage. Data were analyzed using the PROC MIXED procedure of SAS. TM, PM and sperm viability decreased over time ($P < 0.05$); however, there were no differences in TM and PM due to melatonin concentrations at any time point. At 48 h, the addition of 10 m*M* of melatonin to the extended semen had significantly higher PM ($P < 0.05$). At 24 and 48 h, semen extended with 10mM of melatonin had significantly decreased VCL and VAP compared with control ($P < 0.05$). VSL and VAP decreased from 0 to 24 h, but there were no differences in VSL between 24 and 48 h. Overall, addition of melatonin to stallion semen extender did not affect sperm motility and viability during storage at 5°C in this study.

Key Words: stallion, semen, melatonin

TH267 Influence of prebiotic and probiotic supplementation on apparent digestibility in mature geldings at maintenance. J. A. Coverdale*[1], E. D. Lamprecht[2], P. Kropp[3], I. Yoon[3], J. L. Lucia[1], K. N. Winsco[1], A. E. Hanson[1], and C. M. Warzecha[1], *[1]Texas A&M University, College Station, [2]Cargill Incorporated, Elk River, MN, [3]Diamond V, Cedar Rapids, IA.*

Twenty-seven mature Quarter horse geldings (465 to 663 kg BW and 4 to 24 yr old) were utilized in a randomized complete block design to evaluate effect of prebiotic and probiotic dietary fortification on apparent digestibility. Horses were blocked by age and BW and randomly assigned to treatment within block for a 28-d trial. Dietary treatments consisted of whole oats (Oat), an unfortified pellet (Control) without pre- or probiotics and inorganic trace minerals (Cargill, Inc., Elk River, MN), or the same pellet (Fortified) including a prebiotic (14 g per d *Saccharomyces cerevisiae* yeast fermentation culture dehydrated, commercial name Original XPC, Diamond V, Cedar Rapids, IA), probiotic (min 2.3 million cfu/kg feed each of *Lactobacillus acidophilus*, *Lactobacillus casei*, *Bifidobacterium bifidum*, and *Enterococcus faecium* fermentation products dehydrated), and complexed trace minerals. Dietary treatments were offered individually at 0.5% BW (as fed) in addition to 1.5% BW (as fed) of coastal bermudagrass hay (*Cynodon dactylon*) per d. Physical measurements were recorded every 7 d. The final 4 d consisted of total fecal collections. Concentrate, hay, and fecal samples were analyzed for nutrient composition an apparent digestibility determined. Data were analyzed using the PROC MIXED. Treatment means were compared using pre-planned orthogonal contrasts: pelleted concentrate vs. oats (Control + Fortified vs. Oat) and Control vs. Fortified. Rump fat, BW, and BCS were unaffected by dietary treatment. Apparent digestibility of DM, OM, CP, and gross energy was also not influenced by diet. Apparent digestibility of NDF and ADF was greater ($P = 0.03$) for horses fed pellets compared with Oat. Between pelleted concentrates, digestibility of NDF and ADF tended ($P = 0.13$) to be greater for horses fed Fortified compared with Control. In conclusion, digestibility of ADF and NDF is improved when pelleted diets are fed to mature horses and further improved with addition of prebiotic, probiotic, and complexed trace mineral preparations.

Key Words: digestibility, prebiotic, probiotic

TH268 Influence of oral glucosamine supplementation in young horses: Dietary adaptation. J. L. Lucia*[1], K. L. Gehl[1], J. A. Coverdale[1], C. E. Arnold[1], R. A. Dabareiner[1], K. N. Winsco[1], and E. D. Lamprecht[2], *[1]Texas A&M University, College Station, [2]Cargill Incorporated, Elk River, MN.*

Fourteen yearling Quarter horses (351 to 470 kg) were utilized in a randomized complete block design to evaluate absorption of supplemental dietary glucosamine hydrochloride (HCl) and incorporation into plasma and synovial fluid over 98-d. Horses were blocked by BW, age, and sex, and randomly assigned to treatment within block. Dietary treatments included control (no glucosamine HCl; CON) or 30 mg/kg BW/d glucosamine hydrochloride (HCl) powder derived from a non-GMO fungal biomass fermentation product (GLU30; 99.6% purity Regenasure powder; Cargill, Inc., Eddyville, IA). Diets consisted of CON horses (n = 7) fed 1% BW (as-fed) concentrate only or GLU30 horses fed (n = 7) the same concentrate with additional GLU30 offered at 12 h intervals. Horses were maintained in individual stalls and offered approximately 1% BW per d of coastal bermudagrass hay (*Cynodon dactylon*). Plasma and synovial fluid samples were obtained every 14 and 28 d, respectively, and stored at −20°C, before analysis of glucosamine via HPLC. Synovial samples were obtained from both radiocarpal joints and pooled. Data were analyzed using PROC MIXED procedure of SAS. Plasma and synovial glucosamine concentrations tended ($P = 0.10$ and $P = 0.06$, respectively) to increase in response to GLU30 compared with CON. There was also a treatment by time interaction ($P \leq 0.01$), with GLU30 increasing plasma glucosamine concentrations at 28 and 42 d when compared with CON. Similar to plasma, a treatment by time interaction ($P \leq 0.01$) was observed with GLU30 increasing synovial glucosamine levels at d 28 and 84 ($P \leq 0.01$ and $P = 0.05$, respectively). These results indicate that an oral glucosamine supplement is successfully absorbed and results in increased plasma and synovial fluid concentrations of glucosamine when fed to young horses.

Key Words: glucosamine, horse, synovial fluid

TH269 The availability of dietary calcium and magnesium to long yearlings and mature horses. A. L. Fowler*, L. A. Strasinger, T. L. Hansen, B. E. Harlow, S. H. Hayes, and L. M. Lawrence, *University of Kentucky, Lexington.*

When formulating requirements, the NRC (2007) assumes that growing and adult horses have the same ability to digest Ca and Mg. However, very few studies have compared the digestibilities of dietary minerals

by different aged horses. This study examined Ca and Mg digestibility of a forage:concentrate diet fed to long yearlings and adult horses. Four long yearling geldings (19 ± 1 mo; 478 ± 58.9 kg) and 4 mature geldings (10.5 ± 7.5 yr; 541 ± 45.9 kg) were randomly divided into 2 separately studied blocks, each consisting of 2 long yearlings and 2 adult horses. Horses were fed a diet of timothy cubes, alfalfa cubes and a pelleted concentrate. The diet contained 0.73% Ca and 0.25% Mg (dry matter basis). During a 14-d adaptation period, feed intake was adjusted to minimize orts and horses were accustomed to wearing fecal collection harnesses. Then for a 4-d period, total fecal output was collected from each horse. Fecal and feed samples were analyzed for Ca and Mg using atomic absorption and the results were used to calculate Ca and Mg digestibility. The effect of age on Ca and Mg digestibility was evaluated using GLM procedures (SAS 9.2). Apparent Ca digestibility tended to be lower ($P = 0.053$) for the long yearlings (37.16 ± 2.0%) than for the adult horses (42.78 ± 2.1%). Apparent Mg digestibility was not different between the 2 ages ($P > 0.05$) and averaged 39.79 ± 3.2% across the 2 groups. Endogenous fecal losses of Ca and Mg were calculated for mature and growing horses using values reported in NRC (2007) and used to estimate true digestibility. True Ca digestibility tended to be higher ($P = 0.058$) for the long yearlings (78.71 ± 1.2%) than for the mature horses (70.57 ± 3.0%). True Mg digestibility was not different between the ages ($P > 0.05$) and averaged 59.19 ± 3.2% across the 2 groups. The NRC (2007) estimates true Ca digestibility at 50% and true Mg digestibility at 40%. These results suggest that true Ca and Mg digestibility values used by NRC (2007) to calculate Ca and Mg requirements may be underestimated.

Key Words: equine, mineral, requirement

TH270 Changes in fecal microbial species richness during foal heat diarrhea. L. A. Strasinger*[1], A. L. Fowler[1], G. L. Gellin[2], M. D. Flythe[2,1], and L. M. Lawrence[1], *[1]University of Kentucky, Lexington, [2]USDA, ARS, Lexington, KY.*

Foal heat diarrhea affects many newborn foals and typically occurs between 5 and 15 d post-foaling. While this phenomenon is named for its occurrence at the time the mare has her first postpartum estrus, the actual cause is still undetermined. One theory is that foal heat diarrhea is caused by the normal colonization of the neonatal gastrointestinal tract by bacteria. We hypothesized that the fecal microbial species richness in foals experiencing foal heat diarrhea would be greater than in the same foals before diarrhea. Fecal samples were collected from foals (n = 6) 4 d post-foaling and on the first d that foal heat diarrhea was observed. Samples were frozen at −20°C immediately after collection for later analysis using PCR-denaturing gradient gel electrophoresis (PCR-DGGE). Fecal consistency was scored on a scale from 0 to 3 (0 = normal feces, 1 = soft stool, 2 = particulate bundles in a liquid base, and 3 = mostly liquid with very little particulate matter present). Foals with fecal scores above 0 were considered to have foal heat diarrhea. Microbial DNA was extracted from each fecal sample and the small ribosomal subunit (16s rRNA gene) was amplified, then subjected to DGGE using a 40–60% gradient. Comparisons of the foal fecal microbial species richness were made by enumerating bands on gels from fecal samples collected on d 4 (no foal heat diarrhea) and on the first day of foal heat diarrhea. Body weights were measured on 0, 1, 2, 3, 4, 7, 9, 11, 17, 21, and 28 d post-foaling. The initiation of foal heat diarrhea ranged from 7 to 11 d post-foaling (9.7 ± 1.6; mean ± SD) and lasted 4 ± 1.8 d. All foals had fecal scores of 3 on the first day of foal heat diarrhea. The average daily gain (ADG) for foals before the onset of foal heat diarrhea was 2.4 ± 0.6 kg/d but decreased ($P < 0.05$) to 1.1 ± 0.4 during foal heat diarrhea. Foal band count was 22.6 ± 2.4 (mean ± SE) before foal heat diarrhea however, during foal heat diarrhea band count increased ($P < 0.05$) to 32.6 ± 4.3. While foal heat diarrhea is not considered infectious, these observations suggest that this phenomenon does affect ADG and the microbial community of the hindgut.

Key Words: equine, microbial ecology, bacterial flora

TH271 Equine palmar artery, palmar vein and uterine artery express different populations of vasoactive biogenic amine receptors. D. A. Hestad[1], K. J. McDowell[1], and J. L. Klotz*[2], *[1]Deparatment of Veterinary Science, University of Kentucky, Lexington, [2]USDA-ARS FAPRU, Lexington, KY.*

Consumption of endophyte-infected (*Neotyphodium coenophialum*) tall fescue (*Lolium arundinaceum*) seed by horses causes constriction of the palmar artery (PA), palmar vein (PV) and reduced blood flow to the corpus luteum that can be measured in vivo by Doppler ultrasonography. In addition, myograph studies demonstrated that some ergot alkaloids, as well as the biogenic amines norepinephrine and 5-hydroxytryptamine, cause constriction of the PA and PV in vitro, but that the PA and PV have different contractile responses to different alkaloids. The objective of this study was to characterize biogenic amine receptors in the PA, PV, and uterine artery (UA) of horses. Immediately after euthanasia, PA, PV and UA were collected from 14 mixed breed mares. In experiment 1, transcriptomes of the PA, PV and UA were analyzed by PCR for presence/absence of adrenergic (ADR), serotonergic (5-HTR), and dopaminergic (DRD) receptor mRNAs (n = 4, 6, and 5 receptor subtypes, respectively). Of those, 2 ADR, 5 5-HTR, and 2 DRD receptor subtype mRNAs were consistently expressed. In experiment 2, relative abundance of 5-HTR subtype 1B, 1D, 2A, 2B and 7 mRNAs, as well as GAPDH mRNA, were determined using semiquantitative real-time PCR. Quantitation of mRNA expression was conducted using the relative standard curve method with expression normalized to GAPDH mRNA. Expression of receptor types differed across vessels ($P < 0.0001$). Within the PA, 5-HTR2B was more highly expressed ($P = 0.03$), while other subtypes did not differ. Within the PV, 5-HTR2A had relatively more mRNA than 5-HTR1B ($P = 0.01$). In the UA, 5-HTR2B had the greatest relative quantity of mRNA ($P < 0.0001$), while 5-HT2A had a lower relative quantity of mRNA than 5-HT2B ($P < 0.0001$) or 5-HT1D ($P = 0.0003$). Relative differences in vessel receptor types emphasize the different physiological roles of the vessels under normal physiological conditions. Additionally, different receptor types may also contribute to the different capacities of the vessels to respond to, or be protected from, vasoconstrictive effects of fescue toxicosis in horses.

Key Words: equine, fescue, vasoconstriction

TH272 Use of kainic acid as an alternative to commercially available anthelmintics in horses. K. J. Stutts*, J. L. Lucia, M. J. Anderson, S. D. Brooks, and M. L. McMillan, *Sam Houston State University, Huntsville, TX.*

Parasite management is important in any equine program. Traditionally, intestinal parasites have been controlled by the routine use of commercial equine anthelmintics. A potential alternative to these products is the use of natural plant extracts containing kainic acid. The objective of this study was to evaluate the efficacy of kainic acid in mitigating intestinal parasite load in young horses. Prior to the study, all horses were treated with fenbendazole at 6 and 12 mo of age and with ivermectin at 18 mo of age. Twelve 2-year-old Quarter horses were blocked by location in barn and randomly assigned to 1 of 2 treatments. Treatments consisted of a one-time oral dosage of 25 mg of fenbendazole per 45 kg BW (n =

6), or 60 mg of kainic acid per 45 kg BW (n = 6) provided in a pelleted seaweed extract (Acadian Seaplants, Dartmouth, Nova Scotia, Canada) that was delivered in the ration over a 5-d period. All horses were housed in 3 × 3 m stalls, were exercised daily, and received a commercially available 14% pelleted concentrate and approximately 1% BW/d of Coastal bermudagrass (*Cynodon dactylon*) hay at 12-h intervals. Fecal samples were obtained via rectal palpation at d 0 and d 7, 14, 21, 28, and 35 following treatment. All samples were stored at 4°C before fecal egg analysis via the Modified Wisconsin Sugar Flotation procedure. An ANOVA was conducted to determine differences in mean fecal egg counts (FEC) between treatments. No differences were detected in FEC between treatments except at d 35 when the mean FEC for the fenbendazole group (22.50) was lower ($P < 0.03$) than that of the kainic acid group (80.17). Maximum FEC reduction of 85.08% was observed in the fenbendazole group at d 14 post treatment, and maximum FEC reduction of 87.94% was observed in the kainic acid group at d 7 post treatment. These results indicate that the seaweed product containing kainic acid was as effective as fenbendazole in reducing FEC in 2-year-old Quarter horses throughout the majority of the 35-d trial. However, efficacy of fenbendazole may be sustained longer as mean FEC of the kainic acid group was greater on d 35 after treatment.

Key Words: horse, anthelmintic, kainic acid

TH273 Comparison of on-farm and commercial laboratory fecal egg counts to determine internal parasite status of horses.
J. L. Lucia*, K. J. Stutts, M. J. Anderson, S. D. Brooks, and M. L. McMillan, *Sam Houston State University, Huntsville, TX.*

Techniques implementing free-swing centrifugation for fecal egg analysis have been documented as superior methodology for accurate determination of parasite species and egg count. However, determining the efficacy of on-farm methodology is limited. The objectives of this study were to determine the effectiveness of 2 commercially-available anthelmintics, and to determine the efficacy of on-farm evaluation of internal parasite status in horses. Sixteen 2-year-old Quarter horses were blocked by location in barn and randomly assigned to one of 2 treatments. Treatments consisted of a one-time oral dosage of 25 mg of fenbendazole per 45 kg BW (n = 8) or 200 µg ivermectin per kg BW (n = 8). All horses were housed in 3 × 3 m stalls and received a commercially available 14% pelleted concentrate and approximately 1% BW/d of Coastal bermudagrass (*Cynodon dactylon*) hay at 12-h intervals. Fecal samples were obtained via rectal palpation at d 0 and d 7, 14, 21, and 28 following anthelmintic dosing. All samples were stored at 4°C before fecal egg analysis. Samples were sent to a commercial laboratory (MidAmerica Agricultural Research Center, Verona, Wisconsin) and analyzed on-farm for fecal egg counts (FEC) utilizing the Modified Wisconsin Sugar Flotation procedure. An ANOVA was conducted to determine differences in mean fecal egg counts (FEC) between treatments and laboratories. Mean FEC were not different ($P > 0.11$) between anthelmintic treatments at the initiation of the study, however, ivermectin decreased ($P < 0.01$) FEC beginning at d 7 when compared with fenbendazole administration. In addition, mean FEC did not differ ($P > 0.05$) between the commercial and on-farm laboratories. These results indicate that ivermectin was more effective in reducing intestinal parasite load in 2-year-old Quarter horses than fenbendazole. Additionally, the Modified Wisconsin Sugar Flotation procedure is effective in determining internal parasite status of horses on the farm and requires minimal experience by the individual utilizing the technique.

Key Words: horses, anthelmintics, Modified Wisconsin Sugar Flotation

TH274 A survey analysis on comparative growth and reproductive performance of various sheep breeds in alpine pasture and foot hills of northern areas in Pakistan. M. Abdullah*, K. Javed, M. Mudassir, J. A. Bhatti, N. Ahmad, and U. Younas, *University of Veterinary and Animal Sciences, Lahore, Pakistan.*

To investigate perception of pastoralists and adaptation of sheep breeds in their particular environment in northern areas of Pakistan the study was carried out at Kaghan valley of Mansehra district and Haripur by interviewing 150 pastoralists using a pretested questionnaire. The data were analyzed using Epi-info program (version 6.04b) for descriptive statistics. Sheep breeds found in Naran (upland) and Haripur/Attock (lowlands) were Afghani, Kaghani, Ramghani (crossbreed) and Rambouillet (exotic). Average age at puberty for Kaghani, Ramghani, Rambouillet and Afghani breed was found to be 1.36, 1.40, 1.34 and 1.26 years, respectively. Ram replacement was done every 2 years where Afghani breed was given most preference i.e., 44.3% as compared with the other breed rams. Highest twinning rate (9.26%) was found in Afghani breed followed by Ramghani, 6.13%; Rambouillet, 4.2% and 3.81%, in Kaghani breed. Breeding season in all sheep breeds was found to be ranging from September to October with some exceptions during August, November and December with a corresponding lambing season January and February with few lambings during March and April. Average number of ewes conceived, pregnant and parturated per flock per year was higher in Kaghani breed viz. 31.4, 23.0 and 17.2, while lowest in Rambouillet being 19.0, 12.8 and 7.3, respectively. Average weight (kg) of new born lamb was found higher (2.15 kg) in Afghani breed whereas, lowest (1.61 kg) in Kaghani breed. The herders have limited access to health and production extension services and very responsive to these services for improving productive and reproductive performance of their animals.

Key Words: sheep performance, adaptability, northern Pakistan

TH275 Development and comparison of regression models for estimation of live body weight in Lohi and Hissardale sheep using mophometric measurements. M. Abdullah*, K. Javed, U. Younas, M. A. Hassan, N. Ahmad, and J. A. Bhatti, *University of Veterinary and Animal Sciences, Lahore, Pakistan.*

To develop regression models for predicting live animal body weight by linear body measurements for Lohi and Hissardale sheep, data on 762 Lohi, a mutton type and 125 Hissardale, a fine wool crossbred (Merino × Bikaneri) sheep were taken from 2 Livestock Experiment Stations and analyzed for use by small scale farmers of rural areas in Pakistan with no weighing facility. Data on body weight and various body measurements (height at withers, body length, heart girth, neck length, neck width, ear length and ear width) were taken. Animals at each station were divided into 2 groups, i.e., A and B. Group A consisted of the animals of the age of 24 mo and under where as those in group B having having the age over 24 mo. Data were analyzed using SPSS software, version 13.0, to determine the best fitted regression model for prediction of body weight. Step wise multiple regression analysis was used to evaluate these regression models. The body weight for the groups A and B for Lohi sheep was 30.83 ± 3.32, 42.63 ± 5.75 kg, while that of Hissardale in both the groups was 25.57 ± 2.94, 47.10 ± 4.41 kg, respectively. A positive correlation between the body weight and body measurements (height at wither, body length and heart girth) were found ($P < 0.001$) in groups A and B of both the breeds. The correlation coefficients between the body weight and height at withers, body length and heart girth were 0.40, 0.68 and 0.61 for group A and 0.78, 0.86 and 0.81 for group B in Lohi sheep, respectively. The corresponding correlation coefficients for these parameters in Hissardale sheep were 0.73, 0.82, 0.76 and 0.54, 0.46, 0.42 for groups A and B, respectively. All biometrical traits were fitted in the model however combination of height at wither, body length and heart girth ($R^2 = 55.8$) were best suited for the regression model whereas combination of heart girth and body length was the second most suited ($R^2 = 53.9$) for prediction of body weight

Key Words: sheep, body weight, morphometric measurements

TH276 The dairy industry in Malawi—A description of the Malawi milk bulking groups. W. G. Sindani[1,2], S. R. Neba*[1,3], M. T. Correa[1], K. L. Anderson[1], and J. C. Allen[1], *[1]North Carolina State University, Raleigh, [2]Malawi Bureau of Standards, Blantyre, Malawi, [3]Ministry of Agriculture, Salima, Malawi.*

The objective of this research was to describe the milk industry in Malawi (SW Africa) focusing on milk bulking groups (MBGs) to identify areas that need to be addressed to improve the quality and quantity of milk produced by small scale farmers. The Malawi dairy industry (primarily cow milk) is only a very small proportion of the livestock subsector and agricultural sector. Dairy farmers are categorized into large scale producers and small scale producers where small scale makes up a larger proportion and on average keeps up to 10 animals. Small-holder farmers are organized into MBGs that gather milk, store it in cooling tanks, and sell it to processors. Anecdotal evidence suggested that milk produced by farmers and subsequently collected by milk processors is of low quality. Low milk production only meets about 30% of the total capacity of processing plants. In this project, current practices were mapped to desired practices using qualitative data captured through questionnaires that were administered to farmers, representatives of the bulking centers, and participants in a focus group discussion (FGD) in which the MBG participated. The total bacteria count of raw milk was analyzed as an indicator of milk quality and the hygienic conditions under which milk was produced. Results showed that to improve the quality and quantity of milk, the dairy industry needs to move away from use of low quality breeds, lack of extension workers, poor milk marketing that is characterized by low milk prices, lack or absence of insurance on dairy animals and bulked milk, and frequent electric power failures that affect cooling of milk. High bacteria counts (3.4 and 4.7×10^7 cfu/mL in and out of collection centers) indicate that the quality of milk produced by farmers and subsequently collected by processors is of poor quality, which calls for better hygienic measures during milk production and handling. The FGD suggests the following roles for government extension workers: promote breeding to increase yields; improve on-farm milk handling and more rapid cooling; promote mastitis checking to increase milk quality and yield.

Key Words: Malawi dairy industry, milk bulking group, extension goal

TH277 Effects of a new additive on milk performance of water buffalos. M. Lohölter*, A. Lewke, A. Numsri, S. Kirwan, and B. Eckel, *Dr. Eckel GmbH, Niederzissen, Germany.*

Since the early 1990s, the global buffalo population was characterized by a constant growth approximating an annual increase between 1 and 2% and current numbers exceed 180 million head. Traditional systems

comprised draft and meat purposes but currently the production of high solid buffalo milk high increases. Milk fat content is of particular importance for derived products such as mozzarella cheese. Increases in milk yields are accompanied by similar dietary challenges as faced by other high yielding ruminants. In early lactation, energy usage often exceeds energy intake. Meeting the energy demand by an increased use of concentrate is related to a rising risk of subacute ruminal acidosis. The aim of the present study was to investigate the potential of a product based on rumen protected niacin, buffering substances and organic acids on milk yield and composition of lactating buffalos. A total of 24 multiparous lactating water buffalos (*Bubalus bubalis*) were randomly allocated to either a control group or a treatment group fed a nutritionally adequate diet. The treatment group received the basal ration supplemented with 50 g RumenProtect WB per head and day (RumenProtect WB, Dr. Eckel GmbH). In the treatment group, average milk yield was stimulated by 10%. Moreover, the supplementation of the additive was found to increase milk fat content from a high control value amounting 7.01% to 7.7% approximating a 10% rise of the milk solid most susceptible to dietary influences such as higher ruminal acetate concentrations. In conclusion, the present study demonstrated that a combined supplementation of rumen protected niacin, buffering substances and organic acids can increase yield and fat content of water buffalo milk. The inclusion of the evaluated additive in water buffalo diets may be a useful tool to improve milk performance.

Key Words: buffalo, milk yield, milk fat content

Lactation Biology II

TH278 Changes in the mechanical microenvironment of the bovine mammary gland and their effect on mammary function. J. Biet*[1], K. Stelwagen[2], J. Margerison[3], CA Poole[4], A. Cullum[1], and K. Singh[1], *[1]AgResearch Ltd., Hamilton, New Zealand, [2]SciLactis Ltd., Hamilton, New Zealand, [3]Massey University, Palmerston North, New Zealand, [4]University of Otago, Dunedin, New Zealand.*

Mammary gland engorgement leads to changes in cell morphology and has been recognized as a potential key initiator for mammary remodeling processes culminating in a decline in milk production. These changes in the mechanical forces (mechanotransduction) may initiate a cascade of signaling networks involved in mammary involution. The goal of this study is to determine the effects of physical distension of bovine mammary epithelial cells on changes in cell sensing and signaling, and the initiation of the involution process. Multiparous, non-pregnant Friesian cows (n = 8) at peak lactation (78 ± 20 DIM) were milked with prior administration of oxytocin (20 IU per cow; IM) to ensure complete milk removal. Subsequently, one rear quarter was aseptically infused with a sterile iso-osmotic (300 mOsm) saline solution equivalent in volume to 5 h worth of individual milk secretion. Fifteen hours later, mammary gland biopsies were collected from both hind quarters, with the infused and the non-infused glands respectively providing treatment and control samples. Alveolar tissue was fixed, wax embedded, sectioned at 7µm. Histological analysis (haematoxylin and eosin staining) and grading of tissue sections for degree of milk stasis and signs of involution showed morphological differences between the control and treatment tissues. While the control tissues had the appearance of lactating mammary glands, the treatment tissues showed more signs of involution ($P <$ 0.002). Moreover, qRT-PCR results showed a significant decrease in α-lactalbumin expression (1.44 fold, $P < 0.05$) indicating a decline in milk production and volume due to changes in the mechanical microenvironment. Thus, increased udder filling may play a fundamental role in the change of mammary epithelial cell shape which in turn may initiate the involution process

Key Words: mechanotransduction, mammary gland, dairy cow

TH279 Determining the effect of chronic light:dark shifts on dairy cow milk production. J. Crodian*, T. Casey, and K. Plaut, *Purdue University, West Lafayette, IN.*

Photoperiod affects milk production and growth of dairy cattle. However, mechanisms underlying responses to photoperiod are not well understood. Virtually all aspects of physiology are controlled by the circadian system, which coordinates behaviors and physiological processes with the environment. Chronic shifts in light (L), dark (D) cycle disrupt circadian system and are associated with development of metabolic disease in rodents and humans. The objective of this study was to develop a model system to study circadian disruption in dairy cows by determining the effects of exposing mid-lactation dairy cows to chronically shifting LD cycles on feed intake, milk yield, milk composition and mammary gene expression. Six first lactation Holsteins, 90 ± 7.3 d in milk were maintained on a 16 h L: 8 h D cycle and milked at 0500 h and 1600 h for 7d (control). Immediately following control period, cows were exposed to continuous cycles of 8 h L: 8 h D, but were maintained on the same milking and feeding schedule for 7d. Cows were allowed 5d of acclimation; milk yield, composition and mammary gene expression were measured during the last 48 h of each period, and differences were analyzed with paired *t*-test. Exposure to chronic 8 h LD cycles significantly depressed milk yield ($P < 0.05$; 31.5 ± 1.5 versus 30.0 ± 1.3 kg) but did not affect daily feed intake. Percent milk fat, protein and lactose were not different, but milk urea nitrogen (MUN) significantly increased (12.5 ± 0.8 versus 14.8 ± 0.6 mg/dl). On the last day of each period, mammary gene expression was measured using Q-PCR of total RNA isolated from the cytosolic components of milk fat globules. Expression of core clock gene Bmal1 was 38%, beta-casein 68%, alpha-lactalbumin 48%, fatty acid synthase 11% and acetyl CoA-carboxylase 37% of control period level ($P < 0.05$). Disruption of circadian rhythms by alternating LD cycle decreased milk production, decreased expression of genes involved in milk synthesis and increased MUN content of milk. Further, decreased BMAL1 expression supports that alterations of mammary clock genes may be part of the mechanism responsible for photoperiod induced alterations in milk production.

Key Words: photoperiod, dairy cow, milk

TH280 Lipoprotein lipase (LPL), molecular cloning, tissue expression, and regulation of milk fat synthesis in goat mammary epithelial cells. W. S. Zhao, J. Luo*, and S. L. Hu, *Shaanxi Key Laboratory of Molecular Biology for Agriculture, College of Animal Science and Technology, Northwest A&F University, Yangling, Shaanxi, China.*

Lipoprotein lipase (LPL) served as a central factor in hydrolysis of triacylglycerol and uptake of free fatty acid. However, very little data are accessible about the action of LPL on the regulation of milk fat synthesis in goat mammary gland. In this investigation, we described the cloning and sequencing of LPL gene from Xinong Saanen dairy goat mammary gland, along with a study of its phylogenetic relationships. Sequence analysis showed that LPL in goat contributes many similarities with other mammals, including sheep, bovine, human and rat. The presence of mRNA levels for LPL in goat various tissues, using RT-qPCR, revealed the highest mRNA level in the white adipose tissue, less in heart, lung, spleen, rumen, small, intestine, mammary gland, and kidney, following almost undetectable in liver and muscle, respectively. The expression profiles of LPL gene in mammary gland at early, peak, mid, late lactation stages and dry period of Xinong Saanen dairy goat was also accessed. There was a dramatic increase at early lactation, following a rapid decrease in LPL mRNA appearing at peak lactation and mid lactation compared with early lactation and then a slight increase from mid lactation to late lactation, finally arrive at lowest levels at dry period. The expression patterns of LPL were very similar by using Orlistat (an inhibitor of LPL gene) and RNAi of LPL (69% and 31%). RNAi of LPL reduced mRNA abundance of SREBP, FASN, HSL and PPARG by 16%, 17%, 32% and 82%, respectively, and accelerated the expression of PRLR and GPR41 by 266% and and 3390%, without significant effect on ACC gene. Nonetheless, by using Orlistat, the expression of HSL (58%) was dramatically downregulated and the levels of GPR41 (578%) and SREBP (243%) were upregulated sharply. Meanwhile, the level of PPARG (125%) was upregulated, together with the downregulation of ACC (18%) and PRLR (57%).

Key Words: LPL gene, goat mammary epithelial cells, Orlistat

TH281 Use of quantitative real-time PCR for diagnosis of culture negative mastitis cases. K. E. Merriman, J. Laporta, T. L. Peters, M. J. Fuenzalida, P. L. Ruegg, and L. L. Hernandez*, *University of Wisconsin, Madison.*

Mastitis is the most common health problem and greatest source of economic loss in the dairy industry. The current gold standard method for identifying mastitis-causing pathogens is through the use of microbiological testing. To treat mastitis, culturing of milk should be done as efficiently as possible to determine the bacteria causing the infection. However, culturing is not the most reliable method to find the pathogens because 25–45% of milk samples yield no bacterial growth (NBG), even after 48 h of incubation. Quantitative real-time PCR (qPCR) is one option of detecting bacterial DNA in milk samples that do not contain sufficient number of live bacteria to The objective of this study is to assess use of qPCR to detect mastitis-causing pathogens in milk samples that were determined as NBG using standard microbiological testing. Quarter milk samples were aseptically collected from cows that were diagnosed with clinical mastitis at 2 dairy farms. Initial microbiological testing was performed according to NMC specifications. Only samples that were determined to be NBG were further subjected to qPCR testing (n = 51). DNA was subsequently extracted from all milk samples. The DNA from each sample was assessed by qPCR for 9 different bacteria using primer sequences for *E. coli* (EC), *Streptococcus* spp. (SC), *Strep agalactiae* (SAg), *Staphylococcus* spp. (ST), *Staphylococcus* aureus (SAu), *Enterococcus* spp. EG), *Enterococcus faecalis* (EF), *Streptococcus uberis* (SU) and *Klebsiella pneumoniae* (KP). When probed for ST, all milk samples demonstrated a 32-fold increase in gene expression. Only 2 of the milk samples tested for EC demonstrated a 5-fold increase in EC. When tested for EF and KP only one of the samples had increases in gene expression of 2- and 5-fold, respectively. When samples were tested for SU, SAg, EG, and SAu there were no changes in gene expression detected. Despite milk samples being identified as NBG using microbiological techniques, qPCR analysis was able to detect DNA of specific bacteria in milk.

Key Words: mastitis, no bacterial growth, qPCR

TH282 Circulating serotonin (5-HT) concentrations on day 1 of lactation as a potential predictor of transition-related disorders. J. Laporta, SAE Moore*, MW Peters, and LL Hernandez, *University of Wisconsin, Madison.*

Serotonin (5-HT) has been described as a homeostatic regulator of lactation. Recently, it has been determined that 5-HT is involved in regulating calcium and glucose homeostasis during the transition period in rats. It has been shown that 5-HT is important for initiating calcium mobilization from bone during the transition period. Additionally, 5-HT has been demonstrated to affect hepatic and mammary gland energy metabolism during the transition period. Therefore, we investigated the correlation of circulating 5-HT concentrations in relation to circulating calcium and parathyroid hormone related-protein (PTHrP) concentrations on d 1 of lactation, as well as the correlation of circulating 5-HT with the incidence and severity of ketosis in Holstein cows in relation to circulating 5-HT concentrations. Blood samples were collected from 50 multiparous cows on d 1 of lactation at the Emmons Blaine Dairy Cattle Research Center. Serum and plasma were harvested from samples and analyzed for 5-HT, ionized calcium, and PTHrP. Incidence and extent of ketotic events were recorded for all animals during the first 10 d postpartum and ketosis severity was defined as follows: 0 = no signs of ketosis, 1 = mild ketosis with no treatment, 2 = mild ketosis with treatment, 3 = moderate ketosis, and 4 = severe ketosis. Serum 5-HT and ionized calcium were positively correlated ($P = 0.0182$, r = 0.3672), as were serum 5-HT and plasma PTHrP ($P = 0.0419$; r = 0.3562). Additionally, serum 5-HT was negatively correlated with ketosis incidence and severity ($P = 0.0481$; r = 0.3137). These data suggest that 5-HT potentially plays a role in regulating calcium and glucose homeostasis during the transition period in cattle, which has been previously demonstrated in rodents.

Key Words: serotonin, lactation, transition period

TH283 Hormonal regulation of α-tocopherol transfer related molecules expression in bovine mammary epithelial cells. S. Haga*[1,2], Y. Kobayashi[1], M. Nakano[1], H. Ishizaki[1], SG Roh[2], and K. Katoh[2], *[1]NARO Institute of Livestock and Grassland Science, Nasushiobara, Tochigi, Japan, [2]Lab of Animal Physiology, Graduate School of Agriculture Science, Tohoku University, Sendai, Miyagi, Japan.*

α-Tocopherol (α-Toc) is the most biologically active form of vitamin E in animals. α-Toc is the major lipid-soluble vitamin and an important integrant in milk for newborn animals. However, little is known on the secretory mechanism of α-Toc in milk and the regulation of α-Toc transfer protein (αTTP), scavenger receptor class B type 1 (SR-B1) and ATP-binding cassette transporter A1 (ABCA1) in the mammary gland. In this study, therefore, we investigated the mRNA expression levels of αTTP, SR-B1 and ABCA1 in mammary glands among different lactation stages, and the effects of lactogenic hormones (dexamethasone, insulin and prolactin), E2 and GH on these genes expression in cultured bovine mammary epithelial cells (bMEC). The mammary tissues were sampled from 9 dairy cows (peak lactation (n = 3, 2 mo after parturition), late lactation (n = 3, 8 mo after parturition) and the dry-off stage (n = 3, 3 years after parturition). The cloned bMEC were grown until confluence in a collagen type IV coated transwell and treated with lactogenic hormones, E2 and GH at various concentrations for 24 h. Total RNA was extracted from the mammary tissues and the cultured bMEC, and then αTTP, SR-B1 and ABCA1 mRNA were analyzed by Q-RT-PCR. Values were considered to be statistically significant if their P-value was < 0.05 (SAS). In mammary tissues, the expression levels of αTTP and SR-B1 mRNA were significantly higher at lactation stages than at dry off stage. In bMEC, lactogenic hormones increased the expression levels of αTTP, SR-B1 and ABCA1 mRNA. Dexamethasone or E2 treatment significantly upregulated the expression levels of SRB1 mRNA in a dose-dependent manner. The expression level of ABCA1 mRNA was increased by E2, but decreased by GH in dose-dependent manner. These results indicate that hormonal changes in different lactogenic stage differentially regulate the expression of αTTP, SR-B1 and ABCA1 genes related with α-Toc transfer for vitamin E secretion in milk.

Key Words: α-tocopherol, bovine mammary epithelial cell, milk secretion

TH284 Cellular composition and expression of potential stem cell markers in mammary tissue of cows consuming endophyte-infected fescue seed during the dry period and early lactation. R. K. Choudhary*[1], R. L. Baldwin VI[2], C. M. Evock-Clover[2], P. Grossi[3], T. H. Elsasser[2], G. Bertoni[3], E. Trevisi[3], K. R. McLeod[1], and A. V. Capuco[2], *[1]Department of Animal Sciences, University of Kentucky, Lexington, [2]Bovine Functional Genomics Lab, USDA-ARS, Beltsville, MD, [3]Istituto di Zootecnica, Universitá Cattolica del Sacro Cuore, Piacenza, Italy.*

We evaluated the effect of consuming endophyte-infected fescue during late pregnancy on parameters of mammary development in Holstein cows. Cows (n = 16) were fed 10% of their ration as tall fescue seed that was free from (CON) or infected with endophyte (INF) from 90 d before expected calving until 10 d of lactation. Mammary tissue was biopsied during dry period (−32 d) and early lactation (+10 d). The percentage of tissue area that was occupied by epithelium, stroma and lumina was

quantified. Epithelial proliferation was assessed by nuclear expression of the Ki67 antigen, detected by immunohistochemistry. Staining for putative mammary stem cell markers, nuclear receptor subfamily 5 group A member 2 (NR5A2), fibronectin type III domain containing 3B (FNDC3B) and musashi1 (MSI1), was evaluated and expressed as a percentage (% DAB pixels out of DAB plus hematoxylin pixels). Epithelial content of mammary tissue did not differ between CON and INF cows, nor did stromal and luminal areas differ between treatments in dry cows ($P > 0.05$). However, in lactating cows, tissue areas reflected greater milk yield in CON than INF cows (luminal area in CON > INF; stromal area in INF > CON; $P < 0.05$). Proliferation indices did not differ between mammary epithelia of CON and INF cows ($P > 0.05$). Similarly, nuclear staining of NR5A2, FNDC3B and MSI1 did not differ in INF vs. CON. However, there were differences ($P < 0.05$) in staining of all 3 markers between dry period and lactation (−32 d vs. +10 d). FNDC3B staining was greater during early lactation than the dry period ($P < 0.001$) and cytoplasmic staining of myoepithelial cells was observed during lactation. During early lactation, FNDC3B (r = 0.86; $P = 0.13$) staining tended to correlate with milk yield. Data indicate that fescue toxicity did not alter cellular composition of mammary tissue, epithelial proliferation rate, or expression of mammary stem cell markers. Immediate effects of fescue toxicosis on milk yield are likely mediated by influences on mammary differentiation and secretory activity.

Key Words: fescue toxicosis, mammary stem cell, lactation

TH285 Influence of intramammary lipopolysaccharide challenge on milk and plasma adiponectin in dairy cows. S. P. Singh*[1], S. Häussler[1], O. Wellnitz[2], R. M. Bruckmaier[2], and H. Sauerwein[1], *[1]Institute of Animal Science, Physiology and Hygiene Group, University of Bonn, Bonn, Germany, [2]Veterinary Physiology, Vetsuisse Faculty University of Bern, Bern, Switzerland.*

Intramammary LPS infusion induces local and systemic inflammatory responses. Circulating concentrations of the adipokine adiponectin (Aq) decrease during inflammation and Aq was therefore suggested as a negative acute phase protein. Our objective was thus to investigate the changes in milk and blood Aq concentrations after inducing an experimental mastitis by intramammary LPS infusion in dairy cows. Eight lactating, non-pregnant Holstein cows (1st - 6th parity) in wk 18 to 37 of lactation were used. One front and one rear quarter was intramammarily injected with 200 µg LPS from *E. coli* (O26:B6) in 10 mL NaCl (0.9%). Cisternal milk samples were collected before and 8 h after LPS challenge. Skim milk was prepared by centrifugation (3,000 × *g*, 20 min, 4°C). Blood plasma was prepared (3,000 × g, 20 min) from blood samples taken hourly. Skim milk and plasma Aq concentrations were measured by ELISA. The intra- and interassay variation were 7.0% and 11.0%; 4.5% and 11.9% for plasma and skim milk, respectively. The limit of detection was 0.03 ng/mL. Assay accuracy for skim milk was indirectly determined by linearity of serial samples dilutions. Differences in plasma Aq between time points were tested for significance ($P < 0.05$) by repeated measure ANOVA with Bonferroni correction. Wilcoxon signed rank test was used for analysis of skim milk Aq concentrations. The results are presented as means ± SEM. The plasma Aq concentrations (µg/mL) were not different across all times of LPS infusion (average concentrations: 29.8 ± 0.6), whereas milk Aq was significantly increased after 8 h of LPS challenge (0.5 ± 0.7 vs. 1.1 ± 0.5; $P = 0.028$). In view of the fairly constant Aq concentrations in plasma, the Aq secretion from adipose tissue was apparently not affected by intramammary LPS treatment. The increase in milk Aq after LPS challenge probably resulted from transfer of blood Aq through the disturbed blood milk barrier.

Key Words: lipopolysaccharide, milk, adiponectin

TH286 Transcriptomics differences between liver and mammary tissue in mid-lactation dairy cows. D. P. Bu[1], M. Bionaz[2], X. M. Nan[1], and J. Q. Wang*[1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Animal and Rangeland Sciences, Oregon State University, Corvallis.*

Liver and mammary gland are among the most prominent organs during lactation in dairy cows. With the purpose to understand both the different and the complementary roles of those 2 organs during lactation, a transcriptome analysis was performed on liver and mammary tissues of 10 dairy cows in mid-lactation (136 ± 3.7 d). The analysis was performed using a 4 × 44K Bovine Agilent microarray chip. The data were normalized by Lowess and uploaded into ArrayStar. A paired *t*-test with false discovery rate correction (FDR) uncovered 7,813 genes differentially expressed (DEG) between the 2 tissues with an FDR <0.001. The functional analysis was performed using the Database for Annotation, Visualization and Integrated Discovery and the Dynamic Impact Approach (DIA). The most enriched biological terms in DEG more expressed in mammary vs. liver were related to translation, extracellular matrix, cell adhesion, cytoskeleton, and vesicle transport. The mitochondria and related respiration, immune reaction (i.e., complement and coagulation cascades, acute inflammatory response) and metabolism of drugs, fatty acid, and steroid were the most enriched terms in DEG more expressed in liver vs. mammary tissue. The DIA analysis revealed a larger induction of almost all metabolic pathways in liver compared to mammary, with exception of fatty acid biosynthesis. The liver had also overall more induced pathways related to immune, endocrine, and digestive system, peroxisome, and PPAR signaling. The DIA uncovered an overall larger protein synthesis capacity and related signaling pathways (e.g., mTOR), cell communication (including cell adhesions), cell cycle, cellular innate immune system (e.g., toll-like receptor), protein export, and secretion in mammary vs. liver. In summary the transcriptome analysis revealed that the liver is more metabolically active compared to the mammary gland with a larger production of energy through mitochondria and peroxisomes while the mammary gland synthesizes more protein with greater export, cell-to-cell interactions, and proliferative capacity compared with the liver.

Key Words: transcriptomics, mammary gland, liver

TH287 Differential proteome analysis of lactating and nonlactating bovine mammary gland. H. Y. Liu*[1], J. X. Yang[1], X. D. Zhang[2], and J. X. Liu[1], *[1]Institute of Dairy Science, Zhejiang University, Hangzhou, China, [2]Department of Animal Science and Technology, Zhejiang Agriculture and Forestry University, Hangzhou-Lin'an, China.*

The initiation and maintenance of lactation are complex phenomena involving general biochemical and endocrinological processes in the mammary glands. It has been extensively studied over the years at the genetic, physiological and morphological levels. However, only limited data are available concerning proteomic changes of lactating and nonlactating bovine mammary gland. To determine the differentially expressed protein profiles between periods of lactation and nonlactation, the comparative proteomes were analyzed using 2-dimensional gel electrophoresis (2-DE) followed by MALDI-TOF/TOF protein identification. Bovine mammary gland tissues were obtained from 3 healthy multiparous dairy cows in each period, respectively. The analyses of multiple 2-DE gels indicated that a total of 80 protein spots

(corresponding to 59 altered proteins) differentially expressed in both periods, including 56 upregulated proteins and 3 downregulated proteins. Database search and identification of functional protein analysis showed that upregulated proteins were mainly related to transportation, macromolecular biosynthesis, metabolism, protein-folding, apoptotic, secretion and pentose-phosphate shunt. Downregulated proteins were involved in cytoskeleton, transport and lipid degradation. These proteins, through various pathways and actions, may regulate either lactogenesis, galactopoiesis, or involution within the mammary gland. Moreover, 30 corresponding genes of the differentially expressed proteins were quantified by real-time RT-PCR to examine the transcriptional profiles and validate the proteins identified by MS/MS between lactating and nonlactating bovine mammary gland. Thus, this study provides useful dynamic protein-related information to facilitate further investigation of the underlying lactation mechanism of dairy cows.

Key Words: lactation, bovine mammary gland, differential proteomics

TH288 AKT/mTOR and JAK2/STAT5 pathway act synchronously on the synthesis of β-casein in bovine mammary epithelial cells. L. L. Shi, F. Zhao, X. J. Gao, Q. Z. LI*, and N. Zhang, *Key Laboratory of Dairy Science of Education Ministry, Northeast Agricultural University, Harbin, China.*

Both AKT and STAT5 are important to cell apoptosis, survival, proliferation and differentiation, and the latter contributes to milk protein gene transcription in bovine mammary epithelial cells (BMECs), but a role for AKT in mammary epithelial cell differentiation has not been established. A lactogenic phenotype is generally induced in BMECs by the differentiation medium including dexamethasone, insulin and prolactin, referred to as DIP and has typically been assessed by milk protein production. The previous studies have shown that these hormones are necessary in vitro for differentiation and milk protein synthesis of BMECs by activating JAK2/STAT5 and PI3K/AKT1/mTOR pathway. To address the interaction between the 2 key pathways, we inhibited AKT1 or STAT5 expression by RNA interference with DIP+IGF-1, DIP+GH, or only DIP, and detected their effects on the synthesis of β-casein in BMECs. In the presence of the differentiation medium, AKT1 inhibition by RNAi compared with control cells, which led to lower mRNA and protein level of AKT1 and mTOR, but no change in their phosphorylation. Interestingly, reduced STAT5 and β-casein expression were also observed. While the similar downregulation of STAT5 expression occurred when STAT5 was inhibited, the above 3 expression levels of AKT1 and mTOR were decreased synchronously. AKT1, mTOR and STAT5 expression were greater for DIP +IGF-1 or DIP+GH than for just DIP, followed by increasing β-casein mRNA. Overall, PI3K/AKT1/mTOR and JAK2/STAT5 pathway both act on the synthesis of β-casein in BMECs. Although they had been negatively regulated separately, the abundance of β-casein mRNA decreased resulting from the 2 inhibited pathways synergically. IGF-1 or GH can enhance β-casein mRNA expression by upregulated JAK2/STAT5 and AKT/mTOR activity, whereas IGF-1 can't replace GH due to its little effect on AKT1 and mTOR phosphorylation.

Key Words: AKT1, STAT5, β-casein

TH289 The effects of laminin on the proliferation of dairy cow mammary epithelial cells are mediated by α6 and β4 integrin. F. Zhao, C. Liu, X. J. Gao, and Q. Z. LI*, *Key Laboratory of Dairy Science of Education Ministry, Northeast Agricultural University, Harbin, China.*

Laminin is a key extracellular matrix (basement membrane) protein and exerts function by its cell membrane surface receptor integrins to affect cell behavior including cell adhesion, apoptosis, survival and cell differentiation. In bovine mammary gland epithelial cells (BMECs), 2 important integrin heterodimers α6β1 and α6β4 are close related to laminin function. In this study, 14 primiparous Holstein dairy cows were chosen from 7 development stages during lactation cycle. Mammary gland biopsies were taken in virgin (postnatal 12 mo), pregnant (6 mo into gestation), lactating (7, 50, 140, 280 d postpartum), and dry period (30 d after weaning). By immunohistochemistry we found that α6 and β4 subunits collocated in basal side cells toward basement membrane in mammary tissue slices. Both mRNA and protein level of 2 subunits were higher during pregnancy and lactation than during virgin and dry period. The proliferation of mammary epithelial cells which originated from a lactating cow was enhanced with the presence of laminin substrate in comparison with plastic culture surface. In vitro, PRL, GH, IGF-1, IGF-2 or 10% serum affect cell growth differently, and IGF-1 and GH were more effective mitogen. We confirmed that BMECs proliferation with laminin substrate induced by GH, IGF-1 or 10% serum could be dramatically inhibited to the same degree to that without laminin by blocking integrin α6 function, whereas it only had a weak inhibitory effect by blocking integrin β4 function. It could result from the different number of heterodimers, and it has been well known that α6 subunit is involved in 2 heterodimers α6β1 and α6β4, but β4 subunit had been detected only to form the later at present. In conclusion, once cell-matrix and cell-cell junctions have established, α6 integrins will play an important role in mammary epithelial cell proliferation by α6β1 and α6β4 heterodimers mediated signaling from laminin or other mitogen such as IGF-1 and GH. These results allow us understand better the regulation of mammary epithelial cells proliferation associated with integrins.

Key Words: integrin α6, integrin β4, bovine mammary epithelial cell

TH290 Shelf life of fresh pork sausage from immunologically castrated barrows. K. A. Jones-Hamlow*[1], A. L. Schroeder[2], and A. C. Dilger[1], [1]*University of Illinois, Urbana-Champaign,* [2]*Zoetis, Kalamazoo, MI.*

Immunological castration is an emerging technology in the pork industry and determination of quality characteristics of fresh sausage from immunologically castrated pigs is needed. Fat and lean trim was obtained from entire carcasses and pooled by castrate type from immunological castrates (IC) and physical castrates (PC) (n = 10). Sub-samples of trim were collected for proximate analysis. Based on results, trim was mixed into five 15 lbs batches of both IC and PC, targeting 25% fat. Batches were ground, mixed with spices, stuffed into casings and sliced into 1.25 cm patties. Samples were collected from each batch for proximate composition. Patties were placed on trays, overwrapped, and assigned to frozen storage times of: 0, 4, 12 wk. Upon conclusion of frozen storage, packages were placed under constant light (883 lx) at 4°C for 5 d to simulate retail display. Patties were evaluated for color and percent discoloration on d 1, 3 and 5 by a trained 5-person panel. On d 5 of each storage time point, patties were evaluated for sensory characteristics and thiobarbituric acid reactive substances (TBARS). Patties were also evaluated for cooking loss, textural properties (compression and break strength) and cooked proximate composition. Data were analyzed as a one way ANOVA; visual evaluations, sensory characteristics and TBARS were analyzed with repeated measures. Patties from IC were darker (3.30 vs. 2.90, $P < 0.05$, respectively) than PC. Overall, discoloration increased ($P < 0.05$) over time, but there were no differences within each storage week. Sensory characteristics were also similar ($P > 0.05$) between IC and PC. Averaged across all storage times, TBARS from IC were reduced (0.47 vs. 0.22 mg/kg, $P < 0.05$, respectively) compared with PC; however, there were no differences within each storage week. Textural properties ($P > 0.05$), cooking loss ($P = 0.94$) and raw ($P = 0.12$) and cooked ($P = 0.65$) proximate composition were similar between IC and PC. Overall, immunological castration had no detrimental effects on the shelf life, sensory characteristics, or textural properties of fresh pork sausage.

Key Words: immunological castration, sensory, textural property

TH291 Gene expression of lipogenic enzymes present in muscle of young bulls fed ground soybean grain or cottonseed and vitamin E. M. M. Ladeira*[1,2], D. M. Oliveira[1], A. Chalfun Junior[1], M. L. Chizzotti[1], H. G. Barreto[1], T. C. Coelho[1], P. D. Teixeira[1], and E. E. L. Valente[1], [1]*Federal University of Lavras, Lavras, MG, Brazil,* [2]*Purdue University, West Lafayette, IN.*

The objective was to evaluate the gene expression of lipogenic enzymes present in the muscle of young feedlot bulls fed ground soybean grain (SB) or ground cottonseed (CS), with or without the inclusion of the vitamin E (E). Forty bulls, with an initial body weight of 339 ± 15 kg, and an initial average age of 20 ± 1.3 mo were allotted in a completely randomized design using a 2 × 2 factorial arrangement. The diets contained 20.0% of SB or 24% of CS, 6.5% ether extract and corn silage was utilized as forage. Vitamin E was supplemented at a rate of 2,500 IU/hd/d. Bulls were harvested at an average BW of 456 ± 15.1 kg. At 24 h post-mortem, samples of the longissimus dorsi muscle were collected at the 13th rib and stored at −80°C. The genes evaluated were acetyl coA carboxylase (ACC), adipocyte-type fatty acid binding protein ($FABP_4$), stearoyl coA desaturase (SCD), lipoprotein lipase (LPL), glutathione peroxidase (GPX), peroxisome proliferator activator receptor (PPAR-α), and sterol regulatory element binding protein (SREBP-1c). The gene expression was analyzed using qPCR technique and the evaluation of relative quantification was carried by formula $2^{-\Delta\Delta C}{}_{T}$. Data were analyzed using PROC GLM of SAS 9.1. The gene expression of ACC and GPX was greater for the diets SB and SBE. Muscle of the bulls fed SB diet had the greatest gene expression for FABP4. Regarding the SCD, the greatest gene expression occurred when bulls fed CS diet. Otherwise, the LPL was more expressed when the SBE was used. In conclusion, the gene expression of lipogenic enzymes was affected by the oilseed and vitamin E supplementation.

Table 1. Effect of soybean grain (SB) and cottonseed (CS), with or without the inclusion of the vitamin E (E) on gene expression (fold change)

Enzyme	SB	SBE	CS	CSE	SEM	*P*-value
ACC	1.53[a]	1.66[a]	1.00[b]	1.35[ab]	0.13	<0.01
$FABP_4$	2.26[a]	1.28[b]	1.00[b]	1.30[b]	0.14	<0.01
SCD	1.00[b]	1.11[b]	1.93[a]	1.02[b]	0.11	<0.01
LPL	1.86[b]	3.05[a]	1.00[c]	2.10[b]	0.14	<0.01
GPX	1.34[a]	1.46[a]	1.00[b]	1.26[ab]	0.08	<0.01
PPAR-α	2.21[a]	1.95[ab]	1.00[c]	1.40[bc]	0.17	<0.01
SREBP-1c	1.00[c]	1.43[ab]	1.69[a]	1.28[bc]	0.09	<0.01

[abc]Different letters in the same row differ ($P < 0.05$) for the Tukey test.

Key Words: nutrigenomics, mRNA, oilseed

TH292 Effects of frame, forage type and time-on-pasture on carcass traits, LM composition, and meat color in steers. G. Volpi Lagreca*[1], R. Arnoni[1], M. Alende[1], S. K. Duckett[1], R. M. Lewis[2], and J. P. Fontenot[2], [1]*Clemson University, Clemson, SC,* [2]*Virginia Tech University, Blacksburg.*

Angus-cross steers (n = 144; 365 ± 50.9 kg BW; 13.3 mo) were used in a 3-year study (2010–2012) to assess the effects of frame, forage type and time-on-pasture on carcass characteristics, LM proximate composition, and color (L*, a* and b*) at 12th rib. Steers were randomly assigned to 1 of 6 treatments, defined by a 2 × 2 × 2 factorial experiment: frame (medium or large), forage type (PAST -bluegrass (*Poa pratensis*), orchardgrass (*Dactylis glomerata*), tall fescue (*Lolium arundinaceum*) and white clover (*Trifolium repens*) - or ANNUAL -high sugar sorghum-sudangrass (*Sorghum bicolor*)-) and time-on-pasture (155 or 209 d). All interactions were non-significant ($P > 0.05$) except LM L*, subcutaneous (s.c.) b* and LM iron. Increasing time-on-pasture increased ($P < 0.05$) hot carcass weight (268.1 vs. 236.5 kg), s.c. fat thickness (0.47 vs. 0.32 cm), kidney, pelvic and heart fat (1.17 vs. 0.83%), skeletal maturity (171.3 vs. 160.4), and yield grade (2.09 vs. 1.70). Both time-on-pasture and forage type affected LM and s.c. color scores. Longer time-on-pasture increased LM a* (26.8 vs. 26.4) and b* (11.7 vs. 11.2) and s.c. a* (8.7 vs. 7.1) and b* (18.6 vs. 16.8), whereas LM a* and b* were greater ($P < 0.05$) in PAST compared with ANNUAL (26.9 vs. 26.4 and 11.6 vs. 11.3). There was a significant interaction between frame and forage type for LM L*, which was greater ($P = 0.001$, 42.1 vs. 40.5) for large compared with medium with ANNUAL, and for s.c. b*, which was greater ($P < 0.0001$, 18.7 vs. 16.7) for medium compared with large with ANNUAL, but no differences where observed with PAST. Greater time-on-pasture increased ($P < 0.05$) ash (1.39 vs. 1.28 g/100 g LM), zinc (3.27 vs. 3.11 mg/100 g LM) and aluminum (0.24 vs. 0.20 mg/100 g LM), whereas time-on-pasture increased iron ($P = 0.0005$,

1.82 vs. 1.60 mg/100 g LM) with ANNUAL, without differences with PAST. Time-on-pasture affected carcass, LM proximate composition, and tissue color; whereas forage type and frame score had minor effects.

Key Words: beef, forage, grazing

TH293 Fatty acid profile of meat from Nellore young bulls fed crude glycerin and lipid sources. R. A. Silva, J. F. Lage*, E. San Vito, A. F. Ribeiro, L. M. Delevatti, E. E. Dallantonia, M. Machado, L. R. Simonetti, B. R. Vieira, and T. T. Berchielli, *Universidade Estadual Paulista, Jaboticabal, Sao Paulo, Brazil.*

This objective of this study was to evaluate the effects of feeding different lipid sources on diets containing crude glycerin (CG) - 80% glycerol - included on 10% of DM diet on longissimus muscle fatty acid profile of Nellore young bulls finished in feedlot. Forty young bulls (Nellore), with 426.00 ± 30.20 initial BW, were randomly assigned to 4 treatments, with 10 replicates. The diets (30% of corn silage and 70% concentrate) were: 10% of CG being control diet (Cn); 10% of CG plus soybean oil (SO), 10% of CG plus whole soybean grain (SG) or 10% of CG plus bypass fat (BF). The Cn diet had 3.5% of ether extract (EE) and diets with lipid sources had 5.5% of EE. Concentrates were composed of grounded corn, soybean meal, urea/ammonium sulfate, mineral mixture and lipid sources. The diets were isonitrogenous. Animals were assigned to individuals pens, fed 97 d and slaughtered with average of 521.30 ± 44.27 kg BW. All carcasses were chilled at 0°C for approximately 24 h. A boneless longissimus muscle (LM) section 10 cm thick was removed from the posterior end of the wholesale rib. LM samples were individually vacuum-packaged and held at −20°C for analysis. The samples were submitted to lipid extraction and methylation and analyzed by gas chromatography. The experiment was conducted according to a completely randomized design and data were analyzed by the GLM procedure of SAS, and the Tukey test used considering 5% probability. The treatments did not affected the contents of CLA ($P = 0.11$), total saturated fatty acid ($P = 0.67$), total unsaturated fatty acid ($P = 0.67$), total monounsaturated fatty acid ($P = 0.19$), total polyunsaturated fatty acid ($P = 0.40$) and relation n-6:n-3 ($P = 0.45$). The inclusion of lipid sources on diets containing crude glycerin (10% DM) did not alter the fatty acid profile of meat from Nellore young bulls finished in feedlot.

Key Words: beef cattle, glycerol, feedlot

TH294 Visible and near infrared reflectance spectroscopy (Vis-NIRS) to predict tenderness in Nellore cattle. M. N. Bonin*[1], S. L. Silva[1], L. Bunger[2], D. Ross[2], C. Craigie[2], R. C. Gomes[3], A. Figueiredo[1], P. Torralvo[1], J. H. A. Campos[1], V. N. Barbosa[1], F. J. Novais[1], M. H. A. Santana[1], L. S. Oliveira[1], M. Mazon[1], J. B. S. Ferraz[1], *[1]College of Animal Science and Food Engineering, University of Sao Paulo, Pirassununga, SP, Brazil, [2]Scotland's Rural College, Edinburgh, United Kingdom, [3]Embrapa Beef Cattle, Campo Grande, MS, Brazil.*

Visible and near infrared reflectance spectroscopy (Vis-NIR) has the potential of predicting meat quality traits by acquiring scans at early postmortem and in intact samples. This technique has the advantage of being a nondestructive and quickly method that could be used as alternative of destructive, laborious and high cost methods as that used for physical and sensorial evaluation of tenderness. The aim of this study was to evaluate the accuracy of Vis-NIRS for predicting beef tenderness in Nellore cattle. Six hundred and 64 Nellore bulls with 18 to 30 mo of age were used in this study. The animals were slaughtered in 6 batches from September 2009 to November 2010. All carcasses were ribbed at the 5th rib, 48 h postmortem and a sample of the longissimus thoracis (2.5 cm thick) was removed. A Vis-NIR spectra with a wavelength range from 400 to 1400 nm and intervals of 5 nm was collected immediately and the samples subjected to Warner-Bratzler Shear Force (WBSF) analysis. Calibration and validation procedures were performed using Partial Least Squares Regression in the program UNSCRAMBLER (version 10.1, Camo, Trondheim, Norway). For testing the Vis-NIRS accuracy at distributing the samples into classes of tenderness, predicted WBSF values were regressed against actual WBSF values. The WBSF values ranged from 2.82 to 13.14 kg, with mean = 6.95 kg and SD = 2.01 kg. Low coefficients of determination were observed in the calibration ($R_c^2 = 0.29$, RMSEC = 1.70) and in the cross-validation ($R_{cv}^2 = 0.14$, RMSECV = 1.29), indicating a low ability of Vis-NIRS for predicting exact values of WBSF in Nellore cattle. However, when used to classify meat as tender (WBSF <4.5 kg) or tough (WBSF >4.5 kg), Vis-NIRS correctly classified 91.8% of samples. These results are in accordance with other studies that reported the Vis-NIRS as a powerful tool for categorization of meat products, with correct classification of more than 80% of samples. Using Vis-NIRS spectroscopy at deboning may be a powerful technique to distinguish tender from tough meat in industrial routines to add value to meat cuts.

Key Words: *Bos indicus*, intact sample, WBSF

TH295 Influence of season of lamb finshing on meat quality. R. C. Vilarinho[1], U. Souza[1], C. P. McManus[2], and L. Kindlein*[1], *[1]Federal University of Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil, [2]Brasilia University, Brasilia, DF, Brazil.*

The present study aimed to evaluate carcass and meat characteristics of lamb (<18 mo of age) slaughtered in different seasons of the year (spring and summer) reared in semi-intensive systems in Rio Grande do Sul State, Brazil. Several genetic and environmental factors can affect quantitative and qualitative traits of lamb meat. For this experiment, a total of 120 Corriedale were used, 60 finished and slaughtered in spring and 60 in the summer. After slaughter and evisceration, hot carcasses were weighed (HCW) and pH (pH_{0h}) measured. After chilling cold carcass weight was taken (CCW) and final pH (pH_{24h}). A section between the 11th and 13th ribs as taken of the longíssimus dorsi muscle for analysis. Animals slaughtered in the spring had higher weights (HCW, CCW) and rib-eye area (REA) ($P < 0.001$, $P < 0.001$, $P < 0.002$; 18.81 kg, 18.40 kg and 13.72 cm^2, respectively) than those slaughtered in the summer (18.00 kg, 17.92 kg and 12.14 cm^2, respectively). These results were expected as in this region there is greater pasture availability and quality in the spring. Other authors found darker meat in lambs slaughtered in the winter, with less fat deposits than those slaughtered in other seasons. In the present study no differences ($P > 0.05$) were found between seasons for meat quality traits including pH_0 6.50(±0.02) vs. 6.40(±0.01); pH_{24} 5.67(±0.03) vs. 5.70(±0.03); L* 34.17(±2.34) vs. 33.84(±3.72); a* 5.09(±1.45) vs. 4.60(±1.21); b* 6.73(±2.56) vs. 6.82(±2.43); marbling (IMF) 1.68(±0.50) vs. 1.63(±0.60); subcutaneous fat thickness (SF), 0.49 (±0.10) vs. 0.48(±0.12); for spring and summer respectively·. The slaughter season for lambs influences carcass traits with animals slaughtered in the spring showing higher values for HCW (Kg), CCW (Kg) and REA (cm^2) than those slaughtered in the summer but this does not affect meat quality.

Key Words: carcass, lamb meat, marbling

TH296 An Investigation of the black bone syndrome with broiler chickens fed diets supplemented with 25-OH-vitamin D_3. L. Kindlein* and S. L. Vieira, *Federal University of Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil.*

A study was conducted to evaluate the leg bones of chickens presenting color alteration compatible with those reported as in Black bone syndrome (BBS) using Cobb 500 male broilers fed corn-soy diets. BBS in chickens refers to darkened meat along the leg bones. It is associated with an increased bone porosity, which then allows the marrow to leak into the meat. This defect has been observed with broilers presenting adequate levels of Ca, P as well as vitamin D_3 and therefore, it is suspected that the greater porosity arises from marginal deficiencies paralleling the high demand of these nutrients in the modern fast growing broiler. For this experiment, birds were placed in floor pens, 22 per pen and were fed diets using industry requirements in a feeding program from 1 to 7 d (1% Ca, 0.5% Av P, 3200 ICU D_3), 8 to 21 d (0.95% Ca, 0.48% Av P, 3200 ICU D_3), 22 to 35 d (0.9% Ca, 0.45% Av P, 2775 ICU D_3), and 36 to 39 d (0.85% Ca, 0.43% Av P, 1825 ICU D_3). A factorial of diet type and 25-OH-vitamin D_3 supplementation (69 ppb) was used. A diet with a moderate increase in anti-trypsin factors by adding 6% of raw soybeans (Malabsorption) and a diet using 6% toasted soybeans (Regular) were used. Broilers were processed at 39 d and the right tibiae of 8 birds from each pen were collected. Bone-in tibiae were cooked to reach 72°C at the muscle-bone junction and further deboned. Bones were evaluated by their proximal epiphysis visual appearance for the level of BBS as: acceptable (absence of darkening), intermediate (moderate darkening) and unacceptable (accentuated darkening). Tibiae was also submitted to a color evaluation using the L, a*, b* scale using a portable Minolta colorimeter at the midshaft. No tibiae from the Malabsorption diet was classified as acceptable; however, birds fed Malabsorption diet supplemented with 25-OH-vitamin D3 showed similar appearance as those from the Regular diet. The a* (red) color coordinate measured at the midshaft surface of uncooked bones showed lower values ($P < 0.05$) in the birds of Regular diet indicating a higher incidence of BBS with birds fed the Malabsorption diet.

Key Words: black bone syndrome, color meat, malabsorption diet

TH297 Effects of feeding ractopamine to immunologically castrated pigs on carcass cutting yields and fresh meat quality. B. K. Lowe*[1], G. D. Gerlemann[2], S. N. Carr[3], P. J. Rincker[3], A. L. Schroeder[4], D. B. Petry[5], G. L. Allee[2], F. K. McKeith[1], and A. C. Dilger[1], *[1]University of Illinois, Urbana, [2]University of Missouri, Columbia, [3]Elanco Animal Helath, Greenfield, IN, [4]Zoetis, Kalamazoo, MI, [5]Newsham Choice Genetics, West Des Moines, IA.*

Thirty-two pens with 22 pigs per pen were used to evaluate effects of feeding ractopamine (RAC; 5 mg/kg) to physically castrated (PC) and immunologically castrated (IC) pigs on carcass characteristics, cutting yields, and pork quality. Male pigs were randomly assigned to sex treatments at birth and fed the same nursery diets before allotment in a grow-finish barn. Pigs in the PC group were physically castrated at 5 d of age. Pigs in the IC group were administered Improvest at 11 and 18 wk of age (d 65 of study). Diet treatments (control or RAC) were initiated on d 87 of study and final treatment arrangement was a 2 × 2 factorial of sex and diet. Pigs were marketed in 3 groups based on ending live weight (target 136 kg) and 3 pigs closest to the pen mean for each group were identified for cutting yield and quality evaluations. Data were analyzed using PROC MIXED in SAS with fixed effects of sex, diet, market group, and their interaction; carcass (n = 285) was the experimental unit. Feeding RAC increased ($P \leq 0.03$) bone-in lean and total carcass cutting yields by 0.76 and 0.70 percentage units, respectively, while having no effect ($P > 0.05$) on LM color, marbling, firmness, pH, drip loss, and tenderness. Carcasses from IC pigs had greater ($P < 0.05$) boneless lean yields (37.53% vs. 36.34%), bone-in lean yields (58.98% vs. 57.34%), and total carcass cutting yields (72.12% vs. 70.79%) than PC carcasses; however, PC loins had 0.2 units more ($P = 0.02$) marbling, were 0.2 units firmer, and were 0.16 kg more ($P < 0.01$) tender. There was an interaction ($P = 0.03$) between sex and diet for LM composition where control-fed PC loins (2.9%) had more ($P < 0.01$) lipid than all other treatment combinations (AVG = 2.3%). Group 1 carcasses (72.46%) had greater ($P \leq 0.02$) carcass cutting yields than the other market groups (AVG = 70.96%); however, group 1 loins were 0.24 kg less ($P < 0.05$) tender than loins from the other groups. The results from this study demonstrate that RAC and immunological castration are additive in terms of improving carcass cutting yields while having minimal effects on pork quality.

Key Words: Paylean, Improvest, cutting yields

TH298 Effects of temperament on meat lipid content and fatty acid composition of Nellore feeder steers. C. L. Francisco*[1,6], A. M. Jorge[1], A. Cominotte[1], I. M. Padovan[1], F. D. Rezende[2], J. M. B. Benatti[3], R. O. Roca[4], and R. F. Cooke[5], *[1]Universidade Estadual Paulista - FMVZ, Botucatu, SP, Brazil, [2]APTA, Colina, SP, Brazil, [3]Universidade Estadual Paulista - FCAV, Jaboticabal, SP, Brazil, [4]Universidade Estadual Paulista - FCA, Botucatu, SP, Brazil, [5]Oregon State University - EOARC, Burns, [6]FAPESP Proc 2010/09516-1, São Paulo, SP, Brazil.*

Forty-four Nellore (*Bos indicus*) steers were used to evaluate the effect of temperament on meat lipid content and fatty acid composition. Steers were evaluated for temperament at feedlot entry (d 0). Temperament was assessed by chute score and exit velocity. Steers were divided in quintiles according to their exit velocity, and assigned a score from 1 to 5 (1 = slowest steers; 5 = fastest steers). Further, individual temperament scores were calculated by averaging steer chute score and exit score. Steers were also classified according to temperament type [≤3 = adequate temperament (ADQ) or >3 = aggressive temperament (AGR)]. All steers were slaughtered on d 109, whereas LM samples were collected and analyzed for lipid content and fatty acid composition. Samples from ADQ steers tended to have greater ($P = 0.07$) lipid content than AGR steers (2.95 vs. 2.59 g/100g of meat, respectively). Temperament influenced ($P = 0.05$) content of t16 and c15 C18:1 isomers (0.07 vs. 0.10%, and 0.04 vs. 0.05% for AGR and ADQ steers, respectively). No differences ($P > 0.05$) were observed for CLA, however, t10,c12 CLA isomer tended to be reduced ($P = 0.07$) in AGR vs. ADQ steers (0.007 vs. 0.011%, respectively). In addition, temperament had an effect ($P = 0.03$) on c9,c12 C18:2 isomer (6.12 vs. 4.66% for AGR and ADQ steers, respectively), and tended to be higher ($P = 0.13$) to t11,c15 C18:2 isomer in AGR vs. ADQ (0.04 vs. 0.03%, respectively). Total PUFA content was greater ($P = 0.04$), as well as n-6 PUFA ($P = 0.04$) in AGR vs. ADQ steers (9.79 vs. 7.49%, and 2.12 vs. 1.60%, for AGR and ADQ steers, respectively), but, no differences ($P > 0.05$) were detected for ratio of n6:n3 fatty acids. Ratio of PUFA:SFA was higher ($P = 0.04$) in AGR vs. ADQ steers (0.23 vs. 0.17%, respectively). In conclusion, temperament is associated with fatty acid composition in the meat of Nellore feeder steers. This is a new issue and deserves further investigation.

Key Words: chute score, exit velocity, PUFA

TH299 Effects of feeding Next Enhance 300 on carcass characteristics, meat quality, and consumer sensory characteristics of longissimus beef steaks. M. C. Westerhold*[1], Z. D. Callahan[1], M. S. Kerley[1], C. L. Lorenzen[1], W. J. Sexten[1], B. R. Wiegand[1], and T. J. Wistuba[2], *[1]University of Missouri, Columbia, Columbia, [2]Novus International Inc., St. Charles, MO.*

Crossbred steers (n = 98; BW = 413 ± 37.7) were used in a randomized, complete block design to evaluate Next Enhance 300 (NE300, Novus Intl. Inc.) feeding on carcass characteristics, meat quality, and consumer sensory characteristics of LM steaks. Steers were blocked by initial BW and randomly assigned to treatment (TRT), with 5 replications per TRT. Corn based diet dietary TRT consisted of 0 (CON, n = 25), 150(n = 24), 300 (n = 25), and 600 (n = 24) $mg \cdot hd^{-1} \cdot d^{-1}$ of NE300. Five steers/TRT (n = 20) were harvested at the University of Missouri abattoir. At 96 h post mortem (d 0) carcasses were ribbed and a 4 rib section was vacuum packaged. Aged color measurements were taken on d 14 and further quality analysis was performed on 4 steaks (1.54 cm). A quadratic increase ($P = 0.01$) in dressing percent (DP) and a quadratic decrease ($P = 0.05$) in 12th rib backfat (BF) occurred with increasing NE300 levels, with CON steers having the lowest DP and the most BF. NE300 caused a quadratic increase in LM area (LMA) ($P = 0.10$) and LMA/45.4 kg ($P = 0.10$). There was a quadratic decrease ($P = 0.04$) in calculated USDA yield grade (YG) with increasing NE300 inclusion. Due to increased DP and LMA and decreased BF and YG of 150 and 300, a quadratic increase in carcass price/45.4 kg ($P = 0.15$) was observed. However, HCW and marbling score did not differ ($P > 0.05$), thus overall carcass value did not differ. NE300 inclusion did not affect a* or b* color values at d 0 or 14. D 0 L* values were linearly decreased ($P = 0.05$) by NE300, but d 14 L* values were not affected. There was a linear decrease ($P = 0.07$) in cook loss due to NE300. A consumer sensory panel (n = 55) was performed on one steak per steer, with 4–5 panelists evaluating each sample. There was no difference ($P > 0.05$) among TRT for Warner-Bratzler shear force, drip loss, percent moisture, percent fat, or consumer opinion of overall like, liking of tenderness, juiciness, and flavor and level of tenderness, juiciness, and flavor. Feeding NE300 improved DP, BF, LMA, and YG, and had no effect on organoleptic properties of LM steaks from beef steers.

Key Words: essential oil, meat quality

TH300 Incidence of white striping in relation to the weight of broiler breast fillets. T. Z. Ferreira, S. L. Vieira, and L. Kindlein*, *Federal University of Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil.*

The objective of the study was to evaluate the incidence of normal (NORM), moderate (MOD) and severe (SEV) degrees of white striping on broiler breast fillets with different weights. With the increase in growth rate and muscle size, there has been as increase in incidence of pectoral myopathies. One of the recent meat quality problems that have been identified is the appearance of white striping or striations in poultry breast fillets following the direction of the muscle fiber. The condition is mainly associated with heavier birds, and high incidences (>50%) can occur, especially in big birds. For this experiment, 12-thousand Cobb 500 male broilers (42 d-old) of a commercial broiler strain were slaughtered and 144 (12%) broilers breast fillets were collected. The samples were separated according to weight (>310 or < 310 g). The macroscopic classification of the carcasses was performed according to the degree of severity of the stripes apparent on the pectoral muscle considering 3 groups: NORM, MOD and SEV. The data were analyzed using ANOVA. Individual birds were considered as the experimental unit for the entire analysis. Eighty-four percent (121) broilers breast fillets being classified as of moderate degree of white striping, 8.33% (12) SEV, exhibited white lines, parallel to the muscle fibers very visible on the fillet surface, and only 7.64% (11) considered as NORM, did not show any distinct white lines. Seventy-nine broilers breast fillets presented weight > 310 g, being 12.65% (10) considered as SEV, 82.27% (66) as MOD and only 5.08% (3) as NORM, totaling 94.92% of the samples with the presence of white striping. On the other hand, of the 65 samples with weight less than 310 g, 87.7% showed presence of this myopathy, being only 3.08% (2) classified as SEV, 84.62% (55) as MOD and 12.31% (8) as NORM. This study results confirm that there is a relationship between the weight of the fillet with the incidence and degree of white striping, that suggests that the increase in growth rate of poultry, accompanied with the selection for greater growth rates of broilers, could produce a greater incidence of this condition.

Key Words: meat quality, myopathy, white striping

TH301 Evaluation of metabolic, endocrine and meat quality traits in longissimus muscle of beef cattle. M. D. Poleti, A. F. Rosa, C. T. Moncau, S. L. Silva, J. P. Eler, and J. C. C. Balieiro*, *University of Sao Paulo, Pirassununga, Sao Paulo, Brazil.*

The purpose of this work was to evaluate the metabolic, endocrine and meat quality traits in samples of longissimus dorsi (LD) muscle. We used 241 Nelore cattle raised in pasture and finished in feedlot. The animals were slaughtered at approximately 24 mo and with average weight of 508 kg. LD muscle samples were harvested from the carcass and frozen in liquid nitrogen for determination of glycogen and lactate concentrations. Steaks of 2.5 cm LD muscle (between 12° and 13° ribs) were removed at 24 h post mortem, vacuum packaged and kept at 2°C for until 14 d for subsequent Warner-Bratzler Shear Force (WBSF) evaluation. At 1, 7 and 14 d, were removed from refrigeration, allowed to bloom (20 min) and measured for L*, a* and b* objectively by using a portable spectrophotometer. Blood samples to obtain plasma were collected beginning of feedlot (ante-mortem) and at slaughter (post mortem) to determine cortisol and adrenocorticotropic hormone (ACTH) concentrations. The pH after 24 h (pH24hs) greater or equal to 5.8 were considered as potential DFD meat and pH lower than 5.8 were considered regular meat. We observed that 18.7% (n = 45) of the samples had pH24hs greater or equal 5.8. The glycogen and lactate concentrations in muscle ranged from 1.71 to 72.51 μmol/g and 1.54 to 49.53 μmol/g, respectively. However, in samples with pH24hs ≥ 5.8, only 37.8% (n = 17, for glycogen) and 8.9% (n = 3, for lactate) samples showed glycogen and lactate concentrations below 6.13 μmol/g and 6.0 μmol /g, respectively. The pH24hs had significant ($P > 0.05$) effect for color measurements (L*, a*, b*) at all times of aging, as well as, for cooking loss at 1st and 14th days of aging. The pH24hs had not significant effect ($P > 0.05$) for cortisol and ACTH concentrations (ante-mortem and post mortem). In the same way, the shear force values at different days of aging were not influenced by pH24hs. These results suggest that the concentration of glycogen in muscle is one of the factors that determine the appropriate reduction pH 24 h, but not the only one.

Key Words: DFD meat, animal stress, HPA axis reactivity

TH302 Visible and near infrared spectroscopy to predict beef quality traits in *Bos indicus* cattle. S. L. Silva*[1], M. N. Bonin[1], R. C. Gomes[2], M. R. Mazon[1], T. M. C. Leme[1], J. M. Balage[1], L. S. Martello[1], J. B. S. Ferraz[1], and P. R. Leme[1], *[1]University of Sao Paulo, Pirassununga, SP, Brazil, [2]Embrapa Beef Cattle, Campo Grande, MS, Brazil.*

This study was carried out to evaluate the ability of visible and near infrared spectroscopy (VISNIRS) to evaluate beef quality traits of Longissimus muscle (LM) in Nellore (Bos indicus) cattle. Twenty 4 h after slaughter carcasses from 206 Nellore bullocks (n = 103) and steers (n = 103) were quartered between 12th and 13th ribs and the VISNIR spectra (400 to 1,500nm), color measurements (L*,a*, b*)

and pH (pH24) of LM were collected. Following LM samples were collected for Warner-Bratzler shear force (WBSF) and cooking loss (CL) determinations. Samples were grouped in tender (WBSF ≤ 5.5 kg), intermediate (5.57.5 kg) and tough (WBSF ≥ 7.5 kg) meat. The group of animals who had tender samples showed smaller absorbance from 400 to 1,170nm whereas in those of tough group absorbance was greater in near infrared region (1,170 to 1,500nm). Regression equations obtained from VISNIR spectral data explained high portion of variation of WBSF (R^2 = 0.84 and 0.80), CL (R^2 = 0.96 and 0.80), pH24 (R^2 = 0.78 and 0.64), L* (R^2 = 0.93 and 0.82), a* (R^2 = 0.96 and 0.92), b* (R^2 = 0.95 and 0.70) in calibration and validation data sets, respectively. When comparisons were made considering tenderness groups (predicted VS observed WBSF), samples were correctly classified 86% of time. The VISNIRS technology can be used as a nondestructive tool to estimate beef quality traits of fresh meat.

Key Words: beef cattle, meat, tenderness

TH303 Effect of aging on pH and water holding capacity of muscles from Nellore beef cattle. L. R. Simonetti, J. F. Lage, E. E. Dallantonia, E. San Vito*, E. A. Oliveira, M. Machado, L. M. Delevatti, G. M. Delamagna, and T. T. Berchielli, *São Paulo State University, Jaboticabal, São Paulo, Brazil.*

This objective of this study was to evaluate the effects of aging on pH and water holding capacity (WHC) of 5 muscles: biceps femoris (BF), gluteus medius (GM), longissimus dorsi (LD), semitendinosus (ST) and trapezius thoracis (TT) from Nellore young bulls fed in feedlot. Fourteen young bulls (Nellore), with 15 mo of age were confined to individual stalls with feeders and drinkers. The diet was consisted of 40% corn silage and 60% of concentrate (grounded corn, soybean meal, urea/ammonium sulfate, mineral mixture). After 60 d of feed, the animals were harvested and the carcasses were chilled at 0°C for 24 h. The muscles were removed, individually vacuum packaged and chilled at 0°C for 1, 7 and 14 d post mortem. The WHC was measured for the difference between the weights of the sample before and after it was subjected to a pressure of 10 kg for 5 min. The experiment was conducted according to a completely randomized design in a factorial arrangement 3 × 5 (3 aging days × 5 muscles) with 14 replicates. Data were analyzed by the GLM procedure of SAS, and the Tukey test used considering 5% probability. The interaction between aging days and muscles was significant for WHC (P = 0.01). The pH (P < 0.01) and WHC (P < 0.01) from beef evaluated in 7 d was lower (P < 0.01) than beef evaluated in 1 or 14 d. The TT muscle had higher value of pH (P = 0.01) than all muscles evaluated. The BF muscle had higher WHC (P = 0.01) than ST and TT muscles. The aging reduce the pH and the water holding capacity of beef. The biceps femoris muscle showed greater water holding capacity than those muscles semitendinosus and trapezius thoracis.

Key Words: beef cattle, commercial cut, meat quality

TH304 Bone breakage resistance of 25-kg piglets fed diets with phytase containing benzoic or butyric acid. L. M. Rufino, M. Q. Resende*, R. M. Geraldine, J. H. Stringhini, M. A. Andrade, A. G. Mascarenhas, A. C. S. Barnabé, B. P. Mota, and R. C. Nunes, *Universidade Federal de Goiás, Goiânia, GO, Brazil.*

In this paper, bone breakage resistance for 25-kg piglets fed diets containing phytase and benzoic or butyric acid was evaluated. A total of 120 piglets from commercial genetic line, weighing 6.69 ± 0.93 kg were raised until reach 25 kg in a randomized block design with 6 treatments and 5 replicates each. The mashed experimental diets were formulated based on Brazilian tables recommendations. Feed and water were offered ad libitum. Treatments were (1) Control diet with 0.41% available phosphorus; (2) Diet reduced to 0.15% available phosphorus; (3) Diet 2 plus 1.000 FYT/kg of phytase; (4) Diet 2 plus 1.000 FYT/kg of phytase with 0.3% butyric acid; (5) Diet 2 plus 1.000 FYT/kg of phytase with 0.75% benzoic acid; and (6) Diet 2 plus 1.000 FYT/kg of phytase with 0.3% butyric acid and 0.75% benzoic acid. When piglets reached 25-kg live weight, one animal per replicate were euthanized, wright leg was collected to analysis. Bones were dissected, second and third metacarpals were prepared, half of them was boiled and other half tested as a raw bone and dried in air-forced oven at 55°C. Bone breakage resistance was measured in a Instron Corporation IX Automated Materials Testing System equipment, model 4204. Data were submitted to ANOVA and compared by Tukey test (5%) with the computational program Statsoft (2001). Lower bone breakage values ($P < 0.05$) were obtained with animals fed 0.15% phosphorus content diet compared with the ones fed the same diet but added with butyric acid, benzoic acid and phytase. Boiled bones were more resistant to breakage. It is possible to conclude that in reduced phosphorus diets, the inclusion of phytase, butyric acid and benzoic acid do not affected bone breakage.

Key Words: enzyme, organic acid, phosphorus reduction

TH305 Phosphorus digestibility of triticale distillers dried grains with solubles without or with phytase supplementation determined using the regression method in growing pigs. P. C. Xue* and O. Adeola, *Department of Animal Sciences, Purdue University, West Lafayette, IN.*

An experiment was conducted to determine the true total-tract digestibility (TTTD) of phosphorus (P) in triticale distillers dried grains with solubles (DDGS) using regression method and to investigate the TTTD of P of triticale DDGS response to phytase. The triticale DDGS sample that used in this experiment contains 0.69% of total P. Six diets consisting of 3 diets without phytase and 3 diets with phytase (500 FTU/kg of diet) were formulated to contain 3 levels of DDGS (30, 40, and 50%) in which all the P was supplied by triticale DDGS at 0.21, 0.28, and 0.35% in each diet in a 2 × 3 factorial arrangement. Corn starch, sucrose, and soy oil were used to formulate the semi synthetic diets. Limestone was included to maintain the similar Ca:P ratio at 1.25:1 across diets. A total of 48 barrows (initial BW 22.2 ± 1.3 kg) were assigned to the 6 diets in a randomized complete block design. There was a 5-d adjustment period followed by a 5-d total collection period with chromic oxide as a marker to time the initiation and termination of fecal collection. The daily feed intake was adjusted to 4% of the average BW of each block. The results showed that the P intake, fecal P output, and digested P increased linearly ($P < 0.01$) with the increasing level of DDGS in diets. There was a main effect ($P < 0.001$) of phytase on apparent total-tract digestibility (ATTD) of P. In diets without added phytase, the ATTD of P in triticale DDGS were determined to be 65.01, 67.70, and 63.16% for the diets with 30, 40, and 50% DDGS, respectively; the corresponding values for diets with added phytase were 77.30, 76.26, and 75.66%. By regressing daily digested P against daily P intake, the TTTD of P was estimated at 75.37 or 81.08% for triticale DDGS without or with added phytase, respectively. The estimated average endogenous P loss for diets contained phytase or not was 0.172 and 0.080 g/d, respectively. In conclusion, the TTTD of P in triticale DDGS without supplemental phytase was determined to be 75.37 and 81.08% in the presence of phytase at 500 FTU/kg of the diet.

Key Words: phosphorus, triticale DDGS, true digestibility

TH306 Performance of piglets in pre-starter phase fed diets containing organic acids and phytase. L. M. Rufino, J. H. Stringhini, M. Q. Resende*, H. H. C. Mello, A. G. Mascarenhas, N. S. M. Leandro, I. C. Di Castro, M. P. F. Silva, and R. C. Nunes, *Universidade Federal de Goiás, Goiânia, GO, Brazil.*

The addition of butyric acid and benzoic acid in diets containing phytase were studied to evaluate piglet performance from 6.69 ± 0.93 kg until 15 kg mean live weight. A total of 120 castrated male commercial piglets were allotted in a randomized block design with 6 treatments and 5 replicates. Temperature and air moisture were measured twice a day, feed and water were offered ad libitum and animals were individually weighed weekly. Variables were submitted to ANOVA and averages compared by Tukey test at 5% probability (SAS, 2008). Mashed diets were formulated according to Brazilian tables requirements, based in corn and soybean meal, considering the inclusion of butyric acid, benzoic acid and phytase. Treatments were (1) Control diet with 0.41% available phosphorus; (2) Diet reduced to 0.15% available phosphorus; (3) Diet 2 plus 1.000 FYT/kg of phytase; (4) Diet 2 plus 1.000 FYT/kg of phytase with 0.3% butyric acid; (5) Diet 2 plus 1.000 FYT/kg of phytase with 0.75% benzoic acid; and (6) Diet 2 plus 1.000 FYT/kg of phytase with 0.3% butyric acid and 0.75% benzoic acid. Piglets fed diets containing phytase and 0.75% benzoic acid increased ($P > 0.05$) average final weight in 11.5% compared with the animals in the control diet. These same animals showed higher total and daily weight gain compared with the ones fed diets reduced to 0.15% available phosphorus and the control treatments. It is possible to conclude that benzoic acid combined to phytase increase performance of piglets from 6.7 kg to 15 kg mean live weight.

Key Words: enzymes, feed conversion, phosphorus reduction

TH307 Effect of protease on growth performance of nursery pigs fed diets with different soybean meal inclusion. J. Guo*[1], P. Biggs[2], and S. W. Kim[1], *[1]North Carolina State University, Raleigh, [2]BioResource International, Morrisville, NC.*

Versazyme (BioResource International, Morrisville, NC), a native protease found in *Bacllus licheniformis*, has been extensively used in poultry production to improve the digestibility of protein. In vitro data has shown that Versazyme is able to hydrolyze glycinin and β-conglycinin, which are considered the major limitation factors for nursery pigs to digest soybean meal (SBM). This study was to test if dietary supplementation of Versazyme will help the growth of nursery pigs fed diets containing soybean meal to provide adequate or reduced amount of TID Lys (100

or 85% of NRC). One hundred twenty pigs (7.3 ± 0.1 kg) weaned on d 21 were allotted to 4 dietary treatments on d 25 of age based on 2 × 2 factorial arrangement with Versazyme (0.00% and 0.05%) and TID Lys (1.19% and 1.01%). Diets with 2 levels of TID Lys were achieved by the amount of SBM included (33% vs. 27%). The diets were fed for a period of 2 weeks. Each treatment consisted of 10 pens (5 barrow pens and 5 gilt pens) with 3 pigs per pen. ADG, ADFI, and G:F were measured at the end of each week. Pigs fed diets containing 1.19% TID Lys had greater ($P < 0.05$) ADG (267 vs. 215 g/d) and G:F (0.68 vs. 0.58) during wk 1, wk 2, and the entire 2 wk period compared with 1.01% TID Lys. There were interactions ($P < 0.05$) of TID Lys and Versazyme for ADG and ADFI during wk 2 and the entire 2 wk period indicating that ADG and ADFI of pigs in 1.19% TID Lys (33% soybean meal) were further improved by the supplementation of Versazyme whereas they were not for pigs in 1.01% TID Lys (27% soybean meal). Collectively, Versazyme can be helpful with improving ADG (282 vs. 252 g/d) and ADFI (411 vs. 375 g/d) of pigs when consuming a diet with soybean meal as high as 33%.

Key Words: nursery pig, protease, soybean meal

TH308 Effect of enzyme supplementation of mango (*Mangifera indica* L.) seed kernel- based diet on the performance of broiler chickens. A. A. Odunsi*, O. A. Olu-Arotiowa, A. O. Akinwunmi, T. A. Rafiu, T. O. Akande, and A. O. Afolabi, *Ladoke Akintola University of Technology, Ogbomoso, Oyo, Nigeria.*

The utilization of mango seed kernel (MSK) (an agro-industrial by-product) - based diet supplemented with or without exogenous enzymes (Hamecozyme, Hameco Agro Bv Holland or Maxigrain, Polchem Hygiene Laboratories India) as a replacement for maize in the diets of broiler chickens was investigated. One hundred and 20 d old unsexed broiler chicks were randomly distributed into 4 experimental dietary treatments each with 3 replicates and 10 birds per replicate using a completely randomized design. The experimental diets were the control (without MSK or enzyme), diet 2 (10%MSK without enzyme), diet 3 (10%MSK + Hamecozyme) and diet 4 (10%MSK + Maxigrain). The birds were fed the diets for a 28-d period during which data were obtained on ADFI, ADG, G:F, hematology and carcass characteristics. The results showed that broilers fed 10% MSK based diet (without enzyme) had a reduced ($P < 0.05$) ADG (−23.1%) and poorer G:F (−21.5%) when compared with those on the control diet. Addition of Hamecozyme or Maxigrain enzymes positively enhanced ($P < 0.05$) ADG (16.8% or 7.3%), ADFI (8.9% or 5.7) and G:F (7.5% or 2.3%) respectively compared with the un-supplemented group. Carcass measures (breast, neck, back, wing, drumstick and thigh) and relative weights of the kidney, liver, heart and lungs did not significantly ($P > 0.05$) change with enzyme supplementation, and had no clear trends. However, gizzard weights were heavier ($P < 0.05$) in broilers fed MSK compared with those without MSK. Hemoglobin, packed cell volume and red blood cells of broilers were not ($P > 0.05$) influenced by dietary treatments but the white blood cells increased ($P < 0.05$) with the inclusion of MSK and enzyme in broiler diets. Conclusively, the use of Hamecozyme or Maxigrain improved ADG of broiler chicks fed MSK by 16.8 and 7.3% respectively over the unsupplemented and, reduced the amount of maize needed in the diets of starter broiler chickens by 21%.

Key Words: Mango seed kernel, enzyme, broiler chicken

TH309 Effects of exogenous enzyme supplemented to a corn and soybean meal based diets on energy and nitrogen balance in nursery pigs. Y. B. Kim* and S. W. Kim, *North Carolina State University, Raleigh.*

Supplementation of exogenous enzymes to stimulate nutrient digestion has attracted considerable interest in the pig industry. The current study was conducted to determine the effects of dietary supplementation of exogenous enzyme (Enervance, Genebiotch; major enzymes are cellulase: 5,000 U/g; and xylanase: 500 U/g) on digestibility and nutrient balance of DM, energy, and N in nursery pigs fed a corn and soybean meal based diet. Fifteen barrows (11.52 ± 0.52 kg BW) at 35 to 40 d of age were allotted to a repeated 3 × 3 Latin square design with 3 diets and 3 periods. The dietary treatments included (1) a corn and soybean based diet (CON), (2) CON + 0.05% Enervance, and (3) CON + 0.1% Enervance. Daily feed allowances were equal to $0.09 \times BW^{0.75}$ and were given in 2 equal meals. Chromic oxide (0.5 g/kg) was used as a marker. Each period consisted of 5 d of adaptation and 3 d of total fecal and urinal collection. Pigs fed the diet supplemented with 0.1% Enervance had greater ($P < 0.05$) apparent total tract digestibility of DM (81.2%) and GE (88.3%) compared with pigs fed the CON (79.3% and 87.2%, respectively) and pigs fed the diet supplemented with 0.05% Enervance (79.8% and 87.4%, respectively). No differences were found between dietary treatments in apparent total tract N digestibility ($P = 0.106$). Pigs fed the diet supplemented with 0.1% Enervance had greater (84.4 vs. 83.6%; $P < 0.05$) energy retention (percentage of intake) compared with pigs fed the CON. No differences ($P = 0.588$) were found between dietary treatments in N retention. In conclusion, exogenous enzyme mainly containing cellulose and xylanase had beneficial effects on energy utilization but not on N retention in nursery pigs fed a corn and soybean meal based diet.

Key Words: digestibility, energy retention, enzyme

TH310 Effect of a controlled fermentation process on the content of digestible phosphorus in diets for growing pigs. R. Schemmer*[1], B. Drüing[1], G. Stalljohann[2], and K.-H. Südekum[1], *[1]University of Bonn, Bonn, Germany, [2]Agricultural Chamber of North Rhine-Westphalia, Münster, Germany.*

This study determined the effect of controlled fermentation processes on P digestibility in diets for growing pigs. Six diets were formulated and adjusted to a maximum of 2.0 g/kg DM of digestible P to minimize regulatory fecal P excretion. The diets were as follows: 1) basal diet (BD; 64.3% pregelatinized wheat starch, 14.8% dried beet pulp, 8.5% potato protein, 6.5% whole-egg powder, 2.2% cellulose, 1.7% soybean oil, 1.2% premix, 0.8% $CaCO_3$); 2) dry diet (DD)+ 40% BD; 3) fermented diet (FD)+ 40% BD; 4) wheat + 40% BD; 5) barley + 40% BD; and, 6) soybean meal + 50% BD. The DD and FD consisted of (DM basis) wheat (58%), barley (26%), soybean meal (SBM) (15%), and soybean oil (1%). P digestibility values for DD, FD, wheat, barley, and SBM were calculated by subtracting the respective values of BD. The FD was prepared in a batch process at 30% DM (pH, 3.8). Fermentation was induced by a lactic acid bacteria strain and water (25°C). Eight male castrated pigs [(German Landrace × Large White) × Pietrain] from one litter with an initial BW of 24.5 (SD 1.74) kg were used. Each diet was tested simultaneously with 4 pigs using a standardized protocol. Pigs were kept in metabolism cages and consumed their feed in amounts corresponding to 2–2.5 multiples of ME requirement for maintenance. After 7 d for adaptation, feces were completely collected for 7 d to determine P digestibility. Total P concentrations of BD and of wheat, barley, SBM, DD, and FD were 1.84, 3.50, 3.96, 6.81, 4.17, and 4.22 g/kg DM, respectively. The mean (SD) P digestibility values of BD and of wheat, barley, SBM, DD, and FD were 72.7 (3.28), 70.0 (2.54), 51.2 (0.72), 50.9 (5.55), 63.5 (2.87), and 80.8% (1.47), respectively. Fermentation improved P digestibility (DD compared with FD) by 17 percentage units ($P < 0.001$). Furthermore, P digestibility of DD calculated from measured values of ingredients weighted by their dietary inclusion level gave almost perfect accord with measured P digestibility of DD (62.1 versus 63.7%).

Key Words: fermentation, phosphorous digestibility, pigs

TH311 Effects of dietary fat source and feeding pattern on performance, tissue fatty acids composition, and serum insulin and ghrelin dynamics in grower-finisher pigs. J. S. Kim[1], S. L. Ingale[1], K. H. Kim[1], S. Lee[1], J. S. Kim[1], E. H. Kim[2], D. C. Lee[2], and B. J. Chae*[1], *[1]Department of Animal Resource Science, Kangwon National University,, Chuncheon, Gangwon-do, Republic of Korea, [2]Department of Biosystem Engineering, Kangwon National University, Chuncheon, Gangwon-do, Republic of Korea.*

The present study investigated the effects of dietary fat source and feeding pattern on performance, fatty acids composition of various tissues, and dynamics of serum insulin and ghrelin in grower-finisher pigs. A total of 128 grower-finisher pigs (initial BW, 81.23 ± 0.32 kg) were allotted to 4 treatment groups with 8 pigs per pen and 4 pens per treatment. Pigs were fed diets containing linseed oil or animal fat, either ad libitum or restricted in 2 × 2 factorial arrangement for 28 d. For analysis of serum ghrelin and insulin dynamics blood samples was collected 1 h before feeding (−1 h) and 2, 4 and 6 h after feeding. Data were analyzed as a 2 × 2 factorial arrangement of treatments in completely randomized block design and the main effects of fat source, feeding pattern and their interaction were determined by the GLM procedure of SAS. Fat source of diet had no effects ($P > 0.05$) on growth performance and ATTD of nutrients. The ADG and ADFI of pigs fed ad libitum were greater ($P < 0.05$) than restricted fed pigs. The G:F of restricted fed pigs was greater ($P < 0.05$) than ad libitum fed pigs. Pigs with restricted feeding had greater ($P < 0.05$) ATTD of DM, CP, and GE than pigs fed ad libitum. Pigs fed linseed oil diet had greater ($P < 0.05$) concentration of polyunsaturated fatty acids in liver and adipose tissues. Pigs offered ad libitum feed had greater ($P < 0.05$) serum insulin during all samplings and increased after feeding in all treatments. Serum ghrelin concentrations in restricted fed pigs were highest ($P < 0.05$) before feeding and declined 2 and 4 h feeding. Also, serum ghrelin concentration of restricted fed pigs was greater ($P < 0.05$) than ad libitum fed pigs during −1 and 6 h sampling. Serum insulin and ghrelin concentration were not affected by dietary fat source. It is concluded that feeding of linseed oil instead of animal fat improved the polyunsaturated fatty acids content of tissues without affecting performance pigs.

Key Words: animal fat, fatty acid, feeding pattern

TH312 Influence of level of fiber inclusion in the diet two different hygiene conditions in weaned pigs. J. D. Berrocoso*, B. Saldana, P. Guzman, L. Camara, and G. G. Mateos, *Universidad Politecnica de Madrid, Madrid, Spain.*

The effects of including addition of fiber source on performance of weanling pigs reared under different hygiene conditions (“clean” vs. “dirty barn”) was evaluated. There was a control diet based that contained 2.2% crude fiber and 8 extra treatments similar to the control diet that included 4 different sources of fiber (SBP, sugarbeet pulp, STR, cereal straw, OH, oat hulls, and WHM, wheat middling) at 2 levels of inclusion (2.5 and 5%). A first batch of pigs were housed a clean barn and afterward, a second batch of pigs of same origin was housed in the same barn without any cleaning. Data on growth performance and nutrient digestibility was analyzed as a completely randomized design with hygiene conditions and source and level of fiber as main effects. In addition, treatment means were compared using these preplanned non-orthogonal contrasts: (1) control vs. all additional fiber diets, (2) control vs. all additional fiber diets in clean hygiene conditions, and (3) control vs. all additional fiber diets in dirty hygiene conditions. For the entire experiment (21 to 42 d of age), pig reared in the clean environment had higher ADG and ADFI ($P < 0.05$) and lower incidence of post weaning diarrhea (PWD; $P < 0.001$) than pig in the dirty environment. Fiber inclusion did not affect pig growth but PWD was lower ($P < 0.01$) in pigs fed the control diet than in pigs fed the fiber containing diets. CP digestibility was not affected by fiber source. Total tract apparent digestibility (TTAD) of all nutrients was higher ($P < 0.001$) for the SBP diet than for the STR diet with diets containing OH or WHM being intermediate. Also, TTAD of the nutrients was higher ($P < 0.001$) for pigs reared in the clean than for pigs reared in the dirty environment. It is concluded that, piglets reared under high hygiene status showed improved nutrient digestibility and growth performance and reduced PWD as compared with pigs reared under low hygiene status. Also, the inclusion of fiber in the diet increased PWD and reduced nutrient digestibility but had little effect on growth performance

Key Words: dietary fiber, pig, sanitary conditions

TH313 Effects of inclusion of spray-dried porcine plasma in lactation diets on sow and litter performance. S. D. Carter*[1,6], L. I. Chiba[2,6], M. D. Lindemann[3,6], M. J. Estienne[4,6], and G. J. M. M. Lima[5,6], *[1]Oklahoma State University, Stillwater, [2]Auburn University, Auburn, AL, [3]University of Kentucky, Lexington, [4]Virginia Tech University, Blacksburg, [5]Embrapa Swine and Poultry, Concordia, SC, Brazil, [6]S-1044 Committee on Nutritional Systems for Swine to Increase Reproductive Efficiency.*

A cooperative study, utilizing 404 primi- and multi-parous crossbred sows from 5 experiment stations (AL, KY, OK, VA, and Brazil), was conducted to determine the effects of inclusion of 0.50% spray-dried porcine plasma (Appetein, APC Inc., Ankeny, IA) in corn-soybean meal diets on sow and litter performance. Crossbred sows were fed corn soybean meal-based diets containing a minimum of 0.50% SID lysine during gestation. Sows were allotted at farrowing, based on body weight and parity, to 2 dietary treatments. The control (C) diet was a fortified corn soybean meal diet. Appetein (App) was added to the control diet at 0.50% at the expense of soybean meal to formulate the test diet. Both diets were formulated to 0.90% SID lysine and 3,414 kcal/kg ME. A common trace mineral and vitamin premix was used at all stations with the exception of Brazil. Chromium picolinate was added to each diet to provide 200 ppb Cr. Sows were allowed ad libitum access to feed. Sows were weighed within 24 h after farrowing, and all litters were adjusted to >10 pigs/litter by d 2 following farrowing. Average sow parity, number of pigs on d 2, and lactation length for the C and App treatments were, respectively: 2.5 and. 2.3; 11.0 and 10.7; and 23 and 23 d. The ADFI during lactation for C and App diets were similar (5.65 kg/d; $P > 0.10$). Sow weight after farrowing averaged 217 kg ($P > 0.10$). The number of pigs weaned (9.9 vs. 9.7), litter weaning weights (68.4 vs. 69.1 kg), litter weight gains (51.6 vs. 52.2), sow weight change during lactation (−6.0 vs. −8.3 kg), and return-to-estrus interval (7.5 vs. 7.2 d) were not affected ($P > 0.10$) by dietary treatment. There were no station × treatment interactions ($P > 0.10$). Additionally, the data were sorted by parity (<3 vs. 3 and greater), ambient temperature (hot vs. thermoneutral), and season (summer vs. winter). No differences between treatments were observed within any data set. These results indicate no benefit of inclusion of spray-dried porcine plasma in lactation diets for sows nursing > 10 pigs and consuming a corn-soybean meal diet containing 0.90% SID lysine.

Key Words: sow, spray-dried porcine plasma, lactation

TH314 Effects of spray-dried plasma replacement for soy protein concentrate on growth performance of weaned pigs. M. Q. Resende*, A. G. Mascarenhas, R. C. Nunes, E. Arnhold, K. A. Teixeira, K. M. Borges, L. V. G. C. Mota, and H. H. C. Mello, *Universidade Federal de Goiás, Goiânia, GO, Brazil.*

Some research demonstrate improvement on piglets growth performance (GP) by including soy protein concentrate (SPC) on post weaning diets, due to reduction of the hypersensitivity to soy allergens. The aim of this work was to assess the spray dried plasma (SDP) replacement for SPC over GP, small intestine histology and blood leucocytes and lymphocytes of post weaned pigs. A total of 54 pigs, weaned at 21 ± 2 d (initial BW: 6.96 ± 0.80 kg), were randomly assigned to 3 diets, 6 replicate pens per diet, and 3 pigs per pen in a randomized block design by initial BW. Corn-soybean mash diets were isonitrogenous and isocaloric: T1) 0% SPD + 5% SPC; T2) 2.5% SPD + 2.5% SPC; T3) 5% SPD + 0% SPC. Experimental diets were fed in 2 dietary phases (0 – 11 d and 11 – 20 d post weaning), and a common diet were fed through 20 – 45 d post weaning. Pigs were allowed ad libitum access to feed and water throughout the 45 d experimental period. The minimum and maximum ambient temperature was 18°C and 32°C. Animals were weighed at d 0, 11, 20 and 45. Feed intake was recorded at d 11, 20 and 45 post weaning. A pig per pen was euthanized on d 11 to collect small intestine and blood samples. Data were analyzed by ANOVA using the GLM procedure of SAS, and the means of the treatments were compared by Duncan test. T2 showed greater final body weight (9.606, 9.254, 8.659 kg), ADFI (0.324, 0.268, 0.253 g) and ADG (0.212, 0.172, 0.124 g) during 0 – 11 d period, compared with T1 and T3. However there were no statistical differences in GP during 45 d experimental period among treatments. On d 11 no difference were observed in villus height, crypt depth and villus:crypt ratio of duodenum, jejunum and ileum. Related to blood cells, T1 showed fewer leucocytes (13.501, 16.350, 19.638 × 10^3/μL) and lymphocytes (6.869, 9.164, 10.123 × 10^3/μL) counts in blood compared with T2 and T3. This confirms the SDP potential to improve immunity of post weaned pigs, which was not promoted by SPC. We conclude that SDP should not be totally replaced from SPC in piglet diets during the first 11 d after weaning, but the use of both can be recommended.

Key Words: intestinal morphology, lymphocyte, nursery diet

TH315 Growth performance, carcass characteristics and meat quality of pigs fed crude glycerin. C. A. Ordonez-Gomez*[1,3], S. Castaneda[1], H. Florez[1], G. Afanador[2], and C. Ariza-Nieto[1], *[1]CORPOICA, Bogota, Colombia, [2]Universidad Nacional de Colombia, Bogota, Colombia, [3]Universidad Francisco de Paula Santander Ocana, Ocana, Colombia.*

The aim of this study was to evaluate the effect of the inclusion level of crude glycerin in the diet of growing pigs on growth performance, carcass characteristics and meat quality. The crude glycerin presented the following composition: 3696 kcal GE/kg, 3579 kcal ME/kg, 8.29% moisture, 82.0% glycerol, 0.79% crude fat, 1.21% sodium and 16 ppm of methanol. Diets were formulated as isocaloric and isoprotein (3200 kcal ME/kg in all phases, 19.1% CP, 0.879% digestible lysine from 20 to 30 kg BW; 17.7% CP, 0.806% digestible lysine from 30 to 50 kg BW; 16.8% CP, 0.747% digestible lysine from 50 to 70 kg BW; 15.5% CP, 0.663% digestible lysine from 70 to 100 kg BW). A total of 36 pigs (average BW 23.05 ± 2.86 kg) were randomly assigned to one of the 3 treatments: 1) control without crude glycerin; 2) 5% crude glycerin; 3) 10% crude glycerin. Pigs were housed in 12 pens; 4 replicates (pens), 3 pigs/replicate. During the study, pigs in each pen were weighed weekly and feed residuals were used to calculate daily feed intake and feed conversion. At the time of slaughter (100 kg BW), one pig per replicate was selected and slaughtered to determine carcass weight (CW), backfat thickness (BF), loin eye area at the last rib on the right side (LA), and lean meat yield (LMY). Loin samples were cut into chops to determine quality attributes such as color, pH, water retention capacity (WRC), and shear force (SF). Data were analyzed using PROC GLM of SAS (Ver. 9.0, SAS Institute, Cary, NC) as a completely randomized block design. Results showed that crude glycerin inclusion did not affect ($P > 0.05$) growth performance (ADG 848 ± 42 g; ADFI 2361 ± 139 g; feed conversion 2.79 ± 0.2 g/g), carcass characteristics (CW 82 ± 8.5 kg; LWY 37.2 ± 7.5 kg) and meat quality (WRC 6.4 ± 2.1 mm^2/mm^2; SF 5.7 ± 1.5 kg). It can be concluded that crude glycerin inclusion can be used up to 10%, without adversely affecting the performance of growing pigs.

Key Words: crude glycerin, growth performance, pork quality

TH316 Energy concentrations in distillers dried grains with solubles containing different fat concentrations and the effect of corn oil addition on energy concentrations in diets fed to growing pigs . D. Y. Kil[1], J. W. Lee[2], D. M. D. L. Navarro*[2], and H. H.

Stein[2], *[1]Chung-Ang University, Anseong-si, Gyeonggi-do, Republic of Korea, [2]University of Illinois at Urbana-Champaign, Urbana.*

An experiment was conducted to determine apparent digestible energy (DE) and metabolizable energy (ME) concentrations in 3 sources of distillers dried grains with solubles (DDGS) containing different fat concentrations and the effect of addition of supplemental corn oil to the diets containing low-fat DDGS on DE and ME concentrations of the diets. A total of 48 growing barrows were used in 2 separate periods and each period consisted of 24 barrows. Initial body weights of pigs were 17.5 ± 1.19 and 13.2 ± 1.53 kg for period 1 and 2, respectively. Each period consisted of 5-d adaptation period to the diets and 7-d collection period. Pigs were raised in metabolism crates at all times. Three sources of DDGS were conventional DDGS containing high level of fat (HF-DDGS), DDGS containing medium level of fat (MF-DDGS), and DDGS containing low level of fat (LF-DDGS). The basal diet was formulated with 972 g/kg corn and 3 diets were prepared by mixing 480 g/kg corn with 500 g/kg HF-DDGS, MF-DDGS, or LF-DDGS. Two additional diets were formulated by adding 15.0 or 23.0 g/kg corn oil to the diets containing MF-DDGS or LF-DDGS at the expense of MF-DDGS or LF-DDGS. Results indicated that the LF-DDGS diet had less ($P < 0.01$) DE and ME concentrations than the HF-DDGS diet, but the MF-DDGS diets had DE and ME concentrations that were not different from the HP-DDGS diet or the LF-DDGS diet. Addition of corn oil to the MF-DDGS diet or the LF-DDGS diet increased DE and ME concentrations of these diets, which were close to those of the HF-DDGS diet. The DE and ME concentrations of LF-DDGS and MF-DDGS were less ($P < 0.01$) than those of HF-DDGS, but the energy values for MF-DDGS were not different from those for LF-DDGS. In conclusion, low-fat DDGS has less energy value than conventional high-fat DDGS, and therefore, when low-fat DDGS is included in swine diets at the expense of high-fat DDGS, addition of supplemental oil or fat may be required to compensate for decreased energy concentrations in the diets.

Key Words: distillers dried grains with solubles, fat concentration, pig

TH317 Effect of diet complexity and an enzyme-treated soy protein plus yeast on performance in weanling pigs. T. Tsai*[1], H. Kim[1], G. Fitzner[2], J. K. Apple[1], J. J. Chewning[1], and C. V. Maxwell[1], *[1]University of Arkansas, Fayetteville, [2]Hamlet Protein Inc., Findlay, OH.*

Weaned pigs (n = 288; 20.4 ± 1.26 d, BW 6.52 ± 0.02 kg) were used to test the effect of diet complexity on the efficacy of increased replacement of ETSP with ETSP plus yeast (ETSPY) on growth performance. Pigs were blocked by BW into 8 blocks, allotted to gender-balanced pens (6 pigs/pen), and pens within blocks were assigned randomly to 1 of 6 dietary treatments fed during phases 1 (10 d) and 2 (13 d): (1) complex diets (PC) with SBM, fishmeal, plasma protein (PP), whey, and lactose; (2) simple diets (NC) containing SBM, PP, and whey; (3) NC diets with 20 and 15% ETSP, respectively; (4) NC diets with 33% ETSP replaced by ETSPY; (5) NC diets with 67% ETSP replaced by ETSPY; and 6) NC diets with 100% ETSP replaced by ETSPY. All pigs received a corn-SBM diet during phase 3 (14 d). Nursery diets were formulated with 2.6, 2.5, and 2.5 Mcal NE/kg and 1.47, 1.43, and 1.28% SID Lys, respectively. In phase 1, ADG was similar ($P = 0.07$) between PC- and NC-fed pigs, but ADG and ADFI increased linearly with increasing replacement of ETSP with ETSPY. ADG, ADFI, and G:F did not differ among treatments in phase 2. In phase 3, however, pigs previously fed ETSPY and ETSP diets had greater ADG than those previously fed NC. Results suggest that pigs fed ETSPY had improved growth rates over pigs fed ETSP, especially after withdrawal, and diet complexity did not affect performance of weanling pigs.

Table 1.

	Dietary treatment							*P*-value		
	1 (PC)	2 (NC)	3 (100% ETSP)	4 (33% ETSPY)	5 (67% ETSPY)	6 (100% ETSPY)	SEM	Linear 3-6	1 vs. 3-6	2 vs. 3-6
0-10 d										
ADG, kg/d	0.17	0.18	0.17	0.17	0.21	0.21	0.01	0.019	0.093	0.581
ADFI, kg/d	0.23	0.22	0.22	0.22	0.24	0.25	0.01	0.021	0.750	0.312
G:F	0.73	0.82	0.79	0.80	0.84	0.81	0.03	0.336	0.014	0.651
10-23 d										
ADG, kg/d	0.44	0.46	0.45	0.46	0.45	0.45	0.02	0.935	0.465	0.722
ADFI, kg/d	0.59	0.60	0.61	0.62	0.62	0.62	0.02	0.595	0.101	0.258
G:F	0.74	0.76	0.73	0.74	0.72	0.71	0.02	0.281	0.302	0.047
23-37 d										
ADG, kg/d	0.71	0.70	0.74	0.72	0.72	0.75	0.01	0.589	0.251	0.022
ADFI, kg/d	1.08	1.08	1.15	1.08	1.13	1.17	0.03	0.496	0.098	0.142
G:F	0.65	0.64	0.64	0.65	0.64	0.64	0.01	0.956	0.490	0.955

Key Words: diet complexity, enzyme-treated soy protein plus yeast, nursery pig performance

TH318 Low oligosaccharide soybean meal improves nursery pig performance. V. Perez*[1], N. Bajjalieh[2], T. Radke[1], and D. Holzgraefe[1], *[1]ADM Alliance Nutrition Inc., Quincy, IL, [2]Integrative Nutrition Inc., Decatur, IL.*

Data from our lab showed a larger swine ME in low oligosaccharide (LO) soybean meal (SBM) vs. conventional (C) SBM. To assess the value of C vs. LO soybeans and 2 processing approaches (SBM or soybean white flakes [SWF; post-hexane oil extraction]), 200 pigs (6.0 ± 0.3 kg BW; ~21 d old) were used in a completely randomized block design with 5 dietary treatments. Each treatment had 10 block-replicates. The ME in SBM and SWF from C and LO was assumed the same. Treatments were (1) Control, with SBM-C and formulated to have ME, Lys (ileal digestible), and Lys:ME as reported in National Swine Nutrition Guide (2010); (2) with SBM-C and formulated with 110 kcal less of ME/kg of diet, but same Lys as Control (so that AA would not limit growth if LO ingredients contribute with extra energy); (3) as diet 2 but using SBM-LO; (4) as diet 2 but using SWF-C; (5) as diet 2 but using SWF-LO. Experimental diets were fed during 25 d post-weaning, following a feeding program of 5, 6, 7 and 7 d for phases 1, 2, 3 and 4, respectively. Then, treatment 1 phase 4 diet was fed to all pigs for additional 7 d. Dietary inclusion of soy products in treatments 1 vs. 2 to 5 was: 20 vs. 30% in phase 1; 30 vs. 32% in phase 2; 35 vs. 38% in phase 3; and 43 vs. 40% in phase 4. Data were analyzed using the MIXED procedures of SAS; block was used as a random effect in the model. From d 0 to 5, pigs fed soybeans LO ate 18% more ($P = 0.07$) than pigs fed soybeans C. Pigs fed SBM-LO diets had equal or better performance than pigs fed Control diets (Table 1), despite the reduction in ME. Pigs fed SWF had the lowest ($P < 0.05$) G:F to d 25 and 32. In conclusion, SBM-LO is a value added option to replace SBM-C in nursery diets.

Table 1. Effect of soybean meal (SBM) and white flakes (SWF), conventional (C) and low oligosaccharide (LO), on nursery pig performance

Response	Control[1]	SBM-C	SBM-LO	SWF-C	SWF-LO	SEM
ADFI d 0-25, g/d[2]	484[b]	463[b]	522[a]	474[b]	490[b]	17
ADG d 0-25, g/d[2]	369[ab]	355[bc]	388[a]	322[d]	332[cd]	13
ADFI d 0-32, g/d[2]	580[b]	566[b]	621[a]	575[b]	595[ab]	18
ADG d 0-32, g/d[2]	427[ab]	416[b]	444[a]	406[b]	418[ab]	13

[a–d] Within a row, means with different superscripts differ, $P < 0.05$.
[1]Diets had 110 kcal more of ME/kg than the others.
[2]C vs. LO, $P < 0.05$.

Key Words: soybean meal, nursery pig, oligosaccharide

TH319 Growth performance, intestinal morphology, and blood parameters of piglets fed different soy protein concentrate levels. M. Q. Resende*, A. G. Mascarenhas, J. H. Stringhini, E. Arnhold, K. A. Teixeira, H. P. F. Xavier, R. D. Silva, and H. H. C. Mello, *Universidade Federal de Goiás, Goiânia, GO, Brazil.*

Piglet's first contact to soybean antigens (conglycinin and β-conglycinin) leads to a transient hypersensitivity, which usually causes diarrhea, low performance, and morphological changes in the small intestine of post weaned pigs. In the current experiment 72 male weanling pigs (initial BW = 6.92 ± 0.98 kg, 21 ± 2 d old) were used to assess the effects of soy protein concentrate (SPC) inclusion in diets on growth performance, intestinal morphology and blood parameters. Pigs were randomly assigned to 1 of 4 treatments with 6 replicate pens per treatment and 3 pigs per pen, in a randomized block design by initial BW. Corn-soybean meal mash diets were formulated to meet pig requirements according to Brazilian tables. Dietary treatments were diet without SPC (0S); diet with 3% of SPC (3S); diet with 6% of SPC (6S); diet with 9% of SPC (9S). Experimental diets were fed in 2 dietary phases (0–11 d and 11–20 d post weaning), and a common diet were fed through 20–45 d post weaning. Pigs were allowed ad libitum access to feed and water throughout the 45 d experimental period. Animals were weighed at d 0, 11, 20 and 45. Feed intake was recorded at d 11, 20 and 45. One pig per pen was euthanized on d 11 to collect samples of small intestine and blood. Statistical analyses were performed by ANOVA using the GLM procedure of SAS. No differences were observed in ADFI, ADG and G:F ratio ($P > 0.05$) within periods of 0–11 d, 0–20 d and 0–45 d after weaning. Although 6S showed 24%, 15%, 14% higher G:F and 28%, 4%, 28% higher ADG compared with 0S, 3S and 9S, respectively, in 0–11 d period. Intestinal morphology, blood leucocytes and eosinophils did not differ among treatments ($P > 0.05$), what indicates that mucosa atrophy was not avoided with SPC inclusion. Despite the better G:F ratio and ADG in the first period, numerically differences showed by 6S were reduced in the 45-d period, thus performance from all treatments were similar in the 45-d experimental period. We concluded that SPC can be recommended in piglet diets after weaning.

Key Words: anti-nutritional factor, nursery diet, weaned pig

TH320 Effects of cocoa powder as a source of theobromine in diets on performance of weanling pigs. G. L. Cromwell*, M. D. Lindemann, and H. J. Monegue, *University of Kentucky, Lexington.*

Chocolate powders and confectioneries are sometimes used to replace a portion of dried milk or whey products in starter diets for early weaned pigs. Cocoa, a primary component of chocolate, contains methylxanthines; the major one being theobromine (TB) which is known to be toxic in a variety of animals (especially dogs and horses) at relatively low doses. Whether the amount of TB is sufficient to cause reduced performance in weanling pigs when chocolate-containing ingredients are included in diets is unknown. A 21-d experiment involving 225 pigs initially averaging 20.6 d of age and 6.6 kg BW was conducted to evaluate levels of TB on performance of weanling pigs. Pure cocoa powder (International Ingredient Corp., St. Louis, MO) was used as a source of TB. The cocoa contained 95.5% DM, 26.6% CP, 11.2% fat, 0.93% Lys, and 2.07% TB. Typical phase-1 and phase-2 diets were fed for 10 and 11 d, respectively. Cocoa was added to diets at 0, 0.42, 0.85, 1.27, and 1.69%, which supplied 0, 87, 175, 262, and 350 ppm TB. Dietary Lys was 1.38 and 1.26% in the 2 phases. A common phase 3 corn-soybean meal diet (1.18% Lys) was fed to all pigs for 14 d following the 21-d experimental period. Each diet was fed to 9 pens of 5 pigs each. ADG and ADFI during the 21-d experimental period were quadratically ($P < 0.05$) affected by level of cocoa (361, 383, 398, 366, 363 g/d; 552, 558, 616, 553, 543 g/d), but F:G ratios were not affected (1.54, 1.46, 1.55, 1.51, 1.50). Similar quadratic responses in ADG (619, 611, 656, 613, 630 g/d) and ADFI (1072, 1044, 1140, 1058, 1050 g/d) occurred during the 14-d period when a common diet was fed and over the combined 35-d experimental and post-experimental period (ADG: 464, 474, 501, 465, 470 g/d ADFI: 760, 752, 826, 755, 746 g/d), but F:G was not affected (1.64, 1.59, 1.65, 1.62, 1.58). The results indicate that up to 1.69% cocoa which supplied 350 ppm TB in diets did not negatively influence feed intake or growth rate in weanling pigs when compared with a diet without cocoa. These levels of pure cocoa (1.69%) and TB (350 ppm) exceed those commonly found with reasonable inclusion levels of chocolate powders in pig starter feeds.

Key Words: pig, cocoa, theobromine

TH321 Grain replacement value of honey bee slumgum meal in broiler finisher diet. O. O. Ojebiyi*, I. O. Oladunjoye, T. B. Olayeni, and M. D. Shittu, *Ladoke Akintola University of Technology, Ogbomoso, Oyo State, Nigeria.*

The objective of this study was to investigate the effect of replacing corn with honey bee slumgum meal (a waste generated after the processing of honey and bee wax) on the performance and organ weights of broiler chickens at the finisher phase. One hundred and forty-four (144) day-old Marshall strain broiler chicks were used for the experiment. The birds were reared on a common starter diet (0–4 wk). Four experimental diets were thereafter formulated for the finisher phase (5–8 wk) with the control diet (T1) containing zero honey bee slumgum meal (HBSM) and 43.7% corn. Honey bee slumgum meal was used to replace corn in the control diet at 25, 50 and 75% in diets 2, 3, and 4 respectively. At the end of the starter phase, birds were randomly divided into the 4 treatment groups with 3 replicates per treatment at 12 birds per replicate in a completely randomized design. Data collected were used to evaluate ADFI, ADG and F:G. At the end of the study, birds were euthanized and the weights of liver, heart, lungs and spleen were obtained and expressed as percentage of BW. Data were analyzed using the proc GLM procedure of SAS. Although ADFI was not different across treatment groups, the final BW of broilers on the control diet (1816 g) and those fed 25% HBSM (1811 g) were comparable ($P > 0.05$) but higher ($P < 0.05$) than the BW of birds fed 50% HBSM (1562 g) and those fed 75% HBSM (1455 g). Similar trends were observed in the values of ADG which were 46, 46, 38 and 33g for broilers fed the control, 25, 50 and 75% HBSM, respectively. Broilers fed the control diet and 25% HBSM had similar ($P > 0.05$) F:G of 1.84 and 1.9, respectively which were lower ($P < 0.05$) than the values for broilers fed 50% (2.3) and 75% HBSM (2.6). The weights of the liver, heart and lungs were not affected ($P > 0.05$) by dietary treatments but spleen weight of birds fed

with 50 and 75% HBSM was higher ($P < 0.05$) than those of control and 25% HBSM. In conclusion, HBSM can be used to replace 25% of corn in broiler finisher diets without an adverse effect on BW and ADG.

Key Words: broiler, finisher, slumgum

TH322 Use of modified soy protein in aquaculture feeds as a replacement for fishmeal. B. M. Vester Boler*[1], D. M. Gatlin[2], E. A. Koutsos[1], and B. L. Miller[1], *[1]Purina Animal Nutrition, Gray Summit, MO, [2]Texas A&M University, College Station.*

Fishmeal is a commonly used protein source in aquaculture feeds due to its high acceptability and amino acid content. Due to environmental sustainability, availability, and ingredient cost concerns of fishmeal, investigation of other protein sources is needed. Twelve tanks of all-male tilapia fingerling (starting weight 2.5 g) were stocked at normal stocking density (n = 12/tank) in a recirculating system consisting of 38-L aquaria. Tanks were randomly assigned 1 of 3 dietary treatments (n = 4 tanks/treatment) and fed for 10 wk at a constant feeding rate across diets (6% of BW initially and 3% of BW at conclusion of the trial). Diets were isonitrogenous (46% calculated crude protein) and included a control diet containing menhaden fishmeal (FM) as the protein source, a negative control consisting of soybean flour (SF), and a diet containing 50% of protein from modified soy protein and 50% from fishmeal (MSP). Modified soy protein is manufactured by blending defatted soy flake with alcohol and reducing agent, heating it to 90°C and a pressure 10 psig, and finally removing the alcohol through venting. Weight gain and survival were determined at wk 6, 8, and 10. At the end of the study hepatosomatic index, intraperitoneal fat ratio, and feed efficiency were determined. Weight gain, as a percent of initial weight, was lower ($P < 0.01$) in fish fed SF, but did not differ in fish fed MSP compared with FM at any week (Table 1). Survival did not differ among treatments ($P = 0.34$). Hepatosomatic index ($P = 0.37$) nor intraperitoneal fat ratio ($P = 0.11$) differed among treatments. Feed efficiency was lower ($P = 0.03$) in fish fed SF compared with MSP and FM. Fish fed MSP had equal performance to those fed traditional fishmeal-based diets. Modified soy protein has potential use in future aquaculture diets to reduce the amount of fishmeal used.

Table 1. Weight gain (% from initial) in tilapia fed fishmeal (FM), modified soy protein (MSP), and soybean flour (SF) diets

	Treatment				
Week	FM	MSP	SF	SEM	*P*-value
6	687[b]	638[b]	427[a]	3.5	0.002
8	1074[b]	1087[b]	704[a]	3.5	<0.001
10	1602[b]	1547[b]	999[a]	3.5	<0.001

[a,b]Means within a row lacking a common superscript differ ($P < 0.05$).

Key Words: fish meal, aquaculture

TH323 Complete replacement of soybean meal in pig diets with hydrolyzed feather meal with blood by amino acid supplementation based on standardized ileal digestibility. S. D. Brotzge*[1], L. I. Chiba[1], C. K. Adhikari[1], H. H. Stein[2], S. P. Rodning[1], and E. G. Welles[1], *[1]Auburn University, Auburn, AL, [2]University of Illinois, Urbana.*

The possibility of replacing soybean meal (SBM) in finisher pig diets completely with hydrolyzed feather meal with blood (FM) was evaluated. Corn-SBM, positive control (POS) diets were formulated to contain 6.6 and 5.2 g true ileal digestible (TID) Lys/kg during the finisher 1 (F1) and finisher-2 (F2) phases, respectively. Corn-FM negative control (NEG) diets were formulated to be iso-N to the POS diets, and 2 diets were formulated by supplementing the NEG diets with AA based on the 1998 NRC TID (NRC) or determined standardized ileal digestible AA values (SID) in FM to alleviate AA deficiencies. When pigs weighed 50.0 ± 2.9 kg, 32 gilts and 32 barrows (2 gilts or 2 barrows/pen) were randomly assigned to 1 of 4 F1 diets, and they were switched to F2 diets at 79.0 ± 2.0 kg. Pigs had ad libitum access to feed. At 107.7 ± 3.3 kg, blood samples were collected and pigs were slaughtered. Pigs fed the POS diets had greater overall ADFI ($P = 0.083$) and total Lys intake ($P = 0.029$) than those fed the SID diets, which resulted in a slightly greater ADG ($P = 0.094$) in pigs fed the POS diets, but there was no difference in the efficiency of feed or Lys utilization. Pigs fed the SID diets had greater G:F ($P = 0.057$) and gain:total Lys intake ($P < 0.001$) than those fed the NRC diets. Pigs fed the POS diets had greater fat-free lean accretion ($P = 0.020$) that those fed the SID diets, but similar LM area, fat-free carcass %, and the efficiency of lean gain. Serum glucose was not affected by dietary treatments. Pigs fed the POS diets had greater urea-N ($P = 0.003$) and lower cholesterol ($P = 0.002$) than those fed the SID diets. As expected, pigs fed the NEG diet had reduced total protein ($P < 0.001$) and increased urea-N ($P = 0.001$), triglyceride ($P < 0.001$), and cholesterol ($P < 0.001$) compared with those fed the POS diets. The results indicate that pigs fed the SID diets utilized feed and Lys as efficiently as those fed the POS diets, but they had slightly reduced BW and lean gain, perhaps, because of slightly reduced feed and Lys intake.

Key Words: hydrolyzed feather meal, standardized ileal digestible amino acids, pigs

TH324 Hen performance as influenced by dietary *Aspilia africana* leaf. O. O. K. Oko*, E. A. Agiang, and P. O. Ozung, *University of Calabar, Calabar, Cross River State, Nigeria.*

The identification and validation of alternative antibiotic growth promoters is a major research focus in animal production. Phytobiotics also referred to as phytogenic feed additives (PFAs) are a group of plant-derived substances which are currently thought to be the ideal alternatives to antibiotics. Recent studies have reported the positive effects and economic effect of PFAs on feed intake, weight gain and feed efficiency in poultry and pigs. *Aspilia africana* leaf (AaL) is one of such plants with high phytonutrients and bioactive components with potential phytobiotic actions. The study investigated the effects of dietary AaL on the egg production performances of 360 (24 wk-old) laying hens over a period of 24 wk. Four treatments of 90 birds per treatment with 15 birds per replicate of 6 were studied in a completely randomized design. A corn-soybean mash diet was formulated (0%) and 2%, 5% AaL or 0.2% terramycin were added into the basal diet. Egg production traits were measured weekly throughout the experiment and a one-way ANOVA at $P \leq 0.05$ was conducted. Results indicated significant ($P \leq 0.05$) improvement in the production performance of birds fed AaL and terramycin diets. Compared with the control, hens fed AaL diets had 7.20, 6.90, 1.50 and 43.77% increase in hen-day production, shell thickness, yolk weight and yolk color, respectively than those fed terramycin (6.23, 3.45, 0.62 and 23.58%) diets. While feed intake and percentage cracked eggs had decreased ($P \leq 0.05$) by 6.00 and 19.41% in AaL- fed hens against the 4.25 and 16.47% decrease observed in terramycin-fed hens. These findings further demonstrated that *Aspilia africana* leaf has strong egg promoting potentials in poultry.

Key Words: growth promoter, egg quality, bush marigold

TH325 Utilization of high levels of crude glycerin in commercial layer diets. Y. Avellaneda*[1,2], R. Ortiz[1,2], G. Afanador[2], and C. Ariza-Nieto[1], *[1]CORPOICA, Mosquera, Cundinamarca, Colombia, [2]Universidad Nacional de Colombia, Bogota, Cundinamarca, Colombia.*

The objective of this study was to determine the highest level of acceptability of crude glycerin in the feeding systems of commercial layers, for this, an experiment was carry out to evaluate the inclusion of this resource by up to 15% of the diet. The crude glycerin (CG) presented the following composition: 3042 kcal / kg AMEn (determined previously through a balance study), 3453 Kcal / Kg of EB, 8.29% moisture, 82.0% glycerol, 0.79% crude fat, 1.21% sodium and 16 ppm of methanol). Two hundred sixteen 60-wk-old Babcock Brown laying hens were randomly assigned to one of the 6 crude glycerin levels (0, 3, 6, 9, 12 and 15%). Hens were housed in individually cages equipped with an automatic nipple drinker and a feeder channel side during 2 mo and their performance was record every other week during the study. Six hens housed adjacent, sharing the same trough were consider an experimental unit (replicate). During the study, eggs were collected daily and weighed weekly by each replica and feed residuals were used to calculate daily feed intake and feed conversion. The data were analyzed as a completely randomized design, with one covariate (egg production of last month, before the start of the experiment). The linear, quadratic, and cubic effects of crude glycerin level were evaluated using SAS procedures, version 9.0. The results showed that the inclusion of CG up to 15% did not affect hen performance in terms of egg production (94.5 ± 7.0%) or egg weight (67.5 ± 2.4g); however, feed intake decreased linearly with the level of inclusion of CG in diet. Layers supplemented with 12 or 15% of CG consumed ($P < 0.05$) 4.6% less feed compared with the control group and 3% of supplementation. The groups with highest levels of CG presented ($P < 0.05$) a better feed conversion compared with the 3% CG group. In conclusion, CG with low levels of methanol may be used at high levels (up to 15%) without adversely affecting the performance of laying hens.

Key Words: crude glycerin, acceptability, layer diet

TH326 Dietary hop (*Humulus lupulus*) β-acids improve growth performance of weanling pigs. M. Sbardella*, C. Andrade, D. P. Perina, and V. S. Miyada, *Universidade de São Paulo (USP/ESALQ), Piracicaba, SP, Brazil.*

Hop (*Humulus lupulus*) β-acids have shown antimicrobial activity in vitro, as well inhibition capacity of *Clostridium perfringens* in chick gastrointestinal tract. The purpose of this study was to evaluate the effects of dietary levels of hop β-acids on growth performance of weanling pigs. Two hundred 21 d-weaned pigs (6.23 ± 0.32 kg BW) were used in a randomized complete block design experiment with 5 treatments, 8 replications per treatment, and 5 animals per experimental unit (pen). The treatments were: basal diet (based on corn, soybean meal, dried milk and dried plasma) with 40 ppm of colistin (antimicrobial treatment) and basal diet with 0 (negative control), 120, 240 or 360 ppm of hop β-acids. Feed and water were provided ad libitum during all 35 d-experimental period. Statistical analyses were performed by ANOVA using the MIXED procedure of SAS. Polynomial orthogonal contrasts were performed to determine the dose-response to dietary hop β-acids. Added dietary levels of hop β-acids improved linearly ($P < 0.05$) final BW, ADG, and G:F ($P = 0.003$) of weanling pigs (Table 1). The antimicrobial treatment improved ($P < 0.03$) BW, ADG and G:F compared with negative control treatment, but did not differ from any dietary levels of hop β-acids. No effects ($P > 0.05$) of hop β-acids or antimicrobial agent were observed on ADFI. Dietary levels of hop β-acids up to 360 ppm and 40 ppm of colistin improved growth performance, showing that hop β-acids may be used as alternative of antimicrobial growth promoters for weanling pigs.

Table 1. Effects of dietary levels of hop β-acids on growth performance of weanling pigs

	Dietary level, ppm							CV
	Colistin	0	120	240	360	*P*-value	SEM	(%)
Initial BW, kg	6.23	6.22	6.23	6.23	6.23	0.424	0.32	14.87
Final BW, kg[1]	20.94	19.61*	20.51	20.79	21.46	0.043	0.92	13.13
ADG, g/d[2]	425	387*	414	421	441	0.045	18	13.04
ADFI, g/d	693	663	683	689	703	0.550	28	11.71
G:F[3]	0.61	0.58*	0.61	0.61	0.63	0.004	0.01	4.38

[1]Linear effect of β-acids on Final BW (BW = 0.0049x + 19.716; $R^2 = 0.96$; $P = 0.003$).
[2]Linear effect of β-acids on ADG (ADG = 0.14x + 390.51; $R^2 = 0.96$; $P = 0.003$).
[3]Linear effect of β-acids on G:F (G:F = −0.0001x + 0.5863; $R^2 = 0.94$; $P = 0.000$).
*Lower than antimicrobial treatment by orthogonal contrast-test ($P < 0.03$).

Key Words: feed additive, growth promoter, swine

TH327 Type 2 diabetes mellitus increases sensitivity to dietary iron overload in pigs. M. S. Morales*[1], A. Espinoza[1,2], M. Arredondo[2], and F. Pizarro[2], *[1]Facultad de Ciencias Veterinarias y Pecuarias, Universidad de Chile, Santiago, R.M., Chile, [2]INTA, Universidad de Chile, Santiago, R.M., Chile.*

Oxidative stress (OS) due to high levels of iron (Fe) may be involved in type 2 diabetes mellitus (DM2) etiology. We determined effects of high dietary Fe in pigs induced with DM2 by Streptozotocin injection on Fe nutritional status, OS parameters, apoptosis and expression of genes related to Fe metabolism. Four groups of pigs (15 kg BW; 6 pigs/group) were assigned to: Control, a basal diet (120 ppm Fe; C); High Fe, C + 3000 ppm $FeSO_4$ (HFe); DM2 fed C diet (D); and DM2 pigs fed HFe (DFe). Diets were fed for 2 mo; pigs were evaluated weekly for biochemical, Fe metabolism and OS parameters. Pigs were killed, and liver (LI), pancreas (PA) and duodenum (DU) were taken for Fe content and apoptosis. mRNA expression of DMT1, transferrin receptor (RTf), ferroportin (Fpn), hepcidin (Hpc) and ferritin (Fn) genes were measured in LI and DU. Data were analyzed by ANOVA and Tukey test or Kruskal Wallis test. All differences indicated are $P < 0.05$. In plasma OS TBARS was higher only in D at d 60. Apoptosis and 4-HNE in LI, PA and DU were highest in DFe. DMT1 expression in DU and LI was lower in HFe and DFe groups as expected, but in D and C expression was similar; thus, DM2 did not affect DMT1 expression. Hcp gene expression in LI was increased by HFe and DFe as expected for high dietary Fe, but was not modified by DM2. Hcp in DU was downregulated by HFe, thus dietary Fe level caused differential tissue expression of this gene. RTf expression was decreased by HFe in LI as expected. Treatment did not modify expression of Fpn and Fn in DU, but Fn was highly expressed in LI of DFe pigs, reflecting greater Fe storage in DFe pigs with high Fe intake; thus, Fn was differentially expressed as well. HFe on DM2 induced higher OS, apoptosis and differential expression of Fn and Hpc gene.

Key Words: iron, gene expression, pig

TH328 Severe heat stress affects amino acid transporters expression and serum concentration of amino acids in pair-fed pigs. F. Grageola, M. Morales, H. García, B. A. Araiza, N. Arce, and M. Cervantes*, *ICA - Universidad Autónoma de Baja California, Mexicali, BC, México.*

Heat stress (HS) depresses pig performance mainly because of appetite reduction although other factors involved in the cellular availability of nutrients may also contribute to that depression. A 19-d experiment was conducted with 12 pigs (30.3 ± 2.7 kg BW) to examine the effect of severe HS (up to 45°C) on the expression of 2 cationic amino acid (AA) transporters ($b^{0,+}$ in jejunum; $b^{0,+}$ and CAT1 in jejunum, liver, longissimus–LD, and semitendinosus–ST), and myosin in LD and ST, and serum concentration (SC) of AA. Treatments were: Comfort, pigs housed at an average temperature of 22 (±2) °C; and HS, pigs housed in a room with no climate control (21 to 45°C). All pigs received the same wheat-soybean meal diet and had similar daily feed intake. Intestinal mucosa, tissue and blood samples were collected at the end of the trial. Relative expression of $b^{0,+,}$ CAT1, and myosin, and the SC of AA were analyzed. The expression in Comfort and HS pigs were: $b^{0,+}$: jejunum, 2.98, 0.45; liver, 2.24, 0.54; CAT1: jejunum, 0.05, 0.15; liver, 0.001, 0.005; LD, 0.008, 0.006; ST, 0.005, 0.002; myosin: LD, 4.14, 2.73; ST, 1.06, 0.20, respectively. The expression of $b^{0,+}$ in jejunum and liver, and myosin in ST was lower ($P<0.05$); but CAT1 in jejunum and liver was higher ($P < 0.05$) in HS pigs. In jejunum and liver, the average relative expression of $b^{0,+}$ was about 15× higher than that of CAT1 ($P<0.01$), but $b^{0,+}$ was barely expressed in muscles. CAT1 expression in muscles was not affected by HS. The SC of AA in Comfort and HS pigs were: Arg, 567, 552; His, 689, 513; Ile, 341, 470; Leu, 397, 592; Lys, 580, 306; Met, 95, 17; Phe, 214, 310; Thr, 639, 483; Val, 667, 1401 µmol/L, respectively. The SC of Lys and Met were lower ($P < 0.05$) in HS pigs. In contrast, the SC of Ile, Leu, and Val were higher ($P < 0.05$), and Phe tended to be higher ($P < 0.10$) in HS pigs. The SC of Arg, His, and Thr were not affected in HS pigs. These results suggest that HS modifies molecular mechanisms that affect the expression of cationic AA transporters and hence the cellular availability of limiting AA, which in turn may affect the performance of pigs

Key Words: pig, heat stress, expression

TH329 Thyroid function and growth are impaired by *Moringa oleifera* leaf meal in pair-fed growing poultry. J. Ashong* and D. Brown, *Cornell University, Ithaca, NY.*

Moringa oleifera Lam, a popular highly valued fast-growing crop in many tropical and subtropical countries has the potential to be used as high quality nutrient concentrate because of its high content of protein and micronutrients like iron and vitamin A. However, *Moringa oleifera* has been shown to retard growth in poultry. The objectives of the present study were to clarify the mechanism of the growth retardation effects of *Moringa oleifera* leaf meal and to compare thyroid function in growing chickens fed *Moringa oleifera* meal as a protein source. *Moringa oleifera* leaf powder was mixed with soybean as supplemental protein sources in a soybean-corn based chicken diets (based on National Research Council's requirement for white-leghorn type chickens) to formulate 2 isocaloric and isonitrogenous experimental diets—0% (control) and 20% moringa leaf powder. 7-d old chickens were completely randomized and assigned to the diets over a 28 d period as: control ad libitum (CAL), 20% moringa ad libitum (MAL) and control pair-fed (CPF)—chickens fed with control at the same quantity as the feed intake of 20% moringa ad libitum. CAL and CPF had 3 replicates with 5 chickens per replicate. MAL had 2 replicates with 3 chickens per replicate. Daily feed intake and weekly body weights were recorded, and feed efficiency calculated. Serum thyroid hormones were measured at d 14 and 28. Postmortem kidney, liver and heart weights were recorded. Liver tissues were harvested for histopathology. Moringa fed chickens showed heavier liver weight, ($r^2 = 0.64$, $P = 0.003$,), decreased serum thyroxine (T_4), $r^2 = 0.37$, $P = 0.039$ and thyronine (T_3), $r^2 = 0.55$, $P = 0.008$ on d 28. Serum T_4 ($P = 0.79$) and T_3 ($P = 0.25$) were not different on d 14. M. oleifera led to reduced feed intake ($P = 0.003$) leading to 27% and 39% suppression in growth compared with CPF and CAL respectively ($r^2 = 0.26$, $P = 0.0029$). Histopathology results were not different. The results suggest that the growth retardation effects of moringa is likely metabolic and thyroid function might be impaired in chickens fed moringa leaf meal as protein source.

Key Words: *Moringa oleifera*, thyroid hormone, growth

TH330 Effects of immunization against GnRH and feeding allowance on the performance of growing-finishing pigs. O. A. Dalla Costa, G. J. M. M. Lima*, F. C. Tavernari, and L. S. Lopes, *Embrapa, Concordia, SC, Brazil.*

Immunization against GnRH is an innovative technology in swine production because it enhances performance and welfare. The objective of this study was to evaluate the effects of gender and feeding allowance on growing-finishing performance and carcass parameters. This experiment was carried out with 1200 pigs (23.13 ± 3.20 kg) of 2 genders (barrows and intact males), divided into 3 feeding systems (F1 = ad libitum; F2 = 96% feed consumption of F1; F3 = 93% feed consumption of F1). Therefore, there were 6 combinations of factors with 20 replicates of 10 pigs, each, according a randomized complete block design. All animals received the same diets, based on corn, soybean meal and meat and bone meal. Diets were formulated based on the concept of ideal protein, with the following apparent ileal digestible lysine (%) and metabolizable energy (kcal/kg) values: 0.83 and 3189; 0.75 and 3169; 0.75 and 3167; 0.90 to 3164 for growing diets 1 and 2 and finishing diets 1 and 2, respectively. Finishing diet 2 was supplemented with 5 ppm ractopamine and fed during the last month of experiment. The immunization against GnRH occurred at wk 8 and 4 before slaughter. Performance (pig initial and final weights, ADG, ADFI, feed:gain ratio) and post mortem carcass (liver, heart, and kidney weights, meat % in carcass and back fat thickness) parameters were evaluated. There were no significant interactions ($P > 0.05$) between gender and feeding system. Immunized intact males showed better results ($P < 0.05$) on final weight (116.26 vs. 111.96 kg), ADG (0.835 vs. 0.802 kg/d) and feed:gain ratio (2.56 vs. 2.70) compared with barrows during the total period. Final weight (116.19; 113.67 and 112.48 kg), ADG (0.839; 0.814 and 0.803 kg/d), and feed:gain ratio (2.70; 2.62 and 2.58) differed ($P < 0.05$) among F1, F2 and F3 pigs, respectively. Post mortem carcass parameters were not affected ($P > 0.05$) by feed allowance but showed a significant effect of gender ($P < 0.05$). Immunized intact males showed greater means, except for back fat thickness. Immunization against GnRH provides better results and it seems to be independent of the amount of feed provided to animals.

Key Words: feed restriction, carcass, organ

TH331 Effects of melamine in young barrows. B. R. Landers[1], G. Hosotani*[1], D. Y. Kim[2], M. C. Shannon[1], G. E. Rottinghaus[2], and D. R. Ledoux[1], *[1]Animal Sciences Department, University of Missouri, Columbia, [2]Veterinary Medical Diagnostic Laboratory, College of Veterinary Medicine, University of Missouri, Columbia.*

A study was conducted to investigate the toxicity of melamine (MEL) fed to young barrows, and to determine residual levels of MEL in selected tissues. Thirty 14-d post-weaning barrows (initial weight = 10.6 ± 1.2 kg) were allotted to 1 of 6 dietary treatments containing 0, 0.25, 0.50, 0.75, 1.0, or 1.25% MEL. A completely randomized design was used with 5 replicate pens of one pig/pen assigned to each treatment. Compared with controls, BWG and ADG were lower ($P = 0.0205$) in pigs fed ≥1.00% MEL. A decrease in gain to feed with increasing dietary MEL concentrations contained both linear ($P = 0.0076$) and quadratic ($P = 0.0407$) components. Pigs receiving 1.25% MEL had a lower ($P = 0.0427$) gain to feed value than controls. Linear decreases in serum glucose ($P = 0.0124$) and serum calcium ($P = 0.0053$) were observed as dietary MEL levels increased. In contrast, aspartate aminotransferase increased ($P = 0.0049$) linearly as MEL inclusion in the diet increased. An increase in residual MEL levels in the kidney contained both quadratic ($P < 0.0001$) and linear components ($P < 0.0001$). There was a linear ($P < 0.0001$) increase in MEL concentrations in bile with increasing dietary concentrations of MEL. Pigs fed diets containing ≥0.25% MEL had kidney MEL residue levels greater ($P < 0.0001$) than controls, whereas pigs fed ≥0.50% had MEL residue levels in bile and muscle that were greater ($P < 0.0001$) than controls. In summary, results indicate that ≥1.00% MEL was toxic to pigs fed dietary MEL treatments for 21 d.

Key Words: pig, melamine, toxicity

Physiology and Endocrinology III

TH332 Exogenous enzymes and *Salix babylonica* extract affects cellular immune response in growing lambs. N. Rivero[1], A. Z. M. Salem*[1], C. G. Penuelas[1], M. G. Ronquillo[1], H. Gado[2], and N. E. Odongo[3], *[1]Facultad de Medicina Veterinaria y Zootecnia, Universidad Autonoma del Estado de Mexico, Mexico, [2]Animal Production Department, Faculty of Agriculture, Ain Shams University, Qalubia, Egypt, [3]Animal Production and Health Section, International Atomic Energy Agency, Vienna, Austria.*

The aim of this study was to determine effects of an exogenous enzyme of ZADO and *S. babylonica* L. extract on cellular immune response. Twenty 6- to 8-mo-old Suffolk lambs of 24 ± 0.3 kg BW were used. After 2 wk of adaptation to a basal diet, of 70% corn silage and 30% commercial concentrate (DM basis), the lambs were weighed and randomly distributed into 4 groups (n = 5 per group) using a completely randomized design and data of the immunological parameters was analyzed using the MIXED procedure of SAS with repeated measures. Enzyme product of ZADO is commercially available multi-enzyme feed additive in a powder form produced from *Ruminococcus flavefaciens* and manufactured by the Academy of Scientific Research and Technology in Cairo, Egypt. The feeding treatments for lambs were (1) Control: basal diet only; (2) EZ: Control diet plus 10 g of exogenous enzyme; (3) SB: Control diet plus 30 mL of *S. babylonica* L. extract; and (4) EZSB: Control plus 10 g exogenous enzyme and 30mL of *S. babylonica* L. extract. The daily dose of *S. babylonica* L. extract was given orally before the morning feeding while the exogenous enzyme was fed to the lambs mixed with 200 g of concentrate for 20 min and then mixed with the rest of the concentrate and offered for 1h before ad libitum feeding of corn silage. The experiment was 60 d in duration. Blood samples were collected on d 0, 15, 30, 45 and 60 from each animal via jugular venipuncture and flow cytometry analysis was used to assay numbers of T-helper lymphocytes (Th), cytotoxic-T lymphocytes (Tc), granulocytes and monocytes. In general, treatments had no effect on any of the parameters measured, but sampling time decreased Th (5.6 vs. 6.6, SEM = 0.35, linear and cubic effect, $P < 0.01$); and increased Tc (43.7 vs. 37.8, SEM = 1.04, cubic effects, $P < 0.01$), granulocytes (43.3 vs. 38.4, SEM = 0.57, linear and cubic effects, $P < 0.01$) and monocytes (6.2 vs. 5.9, SEM = 0.39, linear and cubic effects, $P < 0.01$). Results suggest that addition of exogenous enzyme and/or *S. babylonica* L. extract have immunosuppressive effects only during the first 15 d on as reflected by the treatment × day interaction.

Key Words: exogenous enzyme, immune response, lamb

TH333 Effects of intravenous β-hydroxybutyrate on the mRNA abundance of genes related to metabolism and immune response in hepatic and mammary tissue in dairy cows. M. Zarrin*[1,2], H.A. van Dorland[1], O. Wellnitz[1], and R.M. Bruckmaier[1], *[1]Veterinary Physiology, Vetsuisse Faculty University of Bern, Bern, Switzerland, [2]Department of Animal Science, Yasouj University, Yasouj, Iran, [3]Graduate School for Cellular and Biomedical Sciences, University of Bern, Bern, Switzerland.*

Increased ketone body synthesis is a frequent metabolic adaptation during negative energy balance (NEB) at simultaneously high glucose consumption by the mammary gland after parturition in high yielding dairy cows. Beyond various metabolic changes the immune system is impaired during NEB and hyperketonemia. Our objective was to study the effects of a 48 h β-hydroxybutyrate (BHBA) infusion on the mRNA abundance of candidate genes related to metabolism and immune response in mammary and hepatic tissue in mid-lactation dairy cows. Thirteen cows were allocated to either intravenous Na-DL-β-OH-butyrate infusion (HyperB, n = 5) to achieve elevated plasma BHBA concentrations (1.7 mmol/L), or saline (0.9%) infusion (Control, n = 8). Liver and udder biopsies were taken one week before the start of the infusion and 48 h after the start of the infusion. Differences of mRNA abundance before and at the end of BHBA infusion were calculated and were tested for significance by a general linear model (GLM) including treatment (BHBA or NaCl) as fixed effect. The mRNA abundance of serum amyloid A (SAA) and haptoglobin (Hp) in the liver increased in both groups. BHBA infusion did not affect mRNA abundance of SAA, Hp, RANTES, and tumor necrosis factor α (TNFα) in the liver, and of acetyl-CoA carboxylase, citrate synthase, fatty acid synthase, β-hydroxybutyrate dehydrogenase 1 and 2, and succinyl-CoA: 3-ketoacid-coenzyme A transferase 1, mitochondrial (OXCT1) in mammary tissue. However, mRNA abundance of SAA in mammary tissue increased (8.97%) during BHBA infusion ($P < 0.01$). Hp mRNA abundance tended to increase (4.7%) during infusion in HyperB, and tended to decrease (1.77%) in the control group ($P = 0.07$). The results indicate that elevated plasma BHBA does not affect metabolism in the mammary gland and immune responses in the liver at a mRNA level. However, effects of BHBA on the mammary immune response could be related to increased susceptibility to infection during hyperketonemia.

Key Words: metabolism, hyperketonemia, immune response

TH334 Effects of bovine plasma handling and storage protocols on concentrations of haptoglobin and ceruloplasmin. P. G. M. A. Martins*, P. Moriel, and J. D. Arthington, *University of Florida, Institute of Food and Agricultural Sciences, Range Cattle Research and Education Center, Ona.*

Our objectives were to evaluate the effects of repeated freezing and thawing cycles, and different storage temperatures on concentrations of haptoglobin and ceruloplasmin using colorimetric procedures within biochemical assays. Briefly, haptoglobin concentrations were assessed via the measurement of haptoglobin/hemoglobin complexing by estimating differences in peroxidase activity, and ceruloplasmin concentrations, via estimation of oxidase activity. Blood samples were collected from 12 Brangus-crossbred steers on d 3 after vaccination against *Mannheimia haemolytica* (One Shot, Pfizer Inc. New York, NY). Blood samples were allocated to 1 of 5 handling protocols: (1) plasma samples were frozen, and thawed only on the day of analysis; (2) 24-h; blood samples were stored at 4°C for 24 h, and plasma was harvested, frozen, and thawed on the day of analysis; (3) 1-time; 1 wk before analysis, plasma samples were thawed for 1 h and re-frozen; (4) 2-time; 1 and 2 wk before analysis, plasma samples were thawed for 1 h and re-frozen; (5) 3-time; 1, 2, and 3 wk before analysis, plasma samples were thawed for 1 h and re-frozen. Each handling scenario was assessed at 1 and 7 mo of storage and at freezing temperatures of −20 and −80°C. Data were analyzed using the MIXED procedure of SAS. Concentrations of both proteins analyzed at 7 mo after blood sampling were greater ($P = 0.01$; 11% and 18% increase for haptoglobin and ceruloplasmin) than results from analysis conducted 30 d after blood sampling, irrespective of thawing and refreezing protocol. Samples subjected to 24-h storage at 4°C, before centrifugation and plasma harvest, had greater haptoglobin concentrations compared with 1, 2, and 3-time handling protocols ($P < 0.05$; 1.07 vs. 0.95, 0.94, and 0.95 mg/mL). For ceruloplasmin, a stor-

age temperature effect was detected with plasma concentrations stored at −80°C being greater than −20°C ($P = 0.05$; 30.1 vs. 28.2 mg/dL). In conclusion, plasma collection protocol, storage time, and storage temperature appear to affect the results of biochemical assays aimed at the quantification of bovine haptoglobin and ceruloplasmin.

Key Words: acute phase protein, beef cattle, stability

TH335 Purinergic signaling gene network expression in bovine polymorphonuclear neutrophils during the peripartal period. J. Seo, J. S. Osorio*, and J. J. Loor, *University of Illinois, Urbana.*

An effective immune response relies on efficient activation of polymorphonuclear neutrophils (PMN). PMN release cellular adenosine triphosphate (ATP) in response to exogenous stimuli such as inflammatory mediators. The peripartal period is characterized by marked changes in inflammatory status that are functionally related with impaired immune responses in the cow. We evaluated the mRNA expression of genes associated with the purinergic signaling in PMN during the peripartal period. Seven multiparous Holstein cows were dried off at d −50 relative to expected calving and fed a controlled-energy diet (NEL = 1.24 Mcal/kg of DM) at intakes to meet and not greatly exceed 100% of NRC requirements. All cows were fed a common lactation diet after calving. RNA from PMN collected at −10, 3, and 21 d relative to parturition were used to measure expression of 22 genes associated with adhesion to endothelium, chemoattractant binding at the plasma membrane, and purinergic signaling. The ANOVA model had day as the fixed effect and cow as the random effect. Differences between days were significant at a $P < 0.05$. The expression of P2RY2, a G-protein coupled receptor of adenosine, increased 2-fold at parturition compared with −10 d suggesting that ATP plays a role in the amplification of chemotactic signals. The expression of genes encoding cell adhesion (SELL and SELPLG), chemoattractant receptors (C5AR1, CXCR1, CXCR, and PTAFR), and adenosine receptors (ADORA1 and ADORA3) decreased at parturition compared with −10 d. The expression of ADORA2A, which is associated with immunosuppression of PMN, was 1.5-fold greater at 3 d than −10 d. The increase in expression of adenosine uptake channels (SLC29A1 and SLC29A2) and ADA after calving suggested that the concentration of extracellular adenosine might be sharply increased compared with pre-partum. This might be a cause of immunosuppression. Overall, our results suggested that the reduction in key immune responses such as cell adhesion and chemotaxis by bovine PMN are partly a function of changes in mRNA expression of genes associated with purinergic signaling.

Key Words: inflammation, PMN, transition cow

TH336 Dynamics of TLR-4 signaling in bovine neutrophils during the periparturient period. M. G. H. Stevens*[1,2], X. Boulougouris[1], C. Rogiers[1], T. McFadden[2], L. Peelman[1], B. De Spiegeleer[1], L. Duchateau[1], and C. Burvenich[1], *[1]Ghent University, Ghent, Oost-Vlaanderen, Belgium, [2]University of Missouri, Columbia.*

During the periparturient period mature blood neutrophils have a lower performance in migration, phagocytosis and respiratory burst assays. These functional alterations have been correlated to an increased risk for severe *E. coli* mastitis. We hypothesize that alterations in TLR-4 signaling may be involved in the functional dysregulation of neutrophils. In this preliminary study blood neutrophils of 11 cows were isolated at −14, 3 and 14 d relative to parturition and stimulated with LPS (10μg/mL). Total RNA was extracted and the expression of TLR-4 related genes was quantified by RT-qPCR. Data were analyzed based on a mixed model with stimulation and lactation stage and their interactions as categorical fixed effects and cow as random effect. Time relative to parturition had an effect ($P < 0.05$) on the expression of TLR4, CD14, RELA, MAPK1, MAPK3, IL8 and IL1β but not on TNFα. The expression of TLR4, CD14 and RELA was on average 25% lower at d-14 compared with d3 and d14. Compared with d-14, IL8 expression decreased with 60% at d3 and increased with 650% at d14. The expression of MAPK1 and MAPK3 increased with 22% at d3 but returned to prepartum values at d14. IL1β expression was similar at d-14 and d3 but increased with 22% at d14. LPS stimulation increased the expression of TLR4, CD14, RELA, IL1β and TNFα ($P < 0.05$) and decreased the expression of MAPK1 and MAPK3 ($P < 0.05$) but had no effect on IL8. The expression of TLR4, IL8, IL1β and TNFα upon LPS stimulation didn't change as a function of time. The effect of LPS stimulation on the expression of CD14, MAPK1 and MAPK3 was lowest at d-14 but was similar between d3 and d14. The effect of LPS on RELA expression was similar between d-14 and d3. At d14 neutrophil expression of RELA increased with 75% compared with d-14. This preliminary study suggests that the constitutive expression of genes related to the TLR-4 pathway changes as a function of time relative to parturition. Moreover, responsiveness of neutrophils to LPS may be altered during the periparturient period due to changes in the activation of the TLR-4 signal transduction pathway.

Key Words: neutrophil, periparturient period, TLR-4

TH337 Expression of niacin receptor GPR109A in bovine oocytes and preimplantation embryos and effect of addition of niacin during embryo culture on development following exposure to heat shock. J. Block[1,2], A. Ruiz[2], A. M. Reeg[1], L. K. Mamedova[3], B. J. Bradford[3], and T. R. Bilby*[4], *[1]OvaTech LLC, Gainesville, FL, [2]Department of Animal Sciences, University of Florida, Gainesville, [3]Department of Animal Sciences and Industry, Kansas State University, Manhattan, [4]Texas A&M AgriLife Research and Extension, Texas A&M System, Stephenville.*

Objectives were to determine whether niacin receptor GPR109A is expressed in bovine oocytes and preimplantation embryos, and to determine whether addition of niacin during embryo culture improves embryo development in the presence or absence of heat shock. In exp. 1, immature cumulus-oocyte complexes were collected from abattoir derived ovaries and used to produce embryos in vitro. Pools of immature oocytes denuded of cumulus cells and embryos at the 2-cell, 8-cell, ≥ 16-cell and blastocyst stages were harvested at the time of collection and 28–32, 68–74, 118–124 and 166–172 h post-insemination, respectively over 2–4 replicates. Total RNA was isolated and quantitative real-time RT-PCR was performed using primers designed for GPR109A and β-actin. Relative mRNA abundance was quantified by the delta C_t method with β-actin used to normalize values. There was a significant ($P < 0.05$) effect of stage of development on the relative expression of GPR109A, with embryos at the ≥16-cell stage having higher levels of GPR109A than immature oocytes or embryos at other stages. In exp. 2, embryos were produced in vitro using abattoir-derived oocytes. At d 3 after insemination, ≥ 8-cell embryos were harvested and randomly cultured with or without 100 μ*M* niacin for 9 h, then exposed to either control (38.5°C) or heat shock (41.0°C) treatments for 24 h. All embryos were then returned to 38.5°C and cultured until d 8. There was a tendency ($P < 0.08$) for niacin to reduce the proportion of ≥8-cell embryos that became blastocysts on d 8 (59.9 vs. 45.2 ± 4.1%). Heat shock significantly ($P < 0.05$) reduced the proportion of ≥8-cell embryos that became blastocysts on d 8 (61.7 vs. 43.4 ± 5.5%). There was no interaction between niacin and heat shock affecting embryo development. Results

indicate that niacin receptor GPR109A is expressed in bovine embryos produced in vitro. However, addition of niacin to embryo culture did not improve embryo development to the blastocyst stage regardless of whether embryos were exposed to heat shock.

Key Words: niacin, receptor, embryo

TH338 Prepartum body condition score changes and the secretion of acute phase proteins in dairy cows. P. Montagner[1,2], E. Schwegler[1,2], M. M. Weschenfelder[1,2], A. R. Krause[1,3], J. Alvarado[1,2], A. S. Maffi[1,2], C. C. Brauner[1,3], A. Schneider[1,4], E. Schmitt*[1,2], E. G. Xavier[5,2], C. F. Martins[1,2], V. R. Rabassa[1,2], F. A. B. Del Pino[1,3], and M. N. Correa[1,2], *[1]Center for Research, Teaching and Extension in Animal Science (NUPEEC), Pelotas, RS, Brazil, [2]Department of Clinical Veterinary, Federal University of Pelotas (UFPEL)-BRA, Pelotas, RS, Brazil, [3]Department of Animal Science, (UFPEL - BRA), Pelotas, RS, Brazil, [4]Departament of Nutrition (UFPEL - BRA), Pelotas, RS, Brazil, [5]Granjas 4 Irmaos, Rio Grande, RS, Brazil, [6]Center for Agroforestry Research of Rondonia - Embrapa CPAF, Rondonia, RO, Brazil.*

The aim of this study was to investigate the effect of body condition (BCS) score changes during the prepartum period on the concentration of acute phase proteins and metabolic parameters in dairy cows. Evaluation of BCS was performed on 20 pregnant Holstein dairy cows (on a 5-point scale with quarter-point divisions), from a commercial herd kept in a semi-extensive system in southern of Brazil. The cows were divided into 2 groups: cows that increased BCS (+0.25) from the third to the first week before the expected calving date (UP-BCS; n = 11) or cows that decreased BCS (−0.8) (LO-BCS; n = 9) in the same time frame. Blood samples were collected from the coccygeal vein on the d 23, 14, 7 and 3 prepartum, on the calving day and at d 3, 6, 9, 16 and 23 postpartum to evaluate the concentrations of nonesterified fatty acids (NEFA), glucose (GLU), albumin (ALB), haptoglobin (Hp) and paraoxonase (PON). Milk yield was recorded daily, and a 5-d average was generated, from 16 to 41 d in milk. Statistical analysis was performed using the SAS software, using the MIXED procedure for repeated measures. Average milk yield was higher for UP-BCS cows ($P < 0.01$; 27.4 kg/d vs. 24.4 kg/d). The UP-BCS cows had higher serum concentration of PON and ALB in the pre and postpartum periods ($P < 0.05$), while the LO-BCS group had higher levels of Hp in both periods ($P < 0.05$). Other variables (GLU and NEFA) were not different between groups ($P > 0.05$). These results indicate that BCS loss in the pre-partum period can affect the pattern of secretion of acute phase proteins in dairy cows in the transition period. In sum, our results indicate that higher BCS loss is associated to increased secretion of HP and reduced secretion of PON and ALB, which can be associated to increased risk of disease development.

Key Words: body condition score, haptoglobin, paraoxonase

TH339 Relationships of birth weight traits with age at first estrus and number of ovulations in Landrace-Duroc-Yorkshire gilts. C. A. Lents*, L. A. Rempel, T. Wise, and D. Nonneman, *U.S. Meath Animal Research Center, Agricultural Research Service, United States Department of Agriculture, Clay Center, NE.*

Selection for increased litter size has resulted in greater within-litter variation in piglet birth weight and a reduction in litter average birth weight; believed to be associated with intrauterine growth restriction as a result of limitations in uterine capacity. This leads to increased preweaning mortality, reduced growth performance, decreased muscle fiber number and reduced carcass quality. Low birth weight gilts have more primordial and fewer primary and secondary follicles suggesting that variation in average litter birth weight could negatively affect reproductive traits. The objective of this study was to examine the effects of birth weight traits with age at puberty and number of ovulations in gilts. Age at puberty, the first standing estrus in the presence of a mature boar, was determined for 2,187 gilts beginning at approximately 140 d of age. The number of ovulations for 2,173 gilts was determined during postmortem examination by counting the number of corpora lutea on the ovary after the first or second parity. Partial correlation coefficients for total born, total born alive, litter average birth weight, CV of litter average birth weight, individual birth weight, and deviation of individual birth weight from litter average birth weight with age at first estrus and number of ovulations were estimated using a model that fit season and line as fixed effects and sire as a random effect. Average age at first estrus and number of ovulations was 195.1 ± 0.4 d of age and 16.3 ± 0.1 ovulations, respectively. Litter average birth weight ranged from 0.79 to 2.45 kg with CV ranging from 23.5 to 44.7%. There were no significant correlations for age at first estrus with any of the birth weight traits examined. The number of ovulations was weakly correlated ($r = 0.08$, $P < 0.001$) with individual birth weight but not any of the other birth weight traits. These data do not support the concept that differences in average litter birth weight contributes to variation in pubertal age or ovulation rate in pigs.

Key Words: birth weight, ovulation rate, puberty

TH340 Determining the effect of scrotal insulation on sperm production in the boar. K. M. Gibbs*, J. R. Schindler, and J. J. Parrish, *University of Wisconsin-Madison, Madison.*

The objective of this study was to develop a model of heat stress in the boar using scrotal insulation to determine which stages of development were most susceptible to damage and apoptotic loss. The experiment utilized sacks that were adhered to the scrotum to produce a localized heat insult. Sacks were either insulated with batting and foil vapor barrier or were of the same design but without insulation material as a sham treatment. Semen was collected and analyzed for motility and total sperm output from the boars on a Monday, Wednesday, and Friday schedule leading up to the treatment and 6 weeks post-treatment. Scrotal sacks, non-insulated or insulated, were adhered to the testes and temperature loggers were attached to the scrotum to measure scrotal temperature over the 48 h treatment period. A significant difference in average temperature was achieved during the treatment between the insulated group (n = 5) and non-insulated group (n = 5) (mean ± SEM, 33.9 ± 0.33°C vs. 32.1 ± 0.43°C; $P < 0.05$). Semen samples were evaluated for motility and total sperm output. Motility was determined using computer assisted semen analysis with Hamilton Thorne motion analysis system. The non-insulated group (n = 4) showed no significant difference in motility compared with the control days (mean ± SEM, 96 ± 0.52%; $P > 0.05$). However, the insulated group (n = 4) showed a significant decrease in motility for d 28,30,33, and 35 compared with the control days (mean ± SEM, 78 ± 5.00%, 69 ± 6.76%, 66 ± 11.85%, 69 ± 9.86% vs. 95 ± 0.89%; $P < 0.05$). Total sperm output was not different for the non-insulated group (n = 5) compared with the control days (mean ± SEM, 35 ± 3 billion; $P > 0.05$). However, there was a trend indicating a decrease in sperm cell output on d 33 for insulated boars compared with the control days (mean ± SEM, 24 ± 6 billion vs. 35 ± 3 billion; $P = 0.06$). The data suggests that an average temperature increase of 1.8°C of the testes can have damaging effects to boar semen quality. Based on the known spermatogenic timeline in the boar, the main cell stage affected by the scrotal insulation treatment was the primary spermatocyte.

Key Words: semen, heat stress, swine

TH341 Influence of fat supplementation on leptin and LH concentration in Nelore heifers. R. S. Cipriano*, M. C. V. Miguel, H. F. Costa, J. S. Souza, L. M. Pavanello, J. L. C. Delfino, D. Giraldo-Arana, D. M. Pinheiro, and G. P. Nogueira, *UNESP, Animal Endocrinology Laboratory, DAPSA, FMVA, Aracatuba, Sao Paulo, Brazil.*

The aim of this study was to verify whether rumen protected fat supplementation, after weaning increase leptin and LH concentration in Nelore heifers (*Bos taurus indicus*). Contemporary heifers (n = 30) with 167 ± 13 kg and 9 mo were sorted into 3 experimental groups: Control Group (CG, n = 10), sugar cane bagasse plus 4.2 kg concentrate and 500g of ground corn; Fat Group (FG, n = 10), sugar cane bagasse, plus 4.2 kg of concentrate plus 200g of Megalac-E per animal (rumen protected fat); and Excess Group (EG, n = 10), sugar cane bagasse plus 4.2 kg of concentrate, 500 g of ground corn and 200g of Megalac-E per animal per day. After an adaptation period, animals remained under nutritional treatments for 92 d (13th to 16th month of age). Blood samples were collected every 4 d, between 9th and 18th month of age, and every 7 d from the 18th until 20th month of age for leptin and LH quantification. The results were evaluated by repeated measures ANOVA and the Duncan's test was the post-test of SAS. After treatment, the EG presented the lowest LH concentration total area (31.18 ± 14.91 ng/mL × day), $P = 0.06$) in comparison with CG (63.20 ± 33.89 ng/mL × day) and FG (82.90 ± 48.50 ng/mL × day), from samples collected every 4 d. There was no difference ($P > 0.05$) in the total area and in the LH concentration maximum amplitude between the groups before and during the nutritional treatments. Before treatment, the EG showed higher leptin concentration amplitude ($P = 0.08$, 2.99 ± 1.62 ng/mL) than CG (1.71 ± 0.77 ng/mL). There was no difference in leptin concentration amplitude between groups either before, during or after treatment ($P = 0.49$, 2.46 ± 0.96, 2.03 ± 1.26 and 1.86 ± 1.20 ng/mL). The FG and EG showed smallest leptin amplitude during and after treatment combined compared with before (FG: 2.03 ± 1.26 vs. 2.87 ± 1.57 ng/mL, $P = 0{,}052$; EG: 1.86 ± 1.20 vs. 2.99 ± 1.62 ng/mL, $P = 0.03$), and the CG showed greatest leptin amplitude after and during combined when compared the period before treatment (2.46 ± 0.96 vs. 1.71 ± 0.77 ng/mL, $P = 0.03$). We concluded that excess treatment decreased the LH concentration area and fat treatment decreased leptin amplitude after supplement period.

Key Words: fat, leptin, LH

TH342 Effect of supplementation of distillers grains during early pregnancy on reproductive performance of beef cows. A. M. Schreiner[1], P. M. Fricke*[2], E. J. Cretney[2], A. E. Radunz[1], and J. S. Luther[1], *[1]University of Wisconsin-River Falls, River Falls, [2]University of Wisconsin-Madison, Madison.*

Crossbred Angus cows (initial BW = 671 ± 8.8 kg; age = 6.3 ± 0.29 yr) were used to evaluate the effects of corn distillers' grains plus solubles (DG) supplementation during early pregnancy on reproductive performance. Cows were randomly assigned to 1 of 3 treatments (n = 33 cows/trt): no supplementation (CON); low supplementation of 2.7 kg of dried distillers grains/hd/d (LDG); and high supplementation of 5.4 kg of DDGS/hd/d (HDG). During the supplementation period, cows were housed in separate pastures of similar forage quality and DG supplementation contained 50% dried DG and 50% modified wet DG on a DM basis. Supplementation of DG began 7 d before artificial insemination (AI, d 0) and ended 20 d later. Body weight (BW) and body condition scores (BCS) were collected at the start (d −7) and end of supplementation (d 20). Blood samples were collected for progesterone (P4) analysis on d 4, 6, 8, 11, 13, 15, 18, and 20. B-mode ultrasonography was used to determine diameter of the dominant follicle (d −1) and corpus luteum (CL; d 13), and pregnancy status (d 33). Cows fed LDG and HDG had greater ($P < 0.001$) BW and greater ($P < 0.05$) BCS at the end of supplementation compared with CON cows. No difference ($P > 0.05$) was observed in follicle diameter among treatments. Cows fed HDG had a greater ($P < 0.05$) CL diameter compared with cows fed CON or LDG. From 4 to 20 d after AI, area under the curve for plasma P4 was greater in cows fed LDG ($P < 0.02$) and HDG ($P < 0.05$) compared with CON cows. Pregnancy rates among CON (73%), LDG (70%) and HDG (79%) cows were similar ($P = 0.69$). Supplementation of DG during early pregnancy improved BW and BCS and increased plasma P4 concentrations, but pregnancy rates did not differ among treatments.

Key Words: distillers grain, beef cattle, reproduction

TH343 Effect of capsicum oleoresin on proliferation and cytokine production in bovine peripheral blood mononuclear cells. J. Oh*[1], S. Walusimbi[1], A. N. Hristov[1], J. Pate[1], and D. Bravo[2], *[1]Department of Animal Science, The Pennsylvania State University, University Park, [2]Pancosma, Geneva, Switzerland.*

The objective of this experiment was to investigate the effect of capsicum oleoresin (CO) on proliferation of, and cytokine production in, activated and non-activated bovine peripheral blood mononuclear cells (PBMC). Peripheral blood mononuclear cells were obtained from blood collected from dry Holstein cows (n = 4). The cells were cultured in the presence or absence of immune cell activating compounds, phorbol 12-myristate 12-acetate (PMA, 50 ng/mL) and ionomycin (1 μg/mL), and treated with CO at 4 concentrations, 0 (control), 40, 160, and 320 μg/mL. Cell viability and proliferation were determined by flow cytometry using propidium iodide (PI) and carboxyfluorescein diacetate succinimidyl ester (CFSE), respectively. There was no effect of CO on cell viability in activated or non-activated PBMC. However, CO at 320 μg/mL increased ($P < 0.001$) the percent proliferating cells (64.9%) compared with the control (4.6%) in activated cells. Cytokine production was detected by intracellular staining and flow cytometry. Brefeldin A (BFA) was added to prevent the cells from releasing the cytokines into the media. Activated and non-activated PBMC treated with CO were labeled with antibodies against tumor necrosis factor α (TNF), interferon gamma (IFNG), and interleukin 10 (IL10). Compared with the control, CO at 160 and 320 μg/mL significantly increased ($P = 0.04$ and 0.01) the production of IFNG in non-activated (1.04 vs. 2.18 and 2.64% positive cells, respectively), but not in activated PBMC. There was no effect of CO ($P = 0.19$ to 0.65) on the production of TNF or IL10. In conclusion, CO at high concentrations induced both proliferation and IFNG production. It is suggested that CO may facilitate activation of the immune system in dairy cows.

Key Words: capsicum oleoresin, cytokine, cell proliferation

TH344 Growth and cardiovascular characteristics between birth and one month of age in dairy calves. B. E. Voelz*, H. M. Kerr, D. K. Hardin, K. A. Barton, C. O. Lemley, and J. E. Larson, *Mississippi State University, Mississippi State.*

Growth characteristics and cardiac function in a young calf may affect health and production characteristics later in life. The objective of this experiment was to determine if growth characteristics and cardiac measurements were correlated between 2 ages in a calf's life or between each other at one time point. Holstein (n = 30) and Jersey (n = 8) calves were evaluated at 2 d (±1 d) after birth (n = 38) and again at 1 mo (±4 d) of age (n = 27). Measurements at birth and at 1 mo of age included blood pressure, heart rate, heart girth, hip and wither height as well as carotid artery hemodynamics measured via Doppler ultrasonography [pulsatility index (PI), resistance index (RI), and vessel diameter]. From

these measurements, mean arterial pressure (MAP), pulse pressure (PP), mean velocity (MnV) and blood flow (BF) were calculated. The CORR procedures of SAS were used to analyze data; means (±SD) are presented. Heart girth (r = 0.774) and hip (r = 0.795) and wither height (r = 0.765) at birth were all ($P < 0.0001$) positively correlated with size measurements at 1 mo of age. Heart rates of calves at birth (128 ± 19 bpm) were significantly ($P < 0.01$) and positively correlated with MAP at 1 mo of age (r = 0.564; 93 ± 15 mmHg). Blood MnV and BF (373 ± 201 mL/min) at birth were ($P < 0.05$) negatively correlated with PP (r = −0.456; 48.6 ± 9.9 mmHg) and RI (r = −0.443; 0.855 ± 0.12), respectively, at 1 mo. RI (r = 0.461; $P < 0.05$) and PI (r = 0.372; $P = 0.06$) at birth were positively correlated with BF at 1 mo of age (426 ± 204 mL/min). Birth hip (r = 0.340) and wither height (r = 0.329) tended to be significantly ($P < 0.10$) and positively correlated with MAP at birth (79.8 ± 8.6 mmHg), indicating larger calves had greater arterial pressure. PI at birth ($P < 0.05$) and at 1 mo (2.8 ± 1.7; $P < 0.10$) were negatively correlated with BF at birth (r = −0.355) and 1 mo (r = −0.326), respectively, giving indication that these data correspond to previous research using Doppler ultrasonography. Further characterization of calf cardiovascular hemodynamics may allow researchers to examine potential neonatal outcomes associated with later life production characteristics.

Key Words: cattle, dairy, Doppler

TH345 Effect of decreased progesterone concentrations during follicular development on oocyte yield and quality. F. M. Abreu*[1], S. Kruse[2], L. H. Cruppe[1], R. S. Cipriano[1], M. L. Day[1], T. W. Geary[3], M. A. Coutinho da Silva[1], B. A. Hicks[4], D. S. Clark[4], and G. A. Bridges[2], *[1]The Ohio State University, Columbus, [2]University of Minnesota, Grand Rapids, [3]USDA ARS Fort Keogh, Miles City, MT, [4]Simplot Livestock Inc., Emmett, ID.*

The objective was to determine if decreased concentrations of progesterone (P4) during early follicular development would affect number and quality of oocytes recovered by transvaginal ultrasound-guided ovum pick-up (OPU). Ovulation was synchronized with the 5 d CO-Synch + CIDR program in postpubertal heifers in 2 groups (n = 18 per group) with d of the 2nd GnRH treatment designated as d 0. On d 5.5 all visible follicles in the ovaries were ablated. Heifers were stratified, within group, by estrous expression (yes or no), weight, age, and antral follicle count to receive either a new CIDR (high P4; H) or a previously used CIDR and 2–25 mg doses of PGF given 8 h apart (low P4; L) on d 5.5. On d 10.5 (OPU-1), all visible follicles were aspirated, new and used CIDR were replaced, and OPU was performed again on d 15.5 (OPU-2). Follicle stimulating hormone (FSH; 50 mg per dose) was administered on d 7.5, 8, 8.5 and 9 and d 12.5, 13, 13.5 and 14. Blood samples for P4 were collected at ablation, OPU-1, and OPU-2. Number of follicles aspirated was recorded at each OPU and oocytes were graded on a 1 to 6 scale (1 = ≥5 layers of compact cumulus and homogenous cytoplasm, 6 = denuded). Concentrations of P4, total follicles aspirated, total oocytes recovered, and oocyte quality were compared with the MIXED procedure of SAS. Concentrations of P4 did not differ on d 5.5, but were lower ($P < 0.01$) at OPU-1 and OPU-2 in the L (3.03 ± 1.92 and 2.00 ± 1.01 ng/mL, respectively) than in the H (5.47 ± 2.06 and 5.36 ± 1.60 ng/mL, respectively) treatment. Across OPU-1 and OPU-2, the L treatment had more ($P < 0.05$) total follicles aspirated (15.3 ± 1.1) and oocytes recovered (9.9 ± 1.2) than heifers in the H treatment (12.1 ± 1.0 and 6.4 ± 0.8, respectively). Furthermore, decreased P4 resulted in increased ($P < 0.05$) number of grade 1–3 oocytes collected per heifer (L: 7.78 ± 1.03, H: 4.81 ± 0.72). In conclusion, lesser P4 concentrations during follicular emergence and early development resulted in collection of a greater number of good quality oocytes per heifer by OPU when compared with heifers with greater peripheral P4 concentrations.

Key Words: progesterone, heifer, oocyte

TH346 Integrating nutritional and reproductive models to improve reproductive efficiency in dairy cattle. S. L. Shields* and J. P. McNamara, *Department of Animal Sciences, Washington State University, Pullman.*

Successful reproduction requires coordination among neural, endocrine and nutritional systems leading to ovulation, insemination and a uterine environment that allows embryonic growth and attachment. However, we still lack, in research and practice, a systems approach to integrating genetics and nutrition to improve reproduction. Therefore, our objective was to integrate 2 existing mechanistic, dynamic models of genetic, nutritional and reproductive processes in the dairy cow. A model of metabolism (Molly, UC Davis); which describes metabolism of glucose, VFA, and amino acids for fat and protein synthesis and degradation and milk component production, as well as energy transactions (ADP/ATP), was integrated with a model of reproductive processes which describes growth and decay of the follicles and corpus luteum, gonadotropin releasing hormone, follicle stimulating hormone, luteinizing hormone, progesterone, estrogen, oxytocin, and prostaglandin F2α over time. The 2 models were integrated at specific points based on available literature data: glucose and IGF-I affect rates of follicle stimulating hormone, luteinizing hormone, and follicular growth; higher glucose supply increases IGF-1 and increases follicular growth. Increasing circulating concentration of IGF1 by 20 ng/ml will increase follicular growth by 1 mm in 18 d (versus an average of 12 mm pre-ovulation), leading to an earlier ovulation. Increasing AtAdv (total ATP conversion to ADP) from 372 to 1488 moles/d decreases peak estrogen from 0.342 to 0.281. Increased metabolic rate from either increased milk production or feed intake decreases estrogen and progesterone concentration. The model responses to energy intake and milk production caused a pattern and direction of response in reproductive processes consistent with available data. This research model should be useful to frame specific hypotheses on control of reproductive processes by genetic and nutritional driven mechanisms and to help develop on-farm decision support tools.

Key Words: systems biology, reproduction, nutrition

TH347 Effect of maternal dietary fish oil supplementation on growth and physiological indicators of stress in pre- and post-weaned pigs. S. A. Lockwood*, H. G. Kattesh, C. J. Kojima, M. P. Roberts, G. M. Pighetti, and A. M. Saxton, *University of Tennessee, Knoxville.*

The aim of this study was to assess whether feeding sows a diet with 0.5% protected fish oil (PFO) 2 wk before farrowing through lactation (CON, n = 2; PFO, n = 4) can reduce the stress response of their offspring due to weaning. Colostrum and milk was obtained on d 0 and 20 of lactation. Upon weaning (d 27), 24 pigs from each treatment were blocked by BW and allocated in groups of 6 to nursery pens and fed a diet consistent with dam dietary treatment. Pigs were weighed on d 17, 27, 34, 41, and blood sampled on d 20, 27, 28, 34, and 41. Blood was analyzed for plasma cortisol (CORT) and corticosteroid-binding globulin (CBG) concentrations, and white blood cell (WBC), red blood cell (RBC), and differential WBC numbers. Free cortisol index (FCI) was calculated from plasma CORT and CBG (nmol CORT/mg CBG). Data were pre-adjusted for age difference by quadratic regression, then mixed model repeated measures ANOVA (SAS) was performed. Triglyceride

concentration was higher ($P = 0.03$) in milk compared with colostrum and was not different due to treatment. Pre- and post-weaning BW and RBC were not different ($P > 0.10$) among treatments. No treatment differences were detected for blood parameters measured on d 20. On d 27, CBG but not CORT was greater ($P < 0.01$) in PFO pigs resulting in a lower ($P < 0.01$) FCI (2.9 vs. 5.0 ± 0.4 nmol/mg). Upon weaning, all pigs exhibited an increase ($P < 0.01$) in CORT, which tended ($P = 0.08$) to be greater for the CON pigs. As a result of lower CBG concentration, the FCI for the PFO and CON pigs did not differ. By d 41, regardless of treatment, CORT returned to pre-weaning level and CBG reached its greatest concentration resulting in the lowest overall FCI value recorded ($P < 0.01$). The WBC was greater ($P < 0.01$) for PFO pigs on d 27 and 28 but less ($P < 0.01$) than that measured for CON by d 41. The N:L ratio measured on d 28 tended ($P = 0.06$) to be greater for the CON compared with the PFO pigs. Supplementation of the sows' diet with a PFO, beginning 2 wk before farrowing and throughout lactation, had minimal influence on modifying the pigs' stress response due to weaning.

Key Words: fish oil, pig, weaning

TH348 Effects of intrauterine infusion of *Trueperella pyogenes* on endometrial mRNA expression of genes associated with luteolysis in dairy cows. F. S. Lima*, J. E. P. Santos, R. S. Bisinotto, L. F. Greco, E. S. Ribeiro, N. Martinez, C. A. Risco, W. W. Thatcher, and K. N. Galvão, *University of Florida, Gainesville.*

Objective was to determine the effects of intrauterine (IU) infusion of *Trueperella pyogenes* (*T. pyogenes*) on endometrial mRNA expression of genes affecting the luteolytic cascade. Fifteen early postpartum healthy Holstein cows had the estrous cycle synchronized with on GnRH d0 followed by $PGF_{2\alpha}$ on d7 and GnRH on d9. Four days after ovulation was confirmed cows were allocated randomly to receive one of 3 treatments: TP (n = 5), IU infusion of 10 mL of saline solution containing 10^9 cfu/ml of *T. pyogenes* (formerly *Arcanobacterium pyogenes*); TNF (n = 5), IU infusion of 10 mL of saline solution containing 1 μg of tumor necrosis factor α (TNFα); and Control (n = 5), IU infusion of 10 mL of saline solution. Uterine biopsies were collected at 6, 12 and 24 h after treatment to evaluate the endometrial mRNA expression of TNF-α, Interleukin (IL) 1β, IL6, IL8, prostaglandin E synthase (PGES), PGFS and oxytocin receptor (OXR). RT-PCR was used to measure mRNA expression. MRPS15 was used as housekeeping gene. The MIXED procedure of SAS was used for statistical analysis. Gene expression of IL1β and IL6, PGES and PGFS was not affected by treatment, time or treatment by time interaction. However, TP cows had higher ($P < 0.05$) mRNA expression of IL1β and IL8 than TNF cows at 24 h. TNFα mRNA expression was lower ($P < 0.05$) for TP cows than TNF cows at 6 h. Overall OXR mRNA expression was higher ($P = 0.03$) for TP cows than Control cows. In conclusion, IU infusion of *T. pyogenes* did not consistently increase endometrial mRNA expression of genes involved in the luteolytic cascade; however, the endometrial expression of OXR was increased for cows infused with *T. pyogenes*.

Key Words: dairy cow, *Trueperella pyogenes*, gene expression

TH349 Correlations between PAG concentrations, pregnancy loss, and milk production in high producing Holstein cows. P. Mercadante*[1], C. Risco[2], and A. Ealy[1,3], *[1]University of Florida, Department of Animal Sciences, Gainesville, [2]University of Florida, Department of Large Animal Clinical Sciences, Gainesville, [3]Virginia Polytechnic Institute and State University of Florida, Department of Animal and Poultry Sciences, Blacksburg.*

Pregnancy-associated glycoproteins (PAGs) are produced by the ruminant placenta and secreted into the maternal circulation during pregnancy. Their concentrations in early gestation may indicate pregnancy failure in cattle. To determine if plasma PAG and P4 concentrations are associated with pregnancy loss and several production variables in high producing cows, 125 multiparous Holsteins were timed AI using semen from multiple sires. Transrectal ultrasonography was used to diagnose pregnancy on d 32, 46 and 74 of gestation. Blood was harvested to determine plasma concentrations of PAG and P4 at d 32. Data was segregated into groups based on whether cows maintained their pregnancies to term (n = 101) or lost their pregnancies between d 32 and 46 (n = 9), d 46–74 (n = 9) or after d 74 (n = 6). The CORR procedure of SAS was used to assess traits associated with PAG and P4 concentrations, GLM procedure was used to determine the relationship of calf gender and pregnancy failure with gestation length, PAG and P4 concentrations. Plasma PAG concentrations at d 32 were lower ($P < 0.05$) in cows that lost pregnancy at d 32–46 and d 46–74 (3.81 vs. 4.83 ± 0.39 ng/mL, respectively) than cows that maintained pregnancy to term (8.64 ± 0.39 ng/mL). Also, there were no difference between cows that retained pregnancy to term and cows that lost pregnancy after d 74 (9.8 ± 0.39 ng/mL). Plasma PAGs were negatively correlated ($P < 0.05$) with parity and age, and positively correlated ($P < 0.05$) with average milk yield. Plasma P4 concentrations at d 32 were lower in cows that lost pregnancy (4.82 ± 0.24 ng/mL) than those that maintained it to term (6.84 ± 0.24 ng/mL). Plasma P4 concentrations were negatively correlated ($P < 0.05$) with parity and age. No correlations were detected between PAG or P4 concentrations and calf gender or gestation length. These observations are consistent with the concept that placental and luteal insufficiencies may be detected in cattle before pregnancy failure. Continued analysis of this data set will explore if peri- and postpartum illnesses affects PAG, P4 and the risk of pregnancy failure in dairy cattle.

Key Words: PAG, dairy, fertility

TH350 Assessment of systematic breeding programs: A comparison between AI after estrus detection and timed AI in lactating dairy cows. A. B. Nascimento*[1], A. H. Souza[2], G. Pontes[1], M. C. Wiltbank[2], and R. Sartori[1], *[1]University of São Paulo, Piracicaba, São Paulo, Brazil, [2]University of Wisconsin, Madison.*

Reproductive management strategies on dairy farms are highly variable with AI either occurring after a fixed time protocol to synchronize ovulation (TAI) or following estrus detection (ED). The first objective of this study was to compare pregnancies per AI (P/AI) at first service in herds using TAI in most of the cows (>80% TAI) versus herds using primarily ED and AI (<20% TAI). The second objective was to evaluate the effect of kg/lactation on P/AI in cows bred after ED or by TAI. Six hundred and 48 herds totaling 83,771 cows were divided into herds using < 20% of TAI and submitted to ED (ED = 25,416) and herds using > 80% of TAI and submitted to TAI (TAI = 58,355). Both categories were divided into 5 levels of milk yield, showed in kg/lactation (P1: 9,072–11,340; P2: 11,341–13,608; P3: 13,609–15,876; P4: 15,877–18,144; and P5: > 18,145). Statistical analyses were performed with logistic regression by PROC GLIMMIX of SAS. There was no difference in overall P/AI at first service between ED (35.4%) and TAI (36.1%). For all cows there was a negative correlation between milk production and P/AI ($r = -0.36$; $P < 0.0001$). Surprisingly, there was no interaction between milk production and AI strategy ($P = 0.85$) as demonstrated by P/AI in ED vs. TAI for P1 (38.0 vs. 37.0%), P2 (37.2 vs. 38.0%), P3 (34.2 vs. 36.0%), P4 (31.3 vs. 34.0%), and P5 (30.5

vs. 29.0%). No advantage of TAI on conception rates over ED-AI was observed, likely due to the great variation in synchronization protocols used in these large herds. In addition, it appears that in this large group of herds, milk production was negatively correlated with P/AI in both cows bred to ED or bred by TAI. Supported by FAPESP, CAPES, and CNPq of Brazil.

Key Words: estrus, TAI, conception rate

TH351 Reproductive outcomes of timed AI or transfer of in vivo- or in vitro-produced vitrified embryos in beef cattle. R. Sartori*[1], A. B. Prata[1], R. S. Surjus[1], A. V. Pires[1], M. C. C. Mattos[2], A. C. Basso[2], J. H. F. Pontes[2], J. R. S. Gonçalves[3], L. G. Lima[3], and T. S. Aguiar[1], *[1]University of São Paulo, Piracicaba, SP, Brazil, [2]In Vitro Brasil Ltda, Mogi Mirim, SP, Brazil, [3]Hildergard G. V. Pritzelwitz Experimental Station, Londrina, PR, Brazil.*

The aim was to evaluate conception rates and pregnancy losses in beef cattle bred by timed AI or that served as embryo recipients. All Nelore (*Bos indicus*) cows (in calf or not) were synchronized with the same protocol within a 3-mo period. On Day 0, cows received i.m. Two mg estradiol benzoate and an intravaginal progesterone device. On Day 8, the device was removed and cows received i.m. treatments of 0.150 mg sodium cloprostenol, 300 IU eCG and 0.6 mg estradiol cypionate. For AI, 346 cows were bred on Day 10 using frozen/thawed semen of 5 bulls. For embryo transfer, cattle received in vivo- (n = 274) or in vitro-produced (n = 573) vitrified embryos on Days 16 to 18 of the protocol after confirming the presence of a corpus luteum. The same groups of cows were used for all treatments. Transfers of in vivo- and in vitro-produced embryos, but not TAI were concurrent, and there were 2 time-periods for AI or ET for each treatment group. Pregnancy diagnosis was performed 30 and 60 d after ovulation by transrectal ultrasound. For in vitro and in vivo embryo production, there were 4 sessions of superovulation or ovum pickup, respectively, 42 d apart in 33 Nelore cows. In vitro embryo production was done using 6 bulls and for in vivo production, 8 bulls were used. There were at least 3 bulls overlapping among AI and ET groups. Grade 1 embryos (IETS) were vitrified using the Cryotop method. Data were analyzed by Chi-squared and are presented below. In conclusion, although having inferior reproductive outcomes as compared with TAI, vitrified embryos produced with oocytes from Zebu cows had promising results as seen by acceptable conception rates and pregnancy losses. Supported by FAPESP, CAPES, and CNPq of Brazil.

Table 1.

	Timed AI	In vivo vitrified	In vitro vitrified
30 d conception, % (no./no.)	50.3 (174/346)[a]	39.4 (108/274)[b]	34.0 (195/573)[b]
60 d conception, % (no./no.)	47.7 (165/346)[a]	35.4 (97/274)[b]	28.6 (164/573)[c]
Embryo/fetal loss (30 to 60 d), % (no./no.)	5.2 (9/174)[b]	10.2 (11/108)[ab]	15.9 (31/195)[a]
Abortion (60 d to calving), % (no./no.)	15.2 (25/165)[a]	6.3 (6/96)[b]	16.5 (27/164)[a]
Peripartum loss, % (no./no.)	2.1 (3/140)[b]	4.4 (4/90)[ab]	9.5 (13/137)[a]

[a,b,c]$P < 0.05$.

Key Words: conception rate, pregnancy loss, vitrification

TH352 Effects of gonadotropin releasing hormone (GnRH) and equine chorionic gonadotropin (eCG) during estrus synchronization and fixed-time artificial insemination of *Bos indicus*-based females on fixed-time artificial insemination and final pregnancy rates. F. R. Gaievski[1], V. R. G. Mercadante[2], G. C. Lamb[2], R. R. Weiss[3], M. A. F. Betiol[3], and L. E. Kozicki*[1], *[1]School of Agricultural Sciences and Veterinary Medicine, Pontifical Catholic University of Parana, Curitiba, PR, Brazil, [2]North Florida Research and Education Center, University of Florida, Marianna, [3]School of Veterinary Medicine, Federal University of Parana, Curitiba, PR, Brazil.*

We determined the effects of GnRH and eCG on fixed-time AI (TAI) and overall pregnancy rates of *Bos indicus* and *Bos indicus* × *Bos taurus* crossbred cows during a 90 d breeding season. A total of 678 females (387 pluriparous and 291 nulliparous females) were assigned randomly (within parity) to 1 of 5 treatments: (1) on d 0 females received a 1.0 mg injection of estradiol benzoate (EB) and insertion of a controlled intravaginal progesterone (P4) releasing device containing 0.558 g of P4, followed on d 9 by P4 device removal and a 0.075 mg injection of prostaglandin $F_{2\alpha}$, a 1.0 mg injection of EB on d 10, and TAI 32 h after EB (TAI1; n = 120); (2) same as TAI1, but inclusion of a 500 µg injection of GnRH at TAI (TAI2; n = 120); (3) same as TAI1, but inclusion of a 400 IU injection of eCG on d 10 (TAI3; n = 120); (4) same as TAI3, but inclusion of a 500 µg injection of GnRH at TAI (TAI4; n = 120); (5) females received no estrus synchronization, but were naturally mated during the 90-d breeding season (natural service; NS; n = 198). Females in the TAI1, TAI2, TAI3, and TAI4 treatments received clean-up bulls for natural service 45 d after TAI, for 45 d. Pregnancy was determined by transrectal ultrasonography on d 45 for TAI pregnancy rates (TAI1, TAI2, TAI3, and TAI4 treatments) and overall pregnancy rates on d 120 after TAI for all treatments. Data was analyzed using the procedure FREQ of SAS (SAS Inst. Inc., Cary, NC). There were no differences (P = 0.61) in pregnancy rates for TAI on d 45 between treatments (TAI1 = 50%; TAI2 = 55%; TAI3 = 58%; TAI4 = 58%). Overall pregnancy rates were greater ($P < 0.001$) for the TAI1, TAI2, TAI3, and TAI4 treatments compared with the NS treatment (85%, 85%, 90%, 93% and 73%, respectively). In conclusion, administration of GnRH or eCG during TAI synchronization did not improve pregnancy rates to TAI; however, exposure of cows to TAI synchronization protocols improved overall pregnancy rates during a 90-d breeding season.

Key Words: artificial insemination, estrus synchronization, *Bos indicus*

TH353 The impact of omission of GnRH at the beginning of 5-d CO-Synch + CIDR program on timed AI pregnancy rate in beef heifers. L. H. Cruppe*[1], G. A. Bridges[2], S. L. Lake[3], R. S. Cipriano[1], F. M. Abreu[1], S. Kruse[2], B. R. Harstine[1], R. Arias[3], R. Raymond[4], W. Kayser[4], M. V. Biehl[1], and M. L. Day[1], *[1]The Ohio State University, Columbus, [2]University of Minnesota, Grand Rapids, [3]University of Wyoming, Laramie, [4]Simplot Livestock Inc, Grand View, ID.*

The objective of this study was to investigate whether the omission of the initial GnRH treatment at the time of CIDR insertion would affect pregnancy rates to timed AI in a 5-d CO-Synch + CIDR program that utilizes a single PGF dose given at CIDR removal. Yearling beef heifers in Ohio (n = 294, Angus × Simmental), Utah (n = 271, Angus × Hereford), Idaho (n = 127, Charolais) and Wyoming (n = 137, Angus) were randomly assigned to either receive 100 µg GnRH (G+, n = 413) or not to receive GnRH (G-, n = 416) at CIDR insertion (d −5). At CIDR removal (d 0 of the experiment), 25 mg PGF2α (PGF; Lutalyse) was administered I.M. to all heifers. All heifers were inseminated by timed AI and given 100 µg GnRH on d 3 (72 h after PGF). In 144 heifers, ovarian ultrasonography was performed on d −5 and 0 to identify CL

present at CIDR insertion and newly formed CL at CIDR withdrawal, respectively. In another subgroup of heifers (n = 269), blood samples for progesterone analysis collected on d 3 (at timed AI) and/or estrus detection were used to assess luteal regression. Pregnancy diagnosis was performed between 32 and 38 d after timed AI. At CIDR withdrawal, presence of a new CL was greater ($P = 0.02$) in the G+ (44.4%, 32/73) than G- (25.3%, 18/71) treatment. In heifers assessed for luteal regression, the G+ (96.3%) and the G- (99.2%) treatments did not differ ($P > 0.1$) in incidence of luteal regression. Timed AI pregnancy rate in the G+ (50.7%) and G- (54.7%) treatments did not differ ($P > 0.1$). In conclusion, omission of the initial GnRH treatment in the 5-d CO-Synch + CIDR program did not influence timed AI pregnancy rate in yearling beef heifers, and the incidence of newly formed CL was only increased by 19.1% with inclusion of the initial GnRH.

Key Words: GnRH, beef heifer, PGF

TH354 The effects of intramuscular or intravenous injections of gonadotropin releasing hormone at fixed-time artificial insemination (TAI) on pregnancies per TAI of *Bos indicus* beef cows. D. Demeterco[1], V. R. G. Mercadante[2], G. C. Lamb[2], F. R. Gaievski[1], B. G. Weiss[1], G. N. Turbay[1], M. S. Segui[1], R. R. Weiss[3], M. A. F. Betiol[3], and L. E. Kozicki*[1], *[1]School of Agricultural Sciences and Veterinary Medicine, Pontifical Catholic University of Parana, Curitiba, PR, Brazil, [2]North Florida Research and Education Center, University of Florida, Marianna, [3]School of Veterinary Medicine, Federal University of Parana, Curitiba, PR, Brazil.*

Our objective was to evaluate the effects of an intramuscular or intravenous administration of gonadotropin releasing hormone (GnRH) at fixed-time AI (TAI) on pregnancies per TAI of crossbred *Bos indicus* beef cows (Nelore × Tabapuã). Pluriparous cows (n = 120) were estrous synchronized as follows: on d 0 cows received a 2.0 mg injection of estradiol benzoate (EB) and insertion of a controlled intravaginal progesterone releasing device containing 0.558 g of progesterone, followed on d 8 by removal of the progesterone device simultaneous with a 0.15 mg injection of prostaglandin $F_{2\alpha}$ (PGF), a 1.0 mg injection of EB, and 400 IU injection of equine chorionic gonadotropin. At 54 h after PGF all cows received a fixed-time AI and a 0.084 mg injection of GnRH (buserelin acetate) administered either via the vena caudalis (n = 60), or via the longissimus dorsi (n = 60). All cows were inseminated with the same AI sire and by a single experienced AI technician. Pregnancy was determined by transrectal ultrasonography on d 60 after AI. Data was analyzed by Chi Square analysis using the procedure FREQ of SAS (SAS Inst. Inc., Cary, NC). Cows receiving the intravenous administration of GnRH had greater ($P = 0.04$) pregnancies per TAI than cows receiving the intramuscular injection of GnRH at the time of AI (65% vs. 46.6, respectively). We concluded that intravenous administration of GnRH at the time of AI improved pregnancies per TAI of crossbred *Bos indicus* beef cows submitted to TAI.

Key Words: gonadotropin-releasing hormone, artificial insemination, intravenous

TH355 Timing of artificial insemination in a 7-d P4-E2 estrous synchronization program in *Bos indicus* postpartum cows. M. V. C. Ferraz Junior[1], A. V. Pires[2], M. V. Biehl*[1], E. M. Ferreira[2], D. D. Nepomuceno[2], V. N. Gouvea[1], R. Sartori[2], J. R. S. Goncalves[3], L. H. Cruppe[4], and M. L. Day[4], *[1]University of Sao Paulo, Pirassununga, SP, Brazil, [2]University of Sao Paulo, Piracicaba, SP, Brazil, [3]Experimental Station Hildegard Georgina Von Pritzelwitz, Londrina, PR, Brazil, [4]The Ohio State University, Columbus.*

The aim of this study was to compare the effect of altering the moment of timed AI (TAI) based upon occurrence of estrus for a 7-d P4-E2 estrus synchronization protocol in Nellore cows. Two hundred and 60 postpartum cows (multiparous, n = 201; primiparous, n = 59; body condition score 2.7 ± 0.01; BW, 434 kg ± 3.8) that were 40 ± 1.2 d postpartum (d 0) were used. On d 0, all cows received 2 mg of estradiol benzoate (Estrogin) and a new CIDR. At CIDR removal on d 7 (designated as h 0), 25 mg of PGF (Lutalyse), 0.6 mg of estradiol cipionate (ECP) and 300 IU of eCG (Folligon) were administered in all cows. Cows were either all inseminated by timed AI (TAI) at h 55 (55h, n = 130) or cows detected in estrus by h 55 were TAI at h 55, with the remainder of cows not detected in estrus by h 55 receiving TAI at h 72 (55/72h, n = 130). Estrus detection was performed using Estrotect patches to either h 55 (55h treatment) or h 72 (55/72h treatment). Blood samples collected 11 d after CIDR removal were analyzed for P4 concentration to confirm ovulation during synchronization. Data were analyzed using GLIMMIX procedures of SAS. Estrus detection rate was greater ($P < 0.01$) for the 55/72h (84.6%) than 55h (67.7%) treatment; probably due to the longer period of estrus detection. Ovulation rate (55/72h, 89.2%; 55h, 91.5%) and TAI pregnancy rate (55/72h, 59.2%; 55h, 55.4%) did not differ ($P > 0.1$) between treatments. No interaction between treatment and parity was detected. In a secondary analysis across treatments, estrus detection rate was greater ($P < 0.01$) in multiparous (81.1%) than primiparous (59.3%) cows. Accordingly, ovulation rate was greater ($P = 0.02$) in multiparous (93.5%) than primiparous (79.7%) cows. In contrast, TAI pregnancy rate did not differ ($P > 0.1$) between multiparous (58.2%) and primiparous (54.2%) cows. In conclusion, the 55/72h approach, in which TAI in cows not detected in estrus within 55 h was postponed until h 72 did not increase TAI pregnancy rate compared with TAI of all cows at h 55.

Key Words: postpartum beef cow, E2-P4 protocol, timing of AI

TH356 Improving embryo recovery from superovulated Holstein dairy cattle: Evaluation of reflushing 30 minutes after the initial flush on embryo recovery. R. W. Bender*, K. S. Hackbart, P. D. Carvalho, A. R. Dresch, L. M. Vieira, M. C. Amundson, G. B. Sandoval, A. H. Souza, J. N. Guenther, and M. C. Wiltbank, *University of Wisconsin-Madison, Madison.*

Non-surgical embryo recovery techniques revolutionized superovulation after introduction in 1976; however, suboptimal embryo recovery continues to be a problem. In experiment 1, superovulated Holstein cows were flushed (n = 156 flushings from 32 lactating and 17 dry cows) with a silicone 2-way catheter in each horn individually using a liter of flush media per horn (SF). Following the initial uterine horn flush, the catheter was moved back to the cervix and flush media was placed in the uterus. After 30 min, cows had their entire uterus reflushed with one liter of flush media (DF). Four experienced technicians performed all flushes and one experienced technician performed all searching of structures. Superovulatory response (CL number using ultrasound) averaged 17.3. A total of 8.4 structures (48.6%; fertilized and unfertilized oocytes) were recovered during initial flushing vs. 9.9 (57.2%) after flush/reflush. Thus, reflush increased yield of structures by 17.9% (1.5 structures). Experiment 2 evaluated whether reflush could be done immediately by doing a full uterine reflush immediately after initial horn flushing, followed by a second reflush 30 min later (n = 14). Superovulation averaged 19.6 CL with 10.1 structures recovered after initial flush (51.5%), with immediate reflush yielding 1.1 structures (5.6%) and later reflush 2.5 structures (12.8%). Combining results from both experiments, reflushing increased ($P < 0.0001$) embryo yield 18.9% with no interaction ($P = 0.36$) between superovulatory response and flush technique on recovery

(<10CL: 38.4% vs. 42.6%; 10 – 20CL: 54.9% vs. 67.8; > 20CL: 47.7% vs. 54.9%, flush vs. flush/reflush, respectively). Surprisingly, cows with low (<50%) structure recovery from the initial horn flush had lower embryo recovery from reflush than cows with high (>50%) initial embryo recovery (0.9 vs. 1.9 additional structures). In conclusion, the reflushing technique increased embryo recovery and could be of value, particularly in donor cows of high genetic merit and cows that have high structure recovery during the initial horn flushing.

Key Words: superovulation, dairy, embryo

TH357 Identifying and resynchronizing open cows and heifers 21 d after AI using CIDR inserts, ultrasonography, and GnRH in dairy cattle. L. Ibarbia, J. H. Bittar, R. Daetz, J. E. Santos, C. A. Risco, and K. N. Galvão*, *University of Florida, Gainesville.*

Reinsemination interval (RINT) is at least 42 d when diagnosing pregnancy on d 32 after AI and using timed AI for reinsemination. Objective was to decrease RI when dairy cows or heifers are inseminated using timed AI programs. Holsteins heifers (n = 153) and cows (n = 204) from one herd were randomly allocated into one of 2 groups: 21dRES (n = 77 heifers and 102 cows) had a CIDR inserted on d 13 and removed on d 20 after AI, and ovaries scanned by ultrasonography. Animals found not to have a CL and to have a follicle ≥ 12 (heifers) or ≥ 15mm (cows) received GnRH and TAI in the morning of d 21. Pregnancy diagnosis was performed on d 32, and nonpregnant 21dRES animals not reinseminated (RINS) on d 21 were started on Ovsynch-56 immediately (cows) or on the 5d-CoSynch (heifers) on d 34. Control animals were RINS after nonpregnancy diagnosis using Ovsynch-56 (cows) or 5d-CoSynch (heifers) starting on d 32 or d 34, respectively. Data were analyzed using PROC GLIMMIX in SAS. Conception rate (CR) for initial AI was similar for 21dRes and Control in heifers (49.4 vs. 51.3%) and cows (32.4 vs. 29.4%). Of the open animals, 59.0% (23/39) of heifers and 37.7% (26/69) of cows in 21dRES were RINS on d 21. Only one pregnant heifer was inaccurately diagnosed open on d 20 and RINS on d 21 (97.4% Specificity). RINT was decreased by 12.2 d (30.1 vs. 42.3 d; $P < 0.001$) in heifers and by 8.7 d (34.6 vs. 43.3; $P < 0.001$) in cows. Overall resynchronized CR was increased for 21dRES heifers compared with Control (57.5 vs. 32.4%; $P = 0.03$) because heifers RINS on d 21 had similar CR compared with Control RINS using CoSynch (43.5 vs. 32.4%; $P = 0.39$), but CR was higher for 21dRES RINS using CoSynch than Control (76.5 vs. 32.4%; $P = 0.003$). Overall resynchronized CR for cows was similar for 21dRES and Controls (30.0 vs. 30.0%; $P = 1.0$). CR was similar ($P > 0.7$) for 21dRES cows RINS on d 21 (26.9%) or using Ovsynch (35.7%) compared with Controls (30%). In conclusion, 21dRES resulted in decreased reinsemination interval, similar CR for initial AI and AI on d 21, and increased (heifers) or similar (cows) overall reinsemination CR compared with Control.

Key Words: reinsemination, timed AI, dairy cattle

TH358 Effects of heat stress and insulin on hepatic progesterone catabolic enzymes cytochrome P450 2C and 3A in lactating cows. V. L. McCracken*[1], G. Xie[1], S. E. Deaver[1], L. H. Baumgard[2], R. P. Rhoads[1], and M. L. Rhoads[1], *[1]Virginia Polytechnic Institute and State University, Blacksburg, [2]Iowa State University, Ames.*

Two experiments were performed to determine the effects of heat stress (HS) and insulin on hepatic mRNA abundance of enzymes responsible for catabolizing progesterone (cytochrome P450 2C and 3A [CYP2C and CYP3A]). To distinguish the direct effects of HS from the inherent effects of decreased DMI, a group of contemporaries was pair-fed (PF) to match the intake of the HS cows during both experiments. In the first experiment, multiparous lactating Holstein cows (n = 12) housed in climate-controlled chambers were subjected to 2 experimental periods (P1 and P2): 1) thermoneutral (TN) conditions (18°C, 20% humidity) with ad libitum intake (TN and well-fed [WF]) for 9d; and 2) either HS conditions (cyclical temperature 31.1–38.9°C, 20% humidity) fed for ad libitum intake (n = 6), or TN conditions, pair-fed (PF) to match the intake of HS animal (n = 6) for 9d. Liver samples were obtained at the end of each period and relative mRNA abundance was measured by real-time RT-PCR. In the second experiment, multiparous lactating Holstein cows (n = 12) were housed and fed as described for the first experiment. Liver samples were obtained immediately before and after an insulin tolerance test on the last day of each period. Gene expression data were analyzed using the Mixed Procedure of SAS. Heat stress caused the hepatic expression of CYP2C to decrease during both experiments ($P = 0.07$ and $P < 0.01$ for experiments 1 and 2, respectively). The relative abundance of CYP3A was not affected by environmental conditions in the first experiment but was reduced by HS in the second experiment ($P < 0.01$). Interestingly, during experiment 2 hepatic CYP3A expression also decreased during PF ($P < 0.05$). There were no effects of insulin treatment nor were there interactions between treatment groups (TN/HS or WF/PF) and insulin. Taken together, these results indicate that HS may affect progesterone catabolism by altering the hepatic expression of CYP2C and CYP3A.

Key Words: progesterone, heat stress, insulin

Production, Management and the Environment: Surveys and Models

TH359 Predicting methane and carbon dioxide emissions using the CNCPS. R. J. Higgs*, K. L. Russomanno, T. F. Christoph, and M. E. Van Amburgh, *Cornell University, Ithaca, NY.*

Food production in the US has received increased consideration from policy makers for its role in greenhouse gas (GHG) emissions. Despite dairy farms contributing < 1% of the annual GHG emissions, future regulations are possible. Integrating prediction equations for GHG emissions into field usable models could provide a tool for farmers and nutritionist to consider GHG emissions during the ration formulation process. In this study, the Cornell Net Carbohydrate and Protein System (CNCPS) was updated to include equations that were derived to predict CO_2 and CH_4 production: CO_2 (g/d) = 821.3 + 126.0 × DMI (kg/d) – 1.18 × milk (kg/d) (Casper and Mertens, 2010); CH_4 (g/d) = 45.98 – (45.98 e(−1((−0.0011 × starch/ADF) + 0.0045) × ME intake)) /55 (Mills et al., 2003). Studies were compiled (n = 4; treatments = 22) that reported CO_2 and CH_4 production from animals in metabolic chambers that also had adequate dietary information to run an evaluation in the CNCPS. Data were analyzed using a mixed model where study was included as a random variable. Observed and model predicted (13,449 ± 1,228 and 12,306 ± 685; 503 ± 29 and 442 ± 37) CO_2 and CH_4 (mean g/d ± SD), respectively, were not significantly different ($P > 0.05$) indicating the equations used could provide reliable estimates of GHG production as long as adequate dietary information was available. Following this evaluation, a data set was compiled using information from commercial farms that represented significant regions of dairy production in the US. The data set included 91 diets from 70 different farms representing 10 states. The CNCPS was used to generate predictions of CO_2 and CH_4 at the cow level. Model predicted emissions (g GHG/kg milk) were regressed against milk yield (kg/cow/d). A negative relationship similar to other literature reports was observed where GHG emissions per unit of milk decreased as milk yield increased ($R^2 = 0.81$ and 0.89; Slope = −5.7 and −0.26 for CO_2 and CH_4, respectively). These data demonstrate the potential for nutritionists to consider GHG production as part of ration formulation in a field usable model to reduce the environmental impact of dairy production.

Key Words: greenhouse gas, dairy, modeling

TH360 Risk measurement for technologies used in cow-calf production system. J. O. Barcellos*[1], T. E. Oliveira[1], C. McManus[1], R. P. Pedroso[2], D. S. Freitas[1], and M. E. Canozzi[1], *[1]UFRGS, Porto Alegre, RS, Brazil, [2]UFPA, Belem, PA, Brazil.*

The selection of a technological innovation requires a decision-making promptly secure that combines the usual empirical selection technologies and a quantitative strategy to assist the rural manager. This association increases the consistency and reliability of choosing which technology will be more fitting for each production system. Therefore, this paper seeks to develop a simple method, capable of assisting rural managers in this decision-making process by indicating the risk of technologies used to increase the pregnancy rate in cow-calf systems. The perceptions of 18 experts were evaluated across 4 dimensions related to the risk of technologies (cost (C), technical knowledge (TK), operational complexity (OC) and flexibility (F)). The 4 dimensions, in addition to their definitions, were presented in questionnaires, in which 32 technologies were appraised in accordance with the dimensions on a 5-level Likert scale (1 = very low; 2 = low, 3 = average, 4 = high, 5 = very high). The experts estimated the risk (ER) or the probability that certain technology does not produce the expected result (pregnancy rate). The dimensions with greater influence on the ER were OC and C and the increase of one unit increased ER by 0.43 points (OC) and 0.28 points (C) (maximum value of 1 point). The values for ER and the risk calculated by the proposed equation were not significantly different from each other (G-test = 43.529; $P = 0.07$) and were correlated (r = 0.81), validating the method. Management practices were least risky when related to nutritional ($P < 0.0001$) and reproductive ($P < 0.0001$) technologies, which showed no difference between each other ($P = 0.13$). Technologies related to inputs showed greater risk than innovations in the production process ($P < 0.0001$) and consolidated practices had lower risk than innovative strategies ($P < 0.0001$). Despite their importance, the technical knowledge and flexibility are usually undervalued in the decision-making process in the rural environment. Therefore, studies able to provide clear information regarding technologies may contribute to disseminate those technologies and improve the system efficiency.

Key Words: efficiency, decision-making, livestock system

TH361 The environmental and economic impact of steroid implant and β-adrenergic agonist use within US beef production. J. L. Capper*, *Livestock Sustainability Consulting, Bozeman, MT.*

Consumers are increasingly aware of food production practices, yet this cogniscence is associated with concerns regarding technology use. This study quantified the effects of steroid implant (SI) and β-adrenergic agonist (βAA) use within US beef production upon environmental and economic metrics. A whole-system environmental model was used to quantify resource inputs and waste outputs per 363 kg of beef (US average hot carcass weight). System boundaries extended from cropping input manufacture to live animal delivery at the packing plant. Four production systems were compared: one system using SI; one system using βAA; one system using both technologies; and one system without technology. Systems were modeled using management practices and production data characteristic of US beef systems. The economic impact of technology use was derived from feed use metrics. The greatest opportunity to reduce environmental and economic metrics resulted from a combination of SI and βAA use (via increased carcass weight and improved growth rate) with SI having a greater effect than βAA alone. Technology use reduced the population size required to produce 363 kg beef from 3.08 (no technology) to 2.92 (βAA), 2.72 (SI) or 2.62 (SI+βAA) animals. Production systems using both SI and βAA used less land (2.71 ha) and water (563,543 L) to produce 363 kg beef compared with SI (2.83 ha and 586,219 L), βAA (2.97 ha and 616,588 L) or a system without technology (3.13 ha and 649,556 L). Carbon emissions per 363 kg beef were reduced from 6,738 kg (no technology), to 6,459 kg with βAA, 6,287 kg with SI and 6,072 kg with SI+βAA (reductions of 5.0%, 7.5% and 10.7% respectively). Economic costs of production followed similar patterns, with decreases of 3.8% (βAA), 7.5% (SI) and 9.9% (SI+βAA) compared with the system without technology. The extra beef produced on one single carcass from the SI+βAA system would supply 7 schoolchildren with their beef-containing school meals for one year. Use of technologies improves environmental and economic sustainability metrics, yet communication of these messages to the consumer will require further investigation.

Key Words: beef, environment, economic

TH362 The environmental and economic impact of withdrawing parasite control (Fenbendazole) from US beef production. J. L. Capper*, *Livestock Sustainability Consulting, Bozeman, MT.*

Consumer concern exists regarding the use of chemicals to control infective disease within livestock systems, yet as the global human population increases, ruminant productivity must be improved to fulfill beef demand. This study quantified the environmental and economic effects of withdrawing a parasite control compound (Fenbendazole) from US beef production. A whole-system environmental model (EM) was used to quantify resource inputs and waste outputs per 363 kg beef (US average hot carcass weight). System boundaries extended from cropping input manufacture to live animal delivery at the packing plant. Two production systems were compared, either with or without Fenbendazole use for parasite control in growing and mature cattle. Systems were modeled using characteristic management practices and production data from US beef systems. Productivity effects of parasite control were derived from peer-reviewed published literature. The economic impact of withdrawing parasite control was quantified from feed use within the EM. Withdrawing parasite control from US beef production reduced herd productivity through decreases in pregnancy rate (81% vs. 91%), weaning weight (227 kg vs. 248 kg) and growth rate from birth to slaughter (1.10 kg/d vs. 1.31 kg/d). A production system without parasite control required a total of 3.07 animals (supporting population plus slaughter animals) to produce one 363 kg carcass compared with 2.61 animals in a population with parasite control. An extra 1,180 kg of feed, 0.43 ha of land and 85,864 L of water were required to produce one 363 kg beef carcass in a system without parasite control. Carbon emissions were increased by 13.4% (6,883 kg per 363 kg beef) by withdrawing parasite control from the beef production system compared with the control (6,072 kg per 363 kg beef). Reduced productivity conferred by withdrawing parasite control incurred an increase of 11.8% in production costs per unit of beef. It is clear that parasite control has significant environmental and economic impacts on beef production; the challenge is to communicate these effects to the consumer, retailer and policy-maker.

Key Words: beef, economic, environment

TH363 The environmental and economic impact of calving rate within US beef production. J. L. Capper*, *Livestock Sustainability Consulting, Bozeman, MT.*

The proportion of cows bearing a live calf is a key productivity metric in cow-calf production. This study quantified the environmental and economic effects of calving rate within US beef production. A whole-system environmental model (EM) was used to quantify resource inputs and waste outputs per 363 kg of beef (average US hot carcass weight). System boundaries extended from cropping input manufacture to live animal delivery at the packing plant. Calving rate varied from the ideal of one live calf per cow per year (100%) to 60% (representative of many South American systems), with systems modeled using management practices and production data characteristic of US beef production. The economic impact of varying calving rate was quantified from feed use within the EM. As calving rate (x) within the cow-calf system decreased from 100% to 60%, the number of animals required to produce 363 kg of beef increased from 2.35 to 3.38 with a trend described by Animals (head) = $0.0047x^2 - 0.0238x + 2.475$ ($R^2 = 0.992$). Land and water use increased with a decrease in calving rate, with the quantity of land required (Land (ha) = $0.0143x^2 - 0.0718x + 6.204$; $R^2 = 0.992$) increasing at a greater rate than water use (Water (L) = $211x^2 - 1062x + 139843$; R = 0.992). At a 60% calving rate, land use was increased by 53.2% per unit of beef, whereas water use was increased by 34.1%. This was due to the differing proportions of land and water attributed to the cow-calf operation within the entire system. As calving rate decreased from 100% to 60%, carbon emissions increased from 5,459 kg per 363 kg beef to 7,945 kg per 363 kg beef, following a polynomial trend with the equation: Carbon (kg) = $11.45x^2 - 57.62x + 5762$. A decline in calving rate from 100% to 60% was associated with a 36.3% increase in production costs per unit of beef. Opportunities clearly exist to reduce environmental and economic impact per unit of beef by improving calving rate, with the greatest returns per unit increase occurring at lower calving rates. Further research should focus on quantifying the proportional contribution of other management practices, including calf mortality and weaning weight.

Key Words: beef, calving, environment

TH364 Comparison of traditional and modern systems for the individual identification of dromedary camels. G. Caja*[1], E. Diaz-Medina[2], S. Cabrera[2], O. Amann[2], O. H. Salama[3], M. H. El-Shafei[3], H. El-Sayed[3], A. A. K. Salama[1,3], R. S. Aljumaah[4], M. Ayadi[4], and M. A. Alshaikh[4], *[1]Grup of Ruminant Research (G2R), Universitat Autonoma de Barcelona, Bellaterra, Spain, [2]Oasis Park-Museo del Campo Majorero, Fuerteventura, Spain, [3]Animal Production Research Institute, Dokki, Giza, Egypt, [4]College of Food and Agriculture Sciences, King Saud University, Riyadh, Saudi Arabia.*

The use of traditional (red iron brands) and modern (plastic ear tags and low radiofrequency boluses) identification (ID) systems were compared in a study done in 477 camel dromedaries of different breeds, ages and exploitation conditions (stabulated and grazing) according to location: Egypt (Maghrebi, n = 83; 1 to 14 yr), Spain (Canarian, n = 304; 0 to 19 yr) and Saudi Arabia (Maghatir, n = 37; Majahim, n = 53; 1 to 15 yr). We evaluated the retention and readability of ID systems and camel health and wellbeing during 2 yr. Iron brands (3 digits, 20 cm) were applied in left flank of 45 Egyptian camels at yearling. Ear tags, made of polyurethane and consisting on double rectangular flaps (15 × 50 mm, 3 g; Egypt) or button tags (28.5 mm diameter, 3.5 g; Spain) were inserted in left ear of > 1 yr age camels at the start of the study. Moreover, 5 types of radiofrequency boluses, varying in specific gravity (SG, 1.5 to 3.6), volume (5.2 to 22.8 mL) and weight (12.7 to 82.1 g), were also orally administered by trained operators across camel ages and locations at the start of the study. Data were analyzed by the PROC MIXED of SAS v.9.1, using a Logit model with the method of maximum likelihood. Iron brands showed healing problems, only 38% brand digits being fully readable which misadvised on their use. Ear tag retention was lower in the rectangular vs. button ear tags (66.0 vs. 81.1%; $P < 0.01$). Administration of boluses was done safely at all ages, but 2 standard sized boluses (21 × 68 mm, 22.4 mL) were blocked at the diaphragmatic hiatus level in 2 camel calves (70 kg BW) and required the use of an esophageal probe to be unblocked. Bolus retention varied dramatically according to SG, the SG <2 being fully lost after 8 mo. On the contrary, despite their volume and weight, SG > 3 boluses were efficiently retained (99 to 100%) at all ages. Under practical conditions, > 99% camel ID at mid-term (>2 yr) can be obtained by administering high SG radiofrequency boluses. Bolus administration needs to be done by trained operators and the use of miniboluses (<15 mL) is hardly recommended in camel calves <90 kg BW.

Key Words: bolus, branding, ear tag

TH365 Prediction of body condition scores in dairy cattle from daily measurements of milk yield, milk composition and body weights. A. De Vries*[1], K. D. Gay[1], L. F. Barbosa[1], F. Du[1], K. Kaniyamattam[1], and E. Maltz[2], *[1]University of Florida, Gainesville, [2]Institute*

of Agricultural Engineering, ARO, The Volcani Center, Bet Dagan, Israel.

The objectives of this study were to develop and compare equations to predict body condition scores (BCS) in dairy cows during their lactation from body weight, milk yield and milk composition measurements obtained, for each cow, twice per day around milking. At the University of Florida Dairy Unit, 338 Holstein cows were scored weekly (1 to 5 scale) from calving until culling or dry off in 2011 and 2012 (n = 15,959). All cows were fed one total mixed ration and housed in freestalls. Body weights, milk yield, fat, protein, and lactose were obtained using commercial sensors (milk meters, on-line milk composition analyzers, and walk through scales). Weekly averages were calculated. The weekly BCS per cow were smoothed with a loess smoother. Thirty-four variables were constructed, including, but not limited to, energy in milk, milk yield, weight, metabolic weight, days in milk (DIM), and their logs, squares and reciprocals. SAS procedure glmselect was used to find the best fitting regression equations constrained to 3, 5, or 7 variables and their 2-way interactions. Results for mean ± SD of BCS at calving, 70, 140, 210, 280, 350 DIM were 3.46 ± 0.29, 2.99 ± 0.55, 3.16 ± 0.51, 3.43 ± 0.51, 3.65 ± 0.41, and 3.89 ± 0.43. The Root MSE of the 3, 5, and 7-variable equations were 0.34, 0.32 and 0.31 BCS. The R squared of the 3, 5, and 7-variable equations were 53%, 60%, and 63%. The 7-variable equation was BCS at t DIM = 3.65 + 0.238 × BCS at calving – 0.083 × Mcal in kg milk per kg metabolic body weight at t DIM × Mcal in milk at 7 DIM – 3.08 × kg milk yield at 70 DIM / Mcal in kg milk at 70 DIM + 2.68 × kg body weight at t DIM / kg body weight at 70 DIM – 0.204 × lactation number × kg body weight at t DIM / body weight at 70 DIM – 827 / kg body weight at t DIM. When the cow has not yet reached 70 DIM, estimates at 70 DIM should be provided. In conclusion, body weight, milk yield, and components were useful for predicting BCS during the course of the lactation. The predictions could be improved with new variables that have not been tested, and should be validated with other BCS data sets.

Key Words: body condition score, weight, milk component

TH366 Evaluating carbon fluxes variability in late lactation organic Jersey cows using a portable automated gas quantification system during the grazing season. A. B. D. Pereira*[1], A. F. Brito[1], S. Zimmerman[2], and N. Antaya[1], *[1]University of New Hampshire, Durham, [2]C-Lock Inc., Rapid City, SD.*

The objective of the current study was to determine methane and carbon dioxide fluxes (J_{CH4} and J_{CO2}, respectively), and carbon emissions variability from 7 primiparous and 3 multiparous lactating organic Jersey cows (200 ± 53 DIM and 13.3 ± 2.4 kg of milk yield). Measurements were taken from July to October 2012 yielding a total of 72 d of data collection. A portable, automated system [i.e., The GreenFeed (GF) system; C-Lock Inc., Rapid City, SD] consisting of air sampling and gas quantification modules powered by solar energy was mounted on a trailer for assessing breath carbon fluxes from grazing cows. The GF uses radio frequency identification and controlled release of pellet concentrates to reinforce voluntary visitations by individual animals several times throughout the day. Cows were moved to a new strip of fresh, cool-season grass-legume herbage mix (predominantly grass) after each milking (a.m. and p.m.) yielding about 17 h of access to pasture daily. Cows were supplemented with a TMR composed (DM basis) of 51% grass-legume baleage, 47% concentrate, and 2% liquid molasses fed via Calan doors. The GF was moved once daily to remain with the cows. Cows had no access to the pasture and the GF from 0430 to 0800 h and from 1400 to 1730 h, which coincided with milking times and TMR feeding. Number of animal visitations to the GF, J_{CH4} and J_{CO2}, within animal J_{CH4} and J_{CO2} coefficient of variation (CV), and between animal CV of 3 d rolling average were calculated. Average herbage DMI (6.5 kg/cow/d) was calculated by subtracting estimated total DMI (14.6 kg/cow/d; NRC, 2001) from measured TMR intake (8.1 ± 2.9 kg/cow/d), yielding a J_{CH4} of 21 g/kg DMI. Each animal averaged 128 ± 30 total visits to the GF. Daily J_{CH4} and J_{CO2} averaged 308 ± 18 g/d and 8,716 ± 519 g/d, respectively. The within animal emissions CV averaged 11.1% ± 2.13 and 8% ± 2 for J_{CH4} and J_{CO2}, respectively, while the between animal emissions CV averaged 5.9% for both J_{CH4} and J_{CO2}. Results suggest that the J_{CH4} and J_{CO2} measurements appear to be reliable and repeatable as indicated by the relatively low CV.

Key Words: methane, carbon dioxide, pasture

TH367 Housing and management characteristics of 53 farms using automatic milking systems. J. A. Salfer*[1], M. I. Endres[1], and D. W. Kammel[2], *[1]University of Minnesota, St. Paul, [2]University of Wisconsin, Madison.*

The objective of this study was to describe housing and management characteristics of farms in Minnesota and Wisconsin using automatic milking systems (AMS). Fifty-three farms using AMS were visited from June to September 2012. Data were collected on facility layout and design. Farms had 2.6 ± 1.6 AMS/farm, with a range or 1 to 8 AMS/farm. Farms averaged 1.4 robots/pen with a range of 1 to 3 robots/pen. The average number of freestalls was 78 ± 31 freestalls/pen. Thirty-four farms built new cow housing facilities and 23 installed AMS units in retrofitted existing barns. Methods of manure removal and number of farms were: automatic alley scrapers (25), scrape manually (14), slatted floor (11) and bedded pack (3). Eleven of the farms had robotic feed pushers that pushed up the ration on a pre-determined schedule. Forty farms had exclusively free flow cow traffic, 12 farms had exclusively guided flow traffic and 1 farm had both a free flow and guided flow cow traffic system in separate barns. Guided flow traffic and number of farms were: freestall to AMS to feed (9), feed to AMS to feed (2), feed to AMS to freestall (2). The majority of the summer forage on 5 farms was pasture, with 4 farms being certified organic. Freestall surface on farms were: mattresses (23), sand (14), or waterbeds (7). Cows on 5 farms had access to pasture and freestalls and 3 farms had a bedded pack. Thirty-five of the farms were naturally ventilated, 11 were tunnel ventilated and 7 were cross-ventilated. Forty-five of the farms had mechanical rotating brushes. Average feed bunk space was 50.5 ± 13.5 cm/cow with a range of 25.9 to 106.7 cm/cow. Open area in front of the robot was 44.7 ± 29.4 m^2 and ranged from 11.1 to 187.3 m^2. Protected AMS exit lane was 3.1 ± 2.4 m and ranged from 0.3 to 8.5 m. Drinking space was 6 ± 2.8 cm/cow and ranged from 0.5 to 11.8 cm/cow. These results indicate that some aspects of AMS barn designs appear to be similar to other types of housing systems.

Key Words: automatic milk system, precision dairy, robotic milking

TH368 Factors affecting expression of estrus of lactating dairy cows using activity monitors. A. M. L. Madureira*, T. A. Burnett, B. F. Silper, N. Dinn, and R. L. A. Cerri, *University of British Columbia, Vancouver, BC, Canada.*

The objective of this study was to determine parameters related to increased physical activity as a result of estrous expression. Estrus expression (795 events) from lactating Holstein cows (n = 305) was recorded. Cows were monitored continuously by an activity monitoring system (Heatime, SCR Engineers) attached to the cow's neck 5 d after calving. Data was recorded in real time every 2 h. The threshold level

was set at SCR index = 35 or approximately 80% increase in physical activity. Upon detection, cows had blood samples and BCS immediately collected and their ovaries scanned by ultrasound (Aloka SSD-500, Aloka Co. Ltd.). Pregnancy per AI, health episodes and milk production data were collected and recorded for the entire experimental period. Data was analyzed using ANOVA logistic regression using procMIXED and GLIMMIX. Mean estrus duration was 11.3 ± 5.3 h with index activity peak of 72.8 ± 20.2 and a pre-ovulatory follicle diameter of 18.8 ± 0.3 mm. There was a positive correlation between duration and peak (r2 = 0.70), with estrus episodes with high peak (66–100) being longer (14.3 ± 0.2 vs 6.2 ± 0.2 h) than those with small peaks (35–65). Estrus duration was affected by parity as multiparous cows expressed it for a shorter period than primiparous (10.8 ± 0.3 vs 12.2 ± 0.3 h). Cows with moderate BCS (>3.00) had longer duration of estrus episodes than cows with low BCS (≤2.75), 13.0 ± 0.4 vs 11.5 ± 0.3 h, respectively. Follicle diameter was not correlated with peak of activity, duration, BCS or disease episodes. Pregnancy per AI was not influenced by parity, follicle diameter, peak of activity and duration of estrus. Estrus expression patterns were not affected by disease episodes during the transition period or by expression of secondary signs of estrus behavior. In conclusion, duration and peak of estrus episodes were quite variable and mainly influenced by parity and BCS. Follicle diameter was not correlated with estrus peak and duration, and no effect on pregnancy per AI was found. Further analyses are needed to define physical activity thresholds correlated with pregnancy per AI and efficiency of activity monitoring technologies.

Key Words: follicle, duration, heat

TH369 Ammonia emissions and carbon and energy footprints of dairy farms in the Northeastern United States and Northern Europe estimated using DairyGEM. A. N. Hristov*[1], A. Rotz[2], P. Huhtanen[3], M. Korhonen[4], and B. Isenberg[1], *[1]Department of Animal Science, The Pennsylvania State University, University Park, [2]USDA-ARS-PSWMRU, University Park, PA, [3]Division of Animal Husbandry, Swedish University of Agricultural Sciences, Umea, Sweden, [4]Farm Services, Valio Ltd., Helsinki, Finland.*

Production system, diet, geographic location, and climate affect the environmental footprint of dairy farms. The objective of this analysis was to estimate ammonia emissions and carbon and energy footprints of dairy farms in the Northeastern United States (US) and Northern Europe (NE). Sixteen US farms [average size 121 ha (SD = 19.7, min = 16 and max = 304 ha)] and 11 NE farms [93 ha (SD = 44.8, min = 26 and max = 201 ha)] were included in the analysis. Parameters were established to simulate all farms with the Dairy Gas Emission Model (DairyGEM). Important input data for each farm were the number of animals including replacement heifers, milk production and milk composition, feeds (forages and concentrates) fed and their nutrient contents, pasture use, crude protein concentration of the diets, housing type, and manure handling practices. Output data were analyzed using the MIXED procedure of SAS with farm as a random effect. Estimated ammonia emissions ranged from 5.1 to 13.6 g ammonia/kg fat- and protein-corrected milk (FPCM) with the emissions on NE farms averaging 36% less ($P < 0.001$) than the US farms (Table 1). Carbon footprints ranged from 0.77 to 1.47 kg CO_2 eq/kg FPCM with the NE farms averaging 17% greater than the US farms. Energy use ranged from 2.45 to 3.81 MJ/kg FPCM with the NE farms averaging 19% greater than the US farms. The lower ammonia emissions for the NE farms were attributed to cooler temperatures, lower dietary protein content, and faster incorporation of manure when applied to fields. Greater carbon and energy footprints of the NE farms were primarily due to an average 16% lower milk production per cow compared with the US farms.

Table 1. Milk production, ammonia emissions, and carbon and energy footprints of US and NE dairy farms

Item	US	NE	SEM	*P*-value
No. of farms	16	11	—	—
No. of cows	195	60	52.4	0.02
No. of heifers	164	55	45.7	0.03
FPCM, kg/yr	10,180	8,569	352.0	<0.001
Ammonia emissions, g/kg FPCM	10.3	6.6	0.64	<0.001
Carbon footprint, CO_2 eq g/kg FPCM	1.03	1.21	0.064	0.03
Energy footprint, MJ/kg FPCM	2.98	3.54	0.137	<0.001

Key Words: carbon footprint, ammonia emission, dairy farm

TH370 Potential impact of climate change on crop yield and nutritive value of dairy farms in Quebec. J. M. Moreno*[1], G. Bélanger[2], H. Côté[3], D. Pellerin[1], V. Bélanger[1], G. Allard[1], R. Audet[2], D. Chaumont[3], and E. Charbonneau[1], *[1]Universite Laval, Quebec, QC, Canada, [2]Agriculture and Agri-Food Canada, Quebec, QC, Canada, [3]Ouranos, Montreal, QC, Canada.*

The projected climate change will likely affect the yield and nutritive value of crops grown in Quebec but their effect on dairy farms has not yet been investigated. Our objective was to determine the effect of climate change on the yield and nutritive value of the major crops used on Quebec dairy farms as the first step of a more comprehensive study at the farm level. Our study was conducted for 2 regions [Centre-du-Quebec (CQ; corn heat unit: 2700) and Bas-St-Laurent (BSL; corn heat unit: 2045)]. Currently used agroclimatic indicators were calculated for the current conditions and projected for 2041–2070 using 2 scenarios of greenhouse gas emissions (SRES A1B and SRES B1). Published results were used along with the agroclimatic indicators to estimate the potential effect of climate change on crop yield and nutritive value, followed by a validation in a focus group of 10 experts in dairy and crop production. The projected climate change is expected to result in increased yields of grain corn (6.1 to 10.2 ton/ha) and soybeans (1.9 to 2.5 ton/ha) in CQ, and the possibility to grow those 2 crops in BSL with yields similar to those in CQ under current climatic conditions. Yields of wheat (2.1 ton/ha) and barley (2.0 ton/ha) are not expected to change with climate change in the 2 regions. An increase in yield is expected for alfalfa (CQ: 5.3 to 9.3 ton/ha; BSL: 3.9 to 6.8 ton/ha) and corn silage (CQ: 13.8 to 16.1 ton/ha; BSL: 11.1 to 13.8 ton/ha) but no changes are expected for timothy (CQ: 4.3 ton/ha; BSL: 3.1 ton/ha). Forage nutritive value is expected to be affected by climate change with a decrease in crude protein concentration of alfalfa (19.3 to 18.5%) and timothy (11.8 to 11.4%) and an increase in fiber concentration for alfalfa (NDF: 44.7 to 46.6%; ADF: 32.8 to 34.3%; ADL: 6.9 to 7.4%). In Quebec, a northern agricultural region, mostly positive variations in crop yields and negative changes in the nutritive value of forages are expected with climate change.

Key Words: climate change, dairy farm, crop production

TH371 Potential impact of climate change on dairy farm profitability and management practices in Quebec. J. M. Moreno*[1], D. Pellerin[1], G. Bélanger[2], V. Bélanger[1], H. Côté[3], G. Allard[1], R. Audet[3], D. Chaumont[3], and E. Charbonneau[1], *[1]Universite Laval, Quebec, QC, Canada, [2]Agriculture and Agri-Food Canada, Quebec, QC, Canada, [3]Ouranos, Montreal, QC, Canada.*

Modifications to crop yield and forage nutritive value with the projected climate change will likely affect management practices and profitability of dairy farms. Our objective was to evaluate the potential effect of

climate change on dairy farm profits and management practices, considering the farm as a single unit of management. The whole-farm model N-CyCLES was adapted and used to evaluate changes in the economic performance of a dairy farm and to optimize the management practices required to maximize profits. Data representative of an average dairy farm from the Centre-du-Quebec region in Quebec were used along with expected modifications to crop yield and forage nutritive value associated with climate change projections (greenhouse gas emission scenarios SRES B1 and A1B; 2041–2070 and assessed with a combination of agro-climatic indices, literature review, and focus groups). For both scenarios, projected higher crop yields and variations in forage nutritive value are likely to result in increased in the proportion of income from crop sales (3.0% to 6.3% and 7.4% for B1 and A1B respectively) and a decrease in purchased grains. The farm profit is projected to increase by $0.38/hL (±2668 $/farm) for A1B. The projected yield increase is less with the B1 scenario with a resulting lower farm profit than under the current situation (−0.06 $/hL). For both scenarios, no modifications in crop rotations were made by the model. To meet the requirements of lactating cows using forages with a lower nutritive value, the proportion of corn silage in the diets was increased. Climate change is expected to result in an increased farm P balance (201 and 197 kg/y with B1 and A1B respectively) but results for N balance variation are different for B1 (1236 kg/y) and A1B (−310 kg/y). These results, as well as sensitivity analysis performed on crop yields, confirm that the effect of climate change can be beneficial for Quebec dairy farms as long as the increase in crop income compensate for higher costs related to crop production and the lower forage nutritive value.

Key Words: dairy farm, whole-farm model, climate change

TH372 Survey of milk production, and feeding and reproduction management on pasture based dairy farms in Florida and Georgia. F. Du*[1], K. Gay[1], M. Sowerby[1], Y. Newman[1], C. Staples[1], C. Lacy[2], and A. De Vries[1], *[1]University of Florida, Gainesville, [2]University of Georgia, Tifton.*

Objective of this study was to document milk production, and feeding and reproduction management on pasture based dairy farms in Florida and Georgia. The survey consisted of 62 questions and covered 7 areas, which included farm business structure, young stock, herd management, pasture and crop management, feeding management, manure and nutrient management and environment and sustainability. The survey focused on the year 2011–2012. Data were collected by personal interview in the fall of 2012. This survey was conducted on 15 dairy farms that were responsible for approximately 12,000 cows and 5,000 heifers. Grazing rotation and pasture management was employed by 10 (67%) respondents. The average milk production was 58 ± 16 lbs/cow/day during the winter and 41 ± 14 lbs/cow/day during the summer. The average rolling herd average was 15,766 ± 4,719 lbs/cow/year. The average somatic cell count was 253,286 ± 73,676 cells/ml during the winter, and 381,467 ± 85,891 cells/ml during the summer. For cows, 4 farms (27%) utilized a year around breeding strategy, while the remaining farms practiced various seasonal breeding strategies. Three farms (20%) employed 100% seasonal breeding. The greatest number of calvings were reported for October (8 farms, 53%) while 13 farms (87%) reported the fewest calvings during the summer. Non-breeding periods were reported by 13 farms (87%). Summer breeding was avoided due to lower pregnancy rates (7 farms, 47%), or breeding during October to November was avoided (10 farms, 67%) to avoid calving during the summer. Feeding from grazing varied widely in different seasons, and the intake from stored feed was high. For lactating cows, the average dry matter intake from stored feed was 33 ± 16 lbs/cow/day during the winter, and 21 ± 19 lbs/cow/day during the summer. For dry cows, the average dry matter intake from stored feed was 12 ± 10 lbs/cow/day during the winter, and 6 ± 11 lbs/cow/day during the summer. Findings from this study will be used to design programs that focus on optimization of reproduction strategies for pasture based dairy farms in the Southeastern United States.

Key Words: pasture, seasonality, survey

TH373 Breeding for polled dairy cows versus dehorning: Preliminary cost assessments and discussion. N. J. O. Widmar*[1], M. M. Schutz[1], and J. B. Cole[2], *[1]Purdue University, West Lafayette, IN, [2]Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD.*

Dairy producers today face labor, equipment, and medical costs associated with dehorning heifers. Further, complications requiring veterinary intervention occur with some probability. The objective of this work is to develop preliminary cost estimates of selecting for polled dairy heifers. Stochastic budgets were developed to analyze the expected costs (EC) associated with polled dairy genetics. Triangular distributions, commonly used to represent distributions with limited data, were used to represent costs for dehorning, added semen costs of polled genetics, the likelihood of treatment of calf, and the cost of veterinary treatment (should it be needed). The minimum, most likely, and maximum costs used for dehorning were $5.00, $7.00, and $15.00; additional polled genetics $0.00, $8.00, $20.00; probability of treatment with dehorning 0.01, 0.03, and 0.08; probability of treatment with polled 0.01, 0.02, and 0.03; and the cost of treatment, held constant across all scenarios, was parameterized by $10.00, $50.00, and $150.00. A total of 10,000 iterations were run using @Risk v 5.7. The minimum expected cost of dehorning and polled breeding, using these simplified parameters, was $5.84 and $0.47, respectively. The maximum EC of dehorning and polled breeding, using these simplified parameters, was $22.89 and $22.50, respectively. Mean EC of $11.79 and $10.73 were found for dehorning and polled genetics, respectively; given the parameters outlined here, sensitivity to individual farms' semen and dehorning costs are likely to outweigh these differences. Beyond on-farm costs, industry-wide discussion may be warranted surrounding the public acceptance and attitude toward polled genetics versus dehorning calves. The value of avoiding dehorning may be (much) larger for the industry, and perhaps some individual farms, than initially suggested if additional value is put on calf comfort, potentially decreased rates of gain if calves are stressed at dehorning, and possible worker aversion to the dehorning process.

Key Words: dairy breeding, polled, cost-benefit

TH374 Environmental impact estimate of dairy cows treated for mastitis. F. M. Goncalves*[1,2], P. A. S. Silveira[1,3], M. E. Lima[1,3], G. N. Bolzan[1,3], J. Halfen[1,3], A. Schneider[1,3], E. G. Xavier[1,4], and M. N. Correa[1,3], *[1]Federal University of Pelotas, Pelotas, RS, Brazil, [2]Nucleo GAPA - Research Group in Environmental management in livestock, MERCOSUL Center, Pelotas, RS, Brazil, [3]NUPEEC - Research, Teaching and Animal Husbandry Extension Center, Veterinary Clinic Dep., Pelotas, RS, Brazil, [4]Granja 4 Irmaos, Rio Grande, RS, Brazil.*

Mastitis is one of the major causes of quality and quantity deficiency in milk production. Brazil has the largest commercial cattle herd in the world using tropical forage as their main diet; due to this, the country has been dubbed "the major methane producer in the world." The aim of this study was to estimate the environmental impact on a dairy herd presenting mastitis episodes. Data collected along 781 d on a dairy farm located in southern Brazil was analyzed using descriptive statistics. The

average number of lactating dairy cows kept under semi-confinement management (concentrate and pasture fed) during this period was 873 animals. Average milk production was 22.5 ± 7.6 kg/cow/day. One thousand three hundred and twenty-seven mastitis episodes distributed between recidivist and new cases were observed but only the number of total episodes was used. Mastitis treatment was performed following a Veterinarian antibiotic protocol and averaged 2.36 ± 1.66 d. Milk discard days were estimated by adding days of treatment to the withholding period. Milk discard averaged 5.36 ± 1.66 d per episode. Upon considering the methane emission estimate proposed by Robertson and Waghorn (2002), the cows emitted 22.5g of methane/kg milk. Milk discard was 120.7 ± 37.5 kg per mastitis episode, corresponding to a total of 159,772.5 kg milk discarded in the period observed. This amount contributed to 3,594.88t of methane emission due to discarded milk. Parameters such as diet metabolizable energy (ME), days of lactation and feeding regimens have been the research focus in methane emission reduction. However, this study showed that the sanitary status of cattle must be taken into account. It was concluded that disease prevention in dairy cattle is a very important measure to reduce the use of therapies that imply milk disposal, which generates an environmental impact without any social or economic benefit to the farmer.

Key Words: environmental impact, mastitis, dairy cow

TH375 Trends in noncompliance with milk quality standards for dairy herd improvement herds in the United States. H. D. Norman* and J. R. Wright, *Animal Improvement Programs Laboratory, USDA-ARS, Beltsville, MD.*

Frequency of herd noncompliance for somatic cell count (SCC) based on current US and European Union (EU) standards as well as for standards proposed by the National Milk Producers Federation (NMPF) was examined for US Dairy Herd Improvement (DHI) herds. For current US standards, regulatory action is taken if bulk-tank SCC (BTSCC) for 3 of 5 consecutive monthly shipments is >750,000 cells/mL. For EU standards, a herd is SCC noncompliant after 4 consecutive rolling 3-test geometric means of >400,000 cells/mL. For proposed NMPF standards, a herd would be SCC noncompliant if 3 of 5 consecutive BTSCC were >600,000 cells/mL (January 2014) or >400,000 cells/mL (January 2015). The SCC for individual cows are derived from somatic cell scores, where $SCC = 2^{(\text{somatic cell score} - 3)}(100{,}000)$. As a BTSCC proxy for determining which herds and milk were SCC noncompliant, herd test-day SCC (HTSCC) were derived by weighting each cow's SCC by her test-day milk yield. Based on HTSCC, noncompliance rates were examined for various milk quality standards, with a focus on trends during the last 2 yr, as the EU standards have been imposed upon many US dairies producing for export. Data were from about 13,000 DHI herds monthly and represented about 50% of US milk produced. Herds included had DHI tests with ≥ 10 cows from April 2009 through October 2010 or from April 2011 through October 2012. Mean monthly herd noncompliance based on current US standards dropped from 0.9 to 0.4% over the last 2 yr. For NMPF proposed standards, herd noncompliance would have dropped from 2.7 to 1.4% for a limit of 600,000 cells/mL or from 14.1 to 9.0% for 400,000 cells/mL. For the EU standard, herd noncompliance would have been reduced from 7.8 to 5.0%. The percentage of milk affected by noncompliance is considerably less than the percentage of herds; only 0.1 and 1.4% of US milk failed current US and EU SCC standards, respectively. Trends indicate a continued improvement in US SCC compliance levels but to satisfy stricter milk standards, US producers will need to continue to emphasize sound milking practices more and cull on SCC more intensively.

Key Words: somatic cell count, milk quality, standard

TH376 Management and outcomes of Sicilian dairy farms enrolled in a team-based milk quality improvement project. G. Azzaro[1], M. Caccamo*[1], P. L. Ruegg[2], J. D. Ferguson[3], M. Gambina[1], and G. Licitra[1,4], *[1]CoRFiLaC, Regione Siciliana, Ragusa, Italy, [2]University of Wisconsin, Madison, [3]School of Veterinary Medicine, University of Pennsylvania, Philadelphia, [4]DISPA, University of Catania, Catania, Italy.*

Sicilian dairy farms (n = 138) were enrolled in a team-based milk quality improvement project funded by Sicilian Region. The aim of the project was to identify and improve management practices mostly affecting milk quality to control and reduce mastitis incidence. At the first milk quality team meeting, a survey was submitted to gather management and financial information from dairy farms and a bulk tank milk sample was collected. Farms were ranked according to their bulk tank milk somatic cell (SCC) and total bacteria counts (TBC). Although not statistically significant, an inverse relationship between milk yield and SCC class was found. Economic loss per liter of milk ranged between 3.4 and 5.1 € cents with increasing SCC class ($P = 0.065$). Adoption of standardized best management practices such as maintaining appropriate vacuum reserve, use of milking gloves, pre and post milking teat disinfection, and dry cow therapy were associated with herds having lower bulk milk SCC. Every 2 mo, each team met, analyzed herd performance and identified milk quality goals, set target dates to reach the goals, created an action plan, and assigned responsibility for specific tasks. Bulk tank milk was also sampled and cows were scored for body condition, teat end, and udder hygiene. After 2 meetings, 31 farms were left out of the project based on their willingness to continue and their ability to achieve the assigned goals. No overall difference was detected in the selection of milk quality goals and actions by breed and bulk milk SCC and TBC at enrollment ($P > 0.05$). However, team members working with herds having very high bulk milk SCC and TBC were more likely to list milking as action areas than were team members with herds having medium or low bulk milk SCC. In general, herds completing the fourth meeting of the milk quality program reported reduced bulk tank milk TBC ($P < 0.10$), and rates of teat end and udder hygiene ($P < 0.001$) scored above 3 compared with the beginning of the program. These preliminary results confirm the effectiveness of such programs in improving milk quality.

Key Words: milk quality, team-based program

TH377 Effect of delaying breeding during the summer on profitability of dairy cows. M. Gobikrushanth*, A. De Vries, C. A. Risco, J. E. Santos, and K. N. Galvão, *University of Florida, Gainesville.*

The objective was to evaluate the effect of delaying breeding during the summer on profitability. Holstein cows (n = 676) that calved between June and September of 2007 and 2008 were used. Cows that calved between Jun 1 and Jul 21 were AI upon estrus detection (ED) after the second PGF of the Presynch between 57 and 63 DIM, or were timed AI using the Ovsynch protocol (TAI) if not detected in estrus. Cows that calved between Jul 22 and Sept 18 were AI after the first or second PGF starting Nov 14 or Nov 21 or were TAI if not detected in estrus. Following this scheme, cows could have a regular (REG; 57–63 DIM; n = 288) or extended voluntary waiting period (VWP; 64–115 DIM), which was divided into medium (MED; 64–84 DIM; n = 224) or long (LONG; 85–115 DIM; n = 164). Overall and daily net return was calculated by subtracting the costs with replacement heifers ($1,850/heifer), feeding costs ($0.30/kg lactating cow diet; $0.25/kg dry cow diet), breeding costs ($2.65/dose PGF; $2.40/dose GnRH; $0.25/injection administration; $10.0/semen straw; $5.0/AI; $3.0/pregnancy diagnosis), and other costs ($3.0/d) from the daily income with milk sales ($0.44/kg milk), cow sales ($1.76/kg live weight), and calf sales ($140/calf). Data was

analyzed using the MIXED procedures of SAS. Models included the effect of VWP group, parity and its interaction. VWP group did not affect ($P > 0.5$) overall or daily net return. Overall/daily net return per cow was \$2079/\$5.3, \$1952/\$5.1, and \$2033/5.2 for REG, MED and LONG, respectively. With the exception of milk income, VWP group affected ($P < 0.05$) all costs and incomes. Feeding/other cost was higher for LONG (\$1162/\$1120) and REG (\$1148/\$1108) than MED (\$1073/\$1043). Replacement cost was higher for MED (\$463) than REG (\$304), while LONG was intermediate (\$379). Breeding cost was higher for REG (\$48) than for MED (\$38) and LONG (\$37). Calf sales income was higher for REG (\$117) than MED (\$105), while LONG was intermediate (\$111). On the other hand, cow sales income was lower for REG (\$123) than MED (\$214), while LONG was intermediate (\$193). Although extending the VWP affected most costs and incomes, it did not affect profitability.

Key Words: delayed breeding, profitability, dairy cow

TH378 Impact of feeding strategies on milk production and profitability on Wisconsin organic dairy farms. C. A. Hardie*[1], M. Dutreuil[1], R. Gildersleeve[2], M. Wattiaux[1], N. S. Keuler[1], and V. E. Cabrera[1], *[1]University of Wisconsin-Madison, Madison, [2]University of Wisconsin-Extension, Lancaster.*

The purpose of this study was to group and compare certified organic Wisconsin dairy farms based on general farm characteristics and their feeding regimens during the course of 2010 and evaluate their productivity and profitability. An on-site survey containing sections on farm demographics, feeding, pasturing, and economics was conducted on 69 organic dairy farms. A non-hierarchical clustering method using 9 variables related to general farm characteristics, feed supplementation, and grazing was applied to partition the farms into clusters. A scree plot was used to determine the most appropriate number of clusters. Farm production and profitability were evaluated using reported milk rolling herd averages (RHA) and calculated monthly milk income minus feed costs (IOFC), respectively. The farms in Clusters 1 (n = 8) and 3 (n = 32), the large and small high-input farms, respectively, had the largest RHA and IOFC (Table 1). Cluster 2 (n = 5), the completely seasonal, extremely low-input farms had the lowest RHA and IOFC. Cluster 4 (n = 24), the semi-seasonal, moderate-input cluster, was third for RHA and IOFC. Results indicate that Wisconsin organic dairy farms differed tremendously in structure and feeding strategies, and farms that supplemented more feed had larger RHA and higher IOFC. Evaluation of other farm costs needs to be conducted before assessing profitability at the whole-farm level.

Table 1. Cluster medians (interquartile ranges) for milk rolling herd average (RHA) and milk income minus feed costs (IOFC)

	Cluster (n=8)	Cluster 2 (n=5)	Cluster 3 (n=32)	Cluster 4 (n=24)
RHA, kg/cow per yr	6,878[a] (1,038)	3,632[b] (783)	7,457[a] (1,754)	5,417[c] (1,760)
IOFC,[1] \$/cow per d	10.17[a] (2.99)	5.07[ab] (2.62)	8.59[a] (4.68)	5.83[b] (2.66)

[a–c]Kruskal-Wallis test ($P \leq 0.001$); Wilcoxon test with Bonferroni correction ($P < 0.05$).
[1]IOFC for lactating cows for Jan–Nov. (clusters 1, 3, 4) and May–Nov (cluster 2).

Key Words: organic, supplementation, cluster analysis

TH379 Whole-farm balance of nitrogen and phosphorous on Costa Rican dairy farms. J. A. Elizondo-Salazar*[1], J. P. Jimenez-Castro[1], and Z. Wu[2], *[1]Estacion Experimental Alfredo Volio Mata, Facultad de Ciencias Agroalimentarias, Universidad de Costa Rica, [2]University of Pennsylvania, New Bolton Center.*

With the objective to determine the whole-farm nitrogen (N) and phosphorous (P) balances; to assess the efficiencies of imported N and P on Costa Rican dairy farms, 11 commercial herds were monitored for 12 mo. Farms differed in land area (1,0 to 116 ha), herd size (106 ± 46 animals), housing (tie-stall, free-stall, outdoors), feeding system (grazing, confinement, semi-confinement), production (19 ± 6 kg/day) and feed source (e.g., grasses, agricultural sub products, citrus pulp, concentrate). The import of N and P was mainly in the form of feeds, animals, inorganic fertilizers, and mineral supplements, and the export was through milk and culled animals. On average, feed, inorganic fertilizer, and mineral supplements accounted for 70 (±19), 16 (±14) and 14% (±8) of the total P imports, respectively. Likewise, 75% (±21) of the N imports was through feeds and 25% (±21) in inorganic fertilizers. The balance (import-export) of N and P varied substantially among farms, but was in excess for all farms. Only 33.0% of the N and 23.0% of the P imported was removed from the farm through milk and animals, with the remaining 67 and 77% staying on farm land for recycling through forages. However, surplus nutrientes may also lead to disturbances of environmental ecosystems. The exports through milk and animals averaged 92 and 8% for P and 94 and 6% for N. As the largest imports of P and N occur in feed, controlling dietary P and N to the requirement level, thus limiting feed purchase is fundamentally important for reducing nutrient losses as well as feed cost.

Key Words: nutrient management, environment, nutrition

TH380 Agreement of dairy cattle replacement policies by two models: Optimization and simulation. A. S. Kalantari* and V. E. Cabrera, *University of Wisconsin-Madison, Madison.*

The objective of this study was to compare proposed replacement decisions of a dynamic programming as an optimization model and a Markov chain as a simulation model. Lactation, month in milk, and pregnancy status were used to describe cow states in a herd in both models. The same economic and management parameters were used in both models. To compare models results the cow value calculated by the Markov chain model and the retention pay-off calculated by the dynamic programming model were used to rank all the animals in a sample herd. Then, the rank correlation (Spearman's correlation) was calculated between results of both models. The overall correlation was 89% (df = 998, P-value <0.0001), which evidenced a strong linear relationship between value ranking of animals from the 2 models. By considering only 10% of lowest ranking cows from both models the correlation increased to 98%. Cows with lower values are the main interest for replacement decisions. Therefore, based on this higher correlation for cows with lower values, we concluded that the final replacement decisions with both models were similar. A post optimality analysis was used to explore the effect of the optimal replacement decisions on the herd dynamics and herd net return. A net return was improved \$6/cow per year by using replacement decisions of both the dynamic programming model and the Markov chain cow value model.

Key Words: optimum replacement policy, optimization, simulation

TH381 The effects of condensed tannin-rich pine bark diet on gastrointestinal parasite infection in meat goats. B. R. Min*[1], S. Solaiman[1], A. Wilson[1], N. Gurung[1], and J. Miller[2], *[1]Tuskegee University, Tuskegee, AL, [2]Louisiana State University, Baton Rouge.*

The objective of this study was to assess gastrointestinal (GI) parasite load and animal performance of goats fed condensed tannin (CT)-containing pine bark (PB) diet. Pine bark is one of the abundant forest by-products in the southern US and contains 11–13% CT on a DM basis. Thirty-two Kiko-cross meat goats (*Capra hircus*; BW = 28.0 ± 1.0 kg) were randomly assigned to 2 experimental diets: (1) 0% PB and 30% wheat straw (WS) and (2) 30% PB and 0% WS. The remainder of each diet was a mix of 85% grain and 15% bermudagrass hay. Animals were dewormed and one half of each diet group was inoculated with 5000 infective stage (L3) Haemonchus contortus larvae (n = 8). Feed intake and performance were monitored for 87 d. Blood samples were taken twice, once at the beginning and once at the end of the experiment. Fecal egg and coccidia oocyst counts (FEC/FOC) were determined approximately every 2 wk. At the end of the experimental period, goats were slaughtered, and GI parasite load was determined. Abomasal worms were identified and counted. Overall, there were no differences ($P > 0.10$) in DMI and BW among diets or inoculation groups. Mean hematocrit (packed cell volume) was greater ($P = 0.03$) for goats fed the PB diets. Mean FEC, FOC, and total number of worms were lower ($P < 0.05$) for goats that were fed PB diet. On d 84, control goats on WS diet had greater ($P = 0.01$) FEC (1186 vs. 508) than PB diet group, respectively. Animals on PB diet had lower ($P = 0.03$) FOC on d 56 and the lowest ($P = 0.0001$) FOC were on d 84 for goats on PB diet. Feeding PB diet reduced both male (486 vs. 1357) and female (571 vs. 1386) worm counts compared with the WS diet, respectively. The results indicate that ground PB as a feed ingredient has the potential to decrease internal parasite infection.

Key Words: tannin, parasite, pine bark

TH382 Effect of six condensed tannin containing plants on the third larval stage of *Haemonchus contortus* in an in vitro system. S. A. Armstrong[1], H. N. Naumann[2], B. D. Lambert*[1,3], and J. P. Muir[2,3], *[1]Tarleton State University, Stephenville, TX, [2]Texas A&M University, Department of Crop and Soil Sciences, College Station [3]Texas A&M AgriLife Research, Stephenville.*

This study was conducted to determine the anthelmintic effectiveness of extracts from 6 condensed tannin containing legumes (*Desmanthus illinoensis*, *Lespedeza cuneata*, *Lespedeza stuevei*, *Leucaena retusa*, *Acacia angustissima* south Texas ecotype and *Acacia angustissima* central Texas ecotype) on the third larval (L3) stage of *Haemonchus contortus* (HC) using an in vitro system to measure percent larval migration inhibition (LMI). Rumen fluid, buffer and extracts (legumes or Ivermectin) were anaerobically incubated in 100 mL flasks (one per treatment) overnight to extract potential plant bioactive compounds. A no CT legume, *Arachis glabrata* (rhizoma peanut) was included as a control treatment. After incubation, fluid was transferred into a 96-well plate containing a 20-µm screen with 10 µL of pure HC L3 larvae (2000–2500/mL). Well plates were incubated anaerobically overnight. Following incubation, the screen was removed and fluid from the bottom of the well plate was placed under a microscope and larvae that migrated through the screen were counted. LMI was calculated with the following equation: (A − B)/A × 100 where A represents the number of larvae migrating through control wells and B represents the number of larvae migrating through treatment wells. Each treatment was replicated in 9 wells per repetition, and 3 repetitions of the experiment were conducted. *Leucaena retusa*, *L. stuevei*, and *A. angustissima* (Central Texas ecotype) resulted in the greatest percent LMI (65.4%, 63.1%, and 42.2%, respectively). *Desmanthus illinoensis* (33.6% LMI), *A. angustissima* (south Texas ecotype; 35.2% LMI), *A. angustissima* (Central Texas ecotype; 42.2% LMI), and *L. cuneata* (30.6% LMI) responded with a similar efficacy to that of the no-CT legume *A. glabrata* (34.3% LMI). Ivermectin showed the lowest percent LMI (12.5%) but was not different than larvae incubated in a control solution (34.3% LMI) or L. cuneata (30.6% LMI). Further evaluation, including in vivo trials, of *L. retusa*, *L. stuevei*, and *A. angustissima* as a suppressor of L3 HC is warranted.

Key Words: small ruminant, *Haemonchus contortus*, condensed tannin

TH383 A modified method for larval migration inhibition. S. A. Armstrong*[1], H. N. Naumann[2], B. D. Lambert[1,3], and J. P. Muir[2,3], *[1]Tarleton State University, Stephenville, TX, [2]Texas A&M University, Department of Crop and Soil Sciences, College Station [3]Texas A&M AgriLife Research, Stephenville.*

Larval migration inhibition (LMI) assays have been conducted using varying methods to determine the anthelmintic effect of different compounds. Previous assays often require more sample than was available for investigative screening studies and sometimes added aerobic conditions with extended incubations, which unnecessarily prolonged and complicated the procedure. This experiment was conducted to determine if sample size of treatment plant tissues could be reduced from those required by existing methodologies, and to compare the effectiveness of a modified method to previously published assays. Rumen fluid, buffer and treatments (control or *Juniperous pinchotii* or Ivermectin) were anaerobically incubated in 100 mL flasks (one per treatment) overnight to extract potential plant bioactive compounds. After incubation, fluid was transferred to a 96-well plate containing a 20-µm screen and inoculated with 10 µL of pure *Haemonchus contortus* (HC) L3 larvae (2000–2500/mL). Well plates were incubated anaerobically overnight. Following incubation, the screen was removed and fluid from the bottom of the well plate was placed under a microscope and larvae that had migrated through the screen were counted. LMI was calculated using the following equation: (A − B)/A × 100 where A represented the number of larvae migrating through control wells and B represented the number of larvae migrating through treatment wells. Each treatment was duplicated in 9 wells per repetition, and 2 repetitions of the experiment were conducted. Percent LMI was then compared with a previously published LMI assay (9 wells per repetition, 2 repetitions) which required a larger plant sample size and exposure to aerobic conditions. The results for LMI between the new and existing assay did not differ ($P = 0.88$) indicating that this method is a viable alternative to investigate anthelmintic compounds in a simplified, streamlined procedure requiring smaller sample sizes.

Key Words: *Haemonchus contortus*, larval migration assay, small ruminants

TH384 Effects of feeding a pelletized diet containing pumpkin seeds (*Cucurbita* sp.) on nematode fecal egg counts and hematocrit of wether goats. E. N. Escobar, J. Rodriguez, A. N. Gideon*, V. Purnell-Cropper, and H. Taylor, *University of Maryland Eastern Shore, Princess Anne.*

This field trial was conducted to evaluate the effect of a pelletized diet containing 21% ground pumpkin seeds (PS) on fecal egg counts (FEC) and blood hematocrit (% PCV) and to evaluate gastrointestinal nematode burden in goats kept in a pasture setting. Thirteen naturally infected meat goat wethers (GWs), average BW = 55 kg, had a mean FEC of 840 eggs per gram (epg) at the beginning of the experiment. A pelletized commercial 15% crude protein diet was used as the control (CTRL) diet. The treatment (TRT) diet was formulated with the same ingredients in the CTRL diet plus 21% PS. To minimize feedstuff selection, PS were ground and incorporated into the pelletized mixture. GWs were kept in 2 separated paddocks (CTRL and TRT paddock) with ad libitum hay, mineral salt and water. GWs were trained to each enter an individual stall to eat the experimental diets until every one finished their ration. The piece of equipment used to individually feed the GWs restrained them until an operator would release them; this action ensured that each goat was eating the allotted feed amount only. During 6 consecutive weeks, 6 wethers were fed the CTRL diet and 7 wethers were fed the TRT diet. The GWs were fed twice daily, up to 400 g of the corresponding experimental diet (total 800 g daily). Weekly, the GWs were restrained to collect rectal fecal samples to determine FEC (epg) using a modified McMaster technique. Also, blood samples were collected via jugular venipuncture and hematocrit (%PCV) was determined in whole blood. The data were analyzed as repeated measures using the SAS statistical package. FEC+100 was natural log-transformed to stabilize variance. No significant difference ($P > 0.05$) was determined between the wethers eating the CTRL diet (623.4 epg) and those eating the TRT diet (515.3 epg). The % PCV was similar ($P > 0.05$) between the goats eating CTRL and TRT (26.8% vs. 25.0%, respectively). PS fed to pastured goats did not affect gastrointestinal nematode burdens as related to FEC or hematocrit.

Key Words: *Haemonchus contortus*, pumpkin seed, wether goat

TH385 Influence of body weight, age, and level of *Haemonchus contortus* infection on measurement of parasite resistance in performance tested rams. B. Allen*, D. Wright, D. Notter, M. McCann, A. Zajac, and S. Greiner, *Virginia Polytechnic Institute and State University, Blacksburg.*

Selection for resistance to gastrointestinal nematode infection is an important consideration for sheep producers. This study was designed to evaluate the effect of age and BW on response to an artificial infection with Haemonchus contortus, as well as evaluate level of artificial infection on egg counts per g of feces (FEC), BW, and ADG in ram lambs. A total of 85 Katahdin rams from 13 flocks participated in a post-weaning evaluation at the Virginia Tech Southwest Agricultural Research and Extension Center. Rams were commingled 21 d before the study and dewormed with 3 classes of anthelmintics to clear any previous parasite infections. Following acclimation (June 27), rams were assigned to 3 management groups based on initial BW (Heavy-HWT, Medium-MWT, Light-LWT; n = 17, 28, and 26, respectively), and each received 5,000 infective larvae. A subset of MWT and LWT rams that received 5,000 larvae (5K; n = 12) were compared with an additional group of contemporaries from the same flock which received 10,000 infective larvae (10K; n = 14). All rams grazed fescue paddocks and received 3% BW grain supplement daily (17% CP, 65% TDN). At 2, 4, 6, 8, and 10 wk after infection, BW, ADG, and FEC were measured. FEC was log-transformed to stabilize variance, and data were analyzed in JMP using repeated measures analysis. Final BW for HWT, MWT and LWT rams were 57.6, 43.3, and 38.2 kg, respectively ($P < 0.01$), and HWT rams were older ($P < 0.01$) than MWT and LWT rams (age = 155 vs. 128 and 123 d). Total ADG did not differ among WT groups. Mean LFEC over the 10 wk period was lowest ($P < 0.05$) for HWT rams. Rams receiving 5K or 10K did not differ in BW or ADG. Mean LFEC was similar ($P > 0.05$) between 5K and 10K infected rams over the 10 wk period. Substantial FEC variation existed across treatments (mean = 593, range 10 to 3480), suggesting selection for resistance is achievable. However, these results indicate that level of infection is affected by age and body weight, and therefore these factors must be taken into account in structured parasite resistance evaluation programs.

Key Words: sheep, *Haemonchus contortus*, resistance

TH386 Effect of continuous suckling/"ewe-rearing" and supplementation on growth performance and degree of parasitism of pasture-raised Katahdin lambs. S. L. Rastle-Simpson*, K. N. D'Souza, A. K. Redhead, Q. S. Baptiste, and M. Knights, *West Virginia University, Morgantown.*

The effects of continuous suckling and supplementation on growth performance and degree of parasitism of pasture-raised, crossbred Katahdin lambs were investigated. Spring-born lambs (n = 103; 20.5 ± 1.0 kg) were randomly assigned within birth-type to be weaned at approximately 75 d or to continuously suckle ewes. All lambs were turned out on pasture, and half of the lambs in each rearing method were randomly assigned to be supplemented (16% crude protein pellet) ad libitum (weaned + supplemented, WS (n = 24); suckling + supplemented, SS (n = 28)) or received no further treatment (weaned + no supplementation, WNS (n = 26); suckling + no supplementation, SNS (n = 25)). All lambs were weighed at birth, at the initiation of the trial, and at approximately biweekly intervals for 3 (3) months. Fecal samples were collected at the beginning of the trial and once every month for the duration of the trial to assess the number of parasitic eggs in feces. ANOVA was conducted using the GLM procedures of SAS. The statistical method included rearing method, supplementation, and the interactions. When interactions were present means were separated using Tukey's HSD. Overall average daily gain (ADG) and total weight gain were significantly higher ($P < 0.001$) in suckling than in weaned lambs (0.18 ± 0.01 and 0.13 ± 0.01 kg/day, and 13.9 ± 0.5 and 10.8 ± 0.6 kg for suckling and weaned lambs, respectively), and in supplemented compared with lambs not receiving supplements ($P < 0.01$; 0.15 ± 0.01 and 0.12 ± 0.01 kg/day, and 13.9 ± 0.5 and 11.1 ± 0.5 kg, respectively). Final weights were higher ($P = 0.05$) in suckling (34.1 ± 0.9 kg) compared with weaned (31.6 ± 1.0 kg) lambs, but were not affected by supplementation. The average number of Trichostrongylid per gram of feces was 2659.71 ± 327.65 and was not affected by treatments. The results of the current study indicate that both ewe-rearing and supplementation independently improve growth performance of pasture-raised lambs. In addition, continuous suckling improved the final weights of lambs.

Key Words: continuous suckling, growth, weaning

TH387 Genetic marker assisted selection for footrot disease resistance in sheep flocks. T. Wuliji*[1], W. Lamberson[2], B. Shanks[1], J. Caldwell[1], C. Clifford-Rathert[1], J. Pennington[1], H. Swartz[1], S. Azarpajouh[1], and A. Bax[1], *[1]Lincoln University, Jefferson City, MO, [2]University of Missouri, Columbia.*

Developing a genetic marker for marker assisted selection of footrot resistance in sheep presents a greater advantage over traditional selection techniques. The aim of this study was to evaluate the feasibility and effectiveness of genetic marker assisted selection for footrot disease resistance in sheep flocks. The genetic markers (footrot gene marker test) developed in New Zealand was adopted to screen for

footrot resistance and susceptibility genotype within Lincoln University experimental flocks. Initially, 120 Katahdin ewes and 16 rams were selected for marker assisted selection of footrot resistance. We screened and evaluated 7 genotypes including 3 sheep breeds (Katahdin, Dorper, and Texel) and their crosses. All animals were blood tested for the DNA marker screening. The crossbreeding of Katahdin x Dorper was conducted and F_1 lambing was completed in May, 2012. Footrot marker test screening was conducted on 192 blood samples of sheep including the footrot resistant selection (n = 82) and control (n = 110) flocks. The preliminary DNA marker screening results were classed into 5 gene allelic marker categories (M) ranging from a high, moderate or low resistance. The allelic frequency distribution by marker category was analyzed using Chi-squared test. The frequency distribution ratios were found differed significantly ($P < 0.01$) among groups (M1, M2, M3, M4, and M5). The sample population marker frequency presented a normal distribution pattern. Therefore, a high selection differential and genetic gain can be achieved once animals were identified for the markers to footrot resistance.

Key Words: footrot, genetic marker, sheep selection

TH389 Effects of male-female ratios and treatment with testosterone. O. Angel-Garcia[1], C. A. Meza-Herrera[3], J. M. Guillen-Munoz[1], P. A. Robles-Trillo[1], G. Arellano-Rodriguez[1], M. Mellado[2], F. G. Veliz[1], and R. Rodriguez-Martinez*[1], *[1]Universidad Autonoma Agraria Antonio Narro, Torreon, Coahuila, Mexico, [2]Universidad Autonoma Agraria Antonio Narro, Saltillo, Coahuila, Mexico, [3]Universidad Autonoma Chapingo, Bermejillo, Durango, Mexico.*

The objective of this study was to evaluate the sexual response out-of-season (March 27, 2012, 26°N) in anovulatory goats through the "male-effect" using different male:female ratios and males treated or not with testosterone (25 mg. im, every 3 d during 3 wk). The study compared 2 mating loads (1:5 or 1:10 buck to doe ratios). A total of 30 multiparous mixed-breed anestrous goats were randomly assigned to one of 2 experimental groups: (1) exposure of 20 goats to 2 testosterone-treated bucks, (2) exposure of 10 goats to 2 testosterone-treated bucks. Variables evaluated were interval from start of mating to estrus, tail wagging, and pregnancy rate. Response variables and pregnancy rates were analyzed by categorical procedures using the GENMOD procedure of SAS (SAS Inst. Inc., Cary, NC) with the logit link function. ANOVA considered the MIXED procedure of SAS comparing the number of days to first occurrence of estrus and tail wagging. Interval from mating onset to estrus was shorter ($P < 0.05$) in the 1:5 group when compared with the 1:10 group (66.1 ± 5.4 h vs. 74.2 ± 2.6 h). The onset of tail wagging occurred about 20 h before the onset of estrus for both groups of goats. Pregnancy rates in the 1:5 and 1:10 groups were 85 and 80%, respectively, with no difference ($P > 0.05$) between experimental groups. Although the 1:5 group showed a better response considering time to estrus onset, this advantage was not necessarily important because pregnancy rates were similar in both groups. In conclusion, testosterone-treated bucks regardless of mating load (1:5 or 1:10) were effective in synchronizing estrus in anovulatory goats; this is a reproductive strategy that should increase goat production efficiency during the out-of-season breeding.

Key Words: anovulatory goat, male-female ratio, testosterone

TH390 Reproductive outcomes of nulliparous and multiparous French-Alpine goats synchronized with prostaglandins. R. Rivas-Muñoz[1], E. Carrillo[1], A. Fabela-Hernandez[2], M. Velazquez-Morales[1], J. A. Garcia[1], J. Cabrera-Reyes[1], C. A. Meza-Herrera[3], R. Rodriguez-Martinez[2], and F. G. Veliz*[2], *[1]Insituto Tecnologico de Torreon, Torreon, Coahuila, Mexico, [2]Universidad Autonoma Agraria Entonio Narro, Torreon, Coahuila, Mexico, [3]Universidad Autónoma de Chapingo, Bermejillo, Durango, México.*

The aim of this study was to evaluate sexual response of nulliparous and multiparous goats subjected to 2 prostaglandin treatments applied at intervals of 5 and 10 d. Goats (n = 20) were divided into 4 groups (n = 5 each); the first 2 groups considered nulliparous goats with Group 1 (N5) receiving prostaglandin at 5 d interval and Group 2 (N10) at 10 d interval, while the last 2 groups considered multiparous goats, with Group 3 (M5) receiving prostaglandin at 5 d interval and Group 4 (M10) at 10 d interval. Application of the first dose of prostaglandins (0.2 mL; 160 µg) was carried out in all groups on October 27. Groups N5 and M5 received a second dose 5 d later. Estrus was detected at 0800, 1200 and 1700 h. Groups N10 and M10 received the second dose of prostaglandins 10 d later. Females detected in estrus were exposed to an adult male and full mounts were confirmed. The ovulation was determined 7–9 d after estrus and 45 d after mating pregnant females were detected. Pregnancy was diagnosed by trans rectal ultrasonography scanning. The percentages of estrus, ovulation and pregnant females was subjected to a χ^2 test, while period of estrous response was analyzed by a "t" test. Sexual response from nulliparous and multiparous goats submitted to 2 prostaglandins treatments (5 and 10 d) was as shown in Table 1. Results indicate that prostaglandins can be used to induce estrous synchronization greater than 50% for French-Alpine goats, regardless of their parity, in Northern Mexico.

Table 1. Reproductive outcomes of nulliparous (N5 and N10) and multiparous (M5 and M10) French-Alpine goats treated with prostaglandins (n = 20)

	N5	N10	M5	M10
Estrus	60% (3/5)	60% (3/5)	60% (3/5)	60% (3/5)
Period estrous response (h)	57±9	52±4	80±26	52±4
Ovulations	100% (5/5)	60% (3/5)	100% (5/5)	80% (4/5)
Pregnancy rate	60% (3/5)	20% (2/5)	60% (3/5)	20% (2/5)

**No statistical differences were detected among treatments for any variable ($P > 0.05$).

Key Words: estrus, prostaglandins, ovulations

TH391 Sexual response from Alpine goats stimulated with vaginal sponges vs. intravulvar progesterone. R. Rivas-Muñoz[1], E. Carrillo[1], JA Garcia[1], M. Velazquez-Morales[1], A. Fabela-Hernandez[2], J. Cabrera-Reyes[2], CA Meza-Herrera[3], R. Rodriguez-Martinez[2], and FG Veliz*[2], *[1]Instituto Tecnologico de Torreon, Torreon, Coahuila, Mexico, [2]Universidad Autonoma Antonio Narro, Torreon, Coahuila, Mexico, [3]Universidad Autonoma de Chapingo, Bermejillo, Durango, Mexico.*

Use of impregnated vaginal sponges to stimulate estrous and ovulatory activity in seasonal anestrous goats has been practiced worldwide. However, a very commonly used traditional hormonal treatment includes the induction of estrous activity using an intravaginal device impregnated with progesterone or a sponge for at least 7 d. The aim of this study was to compare the use of vaginal sponges and intravulvar progesterone application on reproductive performance of Alpine goats. Adult goats (n = 24; 2.5 yr of age) were divided into 2 homogenous groups (n = 12) according to weight and body condition ($P > 0.05$). Group 1 (GE) received vaginal sponges for 7 d; at sponge removal, 500 IU eCG and 25 mg prostaglandins were applied. Group 2 (GP), received 25 mg intravulvar progesterone; 24 h later goats received 500 IU eCG and 25 mg

prostaglandins. Subsequent to eCG application, goats were exposed to 2 sexually active males per group. Variables evaluated included plasma levels of progesterone, period to estrous response, estrous females, and pregnant females. Percentages of estrous and pregnant females were subjected to a χ^2 Test; while period to estrous response was analyzed using a "t" test. Plasma levels of progesterone were superior in GP as opposed to GE during the 2 d following progesterone application ($P < 0.01$). Probably, those progesterone levels (2.83 ± 0.6 and 1.66 ± 0.3 vs. 0.02 ± 0.01 and 0 ng/mL) may be responsible for the observed percentages of estrous females and synchronization rates. Period to estrous response (GE: 132 ± 34 h; GP: 133 ± 6 h; $P > 0.05$), proportions of estrous females (GP = 11/12; 92% vs. GE = 11/12; 92%; $P > 0.05$) and proportions of pregnant females (GE: 11/12; 92% vs. GP: 10/12; 83%; $P > 0.05$) were similar in both experimental groups. In this study, reproductive performance of Alpine goats was similar using either intravulvar progesterone or vaginal sponges in mid-July. Nonetheless, the cheaper cost of the intravulvar device makes it an economically viable and efficient technology for marginal goat production systems.

Key Words: estrous, ovulatory, sexual response

TH392 The effects of P.G. 600 on fertility and fecundity of non-lactating, seasonally anestrous ewes. K. N. D'Souza*, S. L. Rastle-Simpson, A. K. Redhead, Q. S. Baptiste, and M. Knights, *West Virginia University, Morgantown, WV, USA.*

Using exogenous gonadotropins as part of an estrous induction protocol can have beneficial effects on fertility in ewes bred out-of-season. Few studies have evaluated the ability of P.G. 600, which contains 400 IU of equine chorionic gonadotropin (eCG) and 200 IU of human chorionic gonadotropin (hCG) per 5 mL, to increase fertility in ewes bred out-of-season and, in particular, following the pre-treatment with progesterone delivered via CIDR devices. The objective of this study was to evaluate the effects of P.G. 600 on fertility and fecundity of nonlactating, seasonally anestrous ewes. Crossbred ewes (n = 610) from 6 farms in WV and PA received CIDR inserts (between the months of April and July) 5 d before introduction of rams. One d before insert removal, all ewes were assigned randomly to receive either a single IM injection of P.G. 600 (3mL; 240 IU eCG, 120 IU hCG; Intervet) or no further treatment. Rams remained with ewes for 25 – 40 d. ANOVA was conducted using the GLM procedures of SAS, and least squares means were computed. Estrous responses of P.G. 600-treated ewes were not different than those observed for controls ($P = 0.16$). Ewes treated with P.G. 600 had significantly higher conception rates ($P = 0.01$; 51.8 ± 0.04 vs. 39.2 ± 0.04%), pregnancy rates to first service ($P = 0.0007$; 45.8 ± 0.03 vs. 32.0 ± 0.03%), and overall pregnancy rates ($P = 0.07$; 59.9 ± 0.03 vs. 51.7 ± 0.03%) than non-treated control ewes. A greater percentage of ewes lambed in the P.G. 600-treated group than in the control group ($P < 0.0001$; 61.2 vs. 42.2%, respectively), however, prolificacy between the treated group and the control group was not different ($P = 0.56$). In addition, the overall lambing rate in the ewes treated with P.G. 600 was significantly greater than that of the control group ($P < 0.0001$; 92.4 vs. 63.6%). In conclusion, an injection of 3 mL of P.G. 600 one day before CIDR removal significantly increased fertility and fecundity of nonlactating ewes bred outside their normal breeding season.

Key Words: ewe, fertility, P.G. 600

TH393 Body, carcass, and chemical composition of lambs and young goats produced in Alto Camaquã, Brazil. R. Arnoni*[1], M. T. Osorio[2], J. C. Osorio[2], R. Oliveira[1], M. Goncalves[1], M. Borba[3], R. Esteves[1], and S. Duckett[4], *[1]Universidade Federal de Pelotas, Pelotas, RS, Brazil, [2]PVNS/CAPES/UFGD, Dourados, MS, Brazil, [3]Embrapa/Pecuaria Sul, Bage, RS, Brazil, [4]Clemson University, Clemson, SC.*

The objective of this study was to characterize and compare the meat quality of lambs and young goats produced in a natural (wild) system unique to the territory of Alto Camaquã, Brazil. The experimental design was completely randomized with 2 treatments (species). ANOVA was performed by GLM procedure of the statistical package (SAS). Carcasses of lambs (n = 15) and young goats (n = 20) were utilized in this experiment. For body composition, the lambs had higher percentages of shoulder than the goats ($P < 0.05$; 22.44 ± 0.93 vs. 20.43 ± 2.10). Leg percentage was higher on average for goats than for lambs ($P < 0.05$; 37.56 ± 2.20 vs 33.82 ± 1.34). In the shoulder and leg, the subcutaneous fat percentages were higher ($P < 0.05$; 10.86 ± 3.55 vs. 6.32 ± 1.69, shoulder; 6.78 ± 2.41 vs. 5.11 ± 1.71, leg) for lambs than goats. Total muscle percentages in shoulder and leg were higher ($P < 0.05$; 53.07 ± 2.01 and 49.32 ± 2.23, shoulder; 58.59 ± 1.75 and 53.50 ± 3.11, leg) for goats than lambs. The marbling fat in the shoulder was higher ($P < 0.05$; 3.71 ± 1.10 vs. 2.45 ± 0.61) for the lambs than goats. Muscle:bone ratio in both cuts was higher ($P < 0.05$; 2.37 ± 0.23 vs 1.86 ± 0.14, shoulder; 2.91 ± 0.34 vs 2.013 ± 0.21, leg) for goats than lambs. Muscle:fat ratio in both cuts was higher ($P < 0.05$; 6.36 ± 1.71 vs 3.67 ± 1.24, shoulder; 6.30 ± 1.32 vs 5.45 ± 1.56, leg) for goats than lambs. Protein content of the loin was higher ($P < 0.05$; 20.20 ± 0.73 vs 19.02 ± 0.74 g/100g) for goast than lambs. These results show that lambs deposit more subcutaneous fat and marbling fat than goats; whereas goats have increased muscle and higher muscle to bone ratios due to the reduction in fat deposition. The goats demonstrated superiority in carcass yield and a higher proportion of the leg, which is considered the premium cut, than lambs. These differences may be related to greater exercise of the goat due to foraging behavior and specific species development.

Key Words: carcass, goat, lamb

TH394 Influence of dietary cottonseed on carcass and meat quality characteristics of feedlot lambs. R. A. Souza[1], R. S. Gentil[1], E. M. Ferreira[1], D. M. Polizel[1], A. P. A. Freire[1], L. G. M. Gobato[1], M. A. Trindade[2], and I. Susin*[1], *[1]Escola Superior de Agricultura Luiz de Queiroz (ESALQ)/USP, Piracicaba, SP, Brazil, [2]Faculdade de Zootecnia e Engenharia de Alimentos (FZEA)/USP, Pirassununga, SP, Brazil.*

Whole cottonseed is a feed ingredient often used in ruminant diet due to its high protein and fiber content with low cost. However, some abattoirs do not take animals fed cottonseed because of lower consumer acceptability of the meat. In addition, lambs are very selective and may not eat homogenously when whole cottonseed is added to the diet. Grinding could favor a more homogenous eating pattern but could enhance the "off flavor" concern. The objective of this experiment was to determine the effects of feeding high-concentrate diets with whole or ground cottonseed on growth, carcass characteristics, sensory evaluation and meat quality of ewe lambs. Twenty-one White Dorper x Santa Inês ewe lambs (initial BW = 23.6 ± 1.2 kg and 87.7 ± 4.5 d old) were used in a randomized complete block design, according to initial BW and age. The experimental diets were: 1) CS0: control, without cottonseed; 2) WC21: with 21% of whole cottonseed; and 3) GC21: with 21% of ground cottonseed. The diets were isonitrogenous (16% CP) and composed of 90% concentrate and 10% coastcross hay. Diets were fed daily and the trial lasted 62 d. At the end of the performance trial, lambs were slaughtered after a 16-h fasting period and carcass characteristics were recorded. Samples of longissimus muscle were used for meat quality analysis and sensory evaluation. Sensory test was performed by 80 untrained panelists. There was no diet effect on DMI, ADG, dressing percentage, back fat thickness, and longissimus muscle area. Color was different

($P < 0.03$) when control diet was compared with cottonseed (WC21 + GC21) groups (L: 29.6 vs 36.8; a: 9.0 vs 7.5; b: 11.0 vs 8.7). The control group had greater ($P < 0.04$) tenderness (6.6 vs 5.9), succulence (6.8 vs 6.1), acceptability (6.2 vs 5.6), and flavor (6.0 vs 5.6) values compared with cottonseed groups. In conclusion, whole or ground cottonseed fed to feedlot ewe lambs did not impair growth and carcass characteristics. However, there was a detrimental effect on sensory evaluation showing that its use should be restricted.

Key Words: consumer acceptance, high-concentrate diet, sheep

TH395 Impact of spray washing of goats and goat carcasses on microbial counts. C. Harris*, A. K. Mahapatra, G. Kannan, J. H. Lee, and B. Kouakou, *Agricultural Research Station, Fort Valley State University, Fort Valley, GA.*

A study was conducted to investigate the microbiological effect of spray washing goats and goat carcasses with tap water, salt water, electrolyzed water (EO), and ozonated water. Eighty meat goats were slaughtered in 4 groups (replicate) on 4 different days (20 goats per replicate group) at the university abattoir using standard procedures during 2 seasons, summer and winter. Ozonated water was generated from tap water using a Lotus Sanitizing System and EO water was generated by electrolyzing NaCl solution (0.075%) using a Biontech BTM-3000 batch water ionizer. Goats were randomly allotted to one of 5 treatments (4 1-min spray-wash treatments or no wash). Spray-washing of all goats was done by the same individual using a battery-operated backpack sprayer. Blood and skin swab samples were collected from control and treated goats before and after the spray-washing. Muscle pH was recorded at 0 (immediately after skinning) and 24 h postmortem using a portable pH meter with a penetrating probe. Using appropriate serial dilutions, 3M Petrifilm *E. coli* Coliform Count Plates and 3M Petrifilm Aerobic Count Plates were used for enumeration of indicator bacteria. Colonies of treated and untreated samples were counted following 24 h incubation period at 37°C for *E. coli* and aerobic plate counts. Bacterial counts of skin and carcass samples were converted to $\log_{10}$ cfu/mL values. Differences between $\log_{10}$ cfu/mL untreated sample and $\log_{10}$ cfu/mL treated samples were calculated as a log reduction. Loin chops were used to determine the effects of treatment on quality characteristics of goat meat. Color and texture changes after spray washing, and cooking loss were evaluated. The results indicate that bacterial load on goat carcasses can be reduced by innovative pre-slaughter spray washing without significantly affecting the meat quality. The results from this study would be useful for small and very small goat processors and provide consumers with safer meat products.

Key Words: goat, microbial count, spray washing

TH396 Carcass characteristics and yield of lambs fed diets containing crude glycerin. V. B. de Carvalho*, J. M. B. Ezequiel, R. F. Leite, V. C. Santos, E. M. de Oliveira, T. R. Delphino, É. H. Fernandes, L. F. Cremasco, S. F. F. Petrorossi, J. R. Paschoaloto, M. T. C. Almeida, and J. F. Lage, *FCAV, São Paulo State University - UNESP, Jaboticabal, São Paulo, Brazil.*

The goal was to evaluate the effects of crude glycerin (CG) - 83% glycerol - on carcass traits and yield of lambs. Forty-two Santa Ines lambs (initial BW 22.9 ± 4.10 kg) were used in a completely randomized design with 5 treatments: 0% of CG (n = 9), 7.5% of CG (n = 8), 15% of CG (n = 8), 22.5% of CG (n = 8) and 30% inclusion of CG (n = 9) in DM. These animals were housed in individual pens and fed ad libitum twice per day. Diets were isonitrogenous with a concentrate:forage ratio of 82:18, and consisted of Tifton hay, corn, crude glycerin, corn gluten meal, corn oil, urea, sunflower meal, soybean hulls, and mineral salt. Animals were slaughtered at an average weight of 37.82 ± 1.42 kg. After slaughter and evisceration, carcasses were weighed, kept refrigerated for 24 h at 0°C, and then weighed again to determine dressing percentage (DP). Commercial cut yield was measured in the right half of each carcass by separating into neck, shoulder, rib, loin, and leg. The yield of cuts was calculated by relating the weight of cut with cold carcass weight, expressed as a percentage. The rib eye area (REA) and rib fat thickness (RFT) were measured in Longissimus between the 12th and 13th thoracic rib with a digital caliper. The MIXED procedure of SAS was used for statistical analysis of data and were compared using orthogonal contrasts (linear and quadratic) at 5% significance level. The DP decreases with increasing levels of CG in the diet, showing a linear ($P = 0.0153$) pattern. The weights of the neck ($P = 0.5433$), ribs ($P = 0.4164$), leg ($P = 0.0826$) and shoulder ($P = 0.6126$) were not affected by CG inclusion. However, the weight of the loin ($P = 0.0340$) decreased linearly with increasing levels of CG in the diet. The yield of the neck ($P = 0.2192$), ribs ($P = 0.9315$), leg ($P = 0.0727$), shoulder ($P = 0.0944$) and loin ($P = 0.1929$) were not affected by the treatment. REA ($P = 0.8232$) and RFT ($P = 0.1345$) were also not influenced by inclusion of CG. The results suggest that the use of CG in the diet of lambs at high levels can affect carcass yield.

Key Words: byproduct, commercial cut, glycerol

TH397 Evaluation of productivity carcass indicators in Merino and Corriedale lambs. G. A. Rosa, L. A. O. Ribeiro, and L. Kindlein*, *Federal University of Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil.*

The present study was conducted to assess whether objective measures taken in the Longissimus dorsi muscle (rib eye area, REA; maximum rib eye depth, RED; maximum rib eye width, REW) may be used by the meat industry as indicators of productivity through their correlation with cold carcass weight (CCW) in 2 lamb breeds, Merino (wool) and Corriedale (wool and meat). Despite the subjectivity of the quality concept, the meat industry requires specific measurable characteristics to be evaluated by consumers when purchasing the product. Slaughterhouses utilize carcass yield values as indicators of productivity, and as labor and processing costs are fixed, high yielding carcasses optimize production costs. Furthermore, objective measures, such as REA, RED, and REW are characteristics that indicate carcass composition, as they are related to animal muscularity and to cutting yield. For this experiment, 50 male lambs (12 mo old, 25 per breed) were used. The CCW were 14.7, 20.8 and 17.8 kg for Merino, Corriedale, and all animals, respectively. Samples of the Longissimus dorsi were collected for objective measurements. The data showed a positive correlation (R) for all the analyzed variables when all lambs (n = 50) were included: CCW and REA (0.694), REA and RED (0.748), REA and REW (0.726), CCW and RED (0.506), and CCW and REW (0.653). Within breed (n = 25), higher correlations were observed for Corriedale (0.313; 0.839; 0.604; 0.264 and 0.166) compared with Merino (0.199; 0.183; 0.274; 0.304 and 0.135), with the exception of CCW and RED. Differences may be related to the narrower carcass conformation of Merino breed. The results indicate greater muscularity in the Corriedale breed as reflected by the correlation between CCW and REA. There is also a high correlation between REA and RED for Corriedale (0.839), a dual purpose breed, confirming that RED can also be an indicator of meat productivity.

Key Words: carcass, lamb meat, rib eye area

TH398 Influence of zilpaterol (β-agonist) supplementation period on carcass traits of feedlot lambs. J. C. Robles-Estrada*, J. A. Rocha-Yocupicio, B. I. Castro-Perez, A. Estrada-Angulo, and H. Davila-Ramos, *Universidad Autonoma de Sinaloa, Culiacan, Sinaloa, Mexico.*

Forty Pelibuey × Katahdin (37.7 ± 0.67 kg) crossbred male lambs were used in a 43-d feeding trial (5 pens/treatment in a randomized complete block design) to evaluate the influence of zilpaterol supplementation on carcass characteristics. Lambs were fed twice daily with a cracked corn based (60%) experimental diet (2.57 Mcal/kg of ME and 15.2% of CP). The animals were allotted to individual pens (6 m^2) with full shade and ad libitum water. Treatments were (1) control (ZIL-0), no zilpaterol supplementation; (2) zilpaterol for 20 d (ZIL-20); (3) zilpaterol for 30 d (ZIL-30); and (4) zilpaterol for 40 d (ZIL-40). Zilpaterol was supplemented at a rate of 0.15 mg/kg of live weight d^{-1} (as zilpaterol chlorhydrate, Zilmax). The lambs were slaughtered in a local slaughterhouse. Zilpaterol supplementation improved hot carcass weight (6.68%), dressing carcass (1.07%), longissimus muscle area (13.7%, $P \leq 0.01$) and decreased fat thickness (25%) compared with control diet. A similar response was observed when comparing ZIL-30 lambs with ZIL-0 lambs. There were improvements in hot carcass weight (5.78%), carcass dressing (1.82%, $P \leq 0.02$), and longissimus muscle area (10.27%, $P = 0.04$), and reduction in fat thickness (34.5%, $P = 0.03$). Orthogonal polynomial analysis indicated a linear increase for carcass dressing ($P > 0.02$), and a tendency for increase in longissimus muscle area ($P = 0.06$) with increased period of zilpaterol supplementation. The results showed that using zilpaterol in lambs increased muscle mass and reduced fat in the carcass. Carcass weight increased with increasing periods (d) of zilpaterol supplmentation. There were no significant differences between ZIL-20 and ZIL-30 groups. It is concluded that due to the high cost involved, a 20-d supplementation is sufficient to improve carcass traits in lambs by increasing protein and reducing fat. However, zilpaterol supplementation in lambs for longer periods can be considered based on local market needs and economic returns.

Key Words: carcass trait, lambs, zilpaterol

TH399 Effect of zilpaterol hydrochloride on growth and carcass characteristics of Nubian × Criollo weather goats. A. M. Ocampo-Barragan[1], M. A. Lopez-Carlos*[1], J. I. Aguilera[1], H. Rodriguez[1], C. F. Arechiga[1], and R. G. Ramirez[2], *[1]UAMVZ, Universidad Autonoma de Zacatecas, Zacatecas, Mexico, [2]Universidad Autonoma de Nuevo Leon, Monterrey, Mexico.*

The β-adrenergic agonists (β-AA) improve growth performance, reduce adipose accretion, and increase muscle mass in food animals. Zilpaterol hydrochloride (ZH) is probably the most widely studied β-AA in ruminants (cattle and sheep). However, there have been no reports on its potential use for improving growth and meat production in goats. The objective of this study was to evaluate the effect of ZH added to the diet on growth performance and carcass characteristics of wether goats for the last 42 d before harvest. Fourty-8 Nubian × Criollo wethers (27.6 ± 2.9 kg) were blocked by BW and randomly assigned to pens (3 blocks, 12 pens and 4 wethers per pen). Pens within a block were assigned randomly to 1 of 4 dietary treatments which consisted of the ZH supplementation in diet at doses of 0.0 (control), 0.1, 0.2 and 0.3 mg/kg BW. Data analysis was performed using the GLM procedure of SAS. Preplanned orthogonal contrasts were used to test linear and quadratic effects of dose of ZH feeding, and differences between control and ZH administration. Results were considered significant at $P < 0.05$. Growth performance (total gain, average daily gain, and final weight) improved by ZH administration ($P < 0.003$) and increased linearly ($P < 0.001$) as dose of ZH increased. Carcass weight and dressing percentage improved by ZH administration ($P < 0.031$) and increased linearly ($P < 0.009$) as dose of ZH increased. Cooling loss percentage was not affected ($P > 0.05$) by ZH administration. Independent of the dose used, leg circumference increased 5.2% ($P = 0.023$), and mesenteric fat decreased 20.2% for wethers fed ZH diets ($P < 0.009$). In conclusion, addition of ZH to diets of wether goats increased growth performance and carcass characteristics in a similar way as reported for cattle and sheep.

Key Words: goat, growth, zilpaterol

TH400 Influence of zilpaterol (β-agonist) supplementation period on primal cuts of feedlot lambs. J. C. Robles-Estrada, B. I. Castro-Perez*, J. L. Martinez-Martinez, S. A. Serrano-Cebreros, and H. Davila-Ramos, *Universidad Autonoma de Sinaloa, Culiacan, Sinaloa, Mexico.*

Sixty Pelibuey × Katahdin lambs were received at the research facility 30 d before initiation of the trial. Forty Pelibuey × Katahdin (37.7 ± 0.67 kg) crossbred male lambs were used in a 43-d feeding trial (5 pens per treatment in a randomized complete block design, with initial body weight as block factor) to evaluate the influence of zilpaterol (β-agonist) supplementation on primal cuts. Lambs were fed twice daily (2.57 Mcal/kg of ME) with 60% cracked corn, 16% sudangrass hay, 12% soybean meal, 9.5% molasses, and 2.5% mineral premix. Animals were allotted to individual pens (6 m^2) with full shade and ad libitum water. Treatments were zilpaterol supplementation for 20 d (ZIL-20), 30 d (ZIL-30), 40 d (ZIL-40), or 0 d (ZIL-0, no zilpaterol, control). Zilpaterol was supplemented at a rate of 0.15 mg/kg of live weight per day (as zilpaterol chlorhydrate, Zilmax, Intervet México, México City). After carcasses were chilled for 48 h, the weights of the following cuts were obtained: rear quarter, leg, loin, skirt, fore quarter, chuck blade, shoulder, chest, and rib. Zilpaterol supplementation increased the final live weight (3.6%, $P = 0.05$) and cold carcass weight (6.2%, $P < 0.01$). Zilpaterol also increased rear quarter weight (8.86%, $P < 0.01$), chuck blade (6.48%, $P = 0.01$), loin (11.76%, $P < 0.01$) and leg (9.59%). Compared with ZIL-0, ZIL-30 increased rear quarter weight (9.0%, $P < 0.01$), chuck blade (7.0%, $P = 0.02$), loin (12.7%, $P = 0.01$) and leg (10%, $P < 0.01$). In both comparisons, there were no effects of zilpaterol on fore quarter weight. Orthogonal polynomial analyzes did not indicate linear or quadratic effects for zilpaterol supplementation days. In conclusion, zilpaterol supplementation increased cold carcass weight and muscle mass, particularly in the rear quarter, but with no effect on fore quarter cuts.

Key Words: lamb, primal cut, zilpaterol

TH401 Influence of zilpaterol (β-agonist) supplementation period on growth performance of feedlot lambs. J. C. Robles-Estrada, J. A. Garcia-Sandoval, B. I. Castro-Perez, and H. Davila-Ramos*, *Universidad Autonoma de Sinaloa, Culiacan, Sinaloa, Mexico.*

Sixty Pelibuey × Katahdin lambs were received at the research facility 30 d before initiation of the trial. From original group, 40 crossbred male lambs (37.7 ± 0.67 kg) were selected and used in a 43-d feeding trial (5 pens per treatment in a randomized complete block design) to evaluate the influence of zilpaterol (β-agonist) supplementation on growth performance of feedlot lambs. Lambs were fed with finishing diet (2.57 Mcal/kg of ME) containing cracked corn 60%, sudangrass hay 16%, soybean meal 12%, molasses 9.5%, and mineral premix 2.5%, twice daily. Animals were randomly allotted to pens (6 m^2) with full

shade and ad libitum water. Treatments were: 1) control, no zilpaterol supplementation (ZIL-0); 2) zilpaterol for 20 d (ZIL-20); 3) zilpaterol for 30 d (ZIL-30); and 4) zilpaterol for 40 d (ZIL-40). Zilpaterol was supplemented at a rate of 0.15 mg/kg of live weight d^{-1} (as zilpaterol chlorhydrate, Zilmax, Intervet México, México City). Zilpaterol supplementation improved the final weight (3.6%), ADG (15.2%), and feed conversion (10%), compared with control group ($P \leq 0.05$). When compared with ZIL-0, ZIL-30 tended to increase ($P \leq 0.08$) the final weight (4%), ADG (16.9%), and feed conversion (11.2%). However, no significant differences were found between ZIL-30 and ZIL-20. Dry matter intake averaged 1.566 ± 0.042 kg/d and there were no differences ($P = 0.34$) among treatments. The orthogonal polynomials (ZIL-20, ZIL-30 and ZIL-40) had similar responses (linear $P = 0.28$, and quadratic $P = 0.74$). The results showed that there were no differences among zilpaterol treatments, and that zilpaterol supplementation upto 30 d maintained improvement in lamb growth performance. Since there were no significant differences between ZIL-20 and ZIL-30, it is concluded that due to the high cost involved, a 20-d supplementation is sufficient to improve the growth performance in lambs. However, zilpaterol supplementation in lambs for longer periods can be considered based on local market needs and economic returns.

Key Words: growth performance, lamb, zilpaterol

TH402 Effect of prepartum administration of recombinant bovine somatotropin (rbST) on plasma beta-hydroxybutyrate levels in ewes subjected to subclinical ketosis. D. Perazzoli*[1], J. O. Feijó[1], A. C. J. Silva[1], A. M. Oliveira[1], L. Mielke[1], L. G. C. Silva[1], I. Bianchi[1], A. Schneider[1], E. Schmitt[1], C. F. Martins[1], F. A. B. Del Pino[1], C. Brauner[1], M. N. Corrêa[1], S. F. Faria Junior[2], M. B. Ferreira[3], *[1]Federal University of Pelotas, Pelotas, Rio Grande do Sul, Brazil, [2]University Anhanguera-Uniderp, Campo Grande, Mato Grosso do Sul, Brazil, [3]MSD Animal Health, São Paulo, São Paullo. Brazil.*

The aim of this study was to determine the effect of rbST prepartum adminstration on plasma BHB profile of pregnant ewes subjected to subclinical ketosis. Twenty-seven Pantaneiro ewes were divided into 2 groups: rbST (n = 14) and control (n = 13). The rbST group received 2 injections of 1 mg/kg of rbST (Boostin 500 mg, Intervet Schering-Plough, Brazil), in a 14 d interval, with the first application at 97 d of pregnancy, whereas the control group received 2 doses of sodium chloride solution, 0.9% (placebo). Blood samples were collected weekly to evaluate BHB, from d 90 of pregnancy until 20 d before expected lambing (pre-induction). During food restriction (from 20 to 15 d prepartum), blood samples were collected twice a day. From d 15 until lambing (post-induction), blood samples were collected every 3 d. Blood samples were collected weekly for 8 wk postpartum. Statistical analysis was performed using SAS software by ANOVA Mixed Model procedure with Tukey Test. Control groups had significantly higher ($P < 0.05$) BHB (2.19 ± 0.21 mEq/dL) compared with rbST-treated group (1.35 ± 0.20 mEq/dL). From the data obtained in this study, we found that the group that received prepartum doses of rbST had lower BHB levels than the control group. Administration of rbST may promote adaptation to lipid mobilization, decreasing the level of ketone bodies produced postpartum, and therefore may be an alternative for ketosis prevention in ruminants.

Key Words: ewe, peripartum, recombinant bovine somatotropin

TH403 Application of wood model to lactation curves of dairy ewes in an organic production system. J. C. Angeles Hernandez*[1], M. Gonzalez Ronquillo[2], B. Albarran Portillo[2], J. H. Gutierrez[2], and J. P. Rocha Malcher[3], *[1]Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autonoma de Mexico, Ciudad Universitaria, Distrito Federal, Mexico, [2]Facultad de Medicina Veterinaria y Zootecnia, Universidad Autonoma del Estado de Mexico, Toluca, Estado de Mexico, Mexico, [3]Ovinos Especializados en Leche SP de RL, El Marquez, Queretaro, Mexico.*

The Wood mathematical function (1967) has been widely used in the description of the lactation curve of different livestock species. The Wood model (WD) is structured by 3 parameters, where a is the initial milk yield; b and c are the parameters of inclining and declining slopes of lactation curve before and after the peak yield, respectively.The objective of the present study was to assess the degree of fit of Wood's model to the lactation curves of dairy ewes in an organic milk production system in Mexico. A total of 4,861 weekly test-day milk yield (TD) records from 193 lactations of F1 dairy ewes were analyzed to assess their lactation curves. The evaluation criteria were the correlation coefficient between estimated and observed values (R), the coefficient of determination (R^2), and the mean square prediction error (MSPE). Total milk yield (TMY), peak yield (PY), and time at peak yield (TPY) were calculated. The WD model showed an adequate fit (R = 0.95, R^2 = 0.92 and MSPE = 0.024), but is not accurate in predicting PY and TPY, underestimating both due to the presence of atypical curves (51.3%). All WD model parameters had high standard deviations, with higher SD values for parameter b, which indicated high variability in the lactation data used, and a marked polymorphism in the lactation curves due to a high number of atypical curves. There was a negative correlation (−0.39) between parameters a and b, and positive correlation (0.83) between parameters b and c, indicating a high association between different stages of lactation curves. The atypical curves generated model values outside the biological range due to organic system management characteristics, including animal genotype and nutrition.

Key Words: dairy sheep, organic management, atypical curve

TH404 Over-expression of adipose triglyceride lipase (ATGL) gene in mammary gland epithelial cells of dairy goats. J. Li, J. Luo, H. Tian, H. Shi, and W. Wang*, *Shaanxi Key Laboratory of Molecular Biology for Agriculture, Northwest A&F University, Yangling, Shaanxi, China.*

The objective of this study was to analyze tissue expression profile of adipose triglyceride lipase (ATGL) in Xinong Saanen dairy goat, and to detect its effect on lipid metabolism in goat mammary epithelial cells, to further reveal its important roles in the process of lactation. The tissue expressions of goat ATGL gene were analyzed by RT-qPCR. Total RNA of various tissues were extracted with Trizol reagent. The first strand cDNA was synthesized using the PrimeScript RT kit to conduct the real-time expression. The data were analyzed with SPSS to compare the difference. The results showed that the goat ATGL gene mRNA expression level of subcutaneous adipose tissue was the highest among all the analyzed tissues. It was followed by the lung and mammary gland. The mRNA level of ATGL gene in mammary gland was higher in lactating stage than in dry period. To analyze the function of ATGL, the recombinant plasmid pAdTrack-CMV-ATGL linearized by *Pme*I was transformed into *E. coli* BJ5183 competent cells containing the backbone vector pAdEasy-1 to construct vector pAd-ATGL by homologous recombination. pAd-ATGL was linearized by Pac I and transfected HEK 293 cells for packaging. The recombinant adenovirus vector with the titer of virus of 10^9 U/mL was used to infect goat mammary epithelial cells for overexpression of ATGL gene. The results showed that compared with Ad-GFP controls, mRNA level of ATGL increased by 600-fold in Ad-ATGL infected goat mammary gland epithelial cells for

48 h, and significant lipid droplet reduction was observed by Oil Red O staining. While cellular triglyceride mass was significantly decreased ($P < 0.05$), the free fatty acid level, which is closely related to cellular lipolysis, was significantly increased ($P < 0.05$) in Ad-ATGL infected goat epithelial cells. In conclusion, the overexpression of ATGL gene can cause remarkable changes of cellular contents, which suggest that ATGL gene may have a role in the process of steatolysis in lactating mammary gland of dairy goats.

Key Words: adipose triglyceride lipase (ATGL), dairy goat, over-expression

TH405 Feeding behavior of goats subjected to feed restriction. R. F. Leite*, F. O. M. Figueiredo, M. M. Freire, V. B. de Carvalho, L. S. Fonseca, D. C. Soares, A. R. C. Lima, A. K. de Almeida, T. F. V. Bompadre, and I. A. M. A. Teixeira, *FCAV, São Paulo State University-UNESP, Jaboticabal, São Paulo, Brazil.*

The objective of this study was to evaluate feeding behavior of goats subjected to 3 levels of feed restriction. Fifty-three Saanen goats (18 intact males, 17 castrated male and 18 females) with average body weight of 22.5 ± 1.3 kg were subjected to 3 levels of feed restriction (ad libitum, 25% and 50% feed restriction). Feed restriction was calculated according to the consumption of the animals fed ad libitum. All animals were fed the same diet comprised of corn stover and concentrate based on soybean meal and corn with 45.7% of roughage and 54.3% of concentrate. The animals were housed individually with unrestricted access to water. Feeding behavior of animals was evaluated during a period of 24 h by one observer who performed visual measurements every 5 min, and identified the activities of ruminating standing, ruminating lying, eating, drinking, idle standing and idle lying. The experimental design was a randomized complete block in a factorial scheme (3 sex × 3 feed restriction levels), data were analyzed using PROC MIXED and means were compared by Tukey test at 5% probability. No significant interaction between feed restriction and sex ($P > 0.05$) was observed for feeding behavior. Ruminating standing and drinking were influenced by sex ($P < 0.05$), with intact males spending longer periods ruminating and drinking than castrated males and females. The animals subjected to 50% feed restriction remained standing idle for a longer period, compared with animals fed ad libtum ($P < 0.05$), which can be explained by greater discomfort of animals subjected to greater feed restriction. In fact, it was observed that animals subjected to greater feed restriction showed agonistic behaviors in the standing position, which also justifies the longer periods observed for these animals in entertainment. In conclusion, sex influences feeding behavior in Saanen goats. And Saanen goats subjected to feed restriction spend more time standing idle.

Key Words: goat kid, ingestive behavior, sex

TH406 Effects of conditions between periods of studies to evaluate electric fence additions to barb wire fence for goat containment. Y. Tsukahara*, A. L. Goetsch, T. A. Gipson, J. Hayes, R. Puchala, and T. Sahlu, *American Institute for Goat Research, Langston University, Langston, OK.*

Forty Boer (B, 3.7 ± 0.23 yr and 52 ± 1.4 kg) and 40 Spanish (S) does (3.0 ± 0.21 yr and 36 ± 0.7 kg) were used to evaluate effects of treatments between periods (IT) of a Latin square (LS) on behavior (e.g., pen exit and shock) when exposed to pens with barb wire fence and different electric fence strand additions. Breeds were split into 2 sets with 5 groups of 4 does. Five 2.4 × 3.7 m evaluation pens had 1 side of barb wire strands at 30, 56, 81, 107, and 132 cm from the ground. Fence treatments (FT) were electrified strands (6 kV) at 15 and 43 (LH), 15 and 23 (LM), 15 (L), 23 (M), and 43 cm (H). For adaptation, there was weekly short-term exposure to test pens with different electric fence strand additions (B: wk 1 - no electric strands (NES), wk 2 - NES, wk 3 - 1 strand at 0 kV, wk 4 - 1 strand at 2.5 kV, wk 5 - NES; S: wk 1 - NES, wk 2 - 1 strand at 0 kV, wk 3 - 1 strand at 3 kV, wk 4 - 1 strand at 4 kV). The adaptation scheme differed between breeds based on initial behavior to prevent very low or high levels of exit during the experiment. Behavior was assessed 1 h every 2 wk in the 5 × 5 LS with different FT. In the week between measurements, 1 set of each breed was exposed to a NES test pen (IT-Y) and others were not (IT-N). It was thought that periodic exposure to IT-Y might refresh memory of potential pen exit depending on the particular FT. There were interactions ($P < 0.05$) in pen exit between IT and period (28, 38, 18, 0, and 18% with IT-Y and 45, 13, 0, 0, and 0% with IT-N in period 1, 2, 3, 4, and 5, respectively; SE = 4.9), fence treatment (5, 8, 15, 40, and 33% with IT-Y and 5, 3, 18, 23, and 10% with IT-N for LH, LM, L, H, and M, respectively; SE = 4.9), and breed (8 and 32% with IT-Y and 15 and 8% with IT-N for B and S, respectively; SE = 3.8). The IT also affected ($P < 0.05$) does receiving a shock (18 and 10%; SE = 2.4). In conclusion, exposing goats to barb wire fence without electric strands between measurement periods did have some desirable effects but, overall, was not adequate for use of a LS design to evaluate effectiveness of various electric strand additions for goat containment.

Key Words: behavior, goat, fence

TH407 Effects of adaptation and meat goat breed in a method to evaluate electric fence additions to barb wire fence for goat containment. Y. Tsukahara*, A. L. Goetsch, T. A. Gipson, J. Hayes, R. Puchala, and T. Sahlu, *American Institute for Goat Research, Langston University, Langston, OK.*

Forty Boer (B) wethers (150 ± 2.7 d of age and 20 ± 0.7 kg BW initially), 40 B doelings (163 ± 1.5 d and 22 ± 0.4 kg), 33 Spanish (S) wethers (162 ± 1.7 d and 18 ± 0.6 kg), and 42 S doelings (163 ± 1.6 d and 15 ± 0.4 kg) were used to investigate effects of adaptation treatment (AT) on behavior when exposed to barb wire fence with different electric strand treatments. Breeds were divided into 2 sets with 5 groups of 3 to 4 animals. Five 2.4 × 3.7 m evaluation pens had 1 side with barb wire strands at 30, 56, 81, 107, and 132 cm from the ground. Fence treatments (FT) were electrified strands (6 kV) at 15 and 43 (LH), 15 and 23 (LM), 15 (L), 23 (M), and 43 cm (H). After animals experienced exit from evaluation pens without electric strands (NES), AT of different modifications with electric fence strands were imposed 1 time each week for <30 min: wk 1 - 1 strand at 0 kV, wk 2 - LH, wk 3 - LH, and wk 4 - NES for 1 set of each breed (BC and SC); wk 1 - NES, wk 2 - 1 strand at 0 kV, wk 3 - L, and wk 4 - NES for the other set of B (BU); wk 1 - 1 strand at 0 kV, wk 2 - LH, wk 3 - LH, and wk 4 - LH for the other set of S (SU). Based on differences in initial behavior, BU and SU were designed to achieve similar behavior during the experiment, with differences between BC and SC expected. After AT, each group was exposed to 1 FT for 1 h in period 1 and 7 wk later in period 2. The % of animals exiting pens differed ($P < 0.01$) among AT (5.5, 39.9, 60.6, and 0.0% for BC, BU, SC, and SU, respectively; SE = 1.18) and FT (9.1, 2.8, 15.4, 62.4, and 22.6% for LH, LM, L, H, and M, respectively; SE = 1.39). Period affected ($P < 0.05$) animals shocked without exit (4.2 and 12.6% in period 1 and 2, respectively; SE = 2.81) and goats exiting with shock (14.5 and 1.3%; SE = 3.47), but did not affect exit. In conclusion, use of the same AT for B and S resulted in different behavior when later exposed to FT and BU affected pen exit as anticipated. However, SU was highly prohibitive to exit and would not be suitable for a method

of evaluating different electric fence strand modifications of barb wire fence for goat containment.

Key Words: behavior, fence, goat

TH408 Growth and survivability of meat goat kids as influenced by breed of dam and sire and forage type from birth to weaning. L. C. Nuti*[1], H. Soape[2], Y. Jung[1], and G. R. Newton[1], *[1]Prairie View A&M University, Prairie View, TX, [2]Texas A&M AgriLife Extension Service, Gregg County, Longview.*

The objective of this study was to determine the effect of forage type and breed of meat goats in a reciprocal cross between Boer and Spanish breeds on growth performance to weaning. Birth weight (BW), weaning weight (WW), pasture type and kid mortality to weaning were studied in 292 kids. Breed of kids were: BB, SS, BS, SB for pure Boer, pure Spanish, Boer with Spanish sire, Spanish with Boer sire, respectively. Dams and kids were randomly assigned to 4 forage treatments: annual ryegrass (ARG)/vetch, ARG/winter peas, ARG/clover, and native pasture (ARG and clover). The main effects on BW and WW analyzed included kid breed, litter size, litter weight, gender, forage type and parity of dam. Average age at weaning was 82.9 and 84.9 d for kids born to Boer and Spanish does, respectively. Death loss of any kid or dam before weaning was recorded. There was a significant difference ($P < 0.05$) in fecundity between Spanish and Boer does (97.0% vs 84.7%, respectively). Spanish does had significantly ($P < 0.05$) fewer male (0.64 vs. 1.05 sex ratios) kids and a significantly higher percentage of twin kids at weaning (50% vs. 23.4%). BB kids had significantly ($P < 0.05$) heavier birth weights than any of the other kid breeds. SS kids had significantly ($P < 0.05$) smaller birth weights than all other breeds. Birth weights of BS and SB (crossbreds) were not significantly different. Although there was no difference in percentage of kids reared to weaning between Spanish and Boer females (62.8% vs 56.9%, respectively), there was a significant difference ($P < 0.05$) in the number of SS kids over BB kids that made it to weaning (70.1% vs 36.0%, respectively). There was no significant effect on WW due to pasture treatment or parity of dam. Analysis of breed of kid and gender on WW revealed significant differences ($P < 0.05$) only with male kids with BS being significantly heavier than SB at weaning. We conclude that selection of the proper sire/dam breeding combination and mothering ability is critical to the overall economic success of a meat goat operation.

Key Words: goat, heterosis, growth

TH409 Dose response effects of supplementing an algal meal in concentrate diets fed to Canadian Arcott lambs on production performance. S. J. Meale*[1,2], A. V. Chaves[1], and T. A. McAllister[2], *[1]Faculty of Veterinary Science, University of Sydney, Sydney, NSW, Australia, [2]Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, AB, Canada.*

As microalgae are the original source of DHA in the marine food chain, the inclusion of dried marine algae in animal feeds is one strategy to increase the DHA level in foods of animal origin. DHA plays a role in normal cerebral development and function, and has been associated with a reduction in heart disease. Currently, there are very few studies using DHA-Gold, a commercial algal meal (*Schizochytrium* sp.) in ruminant diets, none of which have been conducted with sheep. As such, this study aimed to investigate the effects of supplementing DHA-Gold on growth, carcass characteristics and wool production of Canadian Arcott lambs. Forty-four lambs were blocked by weight and randomly assigned to 4 diets consisting of a barley-based pellet where DHA-Gold replaced flax oil at 0, 1, 2 or 3% DM. Lambs were individually housed with ad lib access to feed with feed delivery and orts recorded daily. Lambs were weighed weekly and slaughtered once they reached 50 kg LW. Carcass characteristics (hot carcass weight, dressing % and grading rule), rumen pH and liver weights were determined post mortem. Wool yield was determined on mid-side patches of 100 cm^2 shorn at d-0 and d-140. Dyebands were used to determine wool growth, micron and staple length. Daily DMI, ADG and G:F were similar among treatments ($P > 0.05$). Neither wool yield, length nor diameter were affected by diet ($P > 0.05$). Carcass characteristics were generally unaffected ($P > 0.05$), except for grade rule values (mm) which showed a quadratic increase (16.1, 21.2, 18.8 and 17.4 ± 1.18 mm for 0, 1, 2 and 3% DM, respectively; $P = 0.01$) with additional DHA-Gold. However, this did not increase the overall value of the carcass ($7.63 ± 0.30/kg; $P = 0.50$). Liver weight increased linearly ($P < 0.001$) and back score tended ($P = 0.08$) to increase with increasing dietary concentrations of DHA-Gold. This suggests that DHA-Gold can be successfully included in the diets of growing lambs at up to 3% DM, with the potential to improve carcass quality.

Key Words: Canadian Arcott lambs, DHA-Gold, production

TH410 Factors affecting post weaning growth of hair-sheep lambs born in winter and managed under semi-intensive husbandry system. R. Fernandez-Mier, M. A. Lopez-Carlos, J. I. Aguilera, C. F. Arechiga*, H. Rodriguez, and R. M. Rincon, *UAMVZ, Universidad Autonoma de Zacatecas, Zacatecas, Mexico.*

A study was conducted to identify main factors affecting postweaning growth between 75 and 145 d of age of hair-sheep lambs born in winter and managed under semi-intensive conditions. Lambs (males and females, n = 208) born during the winter months (December, January and February) were weighed weekly from weaning (d 75 adjusted) until 145 d of age. Date of birth, sex, breed of sire, breed of dam, phenotypic expression (stunted or normal), and litter size (single, double, or triple) were recorded. Data were analyzed as repeated measures using MIXED procedure of SAS. Lambs classified as "slow growing" or "stunted" at the beginning of the experiment had lower ($P < 0.001$) weaning weight and were 12.6 kg lighter than normal growing lambs. During the first 2 wk after weaning, there were no differences ($P > 0.05$) between male and female lambs, although male lambs were up to 3.6 kg heavier ($P < 0.001$) at the end of 145 d. Lambs born from multiple births were 2 kg lighter than single birth lambs, but when they completed 145 d of age, the difference was reduced to only 0.8 kg. Breed of sire (Dorper vs. Katahdin) did not affect the weight of lambs. However, breed of dam influenced weight of the lambs. At 131 d of age, lambs from Dorper, Pelibuey or Katahadin dams showed similar weights of 27.1, 25.8 and 25.2 kg respectively, while lambs form Blackbelly dams weighed 23.5 kg and were lighter ($P < 0.05$) than the rest of lambs. Month of birth significantly ($P < 0.05$) affected lamb weights. Lambs born in February were heavier than those born in January, while the lambs born in December were the lightest. In conclusion, "stunted" lambs had lower growth rate, and farmers should consider whether to keep these animals on the farm or hold for sale at weaning. In addition, factors such as prolificacy, maternal breed, sex, and month of birth should be considered when evaluating the profitability of a farm, as these factors significantly affect lamb development in the post weaning period.

Key Words: growth, hair sheep, lamb

TH411 Mitochondrially targeted antioxidants as a strategy to reduce oxidative stress in pigs. M. R. O'Neil*[1], G. A. Kraus[2], N. K. Gabler[1], S. M. Lonergan[1], and D. C. Beitz[1], *[1]Department of Animal Science, Iowa State University, Ames, [2]Department of Chemistry, Iowa State University, Ames.*

Free radical production by the mitochondria and subsequent oxidative cellular damage is a potential target for management of oxidative stress in animals. Targeting antioxidant compounds to the mitochondria may increase the efficiency with which antioxidants decrease oxidative stress. Thirty weaned barrows (68.9 ± 7.4 kg) were used in a completely randomized design to test the effect of dietary tertiary butylhydroquinone (TBHQ) and the triphenylphosphonium derivatized mitochondrially targeted TBHQ (mitoTBHQ) on measures of oxidative stress and growth. Each barrow was assigned randomly to one of 3 treatment diets–control, TBHQ (control plus 8.546 mg/kg TBHQ per day), and mitoTBHQ (control plus 30 mg/kg mitoTBHQ per day). Barrows were penned individually and fed for 6 weeks. Barrows were weighed and urine was collected weekly, and serum and plasma were collected every 2 weeks. All barrows were evaluated for loin eye area and backfat thickness via ultrasound at the initiation of treatments and before harvest. Barrows did not differ in lean tissue accretion ($P = 0.152$) with control, TBHQ, and mitoTBHQ barrows gaining 12.41, 12.79, and 14.54 kg of lean tissue, respectively. Similarly backfat thickness was unaffected ($P = 0.184$) by treatment with control, TBHQ, and mitoTBHQ barrows having backfat thicknesses of 0.65, 0.69, and 0.63 inches, respectively.

Key Words: oxidative stress, antioxidant, tertiary butylhydroquinone

TH412 Effect of neonatal Ca nutrition on growth, bone development and differentiation of mesenchymal stem cell in pigs. Y. Li*, B. Seabolt, and C. Stahl, *North Carolina State University, Raleigh.*

Dietary Ca content plays an important role in animal growth, bone integrity and behavior of mesenchymal stem cells, especially in the neonatal period. To fully characterize the effects of neonatal Ca nutrition, we conducted a Ca dose response feeding trial for 14 d with 24 piglets (28 ± 6 h of age). Pigs were allotted into deficient, adequate, or excessive Ca treatments, fed with 0.6, 0.9 or 1.3% Ca on a DM basis, respectively. Blood was collected at d7 and d14 to monitor Ca status. Urine and bones were collected at the end of the study for determining Ca metabolism. Also bone marrow derived MSCs were isolated. In vivo MSC proliferation was determined by an oral dose of BrdU 12h before tissue collection. Twenty individual colonies were obtained from each pig, and the most and least osteogenic (O^+/O^-) and the most and least adipogenic (A^+/A^-) clones were selected based on functional staining. The results show that the ADG and ADFI were depressed by Ca deficiency, but not improved by excessive Ca. Bone mineral content ($P < 0.05$) was dose dependent on dietary Ca concentration. With increased dietary Ca, urinary Ca excretion increased ($P < 0.05$) and blood PTH level decreased ($P < 0.05$), while the sera Ca and P levels were stable. Proliferation rate of MSC was increased ($P < 0.05$) by excessive Ca. Bone-forming ability was depressed in MSC from Ca deficient pigs. However, both Ca deficient ($P < 0.1$) and Ca excess ($P < 0.05$) groups improved the fat-forming ability of MSC. There is no treatment effect on differentiation ability in A^+/A^- or O^+/O^-. The data suggest that neonatal Ca nutrition affects bone development by changing the programming potential of MSC.

Key Words: neonatal pig, calcium

TH413 Immunological and growth response in pre-weanling piglets administered an oral gavage of alligator blood. S. Means*, B. Chung, T. Shields, and F. LeMieux, *McNeese State University, Lake Charles, LA.*

The objective of this study was to evaluate the effects of alligator blood administered over a 3 d period on pre and post-weaning growth of pigs. A total of 18 crossbred pigs (Yorkshire × Landrace × Duroc) from 2 litters were randomly allocated to a control (tap water) or treatment alligator blood (AB). Pigs were administered 5 mL of an oral gavage twice daily for a total of 3 d before weaning. Pig weights were recorded at d $^{-}$3, 0, 3, 7, and 14 to determine average daily gain. Additionally pigs were bled at d $^{-}$3 and 0 in relation to weaning to evaluate blood chemistry (glucose, blood urea nitrogen, creatinine, phosphorus, total protein, albumin, and globulin) and ELISA testing was conducted to determine immunoglobulin levels (IgG, IgA, and IgM). Treatment did not affect ($P > 0.10$) growth of pigs. Pigs on control treatment had increased levels of glucose, phosphorus, total protein, albumin, and globulin over the 3 d treatment period. Over the 3 d treatment period pigs receiving AB had a 12.02% decrease in blood glucose compared with an increase of 2.7% for the control pigs. Globulin levels decreased 13.23% in pigs administered AB versus a decrease of 19.24% in the control pigs. After 3d of treatment, serum immunoglobulin levels of IgG were lower ($P < 0.05$) in pigs receiving AB treatment. There was no difference ($P > 0.10$) in IgM levels. Immunoglobulin G levels in pigs receiving alligator blood decreased 32% in a 3 d period. This was double the 14% decrease in pigs receiving control treatments. Immunoglobulin A levels were also lower ($P < 0.05$) in pigs receiving the AB gavage. These results suggest that alligator blood may be a beneficial additive for nursing and weanling pigs.

Key Words: oral gavage, pre-weanling pig, alligator blood

TH414 Effect of in-feed enzymes on ileal and cecal microbial populations of nursery pigs. G. M. Preis[2], M. H. Rostagno*[1], B. T. Richert[2], and J. E. Ferrel[3], *[1]USDA-ARS, West Lafayette, IN, [2]Purdue University, West Lafayette, IN, [3]Elanco Animal Health, Greenfield, IN.*

Exogenous enzymes are increasingly being used as feed additives in swine production to promote growth performance and efficiency of nutrient utilization. However, there is a lack of knowledge on their potential effects on the intestinal microbial populations. A total of 48 pigs (37 d of age; 8.35 ± 0.10 kg of BW) were used to evaluate the effect of 2 strains of β-mannanase enzymes, normal (HC) and heat tolerant (HT), the combination of HC with β-glucanase (HC+G), and alkaline phosphatase (AP) on growth performance and intestinal microbial ecology during a 16 d period. Pigs were allocated in a randomized incomplete block design into individual pens, stratified by litter and initial BW, to 5 treatments, with 9 or 10 pigs/treatment. Dietary treatment enzyme concentrations were: Negative Control (NC; no enzymes); HC, 0.10 MU/kg mannanase; HT, 0.06 MU/kg mannanase; HC+G, 0.10 MU/kg HC mannanase + 0.077 MU/kg glucanase; AP, 0.066 MU/kg. Final BW were similar among treatments (16.73 kg; $P > 0.05$). However, ADG of HC+G pigs tended to be greater than HC ($P < 0.10$), and numerically greater ADG (9.2%) and ADFI (11.9%, $P < 0.10$) than NC pigs. All other treatments were intermediate with no significant feed efficiency difference. Ileal anaerobes, coliforms, and lactobacilli were not affected by the dietary supplementation of enzymes. However, HT increased ileal aerobes ($P < 0.05$), whereas HC increased Bifidobacterium spp. and

Enterococcus spp. ($P < 0.05$). Moreover, HC+G and AP reduced ileal concentrations of *E. coli*, and increased Bifidobacterium spp. ($P < 0.05$). In the cecum, no effects were observed on aerobes, anaerobes, lactobacilli, and Bifidobacterium spp. However, HC increased concentrations of Enterococcus spp. ($P < 0.05$), whereas AP reduced concentrations of coliforms and *E. coli* ($P < 0.05$) in the cecum. It is concluded that the use of exogenous enzymes can affect the intestinal microbial ecology, and therefore, may provide an interesting alternative to manipulate bacterial populations of interest in nursery pigs.

Key Words: enzyme, microbial ecology, swine

TH415 Evaluating postweaning macromineral and organic trace mineral supplementation on performance and tissue mineral status of nursery pigs. R. S. Samuel*[1], J. S. Jolliff[2], and D. C. Mahan[2], *[1]Alltech Inc., Nicholasville, KY, [2]The Ohio State University, Columbus.*

Pigs may be weaned onto diets with greater concentrations of minerals than recommended to attempt to maximize performance. Due to mineral antagonisms, it is important to provide minerals in the appropriate form and balance. The objective of the experiment was to investigate the effects of reduced dietary mineral inclusion in diets fed to newly weaned pigs on growth performance and bone and plasma mineral status. Pigs (n = 180) were weaned onto 1 of 7 dietary treatments as pens of 5 pigs. Pigs were fed diets formulated to contain Normal (0.80% Ca), Mid (0.52% Ca), or Low (0.27% Ca) and available P (2:1 ratio) according to recommendations of NRC (1998). The Mid and Low diets were fed for 0 to 7, 0 to 14, or 0 to 21 d before feeding the Normal diet until 35 d postweaning. All diets were formulated to contain organic trace minerals (Bioplex, Alltech, Inc.) providing Cu, Fe, and Mn at 25% of NRC levels and Bioplex Zn and Sel-Plex (Alltech, Inc.) providing 100% of NRC levels. The ADG of piglets fed the Mid Ca and P diet for 21 d postweaning was numerically greater ($P = 0.14$) from d 21 to 35 than pigs fed only the Normal diet. The ADFI of pigs fed only the Normal diet was greater ($P = 0.03$) from d 7 to 21 compared with the pigs fed the Ca and P restricted diets. Feed efficiency of pigs fed Ca and P restricted diets for 21 d postweaning was greater ($P = 0.05$) than for pigs fed only the Normal diet, indicating compensatory gain after extended mineral restriction. Percent bone ash in the femur was lower ($P = 0.01$) in pigs fed the Low Ca and P diet for 21 d postweaning compared with the other treatments. The resulting significant ($P = 0.01$) treatment x week interaction indicated that the percent bone ash of the femur from pigs fed the Mid diets was not affected by moderately reduced dietary Ca and P. Macro- (Ca, P, Mg, S) and trace mineral (Cu, Fe, Zn, Mn, Se) concentrations in the femur, liver and plasma were not affected by dietary treatment. These results indicate that moderately reduced dietary Ca and P and organic trace minerals at 25% of NRC recommendations was not detrimental to animal performance or tissue mineral status.

Key Words: minerals, weaning, Bioplex

TH416 Zinc source and level on nursery pig growth performance. R. S. Samuel*[1], J. S. Jolliff[2], B. W. James[3], and D. C. Mahan[2], *[1]Alltech Inc., Nicholasville, KY, [2]The Ohio State University, Columbus, [3]Kalmbach Feeds Inc., Upper Sandusky, OH.*

Zinc (Zn) is routinely added to swine diets to prevent disease and improve growth performance. The current recommended dietary inclusion of Zn is 100 ppm and 80 ppm for growing swine up to 11 kg and 25 kg, respectively. Dietary inclusion of ZnO has been demonstrated to reduce postweaning diarrhea and improve weight gain of piglets. The objective of this experiment was to investigate the effects of dietary organic (Bioplex Zn) and inorganic (Zn sulfate) Zn sources and interactions with ZnO on growth performance. Pigs (n = 900) were fed diets in a 3 × 5 factorial arrangement of 3 ZnO levels (0, 1500, or 3000 ppm) and 5 Zn additions (0, 75 or 100 ppm Bioplex Zn or Zn sulfate). Pigs were provided free access to feed and water in a commercial research facility. Diets based on corn and soybean meal were formulated to provide all nutrients, except Zn, at the recommended levels in 3 dietary phases (0 to 7, 7 to 21, and 21 to 42 d). All diets contained a commercially available phytase source. Compared with no added Zn, the addition of at least 75 ppm Zn, from Bioplex Zn or as Zn sulfate, increased ($P < 0.01$) ADG and improved ($P < 0.05$) feed efficiency from 21 to 42 d and overall ($P < 0.01$; 0 to 42 d). The addition of 100 ppm Zn, from Bioplex Zn or as Zn sulfate, increased ($P < 0.05$) ADFI and improved ($P = 0.03$) feed efficiency from 21 to 42 d, compared with no added Zn. Positive effects of Bioplex Zn or Zn sulfate additions on ADG were detected after ZnO was removed from the diets. This observation contradicts observations from a previous experiment performed in this facility in which pigs previously fed ZnO had a decrease in performance after ZnO was removed from the diets. In this experiment, there were no significant interactions of Zn source and ZnO on measured parameters. In conclusion, 75 ppm Zn from Bioplex Zn or Zn sulfate was sufficient to meet the requirement for Zn in conventional nursery diets containing phytase and there were no negative effects on performance due to the removal of ZnO from the diets.

Key Words: zinc oxide, Bioplex, weaning

TH417 Probiotics and enzymes on swine feed: Post-weaning to growing phase effects. L. G. M. Amaral, H. Silveira, F. M. Carvalho Jr., C. A. P. Garbossa, and V. S. Cantarelli*, *Federal University of Lavras, Lavras, Minas Gerais, Brazil.*

The aim of this study was to evaluate the effects of an enzyme pool associated with probiotics on performance, intestinal morphology and incidence of diarrhea in pigs from 24 to 129 d old. The study was conducted at the Swine Experimental Center (SEC), at Federal University of Lavras. Eighty pigs (females and castrated males), weaned at 24 d of age, with initial average weight of 6.04 ± 0.18 kg were used. The experiment was a randomized block design and lasted 105 d. Treatments were: PB - *Bacillus subtilis*; PB + E - Probiotics + Enzymes; ATB - antibiotics; CTR – control (5 rep/trt). Pigs were distributed according to the weaning weight and housed in groups of 4 animals per pen (experimental plot). The data were subjected to ANOVA by SNK test (5%) and the diarrhea incidence to the Kruskal-Wallis analysis. Intestinal morphology was not affected by diet ($P > 0.05$). The ADG, feed conversion and final BW was greater ($P < 0.05$) for ATB pigs compared with PB and PB+E trt from 24 to 66 d. However, the use of PB + E resulted in the same BW at 129 d as pigs supplemented with ATB, while consuming less feed *(*$P < 0.05$). All treatments had high incidences of diarrhea in the first 2 wk of experiment. Animals supplemented with antibiotics had high incidences ofdiarrhea during the exchange diets (45 to 52 d) and at the time of relocation (66 to 70 d). Despite the high percentage of diarrhea in the first week, animals supplemented with B. subtilis showed lower ($P < 0.05$) incidence of diarrhea during the changing in the feed. The additives tested are not as effective as antibiotics at immediately postweaning, but beneficial effects during the growingphase on performance and frequency of diarrhea were observed.

Key Words: swine, feed additive, weaning

TH418 Dose response assessment of a whey and yeast-derived additive for nursery pigs. J. S. Monegue*[1], M. D. Lindemann[1], H. J. Monegue[1], M. Thomas[1], and S. Jalukar[2], *[1]University of Kentucky, Lexington, [2]Varied Industries Corporation, Mason City, IA.*

The use of products containing whey and/or yeast-metabolites as dietary supplements has often demonstrated improved feed efficiency and reduction of scours in nursery pigs. A total of 96 crossbred pigs (mean initial BW, 6.92 ± 0.95 kg) were used to evaluate a novel product (called CAP-110) on nursery pig performance and gastrointestinal health. This product contained a proprietary blend of whey fermentation derived sugars, organic acids, and yeast metabolites. Pigs were blocked at weaning into groups based on sex and bodyweight. Pigs were randomly allotted within blocks to 4 dietary treatments and housed 4 pigs/pen (2 barrows and 2 gilts) for a total of 6 replicates. Pens were left somewhat dirty from the previous nursery group to put greater environmental pressure on the newly weaned pigs (simulating a dirty nursery) with the intent of inducing more diarrhea. The 4 dietary treatments were a control diet and 3 levels (0.025, 0.050, 0.10%; or 0.25, 0.50, and 1.00 kg/metric ton [MT]) of the test ingredient. The study was conducted over a 5-week period with 3 diet phases. Phases 1, 2, and 3 diets were fed for 1, 2, and 2 weeks respectively. Performance measures of ADG, ADFI, and Feed/Gain were determined weekly. Pigs receiving Diet 2 (0.025% test ingredient) were 3.4, 1.5, and 5.9% heavier at the end of the study than those fed Diets 1, 3, and 4, respectively. For the total study period, pigs fed Diet 2 had 4.7% greater ADG (505, 528, 517, 488 g/d; $P = 0.093$; quadratic $P = 0.055$), 3.0% greater ADFI (809, 834, 822, 821 g/d; $P = 0.94$), and 1.4% lower Feed:Gain (1.600, 1.578, 1.588, 1.683; $P = 0.28$) compared with pigs fed the control diet. While the *P*-values varied, observations of all responses across all phases were visually quadratic in nature. Routine fecal scoring of the pigs and pens was conducted on d 1, 3, 7, 10, 14, 21, 28, and 35. There was no diarrhea observed in the study so questions about potential efficacy of the product when diarrhea is present cannot be answered. This new product has potential to improve performance and, because of the responses observed, lower inclusion rates should be examined to determine the optimal inclusion rate.

Key Words: growth, pig, yeast metabolite

TH419 Evaluation of Celmanax SCP supplementation in sow diets on piglet performance at weaning. M. Peng[1], C. Guozhu[2], and S. Jalukar*[3], *[1]Anyou Animal Nutrition R&D Co. Ltd., Huanggang City, Hubei Province, China, [2]All Victors Biotechnololgy Co. Ltd., Wuhan, China, [3]Vi-COR, Mason City, IA.*

A highly concentrated form of enzymatically hydrolyzed yeast and yeast culture was evaluated for its potential to improve sow reproductive performance at a private research farm affiliated to a commercial feed company in Hubei Province, China. Twenty-seven Landrace × Yorkshire × Duroc crossbred sows were allotted to 3 treatments in a completely randomized block design with 9 replicates/treatment. Sow allotment was equalized by parity. Treatments were supplemented 14 d before farrowing and for 21 d post-farrowing during lactation phase. The treatments were: No additive, Celmanax SCP (Vi-COR, Mason City, IA) 100 g/MT and Celmanax SCP 200 g/MT. Feed was available ad libitum during lactation. Feed intake, litter size, litter weight at birth and weaning, mortality and scouring in baby pigs was recorded. Piglets were weighed individually at birth and at weaning. Experimental data was analyzed by SPSS 17.0 software and DuSCPan for comparison. A dose dependent response in improving piglet birth and weaning weights, decreasing scours, and mortality was noted with Celmanax SCP 200g/MT inclusion resulting in the best performance. Feed intake and litter size was not affected by the additives. Piglet mortality at birth was also not affected by the treatments. Individual piglet and litter weight at birth was not affected by the additives. However, when Celmanax SCP was supplemented at 200g/MT, piglet weaning weight was 5.48 kg vs.5.03 kg ($P < 0.01$) and litter weaning weight was 55.93 kg vs. 46.05 kg ($P < 0.05$) compared with control. Scouring score decreased from 8.13% in control to 4.51% ($P < 0.05$) with Celmanax SCP 200 g/MT inclusion rate. Mortality decreased from 16.15% in control to 5.51% ($P > 0.05$) with Celmanax SCP 200 g/MT treatment. In conclusion, supplementation of Celmanax SCP 2 weeks before farrowing and during lactation clearly increased piglet body weight, reduced mortality and improved piglet health at weaning.

Key Words: sows yeast, reproductive performance

TH420 Eating patterns of newly weaned piglets. T. van Kempen*[1,2] and J.-W. Resink[1], *[1]Nutreco, Boxmeer, the Netherlands, [2]North Carolina State University, Raleigh.*

Weaning imposes stress which affects health and thus performance. The prime problem appears to be their adaptation to eating solid feed. To better understand how pigs start eating, 96 piglets were weaned at 25 d of age at 1000 h. Pigs were placed into 8 pens equipped with feeding stations with a measuring accuracy of 1 g. Visits and cumulative feed disappearance were recorded for each piglet: the first 10 g was considered their first meal, and the 2nd 10 g their 2nd meal. Light was on continuously the first 24 h and afterward a 16h light 8h dark pattern was introduced; feeders, however, were permanently lit. Ninety-three piglets visited the feeder on the day of weaning; the remaining 3 the next morning. Seventy-eight piglets consumed their first meal the day of weaning, 9 the next day, and the remaining 9 the 2nd day. The day of weaning the average feed disappearance was 2.6g and the largest feed disappearance recorded was 22g. Despite 24 h light, there were nearly no feeder visits between 2000 and 0400 h the first night (38, compared with 1932 before 2000 h). The next day a clear day-night pattern was discernable as well but there were approximately 10× more feeder visits during night time. 77 piglets finished both their first and 2nd meal the first day. Interestingly, the 2nd meal occurred 50% later than the first meal ($r^2 = 0.98$). Piglets that did not finish their 2nd meal before 20:00 waited with finishing their 2nd meal till the next morning (after 6:00) where again a linear relationship was observed between the time till the first meal and the 2nd meal. Pigs that waited till the 2nd day for their first meal only ate their 2nd meal at the end of the 2nd day or the third day: none of these pigs ate a meal at night. The data show that pigs immediately upon weaning change to a day-night feed intake pattern despite 24 h light in the nursery. Pigs that were hesitant to start eating did so carefully; the lag time between the first 10 g and second 10 g feed disappearance was 50% of the time it took to the first 10 g feed disappearance. The time of day that piglets are weaned may thus well affect their transition time to solid feed.

Key Words: piglet, weaning, feed intake pattern

Breeding and Genetics: Genomic Selection in Dairy II

538 Application of a posteriori granddaughter and modified granddaughter designs to determine Holstein haplotype effects. J. I. Weller[1,2], P. M. VanRaden[1], and G. R. Wiggans*[1], [1]*Animal Improvement Programs Laboratory, Agricultural Research Service, Beltsville, MD,* [2]*ARO, The Volcani Center, Bet Dagan, Israel.*

A posteriori and modified granddaughter designs were applied to determine haplotype effects for Holstein bulls and cows with BovineSNP50 genotypes. The a posteriori granddaughter design was applied to 52 sire families, each with > 100 genotyped sons with genetic evaluations based on progeny tests. For 33 traits (milk, fat, and protein yields; fat and protein percent; somatic cell score; productive life; daughter pregnancy rate; heifer and cow conception rates; service-sire and daughter calving ease and stillbirth; 18 conformation traits; and net merit), the analysis was applied to the autosomal segment with the single nucleotide polymorphism (SNP) with the greatest effect in the genomic evaluation of each trait. All traits except 2 had a significant ($P < 0.05$) within-family haplotype effect. The same design was applied with the genetic evaluations of sons corrected for SNP effects associated with chromosomes besides the one under analysis. Number of significant within-family contrasts was 166 without adjustment and 211 with adjustment. Of the 52 bulls analyzed, 36 had BovineHD genotypes that were used to test for concordance between sire quantitative trait loci and SNP genotypes; complete concordance was not obtained for any effects. Of the 31 traits with effects from the a posteriori granddaughter design, 21 were analyzed with the modified granddaughter design. Only sires with a significant contrast for the a posteriori granddaughter design and < 200 granddaughters with a record usable for genetic evaluation were included. Eight traits had significant within-family haplotype effects. With respect to milk and fat yields and fat percentage, the results on BTA 14 corresponded to the hypothesis that a missense mutation in DGAT1 is the main causative mutation, although other polymorphisms in that gene also modify fat yield and percentage. The positive allele for protein concentration was less frequent, which indicated that selection on that locus could be effective. DNA sequencing of the sires analyzed will be needed to determine the causative mutations.

Key Words: granddaughter design, genetic evaluation, genomic selection

539 Using 90,113 single nucleotide polymorphisms in genomic evaluation of dairy cattle. G. R. Wiggans*, T. A. Cooper, and P. M. VanRaden, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

Accuracy of genomic evaluation is expected to increase when more markers are used because of better tracking of causative genetic variants. However, Illumina BovineHD genotypes based on 777,962 single nucleotide polymorphisms (SNP) have not been used for US genomic evaluation because the small reliability gain achieved did not justify the genotyping cost. In December 2012, the GeneSeek Genomic Profiler HD (GHD) BeadChip was released with 76,867 unique nuclear SNP and 13 mitochondrial SNP. It included 28,376 (63%) of usable SNP from the Illumina BovineSNP50 v2 BeadChip as well as 48,491 BovineHD SNP selected because they had the greatest effects for Holstein net merit. Based on analysis of 1,730 animals with GHD genotypes, 3,153 SNP were not used for genomic evaluation because they were on the Y chromosome or had a low call rate, excess parent-progeny conflicts, or a minor allele frequency of < 1% for Holsteins, Jerseys, and Brown Swiss; 73,714 GHD SNP were usable for genomic evaluation, which added 44,925 to the 45,188 currently used (total of 90,113 SNP). Genotypes for those SNP and August 2009 traditional genetic evaluations for 26,200 Holstein bulls and cows were used to predict December 2012 daughter performance of 29 economically important traits for 4,024 bulls with a traditional evaluation since August 2009. Reliability gains from 90,113 SNP were greater than from 45,188 SNP by 2.2 percentage points for yield traits and 0.9 percentage points for calving traits but less by 0.8 percentage points for fitness traits and 0.5 percentage points for conformation traits. Lower gains may result from imputation errors, which will decline as more animals have GHD genotypes. Imputation from lower density chips to 90,113 SNP was about 0.5% less accurate than to 45,188 SNP. More GHD genotypes are needed to achieve adequate imputation accuracy for Brown Swiss and Jerseys, which have few high-density genotypes. The GHD chip allows additional SNP to be included in genomic evaluation without increasing genotyping cost, but higher imputation accuracy is needed before evaluation accuracy can improve for all breeds and traits.

Key Words: genomic evaluation, reliability, single nucleotide polymorphism

540 Methods for genomic evaluation in a small dairy population and the effect of inclusion of genotyped cows' information in multiple-parity analyses. D. A. L. Lourenco*[1], I. Misztal[1], J. I. Weller[2], S. Tsuruta[1], I. Aguilar[3], and E. Ezra[4], [1]*University of Georgia, Athens,* [2]*Institute of Animal Sciences, ARO, Bet Dagan, Israel,* [3]*Instituto Nacional de Investigacion Agropecuaria, Las Brujas, Canelones, Uruguay,* [4]*Israel Cattle Breeders Association, Caesaria, Israel.*

Methods for genomic prediction were evaluated for a dairy population in which less than 1000 progeny-tested bulls were genotyped. The inclusion of elite cows' genotypes in a single-step method was also evaluated. Two data sets were used: a complete data set with production records of 713,686 cows from 1985 through 2011, and a reduced data set with production of 563,870 cows up to 2006. For each production trait (milk, fat, protein, fat %, and protein %), a multitrait animal model was used to compute genetic evaluation for parities 1 through 3 as separate traits. Evaluations were performed for the 2006 and 2011 data sets. Genomic predictions for bulls in 2006 were obtained using genomic BLUP (GBLUP), a Bayesian linear regression method (BayesC), single-step GBLUP (ssGBLUP), and ssGBLUP considering weights for SNP (WssGBLUP). Predictions with BayesC and GBLUP were either direct or included PA in an index (IND). Genomic predictions when including elite cows' genotypes were obtained using ssGBLUP and WssGBLUP. Predictive ability was assessed by coefficients of determination (R^2) and regressions of predictions of 135 validation bulls with no daughters in 2006 on daughter deviations of those bulls in 2011. The average R^2 (%) among parities for PA, GBLUP, BayesC, GBLUP (IND), BayesC (IND), ssGBLUP, and WssGBLUP, respectively, were 14, 9, 10, 15, 15, 19 and 19 for milk; 7, 12, 14, 10, 10, 13, and 12 for fat; 3, 10, 10, 9, 8, 12, and 12 for protein; 35, 22, 29, 34, 37, 37 and 40 for fat %; 31, 24, 30, 32, 36, 39 and 44 for protein %. The average inflation (%) of GEBV among parities and traits was 24, 17, 25, 22, 7, and 15 for GBLUP, BayesC, GBLUP (IND), BayesC (IND), ssGBLUP, and WssGBLUP, respectively. Adding weights in ssGBLUP helped to improve accuracy of genomic predictions, but further modifications are needed to reduce bias observed in some traits. Adding elite cows' genotypes in single-step

methods removed bias in protein % when weights for SNP were added, and improved the overall R^2 by up to 2% in ssGBLUP and WssGBLUP.

Key Words: genomic evaluation, small populations, single-step method

541 Dissection of genomic correlation matrices using multivariate factor analysis in dairy and dual-purpose cattle breeds. N. P. P. Macciotta*[1], C. Dimauro[1], S. Sorbolini[1], D. Vicario[2], D. J. Null[3], and J. B. Cole[3], [1]*Dipartimento di Agraria, Università di Sassari, Sassari, Italia,* [2]*ANAPRI, Udine, Italia,* [3]*Animal Improvement Programs Laboratory, USDA, Beltsville, MD.*

SNP effects estimated in genomic selection programs allow for the prediction of direct genomic values (DGV) both at genome-wide and chromosomal level. As a consequence, genome-wide (G_GW) or chromosomal (G_CHR) correlation matrices between genomic predictions for different traits can be calculated. Comparison between G_GEN and G_CHR or between different G_CHR may indicate differences in the genetic control of groups of traits. In this work, a method for comparing genomic correlation matrices based on multivariate factor analysis (MFA) is presented. Two breeds were considered: 3,096 US Holstein and 460 Italian Simmental bulls, with DGV for 31 and 12 productive and functional traits, respectively. Factor analysis was carried out on G_GEN and G_CHR within each breed. In Holstein, between 7 and 9 factors were able to explain 70 to 80% of the original variance, whereas in Simmental on average 3 to 4 latent variables explained about 80% of the variance. In US Holstein, latent factors correlated ($r > 0.60$) with milk yield traits, milk composition, udder morphology, strength, and functional traits (productive life, SCS, daughter pregnancy rate) were obtained from G_GEN. Differences were observed at the chromosome level. For BTA14, a single factor correlated with both milk yield and composition traits was observed. For BTA18, sire calving traits and some conformation traits were correlated with the same common factor. In the G_GEN of Italian Simmental, the first latent factor was correlated positively with milk yield and milking traits, and negatively with muscularity; the second with daily gain and size; the third to feet and legs and SCS; and the fourth to milk composition traits. On BTA17, one factor is positively correlated with daily gain and negatively with milk composition. The MFA was able to detect differences in genetic correlation patterns across the genome, as well as on individual chromosomes, and may be used for preliminary identification of genome regions affecting multiple traits.

Key Words: genomic prediction, chromosome, genomic correlation

542 International genomic evaluation of young Holstein bulls. J. H. Jakobsen*[1] and P. G. Sullivan[2], [1]*Interbull Centre, Swedish University of Agricultural Sciences, Uppsala, Sweden,* [2]*Canadian Dairy Network, Guelph, ON, Canada.*

Genomic tested young bulls with no daughter proofs yet are of interest for international trade. A genomic multitrait across country evaluation (GMACE) procedure was applied to Mendelian sampling (MS) deviations of young bulls: national GEBV minus parent average from classical MACE. Fifteen Holstein populations provided GEBV data for as many as 38 traits while classical EBVs for the same traits were included from 31 populations. Only GEBV data passing GEBV validation tests; for minimal bias, and for improvement in accuracy compared with national parent averages, were included in the study. Further, national GEBVs were required to be from the same model and on the same base and scale as the national EBVs of progeny-tested bulls provided for classical MACE. GEBVs of bulls less than 7 years of age and with no classical MACE proof were included for the breeding value prediction while bulls 2–5 years of age were included for genomic variance estimation. Numbers of GEBV included in GMACE were 1.96 for 80,765 bulls for protein, while numbers of EBV for classical MACE were 1.23 for 130,349 bulls. Multiple GEBV of a young bull occur due to sharing of data and genotypes among countries for national GEBV predictions. Such genomic data sharing at the national level was accounted for in GMACE by fitting residual correlations among the national GEBV input data. The residual correlations were based on proportions of common reference (i.e., phenotyped) bulls and cows used for genomic predictions by each country. International GEBV had equal or higher reliability than corresponding national GEBV. For example, protein yield national GEBV reliabilities were generally between 65 and 75, while the international reliabilities ranged between 75- 80. Reliability increases were highest if bulls had multiple national GEBV, and if the GEBV were from countries with less genomic data sharing. Each young bull with one or more national GEBV received international GEBV on all 31 population scales, including the populations with no national GEBV. A first official release of MACE GEBV and MACE GREL of young Holstein bulls is planned for August 2013.

Key Words: GMACE, dairy

543 Whole genome analysis for SNP variation in indigenous cattle population in Pakistan. H. Mustafa*[1], H. Heather[2], K. Javed[1], T. Pasha[1], M. Abdullah[1], I. Mohsin[1], K. Euisoo[2], A. Ali[1], A. Ajmal[1], and T. Sonstegard[2], [1]*University of Veterinary and Animal Sciences, Lahore, Pakistan,* [2]*Bovine Functional Genomics Laboratory, ARS/USDA, Beltsville, MD.*

Although a large number of single nucleotide polymorphisms (SNPs) have been identified from the bovine genome- sequencing project, few of these have been validated at large in Bos indicus breeds. We have genotyped 96 animals, representing 10 cattle populations of Pakistan, with the Illumina Bovine 777K SNP BeadChip. These include 8 Achi, 4 Bhagnari, 13 Cholistani, 10 Dhanni, 10 Dajal, 2 Kankaraj, 13 Lohani, 9 RedSindhi, 14 Sahiwal and 13 Tharparkar breeds. Frequency of minor allele frequency (MAF), distribution, and deviation from Hardy-Weinberg equilibrium (HWE) were estimated. Analysis of 500,393 SNP markers revealed that the mean minor allele frequency (MAF) was 0.23, 0.20, 0.22, 0.22, 0.20, 0.18, 0.20, 0.22, 0.21 and 0.18 for Achi, Bhagnari, Cholistani, Dhanni, Dajal, Kankaraj, Lohani, Red sindhi, Sahiwal and Tharparkar cattle, respectively. Significant differences of MAF were observed in the indigenous Pakistani cattle populations ($P < 0.001$). Across the Pakistani cattle populations, common variant MAFs (≥ 0.10 and ≤ 0.5) accounted for 79% of 500, 939 SNPs. The level of SNP variation identified in this particular study highlights that these markers can be potentially used for genetic studies in indigenous cattle breeds in Pakistan.

Key Words: indigenous cattle, minor allele frequency

544 Increasing the accuracy of genomic predictions of fat yield in New Zealand Holstein Friesians using *DGAT1* genotypes. M. K. Hayr*[1], M. Saatchi[1], D. L. Johnson[2], and D. J. Garrick[1], [1]*Iowa State University, Ames,* [2]*LIC, Hamilton, NZ.*

Accurate genomic estimated breeding values (GEBV) are essential for preventing the accumulation of inaccuracies when unproven parents are selected. This study investigated the effect of including the known large effect *DGAT1* mutation in calculating GEBV. Data were provided by LIC, a New Zealand dairy cattle breeding company, and included Illumina SNP50 (50k) genotypes and deregressed estimated breeding values (DEBV) for fat yield. *DGAT1* genotypes were provided for 1,133 cows and 655 bulls and imputed for the remaining 4,528 cows

and 1,632 bulls in BEAGLE. Three models were run using Bayes C in GenSel and 5-fold cross-validation with 97.5% of SNPs assumed to have no effect on the trait: (1) a model relying on linked 50k markers to pick up the *DGAT1* effect; (2) a model with 50k markers and *DGAT1* as a random effect; and (3) a model with 50k markers and with *DGAT1* genotype as a fixed effect. These models were run separately for bulls and for cows, and repeated, once using animals where *DGAT1* had been directly genotyped and once using all animals. The GEBV accuracy was defined as the correlation between DEBV and GEBV. Regression of DEBV on GEBV was computed to quantify bias in GEBV. Accuracy was lowest when only 50k markers were included in the model and increased when *DGAT1* was included in the model, with the highest accuracy observed when *DGAT1* was a fixed effect. The regression coefficient was sufficiently close to one to assume there is little to no bias in GEBV; nevertheless it was closest to one when *DGAT1* was as a fixed effect. These results suggest that including *DGAT1* genotype as a fixed effect when calculating GEBV both increases accuracy of the GEBV and reduces bias. Differences in using direct versus direct and imputed genotypes could be due to sample size or incorrect imputation.

Table 1. Regression coefficient (b) and correlation (cor) between DEBV and GEBV

		Direct genotypes		Direct and imputed genotypes	
Sex	Model	b	cor	b	cor
M	50k	1.104	0.402	0.908	0.377
	50k + DGAT1 (Random)	1.102	0.406	0.011	0.381
	50k + DGAT1 (Fixed)	1.014	0.425	0.917	0.389
F	50k	1.189	0.559	1.022	0.695
	50k + DGAT1 (Random)	1.187	0.564	1.021	0.698
	50k + DGAT1 (Fixed)	1.090	0.574	1.017	0.702

Key Words: dairy, *DGAT1*, genomics

545 Profitability of combined use of sexed semen and genomic testing in dairy heifers. A. De Vries*[1] and J. A. Salfer[2], [1]*University of Florida, Gainesville,* [2]*University of Minnesota Extension, St. Cloud.*

The objective of this study was to evaluate the profitability of the combined use of sexed semen and genomic testing in dairy heifers. The use of sexed semen may result in more dairy heifer calves than are needed to replace culled cows, allowing increased selection intensity. Genomic testing increases the reliability of selection. Combined, the genetic progress of the selected heifers may offset the costs due to the use of sexed semen, including decreased fertility, and genomic testing. First, an algorithm was developed to determine which heifer calves should be genomically tested based on reliability of pre-ranking for net merit, cost of testing, and selection intensity. The net value of the genetic gain in the selected heifers was used in a herd budget simulation model that mimicked a closed herd including young stock and cows. Surplus dairy heifer calves were sold. Annual cull rate in the cow herd was 39% for all scenarios. Four scenarios were tested: (A) no genomic testing, no sexed semen, (B) optimal genomic testing, no sexed semen, (C) optimal genomic testing, first insemination with sexed semen in all heifers, (D) optimal genomic testing, first and second inseminations with sexed semen in all heifers. Genomic testing increased the reliability of net merit breeding values from 20% to 60%. The surplus of dairy heifer calves in scenarios A to D was 7%, 7%, 18%, and 22% of those born alive. Optimal genomic testing (in the lower pre-ranked heifer calves) in scenarios B to D added $25, $60, and $72 per heifer selected. The cost to raise heifers, including the value of genomic selection, was $627, $616, $621, and $627 per milking cow per year (scenarios A to D). The sale of bull calves and surplus dairy heifer calves resulted in revenues of $38, $38, $46, and $50 per milking cow per year. Considering all costs and benefits, herd profit per milking cow per year was $255, $265, $274, and $273 for scenarios A to D. In conclusion, strategic use of genomic testing and use of sexed semen in first inseminations in heifers was the most profitable scenario and increased profit by $20 per milking cow per year.

Key Words: sexed semen, genomics, profitability

Breeding and Genetics: Genomic Selection Methods I

546 Mixed model methods for genomic prediction and estimation of variance components of additive and dominance effects using SNP markers. Y. Da* and S. Wang, *Department of Animal Science, University of Minnesota, St. Paul.*

Mixed model methods for joint genomic prediction and estimation of variance components for additive and dominance effects using SNP markers were developed based on the quantitative genetics model that partitions a genotypic value into breeding value and dominance deviation. Two sets of formulations were developed for genomic BLUP (GBLUP) and genomic REML (GREML) estimation of variance components of additive and dominance effects using SNP markers. Set 1 of GBLUP and GREML formulations is based on the conditional expectation of breeding values and dominance deviations given phenotypic observations with fixed effects estimated by the best linear unbiased estimator (CE). The CE set of formulations applies to both cases of 'q< m' and 'q>m' and applies to cases with singular genomic additive and dominance correlation matrices, where q = number of individuals and m = number of SNP markers. Set 2 of GBLUP and GREML formulations is based on mixed model equations (MME). GREML formulations based on MME are computationally more efficient for the case of 'q>m' and are less efficient for the case of 'q<m' than the CE formulations. Reliability formulations were derived for GBLUP of breeding values, dominance deviations and genetic values as summation of breeding values and dominance deviations. GREML is an effective tool to assess the exact type of genetic effects and assess the genetic contribution of the whole genome or targeted chromosome regions and genes to the phenotypic variance. GBLUP of total genetic value that includes additive and dominance effects provide prediction of an individual's total genetic potential.

Key Words: genomic prediction, variance component, dominance

547 GVCBLUP 2.1: A computing package for genomic prediction and estimation of variance components for additive and dominance effects using SNP markers. C. Wang*[1], D. Prakapenka[2], S. Wang[1], H. B. Runesha[2], and Y. Da[1], [1]*Department of Animal Science, University of Minnesota, St. Paul,* [2]*Research Computing, The University of Chicago, Chicago, IL.*

GVCBLUP is designed for variance component estimation and genomic prediction for additive and dominance effects using SNP markers. Computing speed of GVCBLUP 2.1 increased by about 10 times running on single-core Windows desktops and increased by about 50 times running on 2~4 core Windows desktops using OPENMP. This new version has 3 programs: GREML_CE, GREML_QM, and GCORRMX. The GREML_CE and GREML_QM programs combined the 24 GREML and GBLUP programs in the previous version. GREML_CE is based on the conditional expectation of breeding values or dominance deviations given the phenotypic observations and applies to full-rank and singular genomic additive and dominance relationship matrices, and GREML_QM is based on mixed model equations and is designed for q > m, where q = number of individuals and m = number of markers. These 2 programs calculate GREML estimates of variance components of additive effects, dominance effects and random residuals, calculate additive and dominance heritabilities as well as heritability in the broad sense, calculate GBLUP of breeding values, dominance deviations and genetic values as summation of breeding values and dominance deviations for individuals in training and validation data sets, and calculate reliability of each GBLUP. Option is available to calculate GREML and GBLUP for additive effects only or dominance effects only, and for using any of the 3 definitions of genomic additive and dominance relationship matrices. GCORRMX is for calculating genomic additive and dominance relationships for 3 definitions.

Key Words: genomic prediction, variance component, dominance

548 Estimating dominance SNP effects using alternative single-step type genomic prediction equations. N. Gengler*, *ULg-GxABT, Gembloux, Belgium.*

Recently a new and alternative derivation of single-step type genomic prediction equations allowing joint estimation of GEBV and SNP effects based on the partitioning of genetic (co)variances was developed. The method was derived from a random mixed inheritance model where SNP and residual polygenic effects were jointly modeled. The derived equations were modified to allow non-genotyped animals and to estimate directly and jointly GEBV and SNP effects. Several other advantages of the new equations were that weighting of SNP and polygenic effects becomes explicitly and that SNP effects were also estimated simultaneously. This method makes better use of High-Density SNP panels and can be modified to accommodate other type of genetic effects. In the present study modifications of the equations were developed to allow the estimation of dominance SNP effects even if not all animals are genotyped and parental sub-class effects are used. Previous research done to estimate dominance effects were not very successful, the rationale being that they were hindered by the weakness of dominance information. However, by estimating dominance SNP effects and subsequently dominance GEBV, the estimation and the exploitation of specific combining abilities would become finally feasible. Recently, by genotyping animals heterozygosity of a given SNP locus is now precisely known. Therefore, through the direct use of this information with these alternative equations dominance SNP effects can be estimated and used to exploit specific combining abilities of given combinations of animal genomes. Finally, though this development the flexibility of these alternative equations combining advantages of single-step and of explicit SNP effect estimation methods to accommodate other types of genetic effects is shown.

Key Words: dominance effect, single step, genomic prediction

549 A comparison of hidden Markov-based imputation algorithms when applied to livestock data. K. Dhakal*[1], J. M. Hickey[4], A. Kranis[3], M. A. Cleveland[2], and C. Maltecca[1], [1]*North Carolina State University, Raleigh,* [2]*School of Environmental and Rural Science, Armidale, NSW, Australia,* [3]*Aviagen Ltd., Midlothian, United Kingdom,* [4]*Genus plc., Hendersonville, TN.*

Several of the pedigree-free imputation algorithms are hidden markov model (HMM) based approaches that approximate the coalescent and capture linkage disequilibrium information. Some pedigree-free algorithms have found use in livestock, mostly because their performance is reasonable, they are easy to use, and because in some instances

pedigree information is not present or suitable in livestock data sets being imputed. The objective of this study was to compare the performance of HMM imputation algorithms in several typical livestock genotyping scenarios with different structures where reference and test panels were different sizes. The data set included genotypes for pigs, and dairy cattle. Three in-silico low-density panels were constructed with densities equivalent to 6,065 (L6k), 3,022 (L3k), and 384 (L384) SNP across the entire genome. Four popular software packages fastPHASE, MaCH (minimac), Impute2, and Beagle were used for imputation, and imputation accuracies were evaluated. Differences in accuracies were found among imputation algorithms and across scenarios, with MaCH (minimac) giving higher accuracy (R-squared >0.85) when L6k and L3k panels were used for both pig and cattle data sets. Accuracy was higher when larger reference sets and test animals in L6k and L3k panels were used. Computational time also varied across scenarios with the MaCH (minimac) algorithm overall being the fastest. In general, the results obtained are helpful in guiding the selection of imputation algorithms for different imputation scenarios and livestock data.

Key Words: genotype imputation, pedigree-free, accuracy

550 Effect of genotype imputation on genome-based prediction of complex traits: An empirical study with mice data. V. P. S. Felipe*[1,2], G. J. M. Rosa[1], H. Okut[3], D. Gianola[1], and M. A. Silva[2], [1]*University of Wisconsin-Madison, Madison,* [2]*Federal University of Minas Gerais, Belo Horizonte, Minas Gerais, Brazil,* [3]*University of Yuzuncy Yil, Van, Turkey.*

High-density molecular marker panels have been used in animal and plant breeding for prediction of genetic merit of selection candidates. The prediction models often contain thousands of SNPs, which are fitted simultaneously using shrinkage-based estimation approaches. Quite often, because of cost constrains only a subset of the SNPs are genotyped in the selection candidate population, and genotype imputation methods are applied. The goal of this study was to evaluate the effect of genotype imputation on prediction accuracy of phenotypes. The hypothesis underlying this work was that all genetic signal and information available in a data set is contained entirely on the observed genotypes. A publicly available data set on mice was used, with information of 1,809 SNPs equally spaced along the genome of 1,881 animals. The traits considered were body weight and body mass index. And, from the full set of SNPs, only 201, 453 or 905 were selected as the genotyped SNPs, with the remaining marker imputed using the Beagle software. Then, Bayesian Lasso (BL), reproducing kernel Hilbert spaces (RKHS) and Bayesian regularized artificial neural networks (BRANN) were fitted using the subsets and the full panel of SNPs before and after genotype imputation. RKHS method showed the best predictive accuracy. Genotype imputation seemed to have the same effect on efficiency of BL and RKHS, whereas BRANN resulted in more sensible predictions due to imputation error. In scenarios which genotype imputation accuracy was good and masking rates of 75% and 50%, the genotype imputation did not bring great benefit. However, when genotype information was sparse (90% masking), genotype imputation brought information about important markers and improved predictive ability. The obtained results show that not always the imputation of unknown genotypes is advantageous for phenotypic prediction. The gain of imputing genotypes will depend on the connectedness between reference population and selection candidates, heritability of the trait, number markers available in the original panel, and the method used to predict marker effects.

Key Words: genomic selection, imputation, predictive ability

551 A fast expectation maximization antedependence model for whole genome prediction. C. Chen*, H. Wang, W. Yang, and R. J. Tempelman, *Michigan State University, East Lansing.*

As whole genome prediction (WGP) becomes based on even higher density single nucleotide polymorphism (SNP) marker panels, computational efficiency becomes a greater consideration such that inference strategies other than Markov chain Monte Carlo (MCMC) might be important. Two such popular alternatives are genomic best linear unbiased prediction (GBLUP) and BayesA,B/LASSO like methods based on the use of the expectation maximization (EM) algorithm. A primary limitation of these models is based on the specification of SNP effects being independently distributed, even though one might anticipate sizeable correlation between effects of SNP in close proximity to a major causal variant. Our group has previously developed such a model based on a first order antedependence covariance structure between adjacent SNP, while basing our inference strategy on MCMC. We have demonstrated that modeling this type of non-stationary correlation improves accuracy of breeding value (BV) prediction compared with models assuming independent SNP effects. We have developed a computationally tractable EM analog of this antedependence model that we dub EM-anteBayesA. In a simulation study involving 30 replicates, each involving just over 1000 SNP markers in linkage disequilibrium (LD) with average pairwise LD $r^2 = 0.30$, we compared EM-anteBayesA with a more conventional EM-based BayesA as well as more conventional implementations of anteBayesA and BayesA based on the use of MCMC. Although the EM-based methods tended to lead to slightly less accuracy in BV prediction than their MCMC counterparts, they were extremely competitive computationally thus rendering them to be tractable alternatives. Specifically, EM-anteBayesA demonstrated significantly higher accuracies than conventional EM-BayesA ($P = 0.02$). We also demonstrate the 4 models/inference strategies on the publicly available Wellcome Trust heterogeneous stock mice data. We conclude that EM-anteBayesA is a promising alternative for improving accuracy of WGP compared with other computationally efficient WGP implementations.

Key Words: computational efficiency, genomic selection, expectation maximization (EM)

552 Unknown-parent groups and incomplete pedigrees in single-step genomic evaluation. I. Misztal*[1], Z. Vitezica[2], A. Legarra[3], I. Aguilar[4], and A. Swan[5], [1]*University of Georgia, Athens,* [2]*Université de Toulouse, Castanet-Tolosan, France,* [3]*INRA, Castanet-Tolosan, France,* [4]*INIA, Las Brujas, Uruguay,* [5]*University of New England, Armidale, Australia.*

In single-step genomic evaluation using best linear unbiased prediction (ssGBLUP), genomic predictions are calculated with a relationship matrix that combines pedigree and genomic information. For missing pedigrees, unknown selection processes, or inclusion of several populations, a BLUP model can include unknown-parent groups (UPG) in the animal effect. For ssGBLUP, UPG equations also involve contributions from genomic relationships. When those contributions are ignored, UPG solutions and genetic predictions can be biased. Several options exist to eliminate or reduce such biases. First, mixed model equations can be modified to include contributions to UPG elements from genomic relationships (greater software complexity). Second, UPG can be implemented as separate effects (higher cost of computing and data processing). Third, contributions can be ignored when they are relatively small but they may be small only after refinements to UPG definitions. Fourth, contributions may approximately cancel out when genomic and pedigree relationships are constructed for compatibility; however, different construction steps are required for unknown parents from the

same or different populations. Finally, an additional polygenic effect that also includes UPG can be added to the model (slower convergence rate). Chosen options need to reflect different origins of UPGs: missing pedigrees in a closely selected population, multiple breeds, external lines or combinations of origins. Incomplete pedigrees may also cause biases and convergence problems even when UPGs are not in the model. In such cases, choices include restoration or truncation of pedigrees. Severity of problems with UPG and incomplete pedigrees greatly depends on the population structure. The problems are small in large purebred populations that include many high-accuracy sires (e.g., in dairy). The problems are larger in multi-line/multi-breed populations especially with few high-accuracy animals (e.g., in sheep).

Key Words: bias, genomic evaluation, unknown-parent group

553 Efficient inversion of a large genomic relationship matrix stored on a disk using a multi-core processor and graphic processing units. Y. Masuda* and M. Suzuki, *Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Japan.*

The objective of this study was to develop new software for quick computation of the inverse of a large genomic relationship matrix stored on a disk by a hybrid system with graphic processing units (GPUs) and multi-core central processing unit (CPU). The matrix was split into submatrices called "panels," whose elements were stored on a solid state drive (SSD). The process of inversion was described as a set of multiplications and additions between panels. The panels were loaded into main memory and updated if required. The updated elements were immediately written back to the disk. The optimized BLAS libraries, OpenBLAS and CUDA BLAS, were employed for matrix operations. Some computations on GPUs and accesses with the file were parallelized by OpenMP. Our software was written in Fortran 2003 and compiled with GFortran 4.7.2. The program were benchmarked on a computer with Intel Core i7–3770 (quad-core 3.4GHz), 32GB main memory, and NVIDIA GeForce GTX 580 with 1.5GB RAM, running Linux (x86_64). When the matrix had 50,000 of the order and it stored on the disk, the computing time for the inversion was 5.6 min in single precision and 15.0 min in double precision arithmetic. When enough memory was available on GPUs, the computing time was reduced by approximately 30% in single precision and 10% in double precision arithmetic. Although, the matrix was stored on the disk, our implementation completed the inversion 1.8 times (single precision) or 1.3 times (double precision) faster than a system where all data were loaded into main memory and processed by the optimized LAPACK subroutine (DPOTRF/DPOTRI) with a multi-core CPU only. The inversion for a matrix of 110,000 order in single precision (or 80,000 in double precision) was completed within 1 h. This technique is especially useful when the number of genotypes is up to 200,000 because the inverse of genomic relationship matrix can be directly obtained and used for the calculation of genomic predictions and their reliabilities without modifications to existing software.

Key Words: computing, software, GPU

554 Impact of genetic drift on developing access and benefit sharing guidelines under the Nagoya Protocol: The case of Meishan pigs imported into the United States. H. D. Blackburn*[1], Y. Plante[2], E. W. Welch[3], G. A. Rohrer[4], and S. R. Paiva[5], [1]*National Animal Germplasm Program ARS-USDA, Ft. Collins, CO,* [2]*Agriculture and Agri-Food Canada, Saskatoon, Saskatchewan, CA,* [3]*University of Illinois, Chicago, Chicago,* [4]*US Meat Animal Research Center ARS-USDA, Clay Center, NE,* [5]*EMBRAPA Secretariat International Affairs, Brasilia, Brazil.*

The Convention on Biological Diversity developed the Nagoya Protocol (NP) on access and benefit sharing (ABS) for international exchange of genetic resources. Concerns are NP will impose new costs for exchanging livestock genetic resources and interfere with private treaty contracts which dominate the sector. NP was developed without evaluating sectoral exchange practices or genetic change among imported populations. This study evaluated how allele frequencies of an imported population changed over time and how those results may affect ABS formulation under the NP. Thirty-five microsatellites were used to evaluate the effect of genetic drift (GD) on Meishan pigs. Samples included Meishan from: China (M-China, 22 hd; samples originally imported in the 1989) and US (M-US, 42 hd). The M-US was subdivided by herd of origin; US Meat Animal Research Center (M-MARC, 18 hd) and Iowa State University (M-ISU, 24 hd). Both herds were maintained for ~8 generations as randomly bred controls. Meishan-US, M-MARC and M-ISU were compared with M-China throughout the analysis. Measures of genetic diversity and GD were computed with GENALEX and TempoFs genetic software. Across markers TempoFs analysis showed a mean shift in allele frequency of 0.11(se = 0.019) due to GD for M-US vs M-China. Evaluating M-MARC and M-ISU the mean and standard error allele frequency shifts due to GD were 0.169 (0.034) and 0.214 (0.036), respectively. Principal coordinate analysis confirmed separation of M-US, M-MARC, M-ISU from M-China. The results show that among M-US substantial changes in allele frequency due to GD occurred in a relatively short time frame. If GD is coupled with directional selection differences between founder animals and subsequent generations would increase at a faster rate. The dynamics of genetic change over time plus dispersed ownership of resulting progeny of livestock suggest that current genetic exchange practices of the livestock sector (private contracts) be the basis for livestock genetic resource exchange and any ABS arrangement be considered at the time of purchase.

Key Words: Nagoya Protocol, genetic drift, Meishan

555 Vermont dairy farmer perceptions regarding farm access control. J. M. Smith*, R. Standish, M. Quaassdorff, M. Mills, L. Powell, and L. Weglarz, *University of Vermont, Burlington.*

Movements across the farm gate were important for the spread of foot-and-mouth disease in the United Kingdom in 2001; thus farm access may be an important control point. To better understand the perceptions of Vermont dairy farmers regarding control of farm access, a series of interviews was conducted. Twenty-six farmers, recruited by snowball sampling in one county, were interviewed in 2011. An additional 4 interviews were conducted in 2012. Several key themes emerged. Although many stated that knowing who comes onto the property is very important to protecting the health of the animals, keeping a record was not viewed as necessary. Service providers, such as the veterinarian or AI technician, who have regular contact with animals were trusted to practice effective sanitation of boots and equipment between farms. Farmers generally trusted that no one would go out of their way to intentionally harm the animals, and believed there was not much they could do to prevent an intentional biological attack. Another farmer noted that humans are not the only vectors for disease, and, since keeping birds and rodents away is nearly impossible, if neighboring farms became infected with a highly contagious disease, it would be hard to avoid even if stringent biosecurity measures were followed. Many farming operations have a fairly lax visitor policy because they want to be open to visitors. Many farmers seemed to think that if a visitor policy involving booties, boot washing, and little contact with animals was put in place and enforced, then recording visitors would not be necessary. Recording visitors by hand seemed unnecessary for small farmers who knew most of the visitors that came to the farm personally and impractical for larger farms with deliveries and visitors around the clock. Video surveillance as an option was generally well-received if the cost was not borne by the farmer. Themes identified in these qualitative interviews can form the basis of quantitative surveys to more accurately evaluate the extent to which various perceptions are held by dairy farmers. Such data can assist the development of a social marketing strategy to promote access control on dairy farms.

Key Words: dairy, biosecurity, access control

556 Profit in practice: Understanding the role of human resource management in dairy farm efficiency. J. E. Johnson*, N. Popp, and G. J. Lascano, *California Polytechnic State University, San Luis Obispo.*

The effect of employee selection, assessment, training, rewards and retention is not well understood on California dairy farms (F). A qualitative approach was utilized to address 3 objectives: (1) determine the frequency of Human Resource Management (HRM) policies and practices, (2) identify and categorize effective managerial behaviors, and (3) suggest strategies for finding and educating current and future dairy managers. Eight F were selected based on size (>1000 milking cows) and accessibility (willing to be interviewed) to participate in semi-structured interviews. Dairy owners discussed the history, structure, HRM practices, and perceived effectiveness of HRM practices on their dairies. Participating dairies had 1000–4350 milking cows and 10–90 full time employees. Qualitative codes were identified and defined to allow for analysis of the 3 objectives. Frequency and effectiveness varied considerably. Although all F utilized employment applications, only 25% considered them effective. Alternatively, employee referrals were perceived as highly effective. Employee training was also undertaken in all F, but only 50% considered this practice effective. Although farm-level productivity was evaluated in all cases, individual employee performance was evaluated in only 25%. Extrinsic motivation (pay, bonuses) was used twice as often as intrinsic motivation (empowering employees, offering praise) despite the greater financial cost. Implementation of exemplary HRM strategies included a hiring and 90 d orientation process; regular training offered to all employees to understand dairy SOPs; and a bonus incentive program for individual performance. Key managerial characteristics identified were bilingualism (100%), combining agricultural skills with education (100%), taking initiative (75%), and interpersonal skills (63%). Finally, suggestions for meeting personnel needs on F going forward included offering managerial, technology and language training to students in agricultural programs, utilizing practical examples to

facilitate transfer of training, and offering related extension seminars for those already working on farms.

Key Words: dairy farm, human resources, management

557 Tools to exploit sequence data to find new markers and disease loci in dairy cattle. D. M. Bickhart*[1], H. A. Lewin[2,3], and G. E. Liu[4], [1]*United States Department of Agriculture, Agricultural Research Service, Animal Improvement Programs Laboratory, Beltville, MD,* [2]*Department of Evolutoin and Ecology, University of California, Davis,* [3]*Institute for Genomic Biology, University of Illinois at Urbana-Champaign, Urbana,* [4]*United States Department of Agriculture, Agricultural Research Service, Bovine Functional Genomics Laboratory, Beltsville, MD.*

The decrease in cost of next-generation sequencing has brought the technology into the realm of practical applications in livestock genomics. Recently, the 1000 Bulls Project has heralded the possibility of using full sequence data to improve imputation and detect disease loci within select founder bulls. Sadly, informatics tools designed to utilize such data have not yet reached maturity, as many currently available programs are hard-coded to call variants only in human subjects or take an inordinate amount of time for analysis. With these challenges and prospects in mind, we have developed a comprehensive variant detection pipeline that uses a variety of information derived from sequence data to call SNP, INDEL and structural variants within the genomes of individuals. The pipeline is designed to be fully automated, is capable of being restarted in the case of errors and can be run on different computing architectures. We have run our pipeline on sequence data derived from a famous Holstein bull. Despite having 87 gigabases (30× coverage of the genome) of sequence for this bull, our pipeline took only 48 h to fully analyze the data using 20 processor cores and less than 32 gigabytes of ram. Initial filtering of this data has revealed one million candidate SNP and 759 copy number variants (CNV). An annotation program incorporated into the pipeline has also revealed putative functional effects of these variants and has identified more than 17,000 non-synonymous SNP that could alter protein function in this individual. The pipeline provides an efficient and freely available tool for researchers to process cattle genomic sequence data to detect genetic variants for use in the dairy industry.

Key Words: SNP, sequencing, genomics

558 In situ evaluation of NDF digestion in a large-scale biogas power plant. A. Palmonari*, M. Fustini, G. Canestrari, N. Panciroli, and A. Formigoni, *DSMVET, University of Bologna, Bologna, Italy.*

Optimization of renewable sources is a key point for the modern energy production systems. One of these energy sources, are biogas power plants (BPP). Inside the reactors, cellulosic substrates are fermented by bacteria and fungi to produce methane, which is then burned and converted to electric energy. Since the main BPP methanogenic bacterial species were identified, substrates characterization takes place in small – scale laboratory fermenters, not completely representative of the whole BPP system. An accurate substrate analysis is extremely required to estimate the amount of methane that can be produced. Objective of this study, was to set up and test a potentially useful system to evaluate the fiber (NDF) digestion dynamics directly inside the BPP. Adapting the procedure of ruminal in situ fermentations, 48 samples (8 corn silages, 8 alfalfa hay, 8 grass hay, 8 sorghum, 4 straw, 4 corn stover, 4 soybean hulls and 4 triticale) were placed inside the BPP and collected after several digestion time points (5, 10 and 20 d). Using acid insoluble ashes as internal markers, NDF digestibility was evaluated. We observed an extremely slow process: in 5 d, NDF digestibility was 32.8 ± 3.1% in corn silage, 31.6 ± 2.5% for alfalfa hay, 22.4 ± 1.2% straw, 20.5 ± 0.8% corn stover, 33.3 ± 5.8% soybean hulls, 31.2 ± 4.6% sorghum, 24.3 ± 1.2% triticale. After 20 d NDF digestibility reached higher values: 64.7 ± 4.2%, 57.9 ± 3.6%, 54.7 ± 3.8%, 47.2 ± 2.7%, 49.7 ± 1.7%, 82.8 ± 4.1%, 63.8 ± 3.8%, 59.1 ± 5.3% for corn silage, alfalfa hay, grass hay, straw, corn stover, soybean hulls, sorghum and triticale, respectively. In conclusion, BPP, due to their microflora, are able to digest cellulose to produce substrates required for methane synthesis; however, this process is particularly slow. These data suggest that the novel system is useful to nutritionally characterize several feeds, and moreover, that further analysis could be done to investigate the BPP major digestion dynamics.

Key Words: biogas power plant, biogas fistula, NDF digestibility

559 Dairy cow handling facilities and the perception of beef quality assurance on Colorado dairies. A. E. Adams*, I. N. Roman-Muniz, T. Grandin, D. R. Woerner, and F. J. Olea-Popelka, *Colorado State University, Fort Collins.*

A survey was conducted on Colorado dairies to assess attitudes and practices regarding dairy beef quality assurance (BQA). The objectives were (1) to assess the need for a new handling facility that would allow all injections to be administered via dairy BQA standards; (2) to establish if Colorado dairy producers are concerned with dairy BQA; and (3) to assess the differences in responses between dairy owners and herds-personnel. Of the 95 dairies contacted, 20 (21%) agreed to participate, with a median herd size of 1178. When asked to rank in order of importance 7 traits when designing a new handling facility (efficiency, animal safety, human safety, ease of animal handling, ease of operation, inject per BQA, and cost), 70% ranked human safety as first or second in priority (35% each) and 55% ranked animal safety as first or second (20 and 35% respectively), while being able to administer injections per BQA standards ranked second-to-last or last for 75% of producers (35 and 40% respectively). Respondents estimated the average annual income from the sale of cull cows to be 4.6% of all dairy income, with 50% receiving at least one carcass discount or condemnation in the past 12 mo Ninety-five percent of owners and 93% of herds-personnel stated the preferred location for SC injections was the neck region, with 53 and 50% respectively stating that all SC injections were always administered in that location. Similarly, 79% of owners and 73% of herds-personnel stated the preferred location of all IM injections was the neck region, with 20 and 25% respectively stating that the neck region was used for all IM injections. Results suggest the need for a handling facility that allows for the safe and efficient administration of all drugs according to dairy BQA guidelines. In addition to improved handling facilities, the need for educational opportunities that highlight the impact of improved dairy BQA on profitability and consumer confidence exist. Just as dairy producers are committed to producing safe and nutritious milk, they should be committed to producing the best quality meat as well.

Key Words: dairy beef quality assurance, dairy cow, dairy handling facilities

560 Physico-chemical characterization of casein micelles cross-linked by genipin. N. Nogueira Silva[1], A. F. de Carvalho[2], M. Piot[1], and F. Gaucheron*[1], [1]*INRA UMR STLO, Agrocampus-Ouest, Rennes, France,* [2]*University of Vicosa, Minas Gerais, Brazil.*

The creation of new structures-functionalities of casein micelles is a challenge for the dairy sector. In this context, the new physico-chemical properties of casein micelles (CM) were evaluated after their reactions with genipin (5, 10 and 25 m*M*) in buffer solution (25 m*M* HEPES and 2 m*M* $CaCl_2$, pH 7.15) at 50°C during 24 h. The reaction was spectroscopically monitored between 190 and 900 nm. The reacted products were evaluated by reversed-phase liquid chromatography (RP-LC) and electrophoresis. The reaction level was estimated by the measurement of the available lysine and arginine. The consequences of the reaction on the physico-chemical characteristics of CM were investigated by measuring their zeta potentials, size, hydrations, viscosity, and surface tension. The reaction between genipin and casein molecules was characterized by formation of blue pigmented products, presenting a maximum absorption at 600 nm. The RP-LC profiles showed that above 5 mM of genipin, individual casein molecules were not separated. Electrophoresis revealed that casein molecules formed polymers with molecular weights greater than 200 kDa. Lysine was mainly involved in cross-linking, with a minor participation of arginine. By comparing to control sample, the % reduction in the concentrations of lysine and arginine reached 95 and 12%, respectively, for 25 m*M* of genipin added. The zeta potential and hydration values of CM were gradually reduced, indicating changes in their surface properties. The size distribution did not revealed major changes regarding the diameter of the CM. Internal cross-linking was confirmed by submitting the CM to dissociation conditions. Regarding the viscosity, all the samples behaved as Newtonian fluids, nevertheless the values decreased progressively according to cross-linking intensity. Contrarily, the final values of surface tension as well as the adsorption rates at air/water interfaces increased gradually. Thanks to this new reagent, it was possible to create originally modified CM. Further researches are necessary to elucidate the modifications in their internal structure and the consequences in their functional properties.

Key Words: casein micelle, genipin, structure

561 Destabilization of UHT milk induced by different strains of *Pseudomonas fluorescens*: Role of AprX protease. F. Bagliniere[1], G. Tanguy[1], A. Mateos[2], J. Jardin[1], F. Rousseau[1], B. Robert[1], G. Humbert[2], A. Dary[2], J. L. Gaillard[3], C. Amiel[3], and F. Gaucheron*[1], [1]*INRA 1253 UMR STLO, Agrocampus-Ouest, Rennes, France,* [2]*URAFPA, University of Nancy, Nancy, France,* [3]*ERPCB, University of Caen, Caen, France.*

Destabilization of UHT milk (gelation or sedimentation) due to the proteolysis of casein micelles can be observed. In this context, the objectives of this work were to (1) Appreciate the variability of this destabilization with 9 strains of *Pseudomonas fluorescens*; and (2) Understand the physico-chemical modifications of casein micelles induced by these strains and also by AprX, an extracellular protease produced by one of these strains (*Pseudomonas fluorescens* F). Before UHT treatment, raw milk was inoculated either by different strains of *Pseudomonas fluoresecens* or by the purified AprX protease at different concentrations. Milk destabilization was then determined at macroscopic, colloidal and molecular levels. For experiments testing the strain variability in their proteolytic activities, 5 on the 9 strains were highly destabilizing. For experiments with the purified AprX enzyme, destabilizations were also observed. In all these cases, instabilities were visual (presence of sediment) and increasing as a function of time (after several days or weeks depending on the strains and the concentrations of added enzyme). The analyses of the destabilized UHT milks revealed the presence of aggregates. The zeta potentials and hydrations of casein micelles decreased. At molecular level, we noticed a significant proteolysis. The determination of one part of the released peptides, by liquid chromatography coupled to mass spectrometry, indicated that the α_{S1}-, α_{S2}-, β- and κ-caseins were hydrolyzed with a quantitative preference for β-casein. The nature of the different peptides released was similar for all destabilized UHT milks. The decrease in the stability of casein micelles will be discussed in relation with the modifications of structure and the observed proteolysis. Potential application of this research in term of detection of unstable UHT milks will be proposed knowing that this enzyme is heat-resistant and its implication in the destabilization of UHT milk during its storage is often evoked.

Key Words: casein micelles, UHT, *Pseudomonas*

562 Effect of adding chelators during skim milk powder manufacturing on the physico-chemical properties. V. Sikand*[1], P. Tong[1], S. Vink[1], A. Zeng[1], K. Sikand[1], and S. Roy[2], [1]*Dairy Products Technology Center, California Polytechnic State University, San Luis Obispo,* [2]*Statistics Department, California Polytechnic State University, San Luis Obispo.*

Functional properties of skim milk powders (SMP) can be tailored by processing treatments before spray drying. The objective of this study was to determine the effect of chelator addition during SMP manufacture on reconstituted SMP's solubility, opacity and heat stability (HS). This study was conducted by adding 5, 15 and 25 m*M* sodium citrate dihydrate (SCD), sodium polyphosphate (SPP) and disodium EDTA (DSE) respectively to skim milk concentrate and adjusting its pH to 6.65 before spray drying. Samples were tested for solubility index (SI) and reconstituted to contain 9% total solids and tested for opacity using a colorimeter. Heat stability was determined by measuring the heat coagulation time (time for visible flocculation at 140°C). Samples were adjusted to pH 7.0 with either 0.1 *N* NaOH or 0.1 *N* HCl for HS measurements. Lower values for SI were observed for samples with 5 m*M* SPP and DSE (0.13 mL) as compared with control samples or samples with 5 m*M* SCD (0.3mL). Furthermore, lower SI values were observed with an increasing level of chelating agents regardless of chelator type. A decreased opacity (L* value) or an increase in the lightness of samples was found with increasing levels of mineral chelating salt treatment ($P < 0.001$) and may be associated with dissociation of caseins from micelles. The extent of increased lightness was dependent on concentration and type of chelator. Heat stability studies showed that SMP samples (pH 7.0) treated with 5 m*M* DSE or 5 m*M* SCD had higher HS (>30 min) than HS of 5 m*M* SPP samples (16 min) and HS of control samples (10 min) ($P < 0.001$). Samples with 15 m*M* SPP showed significantly higher HS (20 min) as compared with samples with 15 m*M* SCD or 15 m*M* DSE (<7 min). Samples showed poor HS (<3 min) regardless of chelator type at 25mM chelator usage level.

Key Words: SMP, chelator, solubility

563 Effect of succinylation of skim milk on its plasmin-induced hydrolysis. H. Bhatt*[2,1], A. Cucheval[1], C. Coker[1], H. Patel[3], A. Carr[2], and R. Bennett[2], [1]*Fonterra Research & Development Centre, Palmerston North, Manawatu, New Zealand,* [2]*Institute of Food, Nutrition and Human Health, Massey University, Palmerston North, Manawatu, New Zealand,* [3]*Dairy Science Department, South Dakota State University, Brookings.*

One of the biggest causes of a reduction in the shelf life of dairy products, e.g., through proteolysis, gelation, and bitterness, is the presence of plasmin and its heat stability. It is therefore crucial to control the activity of plasmin in dairy products. Several approaches have been investigated in pure casein system; the present work explores the use of succinylation for the inhibition of plasmin-induced hydrolysis in a skim milk (miceller) system. Protein modification was achieved by attaching a succinate group at the ε-amino group of lysine residues, leading to the formation of succinyl-lysine. The target sites were identified using liquid chromatography-tandem mass spectrometry. The effects of different levels of succinylation on the particle size in skim milk and on the dissociation of casein from the casein micelles were determined using a Zetasizer and sodium dodecyl sulfate PAGE, respectively. The subsequent plasmin hydrolysis was monitored by quantifying the hydrolyzed product using reverse-phase high performance liquid chromatography. Although succinylation had an inhibitory effect on plasmin-induced hydrolysis, similar to that in a pure β-casein system, the trend was not linear. The non-linearity was explained by 2 competing effects. (1) Dissociation of β-casein from the casein micelle resulted in an increase in the micelle size, extensive unfolding, and expansion of the polypeptide chain on succinylation, which collectively reduced steric hindrance and made the protein more readily hydrolyzed by plasmin. (2) The formation of succinyl-lysine rendered β-casein unrecognizable to the substrate-binding pocket of plasmin, as observed for the pure β-casein system. The latter effect dominated the overall behavior and ultimately resulted in a decrease in the rate of hydrolysis with an increase in the level of succinylation. These results indicated the importance of miceller structure and it is possible to control plasmin-induced hydrolysis of milk proteins by succinylation. The present work can be useful in developing food grade approach i.e lactosylation, to control plasmin-induced hydrolysis.

Key Words: plasmin, succinylation, skim milk

564 Antioxidative activity and resilience of Cheddar and Edam whey as determined from total radical trapping potentials (TRAP). Z. Z. Haque*, D. Mukherjee, S. Mukherjee, and S. Chang, *Mississippi State University, Mississippi State.*

Both Cheddar and Edam whey (CW and EW, respectively) possess remarkable antioxidant properties, and thus can potentially be used as components of edible coating films for preserving a variety of food items from oxidative degradation. In the current study, we have investigated the antioxidative activity and persistence of EW and CW based on total radical trapping potentials (TRAP), with an objective of identifying the one with better suitability to be used for preservative purposes. We hypothesize that these 2 types of sweet whey differ considerably regarding their TRAP efficiencies based on differences in processing conditions and reported peptide content. Hydroxyl radicals generated in vitro by pyrolysis of ABAP (2,2′-Azobis[2-methylpropionamidine] dihydrochloride) and unquenched radicals detected by chemiluminescence of luminal was used to determine the TRAP of the whey samples (0.25, 0.5, 1, 2 and 3%, w/v). When generation of the hydroxyl radicals as indicated by the lack of chemiluminescence of control, a second luminescence curve was initiated by reinduction of pyrolysis of ABAP. The luminescence of the test samples at the time point of luminescence maximum of the control ($Lu_{Max}C$) was ascertained to derive of the luminescence at maximum free radical generation (Lu_{MaxFR}). This was done for both the initial (Ini) and final (fin) reactions. The difference between ${}_{Ini}Lu_{MaxFR}$ and ${}_{Fin}Lu_{MaxFR}$ gave the resilience whereas ${}_{Ini}Lu_{MaxFR}$ by itself gave the antioxidative activity of the test sample. The ${}_{Fin}Lu_{max}C$ of EW was observed at 16:30 min in the second reaction and found to be 1279.2 RLU (relative light unit), whereas those of the samples at various concentrations were 182.1, 173.8, 114.4, 86.9 and 84.8 RLUs, respectively. For CW, ${}_{Fin}Lu_{Max}C$ was recorded at 19:30 min and noted to be 1140.3 RLU, whereas ${}_{Fin}Lu_{Max}$ of the different samples were 654.4, 288.9, 235.5, 118.9 and 95.2 RLUs, respectively.The study exhibits the markedly enhanced antioxidative efficacy of EW both in terms of activity and resilience. It is also showed that both EW and CW show a dose-dependent increase in TRAP efficiency.

Key Words: chemiluminescence, free radical, antioxidant.

565 Effect of detergents on the antioxidative efficacy of sweet whey. Z. Z. Haque*, D. Mukherjee, and S. Chang, *Mississippi State University, Mississippi State.*

This study was conducted as part of an investigation to understand the molecular basis for the antioxidative efficacy of similar sweet wheys, Cheddar and Edam whey (CW and EW, respectively). The hypothesis was that the reportedly higher process induced peptide content of CW than EW would make it behave differently. Whey samples (1, w/v) in combination with various concentrations (nil, 0.01, 0.02, 0.05 and 0.1%, w/v). Non-ionic detergent Triton X-100 (TX100) was subjected to hydroxyl radicals generated in vitro by pyrolysis of 2,2′-Azobis(2-methylpropionamidine) dihydrochloride (ABAP). Radicals, that were not quenched by the test samples, were detected by chemiluminescence of luminal. When generation of the hydroxyl radicals had ceased, as evidenced by the lack of bioluminescence of the control, a second luminescence curve was generated by reinduction of pyrolysis of another doze of ABAP. The luminescenceluminescence of the test samples at the time point of luminescence maximum of the control ($Lu_{Max}C$) was ascertained recorded to derive of the luminescence at maximum free radical generation (Lu_{MaxFR}) at . This was done for both the initial (Ini) and second final (Fin) ABAP induced reactions. The difference between ${}_{Ini}Lu_{MaxFR}$ and ${}_{Fin}Lu_{MaxFR}$ gave the resilience whereas ${}_{Ini}Lu_{MaxFR}$ by itself gave the antioxidative activity of the test samples. The IniLuMaxC in case of CW of 746.2 relative light unit (RLU) was observed at 25:30 min. The neutral detergent TX100 had a significantly detrimental effect at all concentrations of CW studied both in terms of antioxidative activity and resilience. However, in case of EW, this trend was reversed and all TX100 containing samples showed better antioxidative activity and resilience. This study shows that detergents induced change in association tendency affected antioxidative efficacy of whey differently depending on the type of whey.

Key Words: antioxidative acitivity, antioxidative resilience, Edam whey

Graduate Student Symposium: How to Communicate Science Successfully Using Media Outlets

566 Proper media preparation and how to successfully sell your science to the public. M. E. McCurry-Schmidt*, *American Society of Animal Science, Champaign, IL.*

The objective of this presentation is to teach graduate students the skills to effectively present animal science and agricultural issues to the media. Scientists and producers see misrepresentations of agricultural production in blog items, news articles and across social media. Misconceptions about animal production have led to non-science-based policy decisions at the state and federal levels. To effectively reach the public, animal scientists must be prepared to speak with the media. Scientists must translate their research into "lay" terms and prepare speaking points before giving interviews. Scientists can offer lab tours and multimedia resources to show how science affects the public. Scientists should also ask reporters questions to make sure their science will not be misreported. With the right preparation, scientists can serve as valuable resources for the media, the public and policy makers.

Key Words: media, communications, outreach

567 Communicate by better listening. R. F. Roberts*, *The Pennsylvania State University, University Park.*

Communication is about exchanging thoughts and ideas and involves the activities of both transmitting and receiving. A focus on your message allows you to tell your story, that is, to "transmit" effectively. But this is only half of the process. Listening, the "receiving" portion of communication is equally as important. Listening requires focus and energy. One of the most difficult parts of really listening is laying aside potential distractions; that is, the smartphone or the computer screen. Nothing tells someone you aren't listening faster than a glance at the screen! Another common issues leading to a "failure to communicate" occurs when both parties are trying to "transmit" at the same time. This occurs when we want to show how smart we are by having a ready answer to every question that is asked (or we think will be asked) or a quick question to prove we are engaged. The result of this behavior is that rather than listening to what is being said, we are in the process of formulating our response, or preparing our question. The end result of this is that we may end up "directing" the conversation down the path we want to go, rather than the path the "transmitter" intended. By focusing more on what is being said, we will foster much deeper communication. Techniques that can be used to enhance communication will be discussed during this presentation.

Key Words: listening, communication

568 Know your story and how to tell it. K. A. Devaney*, *Dairy Farmers of America, Mooresville, NC.*

The average American is 3 to 4 generations removed from the farm and less than 2 percent are involved in agriculture. As consumers become more interested in how their food is produced, the dairy industry needs to tell the story of sustainable and responsible dairy farming. Regardless of one's role in the industry, everyone can be an effective dairy advocate. Participants will learn how to communicate science so that it is clear to any audience, how to speak with one voice as an industry, use various media interview techniques and several ways to reach out to the community on behalf of the dairy industry. Communicating research is extremely important but can be difficult with complex topics. These tips will take the mystery out of communicating clear, concise messages that will resonate with any audience.

Key Words: dairy advocate, communication

569 Growth hormone stimulates liver growth by increasing the size of hepatocytes. D. Jia* and H. Jiang, *Virginia Polytechnic Institute and State University, Blacksburg.*

High levels of growth hormone (GH) are known to cause a disproportional increase in liver weight relative to body weight. The mechanism by which GH stimulates liver growth is not clear. In this study, we determined whether GH stimulates liver growth by increasing the number or the size of hepatocytes. We conducted the study in the lit/lit mouse model. The lit/lit mice lack normal GH production because of a mutation in the growth hormone releasing hormone receptor gene. Lit/lit male mice (n = 6), 12–13 weeks of age, were injected (s.c.) daily with 1 mg/g body weight of recombinant bovine GH or an equal volume of vehicle (0.01 *M* $NaHCO_3$) for 2 weeks. Heterozygous (lit/+) male littermates (n = 6) injected with an equal volume of vehicle (0.01 *M* $NaHCO_3$) were used as normal GH controls. Two hours before euthanasia, mice were injected (i.p.) with 5-bromo-2'-deoxyuridine (BrdU) to label the proliferating cells. Both lit/+ mice injected with $NaHCO_3$ and lit/lit mice injected with GH had greater body weight gains ($P < 0.05$) and greater liver weight/body weight percentages ($P < 0.05$) than lit/lit mice injected with $NaHCO_3$. Based on immunohistochemistry, percentages of BrdU-stained hepatocytes were not different between the 3 groups of mice ($P > 0.10$). However, lit/+ mice injected with $NaHCO_3$ and lit/lit mice injected with GH had 30% and 16% less cells per unit liver area than lit/lit mice injected with $NaHCO_3$ ($P < 0.05$), respectively. Hepatocytes in lit/+ mice injected with $NaHCO_3$ and lit/lit mice injected with GH were 43% and 18% larger than those in lit/lit mice injected with $NaHCO_3$ ($P < 0.05$), respectively. Taken together, these data suggest that GH stimulates liver growth not by increasing the number but by increasing the size of hepatocytes.

Key Words: growth hormone, liver, hepatocyte

570 Insulin and insulin-like growth factor-I (IGF-I) receptor phosphorylation in μ-calpain knockout mice. W. Oliver*[1], A. Chishti[2], and C. Kemp[1], [1]*USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE,* [2]*Tufts University, Boston, MA.*

Numerous cellular processes are controlled by insulin and IGF-I signaling pathways. Due to previous work in our laboratories, we hypothesized that insulin (IR) and type 1 IGF-I (IGF-IR) receptor signaling is decreased due to increased protein tyrosine phosphatase 1B (PTP1B) activity. C57BL/6J mice heterozygous for the μ-calpain deletion were bred and aged-matched control (C) and μ-calpain knockout (KO) mice were killed at 3, 5, and 10 wk of age (n = 48; 24 females and males per age group). Mice studied at 5 and 10 wk were weaned at 21 d of age, housed individually, and given free access to food and water. Mice were killed via cervical dislocation while fasted or allowed to re-feed for one h before sample collection. Trunk blood was collected for insulin and glucose analysis and hind limb muscles were dissected, pooled, and snap frozen in liquid nitrogen. Skeletal muscle abundance of the IR, IGF-IR, and PTP1B and phosphorylation of the IR and IGF-IR were determined. Activity of PTP1B was also analyzed. Feeding increased insulin levels ($P < 0.01$) and the increase was greater at 10 wk of age compared with 3 and 5 wk of age ($P < 0.03$), regardless of sex and genotype. Serum glucose was unchanged by age ($P > 0.43$), but was higher in males compared with females ($P < 0.05$). Glucose was greater in fed compared with fasted mice at 5 and 10 wk of age ($P < 0.001$), but not at 3 wk of age ($P > 0.62$). At 10 wk of age, the feeding-induced increase in glucose was greater in KO compared with C mice ($P < 0.01$). Total IR and IGF-IR was unaffected by genotype, age, sex, or fed status ($P > 0.49$). The phosphorylation of the IR and IGF-IR was unaffected ($P > 0.33$) by age or sex, but feeding increased ($P < 0.01$) phosphorylation of both receptors. IGF-IR phosphorylation was unaffected by genotype ($P > 0.18$). However, IR phosphorylation was decreased in KO mice ($P < 0.01$). In addition, the protein abundance ($P < 0.04$) and activity ($P < 0.01$) of PTP1B was increased in KO mice. These data indicate that μ-calpain regulates phosphorylation of the IR through changes in the activity of PTP1B, which may have implications in glucose metabolism.

Key Words: μ-calpain, insulin receptor, protein tyrosine phosphatase 1B

571 Ractopamine hydrochloride and estradiol/trenbolone acetate implants alter live performance and carcass components of heifers during the finishing phase. M. A. Jennings*[1], T. R. Young[1], J. T. Cribbs[1], B. C. Bernhard[1], A. D. Hosford[1], T. L. Harris[1], M. J. Anderson[1], G. J. Vogel[2], J. A. Scanga[2], M. F. Miller[1], and B. J. Johnson[1], [1]*Texas Tech University, Lubbock,* [2]*Elanco Animal Health, Greenfield, IN.*

Objectives were to evaluate the interaction of ractopamine hydrochloride (Optaflexx, RH) and timing of terminal implant administration on growth performance, carcass characteristics, and meat quality of finishing heifers. A 2 × 3 factorial complete block design was used with 2 levels of RH and 3 terminal implant windows. British x Continental heifers (n = 216; initial BW = 341.6 kg) were blocked by BW and randomly allotted to 54 pens (9 pens/treatment; 6 pens/block; 4 heifers/pen). Main effects were time of implant [TE-200 with Tylan® (200 mg TBA + 24 mg E_2) administered 140 d from slaughter (TI140); 100 d (TI100); or 60 d (TI60)] and RH (0 or 200 $mghd^{-1}d^{-1}$). Individual BW and DMI were collected at 0, 40, 80, 112, and 140 d. No interactions ($P > 0.10$) between main effects were detected. Average daily gain (0.14 kg/d), predicted carcass ADG (0.24 kg/d), HCW (5.6 kg) were increased ($P < 0.05$) by RH, but DMI was unchanged ($P > 0.10$). Heifers fed RH tended ($P \leq 0.09$) to have a larger LM area (2.45 cm^2 difference) and reduced marbling score. Prime and Choice carcasses were decreased ($P < 0.05$) by 16.5% with RH supplementation. No affect of RH was found on 12th-rib fat and KPH ($P > 0.10$). No differences ($P > 0.10$) in Warner-Bratzler shear force (WBS) were detected at 3, 7, and 21 d aging postmortem however WBS values of RH steaks at 14 d were higher (0.45 kg; $P < 0.05$). From 0 to 40 d, ADG of TI140 (0.34 kg/d) and TI100 (0.18 kg/d) groups was increased ($P < 0.05$) compared with TI60. From 40 to 80 d, TI100 had a greater ADG ($P < 0.05$) than all implant groups. The TI60 had a higher ADG ($P < 0.05$) than TI100 and TI140 from 80 to 112 d. Predicted carcass ADG mirrored live ADG advantages ($P < 0.05$). No differences ($P > 0.10$) in DMI, final BW, carcass characteristics, or WBS values across all aging periods were observed among implant strategies. Results from this study demonstrated that heifers fed RH had increased ADG, carcass ADG, and HCW. Also, this study indicated the terminal implant window, before RH feeding, did not affect performance or carcass quality.

Key Words: anabolic steroid, beef cattle, β-agonist

572 The use of terminal implants and β-agonists to alter blood components and myogenic mRNA and protein levels. T. L. Harris*[1], A. D. Hosford[1], M. A. Jennings[1], M. J. Anderson[1], G. J. Vogel[2], and

B. J. Johnson[1], [1]*Department of Animal and Food Sciences, Texas Tech University, Lubbock,* [2]*Elanco Animal Health, Greenfield, IN.*

Two commonly used growth promotants in the beef industry are β-agonists and anabolic steroid hormones. Each has been shown to increase lean muscle deposition in cattle, but much is unknown on how steroid implants and β-agonists work in combination. We provided a terminal implant [TE-200 with Tylan (200 mg TBA + 24 mg E_2)] to heifers at 140 d (TI140), 100 d (TI100), or 60 d (TI60) from slaughter in a 140 d trial (TI100 and TI60 animals were also implanted on 0 d with Component TE-IH). Cattle were then treated with ractopamine hydrochloride (Optaflexx RH) the final 28 d of the trial. Heifers either received 0 mg/head/d RH or 200 mg/head/d of RH. Five animals/treatment were subjected to longissimus muscle (LM) biopsies on 0, 40, 80, 112 d and at slaughter on 140 d, and were used to isolate mRNA of myogenic related genes and protein quantification of the β_1-adrenergic receptor (β1 AR) and β_2-adrenergic receptor (β2 AR). On the same days, blood samples were taken from 18 animals/treatment to assess changes in plasma blood urea nitrogen (BUN), nonesterified fatty acids (NEFA) and progesterone due to treatments. Relative mRNA levels of myosin heavy chain (MHC) IIX, AMPKα, and IGF-I were increased ($P < 0.05$) in animals receiving TI100 over the other 2 implant dates after RH was fed to animals. After RH administration MHC IIA mRNA levels tended to decrease ($P = 0.09$) due to RH. An interaction between TI d and RH administration caused an increase ($P < 0.05$) in MHC IIA mRNA level in the TI60/RH treatment group over all other treatments except the TI100/no RH treatment group. Protein intensity of the β2 AR was decreased ($P < 0.05$) by the latest TI d (TI60) during RH feeding, while β1 AR protein intensity tended to be lower ($P < 0.10$) in animals fed RH. Plasma urea nitrogen levels were reduced ($P < 0.05$) after terminal implants and RH feeding, while progesterone was decreased ($P < 0.05$) by RH alone, and NEFA levels were unaffected. Treatments were shown to cause a biological response to muscle growth by showing a possible shift toward the more efficient MHC IIX, decreasing plasma urea nitrogen, and increasing β2 AR levels.

Key Words: β-agonist, implant, muscle growth

573 Transcriptional regulation of M. longissimus dorsi during nutritional restriction and compensatory growth in Aberdeen Angus × Holstein Friesian steers. S. M. Keady, A. G. Doran, C. J. Creevey, D. A. Kenny, and S. M. Waters*, *Teagasc, Animal and Bioscience Department, Grange, Dunsany, Co. Meath, Ireland.*

The objective of this study was to examine changes in muscle gene expression of growing steers during a period of dietary energy restriction followed by a period of realimentation. Crossbred Aberdeen Angus × Holstein Friesian (n = 24) steers were assigned to one of 2 feeding treatments. Over a 99-d period, 1 group (n = 12) was offered a high energy control diet consisting of concentrates ad libitum and 7 kg of grass silage per head daily. The second group (n = 12) was offered an energy restricted diet consisting of grass silage ad libitum plus 0.5 kg of concentrate per head daily. From the end of the differential feeding period (99 d), both groups of animals were offered a total mixed ration (grass silage:concentrate ratio of 80:20) for 200 d (viz, the realimentation period). Muscle biopsies were collected at 2 time points (end of the differential feeding period (d 99) and during the realimentation period (d131)). RNA was extracted and the muscle transcriptome was examined using RNaseq. Sequence reads were aligned to the Bovine genome. Differentially expressed genes and over-represented pathways were identified using the DESeq and GOseq respectively. During the differential feeding period, 17 over-represented pathways were identified including the peroxisome proliferator activated receptor signaling, glycolysis/gluconeogenesis and lipid/lipoprotein metabolism pathways indicating reduced energy intake and fat tissue accumulation occurring in muscle tissue during the restriction phase. During the realimentation period, 164 differentially expressed genes were annotated to 9 over-represented pathways including starch and sucrose metabolism, carbohydrate digestion and absorption and TGF-β signaling pathway. It is hypothesized that the signaling effects of the TGF-β pathway were reduced thereby promoting accelerated cell growth and proliferation in muscle tissue of animals experiencing compensatory growth. This information can be exploited in genomic breeding programmes to assist selection of cattle with a greater ability to compensate following a period dietary restriction.

Key Words: ‘ruminant nutrient, muscle, mRNA expression

574 Ruminal and adipose gene expression in beef steers selected for diverse feed intake and gain phenotypes. A. K. Lindholm-Perry*, L. A. Rempel, K. E. Hales, W. T. Oliver, H. C. Freetly, and L. A. Kuehn, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Limited information exists regarding genes responsible for phenotypic variation in feed efficiency. To determine whether cattle feed intake or growth phenotypes are related to transcript abundance of genes expressed in rumen and adipose, variation in 5 candidate genes from 2 seasons (fall and spring 2012) of steers (n = 32) with differential feed intake and gain phenotypes was examined. Gain and intake were plotted against each other within season and the 4 most extreme animals were selected from each of the 4 Cartesian quadrants relative to the mean of the 2 traits (ADFI: 6.8 to 17.3 kg/d; ADG: 1.0 to 2.4 kg/d). Transcript abundance of candidate genes fatty acid snythase (FASN), fat mass and obesity (FTO) and DNA protein kinase (DNA-PK) in subcutaneous adipose tissue collected near the tailhead and Rho-gamma (RHOG), and protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2) in the papillae collected from the cranial sac of the rumen was analyzed. Total RNA was extracted and transcribed into cDNA for use with quantitative real-time PCR. Raw data was normalized with a standard curve generated from a pooled sample from adipose tissue (FASN, FTO, DNA-PK) or was normalized against a housekeeping gene using a pooled sample from rumen tissue (RHOG, PRKAG2). Resulting data were analyzed by season for relationships between transcript level and gain or intake. Relative expression of FASN, FTO and DNA-PK was correlated with each other in adipose tissue (r = 0.63–0.83, $P \leq 0.002$), while rumen expression of RHOG and PRKAG2 was not correlated (r = 0.228, $P = 0.2$). Data were blocked by season to account for diet contribution of either dry rolled corn or high moisture corn. In fall animals on a dry rolled corn diet relative expression of PRKAG2 in the rumen and FTO in adipose was correlated ($P \leq 0.04$) with intake. In spring animals on a high moisture corn diet, RHOG in the rumen was correlated with intake ($P = 0.02$). Variation in response by season is likely due to a change in diet between season affecting rumen function and adipogenesis. USDA is an equal opportunity provider and employer.

Key Words: beef cattle, feed intake, gain

575 Identification of the SH3 and cysteine-rich domain 3 (STAC3) gene as a novel regulator of myogenesis in cattle. Y. Zhang*, X. Ge, D. E. Gerrard, and H. Jiang, *Virginia Polytechnic Institute and State University, Blacksburg.*

Myogenesis is the process of formation of myofibers from myoblasts. The objective of this study was to identify novel regulators of this

process in cattle. We searched the gene expression databases for genes preferentially expressed in skeletal muscle but without known functions. This search led to the identification of the SH3 and cysteine rich domain 3 (STAC3) gene. Through RT-PCR, we confirmed that STAC3 was exclusively expressed in skeletal muscle in adult cattle. We next determined the effect of STAC3 gene knockdown on the differentiation of bovine satellite cells into myotubes in culture. Bovine satellite cells were isolated from adult cattle skeletal muscle by Pronase digestion, expanded in medium containing 10% fetal bovine serum, and were then transfected with STAC3 small interfering RNA (siRNA) or scrambled siRNA. Immediately following the transfection, bovine satellite cells were induced to differentiate into myotubes in medium containing 2% horse serum. At d 3 of differentiation, the cells were stained with Giemsa and 4',6-diamidino-2-phenylindole (DAPI) to qualify fusion rates. In addition, total RNA and total protein were isolated to quantify gene expression. Analyzed by a real-time RT-PCR analysis, STAC3 siRNA caused a 92% reduction in STAC3 mRNA expression compared with scrambled siRNA in bovine satellite cells ($P < 0.01$). Analyzed by a Western blotting analysis, STAC3 siRNA caused a 76% reduction in STAC3 protein expression compared with scrambled siRNA ($P < 0.01$). Of those cells transfected with STAC3 siRNA, 57% formed myotubes, whereas 42% of those transfected with scrambled siRNA formed myotubes by d 3 of differentiation ($P < 0.01$). Furthermore, bovine satellite cells transfected with STAC3 siRNA had greater mRNA expression of myotube markers, myogenin, myosin heavy chain 3, and myosin heavy chain 7, compared with those transfected with scrambled siRNA ($P < 0.01$). These data together suggest that STAC3 is an inhibitory regulator of differentiation of bovine satellite cells.

Key Words: satellite cell, cattle, differentiation

576 Metabolomic profile of the small for gestational age piglet following arginine supplementation. C. M. Getty*, A. A. Baratta, and R. N. Dilger, *University of Illinois, Urbana.*

Large profit losses in the swine industry can be attributed to morbidity and mortality of piglets before weaning, especially in the small for gestational age (SGA) piglet (Sus scrofa). Recent evidence suggests sow's milk contains insufficient concentrations of arginine to support optimal growth and health of piglets. Thus, our objective was to assess global metabolomic profiles and the potential for arginine supplementation to promote growth of SGA (≤0.9kg body weight) and average for gestational age (AGA, 1.3–1.5 kg body weight) piglets. Piglets were selected in littermate pairs at processing to receive either L-arginine (Arg, n = 8) or an isonitrogenous control (L-alanine, Ala, n = 8), weighed daily to assess growth rate, and blood was collected at 15–17 d of age. Overall, differences ($P < 0.05$) were noted between treatments for metabolic pathways involving energy (i.e., TCA cycle), amino acids, nucleotides, and fatty acids. Interestingly, serotonin levels in SGA-Arg piglets were lower than in any other group, which may be explained by altered tryptophan metabolism as compared with the SGA-Ala piglets. Although fatty acid oxidation was higher in SGA piglets, Arg supplementation reduced phosphatidylcholine hydrolysis in the SGA-Arg piglet, which may indicate impaired cell membrane formation. Increased nucleotide turnover, indicating an increase in DNA damage and cell death, was also noted in the SGA piglet. However, Arg supplementation reduced these effects to levels comparable to the AGA piglet. Moreover, changes in glucose metabolism suggested the ability to extract energy from dietary sources may have been compromised in the SGA piglet, but partially rescued by Arg supplementation. In terms of growth, piglets dosed with Arg weighed 22.3% and 12.7% ($P = 0.0032$) less at d 16 compared with Ala-dosed piglets in both the SGA and AGA groups, respectively. We conclude that a reduction in the growth potential of SGA piglets is associated with alterations in multiple metabolic pathways, and further reduction due to Arg supplementation may have resulted from perturbations in phospholipid and tryptophan metabolism.

Key Words: arginine, intrauterine growth restriction, metabolite

Meat Science and Muscle Biology Symposium: Pre-Harvest Factors Affecting the Prevalence of Pathogens in Livestock and Meat

577 Diet, fecal microbiome and *Escherichia coli* O157:H7 shedding in beef cattle. J. Wells*[1], M. Kim[1], J. Bono[1], L. Kuehn[1], and A. Benson[2], [1]*USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE,* [2]*University of Nebraska, Lincoln.*

Shiga-toxigenic *Escherichia coli*, such as *E. coli* O157:H7, are foodborne zoonotic pathogens that can cause severe illness and death in humans. The gastrointestinal tract of ruminant animals has been identified as a primary habitat for *E. coli* O157:H7, and in cattle the terminal gastrointestinal tract appears to be a primary site for colonization. This pathogen has been found in cattle feces, on cattle hides, and in the production environment, and transmission to humans has occurred as a result of consumption of contaminated ground beef, water, and produce. Interventions to reduce the pathogen at beef harvest have significantly reduced the occurrence of the pathogen, but outbreaks and recalls due to the pathogen still occur for beef products. Interventions before harvest in the feedyard have had little success, but critical control points for implementing interventions are limited compared with the beef plant. The percentage of animals shedding *E. coli* O157:H7 in the feces can be highly variable from pen to pen, and the levels in the feces can vary from animal to animal. Animals colonized and shedding *E. coli* O157:H7 at high levels are a small fraction of animals in a pen, but are important source for transferring the pathogen among the penmates. Recent research has indicated that diet may greatly influence the shedding of *E. coli* O157:H7. In addition, diet can influence the microflora composition in the feces. However, little is known about the interaction between the indigenous microflora and fecal shedding of *E. coli* O157:H7. Understanding the influence of indigenous microflora on the colonization and shedding of *E. coli* O157:H7 will provide an avenue for intervention in the preharvest production environment not yet exploited.

Key Words: Shiga-toxigenic *E. coli*, pathogens, feces

578 Ecological and dietary impactors of foodborne pathogen prevalence and methods to reduce colonization in cattle. **T. R. Callaway*,** *Agricultural Research Service/USDA, College Station, TX.*

Foodborne pathogenic bacterial infections are a significant drain on the GDP of our nation. Cattle gastrointestinal tracts are colonized by a microbial ecosystem that can be considered as a "microbial organ," but too often this microbiome is penetrated and colonized by foodborne pathogens. While foodborne pathogenic bacteria populations are reduced by processing plant treatments, not all pathogens are eliminated from the food supply. Furthermore, humans can be exposed to foodborne pathogens in water supplies and by direct animal (or feces) contact, such as at petting zoos or open farms. Thus if the burden of pathogens found in food animals can be reduced, then human public health can be enhanced. As a result, researchers have begun examining methods to reduce these pathogens in live animals on the farm. Strategies range from simple management practice changes to the effects of diet on the microbiome and water management to the addition of exogenous treatments to specifically target pathogens. Many of the approaches attempt to harness the powerful microbial population to exclude pathogens, either through probiotics, DFM, prebiotics or bacteriophage treatment. Other exogenous treatments have been utilized as well, such as vaccination and sodium chlorate utilization that directly inhibit or eliminate pathogens. No matter what, pre-harvest strategies will not eliminate the need for good sanitation and procedures in the processing plant and during food preparation and consumer handling. Instead, live-animal management interventions must be implemented as part of a multiple-hurdle approach that complements the in-plant interventions, so that the reduction in pathogen entry to the food supply can be maximized. Furthermore, pathogen reduction strategy implementation comes at an economic cost, therefore pathogen reduction methods that can enhance production efficiency will be implemented in the industry most efficaciously.

Key Words: food safety, cattle, pathogen

814 See TH220

815 See TH227

579 Effects of 5.4 or 9.6% oil dried distillers grains with solubles on finishing pig growth performance and carcass characteristics. A. B. Graham*, R. D. Goodband, M. D. Tokach, J. M. DeRouchey, S. S. Dritz, and S. Nitikanchana, *Kansas State University, Manhattan.*

A total of 1198 pigs (PIC 337 × 1050, initially 46.1 kg) were used to determine the effects of 5.4 or 9.6% oil corn dried distillers grains with solubles (DDGS) in finishing diets on growth performance and carcass characteristics. Pigs were allotted to a corn-soybean meal–based control diet or diets with 20 or 40% 5.4% oil DDGS (29.53% CP, 8.90% ADF, and 21.75% NDF) or 9.6% oil DDGS (29.63% CP, 15.25% ADF, and 28.58% NDF). There were 26 or 27 pigs per pen and 9 replications per treatment. Data were analyzed using the PROC Mixed procedure of SAS as a 2 × 2 factorial plus control with main effects of DDGS source and level and their interactions. From d 0 to 82, ADG was unaffected by DDGS source or level. However, there was a DDGS source by level interaction ($P < 0.01$) observed for G:F. Increasing 5.4% oil DDGS linearly decreased ($P < 0.01$) G:F, whereas there was no change in G:F in pigs fed 9.6% oil DDGS. Two pigs per pen were slaughtered (n = 9) for IV analysis. The remaining pigs (n = 9) were slaughtered to calculate carcass yield (farm weight/plant weight) and HCW. Regardless of DDGS source, carcass yield and HCW decreased (linear, $P < 0.04$) with increasing DDGS. There was also a DDGS source by level interaction ($P < 0.01$) observed for jowl iodine value (IV). Increasing DDGS increased jowl IV, but the magnitude was greater in those fed the 9.6% oil DDGS compared with those fed 5.4% oil DDGS. In summary, the two DDGS sources used in this experiment resulted in similar ADG and reduction in carcass yield. However, pigs fed low oil DDGS also had reduced G:F relative to pigs fed the high oil diets.

Table 1.

	DDGS source and % of diet					
	Control	5.4% oil		9.6% oil		
Item	0	20	40	20	40	SEM
ADG, kg	1.03	1.04	1.02	1.03	1.03	0.10
G:F[1]	0.398	0.386	0.370	0.398	0.390	0.004
Final BW, kg	129.6	129.8	128.5	129.4	129.9	1.1
Carcass yield, %[2]	76.2	76.0	74.3	75.4	75.2	0.46
HCW, kg[2]	95.4	94.0	92.9	93.3	93.8	0.81
Jowl IV[1]	66.6	70.7	75.0	71.1	77.4	0.53

[1]DDGS source × level interaction, linear $P = 0.01$.
[2]DDGS linear, $P < 0.05$.

Key Words: corn, DDGS, pig

580 Effects of 9.4 or 12.1% oil dried distillers grains with solubles on finishing pig growth performance and carcass characteristics. A. B. Graham*, R. D. Goodband, M. D. Tokach, J. M. DeRouchey, S. S. Dritz, and S. Nitikanchana, *Kansas State University, Manhattan.*

A total of 270 pigs (PIC 327 × 1050, initially 46.5 kg) were used to determine the effects of 9.4 or 12.1% oil corn dried distillers grains with solubles (DDGS) on finishing pig growth performance and carcass characteristics. Pigs were allotted to a corn-soybean meal–based control diet or diets with 20 or 40% 9.4% oil DDGS (29.40% CP, 19.57% ADF, and 34.50% NDF, as-fed) or a 12.1% oil DDGS (28.53% CP, 17.57% ADF, and 31.38% NDF, as-fed). There were 8 pigs per pen and 7 replications per treatment. Diets were fed over 3 phases (47 to 73, 73 to 100, and 100 to 122 kg). Data were analyzed using the PROC Mixed procedure of SAS as a 2 × 2 factorial plus control with main effects of DDGS source and level and their interactions. From d 0 to 75, increasing 9.4% oil DDGS increased then decreased ADG but it was not different among pigs fed 12.1% oil DDGS (quadratic interaction, $P < 0.02$). Increasing DDGS tended (linear, $P < 0.07$) to decrease ADFI and increase G:F. All pigs were slaughtered (n = 7) on d 75 for calculation of carcass yield (farm weight/plant weight), HCW and jowl iodine value (IV). Regardless of source, increasing DDGS decreased (linear, $P < 0.05$) carcass yield and HCW. Increasing DDGS increased (linear, $P < 0.01$) jowl IV. In summary, increasing the two DDGS sources (9.4 and 12.1% oil) used in this experiment resulted in reduced carcass yield and HCW but increased jowl IV.

Table 1.

	DDGS source and % of diet					
	Control	9.4% oil		12.1% oil		
Item	0	20	40	20	40	SEM
ADG, kg[1]	1.01	1.05	.98	1.00	1.00	0.16
ADFI, kg[2]	2.85	2.81	2.68	2.76	2.73	0.05
G:F[2]	0.355	0.375	0.366	0.363	0.378	1.01
Final BW, kg	122.0	125.1	119.9	121.6	121.9	1.68
Carcass yield, %[3]	72.6	71.9	71.0	72.3	71.2	0.18
HCW, kg[3]	88.6	89.2	84.7	87.6	86.8	1.11
Jowl IV[3]	66.8	73.1	77.5	73.4	80.0	0.42

[1]DDGS source × level interaction, quadratic $P = 0.02$.
[2]Linear effect of DDGS, $P < 0.07$.
[3]Linear effect of DDGS, $P < 0.05$.

Key Words: corn, DDGS, pig

581 Effects of mix time on nutritional value of diets without and with inclusion of DDGS and wheat midds when fed to finishing pigs. M. E. Morts*, J. D. Hancock, K. L. Kohake, and J. D. McAtee, *Kansas State University, Manhattan.*

A total of 200 finishing pigs (avg initial BW of 76 kg) were used in a 54-d growth assay to determine the effects of mix time in diets without and with inclusion of cereal grain co-products. The pigs were sorted by sex and ancestry and assigned to pens (5 pigs/pen and 10 pens/treatment) in a completely randomized design. Treatments were arranged as a 2 × 2 factorial with main effects of mix time (60 and 420 s) and inclusion of cereal grain co-products (without and with 30% DDGS and 10% wheat middlings). All diets were formulated to be at least 120, 120, and 110% of requirements for essential amino acids, vitamins, and minerals, respectively, as suggested in the 2012 National Research Council guidelines for swine feeding. Feed and water were consumed on an ad libitum basis until the pigs were harvested (avg BW of 134 kg) at a commercial abattoir for collection of carcass data. As for results, there were no interactions among mix time and inclusion of cereal grain co-products ($P > 0.08$) for ADG, ADFI, G/F, hot carcass weight (HCW), dressing percentage (DP), or fat thickness at the last rib (BF). As for main effects, increasing mix time from 60 to 420 s did not affect measurements of growth performance or carcass value ($P > 0.43$). However, pigs fed diets with DDGS and wheat middlings had reduced ($P < 0.05$) ADG, HCW, DP, and BF compared with pigs fed the simple corn-soy diet. In conclusion, increasing mix time from 60 to 420 s did not change

the negative effects of DDGS and wheat middlings on rate of gain and carcass yield in finishing pigs.

Table 1. Results by diet and feed mix time

	Corn-Soy		DDGS-Midds		
	60 s	420 s	60 s	420 s	SE
ADG, g	1,011	1,014	966	954	17
ADFI, kg	3.41	3.49	3.52	3.33	0.14
G/F, g/kg	297	291	274	287	13
HCW, kg	100.4	100.8	97.6	97.7	3.8
DP, %	74.2	74.2	73.8	73.8	0.7
BF, mm	26.3	26.9	23.6	22.7	1.4

Key Words: mix time, DDGS, pig

582 Impact of dietary leucine levels on the optimal valine to lysine ratio in diets for 10 to 25 kg pigs. J. K. Htoo*[1], C. F. M. de Lange[2], and C. L. Zhu[2], [1]*Evonik Industries AG, Hanau, Germany,* [2]*University of Guelph, Guelph, Canada.*

Feeding diets containing excess Leu can reduce feed intake and performance of pigs, which is attributed to interactions with the other branch-chained AA, Ile and Val. The objective of this study was to test if dietary Leu levels affect the dietary Val requirements (Val:Lys ratio) to optimize growth performance of 10 to 25 kg pigs. A 3-wk study was conducted with 144 Yorkshire pigs (initial BW 10.4 ± 1.1 kg) with 6 pen replicates (2 barrows and 2 gilts per pen) per treatment according to a 2 × 3 factorial design with 2 levels of Leu (adequate and excess) and 3 levels of Val (slightly below, at or slightly above estimated requirement). Diets were formulated based on barley, wheat, soybean meal, corn gluten meal and using analyzed AA contents and published standardized ileal digestibility (SID) of AA in the protein containing ingredients to exceed requirements for other AA. Contents of SID Lys and Ile were similar across all diets at 1.13 and 0.68%. Diets 1 to 3 were formulated to contain 1.18% SID Leu (64, 68 and 72% SID Val:Lys) and L-Leu was added to diets 4 to 6 to contain 1.80% SID Leu (64, 68 and 72% SID Val:Lys). The corrected SID Val:Lys ratios in diets 1 to 6 based on the analyzed AA in the diets were 67, 72, 73, 66, 70 and 73%, respectively. Pigs had free access to pelleted feed and water. There were no interactive effects ($P > 0.10$) of dietary Leu and Val:Lys on growth performance. During wk 1, ADG (454 vs. 411 g/d for adequate vs. excess Leu,) and G:F (0.67 vs. 0.61 for adequate vs. excess Leu) were influenced ($P < 0.01$) by dietary Leu but not by the Val:Lys ratio ($P > 0.10$). Feed intake was not affected ($P > 0.10$) by treatment during wk 1, 2, 3 or wk 1–3. During wk 1–3, ADG was not affected by treatment (600, 577, 567, 562, 556 and 580 g/d for diets 1 to 6) while G:F was higher ($P < 0.05$) for pigs fed diets with adequate Leu vs. excess Leu (0.64 vs. 0.62), and there was a tendency ($P = 0.06$) toward a negative effect of increasing SID Val:Lys on G:F. These results suggest that the lowest Val:Lys ratio (67%) was optimal while dietary Leu did not affect the requirement for Val in 10 to 25 kg pigs.

Key Words: leucine, lysine, performance

583 Effects of graded corn cob levels on physicochemical properties of digesta and visceral organs in growing pigs. A. Wate*, S.P. Ndou, and M. Chimonyo, *University of KwaZulu-Natal, Pietermaritzburg, South Africa.*

The objective of the study was to investigate the effects of graded levels of corn cob (CC) meal incorporated in the diet on the physicochemical properties of digesta and sizes of gastrointestinal (GIT) organs of growing pigs. Understanding changes in physicochemical properties of digesta assists feed compounders to identify appropriate fiber inclusion levels that minimize nutrient losses through excretion or overfeeding. A total of 18 pigs with initial body weight (BW), 14 ± 1.2 kg were allocated each to one of the 5 corn cob levels (80, 160, 240, 320 and 400 g/kg DM) and a control diet. The control diet contained 18.09 MJ/kg DM and crude protein of 24.78 g/kg DM. After 4 weeks, weights of the GIT compartments were recorded and the contents were sampled for analyses of water concentration, water holding capacity (WHC), swelling capacity, nutrient contents and short chain fatty acids (SCFA) concentrations. Proc GLM (SAS, 2009) was used to determine the effects of inclusion level of CC on physicochemical measures of digesta and size of GIT organs and means were compared using PDIFF. The sizes of visceral organs of pigs feeding diets with less than 240 g/kg DM were not different. Pigs fed on diets containing at least 240 g/kg CC diets had higher ($P < 0.001$) stomach and the colon weights, compared with the control. Water holding capacity was lowest in the stomach and highest in the cecum. From the stomach to the distal colon, the WHC of digesta was higher compared with the control diet ($P < 0.05$). The neutral detergent fiber (NDF), acid detergent fiber (ADF) and WHC of diets containing less than 240 g/kg DM of CC did not change markedly along the digesta. Propionic and acetic acid concentration was higher ($P < 0.05$) in the colon of pigs that consumed a diet based on 80 and 160 g/kg DM of CC. In conclusion, high increment levels of CC beyond 240 g/kg DM increase the size of GIT organs as well as bulkiness of digesta during transit in the gut of growing pigs.

Key Words: bulky content, physicochemical properties, dietary fiber

584 Effect of dietary supplementation of fermented Hamcho (*Salicornia herbacea*) on growth performance and meat quality in broiler chicks. M.-J. Ku*[1], S.-W. Kim[1], K.-S. Kim[1], S.-K. Lee[1], D.-Ju. Yu[1], Y.-S. Choi[1], A.-A. Yun[1], D.-H. Park[1], S.-S. Lee[2], and W.-H. Kim[1], [1]*Livestock Research Institute, Jeollanamdo Agricultural Research & Extension Service(JARES), Gangjin-gun, Jeollanam-do, Republic of Korea,* [2]*Sunchon National University, Suncheon, Jeollanam-do, Republic of Korea.*

Hamcho (*Salicornia herbacea*), known as Ginseng of the Sea, grows around mudflats and salt marsh in Korea's islands touched by sea water. It contains dozens of nutrients including minerals and amino acid. The study was conducted to investigate the effect of dietary supplementation of fermented Hamcho (FH) on growth performance and meat quality in broiler chickens. Total of one hundred eighty 1-d-old Ross male broiler chicks were divided into 3 groups and fed control (basal diet), antibiotic (basal diet + oxytetracycline 5 ppm) or FH (basal diet + FH 0.5%) diet for 5 weeks, respectively. The birds were arranged in a completely randomized design having 4 replications with 15 chicks per replication. The feed intake and feed conversion rate in the group fed diets containing 0.5% FH were improved by 12.7% and 11.7% as compared with those of control ($P < 0.05$). For the analysis of meat quality, we used chicken breast from slaughtered chickens. The method employed in the analysis is as follows: 1; Water holding capacity was determined by Hamm (1960). 2; Shear force by Yoon (2003). 3; Fatty acid content by gas chromatography (Agilent Technologies, USA) after fatty acid methyl ester (FAMEs). The FH group showed the highest and lowest values, 60.31 ± 1.61 and 1.86 ± 0.08, in water holding capacity and shear force indicating keeping quality parameters ($P < 0.05$). Oleic acid (18:1n-9) and α-linolenic acid (18:3n-3) content were higher in the FH group (45.356 ± 0.48 and 0.706 ± 0.03) than those of the other groups ($P < 0.05$). Also, docosahexaenoic acid (DHA, 22:6n-3) was

only detected in the FH group (0.206 ± 0.07). The results demonstrated that the fermented Hamcho used in this study enhanced the productivity and the meat quality, thus can be used as broiler feed additives for stimulating growth and feed efficiency.

Key Words: broiler chick, fermented Hamcho (*Salicornia herbacea*), growth performance

585 In vitro degradation and fermentation characteristics of expeller-pressed canola meal and cold-pressed canola cake simulating the pig intestine. T. A. Woyengo*[1], R. Jha[2], E. Beltranena[1,3], and R. T. Zijlstra[1], [1]*University of Alberta, Edmonton, AB, Canada,* [2]*University of Hawaii at Manoa, Honolulu,* [3]*Alberta Agriculture and Rural Development, Edmonton, AB, Canada.*

Expeller-pressed canola meal (EPCM) and cold-pressed canola cake (CPCK) serve as sources of protein and energy in pig feeds. However, limited or no information exists on their fermentation characteristics in the pig intestine; this information is important for understanding contribution of a feedstuff to energy needs of pigs via hindgut fermentation. Thus, a study was conducted to determine in vitro fermentation characteristics of EPCM and CPCK in comparison with soybean meal (SBM). Samples were hydrolyzed using pepsin at pH 2.0 for 2 h, and then with pancreatin at pH 6.8 for 4 h. Residues were then incubated in a buffer solution with minerals and fresh pig feces as inoculum. Accumulated gas production was measured for 72 h, and the measured gas production was modeled to estimate kinetics of gas production. Concentration of VFA was measured in fermented solutions using gas chromatograph. Data were subjected to ANOVA and means were separated by probability of difference. On DM basis, SBM, EPCM, and CPCK contained 51, 35, and 30% CP; 1.5, 12, and 23% ether extract; and 9, 21, and 18% NDF, respectively. In vitro DM degradability for SBM, EPCM, CPCK were 82, 68, and 70% ($P < 0.05$), respectively. Total gas production for SBM, EPCM, and CPCK were 207, 114, and 99 mL/g DM ($P < 0.05$), respectively. Total VFA production was higher ($P < 0.05$) for SBM than for CPCK or EPCM (4.10 vs. 2.04 vs. 2.47 mmol/g DM). In conclusion, the in vitro degradability and fermentability of SBM were higher than those for CPCK or EPCM likely due to the lower fiber content. The CPCK had higher in vitro DM degradability, but lower in vitro fermentability than EPCM. Thus, CPCK or EPCM compared with SBM contribute less energy to pigs via hindgut fermentation. EPCM may contribute more dietary energy to pigs via hindgut fermentation, but it contributes lower dietary fat than CPCK.

Key Words: canola meal, canola cake, in vitro fermentation

586 Comparative utilization of processed chicken offal and blood meals in diets of young pigs containing maize offal. A. O. K. Adesehinwa*[1] and B. Adebayo[2], [1]*Livestock Improvement Programme, Institute of Agricultural Research & Training, PMB 5029, Moor Plantation, Ibadan, Oyo State, Nigeria,* [2]*Nigerian Institute of Animal Science, Southwest Zonal Office, Moor Plantation, Ibadan, Oyo State, Nigeria.*

One hundred eight young pigs weighing 8.86 ± 0.2kg body weight, randomly assigned to 6 isonitrogenous (20%CP) dietary groups were used to evaluate responses to 0, 25 and 50% inclusions of maize offal (a by-product of maize milling consisting mainly of the aleurone layer and some adulterants of germs and endosperm) as a replacement for maize in diets supplemented with either chicken offal meal (COM) (ground dried poultry processing by-product comprising heads, viscera, feathers, beaks etc) or blood meal (BM) (ground dried animal blood in a factorial design. Each treatment group comprising 18 pigs had 6 replicates of 3 pigs/replicate. Weekly record of feed intakes and weight gains were taken for the 56-d trial period. Two pigs/replicate were randomly selected and bled at the first and last weeks of the trial to determine the serum total proteins, albumin, globulin, creatinine, urea, cholesterol and glucose. All statistical data were subjected to ANOVA and where statistical significance were observed, the means were compared using the Duncan's multiple range test (SAS). The results showed that the dry matter intake was neither affected ($P > 0.05$) by the maize offal nor the protein sources. The performance of the pigs fed diets supplemented with COM were superior ($P < 0.05$) in terms of DWG (0.49, 0.47 and 0.38 kg), F:G (1.75, 1.82 and 2.22) and metabolizable energy intake per gain (6205, 6366 and 7779 kcalME/kg compared with 0.37, 0.37 and 0.32 kg; 2.25, 2.33 and 2.90 and 7927, 8046 and 10066 kcalME/kg obtained for pigs fed BM-supplemented diets respectively. The results obtained at the 0 and 25% were comparable, but superior ($P < 0.05$) to that obtained at 50% for both protein sources. The serum metabolites were neither influenced ($P > 0.05$) by maize offal nor the protein sources, except the urea (33.3, 30.5 and 29.5 mg/dL for COM; 24.0, 22.8 and 26.5 mg/dL for BM) and globulin (2.88, 3.43 and 3.53g/dl for COM; 2.88, 3.15 and 3.28 g/dL for BM) contents. It could therefore be concluded that up to 25% maize can be replaced with maize offal in diets of young pigs, with better performance obtained with COM.

Key Words: unconventional feed source, young pig, feed utilization

587 Tamoxifen treatment affects morphological characteristics and gene expression within the reproductive tract of prepubertal Holstein heifers. A. Y. Wood*, H. L. M. Tucker, V. L. McCracken, S. E. Deaver, B. M. Brown, R. M. Akers, and M. L. Rhoads, *Virginia Polytechnic Institute and State University, Blacksburg.*

Reproductive responses to steroid hormones during the prepubertal period of heifers are poorly understood. This experiment was conducted as a first step toward understanding the significance of estrogen receptor signaling within the reproductive tissues during the prepubertal period. As such, tamoxifen (TAM) was administered to heifers (n = 8) daily (0.3 mg/kg subcutaneously) from approximately 28 to 120 d of age. Control heifers (CON; n = 6) received an equal volume of excipient. Gross measurements and samples of reproductive tract tissues, and plasma were collected upon sacrifice at 120.7 ± 0.3 d of age. TAM did not affect final body weight, hip height or plasma estradiol concentration. Irrespective of body weight, TAM dramatically decreased overall weight of the reproductive tract (42.04 ± 3.96 g vs 26.32 ± 3.43 g; $P = 0.01$). This difference was due to concomitant decreases in weight of the ovaries (5.89 ± 0.95 g vs 3.09 ± 0.58 g; $P < 0.05$) and uterus (34.45 ± 5.44 g vs 23.23 ± 3.33 g; $P = 0.11$). Interestingly, the number of ovarian follicles did not differ between CON and TAM animals. Expression of estrogen receptor (ER) α in the uterus of the CON animals was nearly double that of TAM animals (30359.60 ± 3053.27 cn vs 15794.12 ± 2644.21 cn; $P < 0.01$) whereas ERα merely tended to differ in the oviduct ($P < 0.15$) and did not differ in the ovary. Abundance of the β form of the ER did not differ in uterus, oviduct or ovary. Conversely, progesterone receptor (PR) expression in the uterus (43465.99 ± 5994.86 cn vs 59990.13 ± 5191.70 cn; $P = 0.06$) and oviduct (12495.22 ± 3433.85 cn vs 26570.15 ± 3179.13 cn; $P = 0.01$) was increased by TAM while ovarian expression of PR was similar between groups. In summary, the selective estrogen receptor modulator, TAM affected the morphological development of the entire reproductive tract. Effects of TAM on the sex steroid receptor expression, however, were most apparent in the uterus and oviduct. These results demonstrate that alterations in ER signaling influence reproductive tract characteristics of heifers during the prepubertal period.

Key Words: tamoxifen, prepubertal, estrogen

588 No evidence of a systemic mRNA biomarker of early pregnancy using RNAseq of whole blood on day 20 of pregnancy in dairy cattle. M. P. Mullen*[1,2], P. McGettigan[2], J. A. Browne[2], S. Scully[2], M. G. Diskin[1], A. C. O. Evans[3], and M. A. Crowe[2], [1]*Teagasc, Athenry, Co. Galway, Ireland,* [2]*School of Veterinary Medicine, University College Dublin, Dublin 4, Ireland,* [3]*School of Agriculture and Food Science, University College Dublin, Dublin 4, Ireland.*

Early and accurate pregnancy diagnosis in dairy cattle is a requirement for efficient herd management. However, most of the currently available methods involve pregnancy diagnosis at or after 28–30 d of gestation, which is too late to re-breed at the next cycle. Therefore, the objective was to evaluate if any potential biomarkers of early pregnancy in dairy cattle could be discerned in blood by d 20 post insemination (AI) at the mRNA level using RNaseq technology. Whole blood samples were collected on d 20 post-AI from 22 dairy cows. Plasma samples were also taken daily from d 16 to 21 and on the date of pregnancy determination to generate progesterone profiles. Pregnancy status was determined between Days 30 to 35 post-AI by transrectal ultrasonography and resulted in the classification of 14 pregnant and 8 nonpregnant cows. Total RNA was extracted from whole blood using the TEMPUS blood RNA stabilization and extraction protocol. Eighteen 100-bp paired-end strand specific RNA libraries were prepared for n = 10 pregnant and n = 8 non-pregnant cows and sequenced on the Illumina HiSeq2000 platform. After quality control, 432,693,725 million 100-bp paired-end reads were generated, of which 94.6% mapped to the bovine UMD 3.1 genome assembly. A total of 12,108 genes were deemed to be expressed (>4 reads per gene per animal). Despite 171 genes showing nominal differential expression ($P < 0.01$), none remained significantly differentially expressed between the pregnant and non-pregnant groups after correction for multiple testing (FDR $P < 0.05$). While it is possible that subtle changes in the systemic transcriptome may be occurring due to the presence of a developing conceptus, which may warrant further targeted investigation into the data set, no significant biomarker at the mRNA level could be discerned using RNaseq of the whole blood on d 20 of pregnancy in dairy cattle. Funded by Science Foundation Ireland 07/SRC/B1156.

Key Words: pregnancy diagnosis, transcriptomics

589 Influence of post-insemination nutrition on embryonic development in beef heifers. S. G. Kruse*[1], B. J. Funnell[1], S. L. Bird[1], H. P. Dias[2], S. L. Lake[3], R. P. Arias[3], G. A. Perry[4], O. L. Swanson[4], E. L. Larimore[4], and G. A. Bridges[1], [1]*North Central Research and Outreach Center, University of Minnesota, Grand Rapids,* [2]*São Paulo State University, Botucatu, São Paulo, Brazil,* [3]*University of Wyoming, Laramie,* [4]*South Dakota State University, Brookings.*

Previous results have demonstrated that a reduction in nutrition immediately following AI reduces pregnancy rates. The objective of this experiment was to determine if nutrient restriction following AI affects early embryo development. Beef heifers in 3 replications (Rep; Rep 1; n = 44, Rep 2; n = 44, Rep 3; n = 50) were developed in a dry-lot and fed approximately 125% NRC requirements from weaning to timed-AI (d 0). Heifers were timed-AI to a single sire in all replications. Immediately following AI, heifers were assigned based on age and weight to one of 2 post-AI nutritional treatments. Half the heifers in each replication continued on the pre-insemination diet allowing weight gain (GAIN) and the remaining heifers were restricted fed to result in weight loss (LOSE). On d 6, embryos/ova were collected and recovered embryos/ova (LOSE; n = 42, GAIN; n = 46) were evaluated to determine quality (IETS standards; 1–5; 1 = excellent, 5 = degenerate) and stage (1–9; 1 = unfertilized, 9 = expanded hatched blastocyst). Embryos were then stained and evaluated to determine the number of dead cells (propidium iodide) and total blastomeres (Hoechst 33342). In Reps 1 and 2, concentrations of IGF-1 were assessed on d 0 and 6 and progesterone concentrations on d 4 and 6. Data was analyzed using the Mixed procedures of SAS. There were no treatment by Rep interactions for any data evaluated, thus all data were pooled. Embryo stage and quality were improved ($P < 0.05$) in the GAIN (4.6 ± 0.1, 2.0 ± 0.2, respectively) compared with LOSE treatment (3.8 ± 0.2, 2.8 ± 0.2, respectively). Embryos in the GAIN treatment had greater total blastomeres ($P = 0.03$; 70.6 ± 5.6) and percentage of live cells ($P = 0.01$; 83.3 ± 3.0%) compared with LOSE (48.9 ± 3.9; 71.1 ± 4.1%). Progesterone and IGF-1 concentrations did not differ between treatments nor were IGF-1 concentrations correlated with embryo parameters. In summary, nutrient restriction for 6 d immediately following AI resulted in poorer quality embryos that were retarded in stage, suggesting that immediate changes in nutrition can alter early embryonic development.

Key Words: embryo, nutrition, beef heifer

590 Effects of maternal nutrient restriction followed by realimentation on uterine blood flow during mid-gestation on beef cows. L. E. Camacho*[1], C. O. Lemley[2], L. Prezotto[1], K. C. Swanson[1], and K. A. Vonnahme[1], [1]*Department of Animal Sciences, North Dakota State University, Fargo,* [2]*Department of Animal and Dairy Sciences, Mississippi State University, Mississippi State.*

The objective of this study was to examine the effect of maternal nutrient restriction followed by realimentation during mid-gestation on uterine blood flow (BF). Lactating, multiparous Simmental beef cows (n = 10) were placed in a pen equipped with Insentec B. V. roughage individual intake control system feeders. On d 30 of pregnancy, cows were randomly assigned to treatments: control (CON; 100% NRC; n = 6) and nutrient restriction (RES; 60% NRC; n = 4) from d 30 to 140 (period 1) and thereafter being realimented to CON until d 198 of gestation (period 2). Calves were weaned at d 90 of dam gestation. Uterine artery measurements ipsilateral (i) and contralateral (c) to the conceptus were obtained on d 30, 58, 86, 114, 140, 152, 159, 166, and 198 of gestation via Doppler ultrasonography and included BF, pulsatility index (PI), and resistance index (RI). There was a treatment × period interaction ($P = 0.02$) on iBF where BF was similar ($P = 0.77$) between groups during period 1 but during period 2 iBF was greater ($P = 0.03$) in RES vs. CON. There were no treatment × day × period interactions ($P \leq 0.36$) for iPI and iRI but both decreased ($P < 0.01$) as gestation proceeded. There was a treatment × day × period interaction ($P = 0.06$) tendency for cBF. From d 30 to 114 cBF was similar between groups and by d 140 until 198 CON had greater cBF vs. RES. For cPI, there was a treatment × day × period interaction ($P = 0.02$) where both groups were similar from d 30 until 114, but on d 140 cPI was greater in RES vs. CON. From d 152 to 159 cPI was similar in both groups and by d 166 cPI was greater in RES vs. CON. Contralateral RI was not affected by treatment or period ($P = 0.60$). Both cPI and cRI decreased as gestation proceeded. There was no treatment × day × period interaction ($P = 0.98$) for total BF; however, there was an exponential increase in BF through gestation. Nutrient restriction during mid-gestation followed by realimentation affects uterine BF in pregnant beef cows without affecting resistance indices. Further investigations in uterine and placental vascular reactivity are warranted.

Key Words: nutrient restriction, pregnancy, uterine blood flow

591 Nutritional genomics: Effect of maternal methionine supplementation on the transcriptome of day 7 embryos from superovulated lactating dairy cows. F. Peñagaricano*[1], A. H. Souza[1], P. D. Carvalho[1], A. Driver[1], R. Gambra[1], J. Kropp[1], K. S. Hackbart[1], D. Luchini[2], R. D. Shaver[1], M. C. Wiltbank[1], and H. Khatib[1], [1]*University of Wisconsin-Madison, Madison,* [2]*Adisseo, Alpharetta, GA.*

The aim of this study was to assess the effect of maternal methionine supplementation on the transcriptome of d 7 embryos. Holstein cows were assigned to 1 of 2 treatments differing in level of dietary methionine from calving until embryo flushing (around 70 DIM). The treatments were (1) Methionine; diet formulated to deliver 2875 g MP with 6.8 Lys %MP and 2.43 Met %MP; (2) Control; same basal diet but formulated to deliver only 1.89 Met %MP. Cows were superovulated with a modified 5 d-Double Ovsynch with 4d of decreasing FSH (400 mg/cow) doses and flushed 6 d after synchronized ovulations. Cows with at least 4 grade 1 or 2 embryos were selected for the study (4 cows per group). Embryos from an individual cow were pooled (2–4 embryos per pool, 2 pools per cow) and analyzed by RNA sequencing. Total RNA extraction, amplification, library preparation, and sequencing were performed following Illumina mRNA-Seq protocol. Sequencing reads were mapped to the bovine reference genome (bosTau7) using Tophat. The resulting alignments were used to reconstruct transcript models by Cufflinks. Differential gene expression was analyzed using the edgeR package in R. In addition, gene set enrichment analysis was performed using a test of proportions based on the cumulative hypergeometric distribution. A total of 276 genes out of 10,662 showed differential expression between treatments (q-value <0.10). Some of the most significant genes are related to embryo development (e.g., VIM and TBX15), regulation of apoptosis (e.g., IFI6, BCL2A1), and immune system (e.g., BLA-DQB, LCP1, TYROBP). Some uncharacterized genes and novel transcripts also had differential expression. Pathway analysis revealed that several Gene Ontology terms (n = 33), InterPro entries (n = 12), and one KEGG pathway were enriched (q-value <0.05) with differentially expressed genes. Interestingly, many pathways closely related to the immune system were found to be significant. Overall, our results support the hypothesis that maternal methionine supplementation affects the transcriptome of bovine preimplantation embryos.

Key Words: methionine, embryo transcriptome, dairy cow

592 Activation of the transcription factor nuclear factor kappa B (NFKB) by recombinant porcine cytokines in the uterine epithelium. D. J. Mathew*, R. D. Geisert, and M. C. Lucy, *University of Missouri, Columbia.*

Embryonic mortality in the pig is temporally associated with conceptus elongation. Embryos undergoing elongation secrete estrogen for maternal recognition and interleukin 1 β (IL1B) to induce an inflammatory reaction in the uterus. There are 2 interleukin 1 β (IL1B) genes in the pig. IL1B is expressed by macrophages and the novel embryonic IL1B (IL1BE) is expressed by the pig conceptus. Within the uterus, IL1BE is believed to activate NFKB, a transcription factor needed for establishment of pregnancy. NFKB, in turn, controls cyclooxygenase-2 (COX2) expression. The objective was to test the capacity of IL1BE to activate NFKB and increase COX2 mRNA expression in porcine endometrium. Endometrium was dissected from 3 gilts and cultured in MEM for 4 h at 37°C. The tissues were then left untreated (negative control) or treated with a low, medium, or high dose of LPS (positive control; 1, 10, or 100 μg/mL), or recombinant β galactosidase (negative control), human IL1B or immature and mature forms of porcine IL1B and IL1BE (10, 100, or 1000 ng/mL). Tissues were frozen for mRNA expression analyses (RTPCR) or fixed and stained for NFKB localization. For NFKB, luminal epithelial cell nuclear vs cytoplasmic NFKB ratio was calculated. Within the uterine epithelium, there was an effect of treatment ($P < 0.001$) and concentration ($P < 0.05$) on NFKB activation. Untreated and negative control-treated epithelium had the least (0.48 and 0.51, respectively; SEM = 0.01) and mature pig IL1B, LPS, mature human IL1B and mature pig IL1BE treated had the greatest (0.82, 0.72, 0.69, and 0.69, respectively; SEM = 0.01) NFKB activation. For COX2 mRNA expression, there was an effect of treatment ($P < 0.05$). Untreated, immature pig IL1B and IL1BE treated had the least COX2 expression (0.70 ± 0.45, 0.99 ± 0.30, and 1.00 ± 0.30, respectively) and mature pig IL1B, human IL1B and pig IL1BE treated had the greatest COX2 expression (2.42 ± 0.35, 1.51 ± 0.30, and 1.43 ± 0.35, respectively). IL1BE may be involved in the establishment of pregnancy in the pig through its capacity to activate NFKB and increase COX2 expression in the uterine endometrium.

Key Words: pig, pregnancy, expression

593 Effects of prenatal transportation stress on preweaning temperament and growth of Brahman calves. B. P. Littlejohn*[1,2], D. M. Price[1,2], J. P. Banta[2], A. W. Lewis[2], D. A. Neuendorff[2], J. A.

Carroll[3], R. C. Vann[4], T. H. Welsh Jr.[1], and R. D. Randel[2], [1]*Texas A&M Department of Animal Science, College Station,* [2]*Texas A&M AgriLife Research and Extension Center, Overton,* [3]*Livestock Issues Research Unit, USDA-ARS, Lubbock, TX,* [4]*MAFES- Brown Loam, Mississippi State University, Raymond.*

The objective of this experiment was to examine the effects of prenatal stress on preweaning temperament and 180-d adjusted weaning weight of Brahman calves. Mature cows were assigned to receive 1 of 2 treatments, which consisted of a control group (n = 42) and a prenatally stressed group (n = 43). Cows in the prenatally stressed group were subjected to 2 h of transportation at 60, 80, 100, 120, and 140 d of gestation. Relative to weaning (d 0 = weaning), pen score (PS; 1 = calm and 5 = excitable), exit velocity (EV; m/s) and temperament score [TS = (PS+EV)/2] were recorded for each calf at d −112, −84, −56, −28, and 0. All data were analyzed using Mixed Models procedures of SAS. Treatment, sex, and day, were included as fixed effects; sire and weaning group were included as random effects. The 180-d adjusted weaning weight was not influenced by treatment ($P = 0.17$) or the sex × treatment interaction ($P = 0.28$). However, male calves (220.35 ± 5.14 kg) were heavier than female calves (201.13 ± 5.27 kg; $P < 0.01$). No interactions were significant for EV, PS, or TS. Pen score tended ($P = 0.06$) to be greater for prenatally stressed (2.83 ± 0.40) as compared with control calves (2.37 ± 0.40). Exit velocity was greater ($P = 0.02$) for prenatally stressed (2.24 ± 0.19 m/sec) as compared with control calves (1.76 ± 0.20 m/s). Temperament score was also greater ($P = 0.03$) for prenatally stressed (2.53 ± 0.28) relative to control calves (2.07 ± 0.28). Of these 3 measures of temperament, there was no effect of calf sex. However, there was an effect of day for each measure of temperament, as shown in the table below. In general, temperament decreased with time. Prenatal stress resulted in increased excitability of calves; however, prenatal stress did not influence preweaning growth rate or weaning weight.

Table 1.

	d −112	d −84	d −56	d −28	d 0	SE	*P*-value
Exit velocity	2.36 [a]	2.04[b]	1.95 [b]	1.81 [b]	1.82 [b]	0.18	0.0007
Pen score	2.80 [a]	2.64 [a]	2.60 [a]	2.43 [b]	2.53 [ab]	0.39	0.0455
Temperament score	2.58 [a]	2.34 [b]	2.28 [b]	2.12 [c]	2.17 [bc]	0.26	<0.0001

Key Words: prenatal stress, calf, temperament

594 Effects of dietary fiber type and inclusion level on the physico-chemical composition of excreta of pigs. C. T. Mpendulo* and M. Chimonyo, *Animal and Poultry Science, College of Agriculture, Engineering and Science, University of Kwazulu-Natal, Pietermaritzburg, South Africa.*

The objective of the current study was to determine whether including varying fibrous ingredients of varying inclusion levels would change the physico-chemical composition of pig excreta. Dietary fiber inclusion to pig rations alters the physico-chemical components of pig excreta. Pigs weighted 20 and 40 kg, on average, at the start and end of the trial. Dietary fiber sources used were grass hay (GH), alfalfa hay (AH), corn cob (CC), corn stover (CS) and sunflower husk (SH). The fibers were included at 0, 80, 160, 240, 320 and 400 g/kg inclusion level. Each treatment had 4 pigs. The pigs were fed ad libitum, and were adapted to the diet for 10 d. Dietary fiber inclusion influenced nutrient removal patterns of both the feces and urine. Fecal nitrogen was lowest in pigs fed on CC and the AH containing diets (2.21 ± 0.082) and (2.11 ± 0.082) ($P < 0.01$). Neutral detergent fiber and acid detergent fiber contents were highest in pigs fed on rations containing GH and CS (1805 ± 25.8) and (1335 ± 25.8), respectively ($P < 0.01$). Pigs fed on high fiber content excreted more feces and produced less urine than those on the control diet ($P < 0.05$). It was concluded that as dietary fiber content was increased, fecal nitrogen increased, resulting into a shift of nitrogen from urine to feces.

Key Words: dietary fiber, pig excreta, pig

595 Effects of cinnamon extracts on urease activity and emission of NH_3 and H_2S of piglet slurry. A. Chen*, Y. Xiao, C. Li, Q. Hong, and C. Yang, *Zhejiang University, Hangzhou, Zhejiang, China.*

The emission of NH_3 and H_2S from the slurry in pig farm is a severe challenge to the habitat and inhabitant. This study was conducted to investigate the effects of cinnamon extract (CE) on urease activity, inhibition of bacteria related to urease production, and emission of NH_3 and H_2S in piglet slurry in vitro and in vivo. In Exp. 1, CE was dissolved in 95% ethanol at the following concentration: 0, 125, 250, 500, 1000, 2000 mg/L. Then they were respectively added to urease solution and the culture medium of *Escherichia coli*, Proteus vulgaris and Staphylococcus aureus to evaluate the inhibitory effect. In Exp. 2, CE was added to the mixture of urine and feces, the time-course of concentrations of urea nitrogen (UN), NH_3, and H_2S were analyzed from 6 h to 168 h. In Exp. 3, 144 piglets of 35 d were assigned to one of the 2 dietary treatments, representing supplementation with 0 or 350mg/kg CE to the basal diet. Feces and urine were collected from d 33 to 35, and blood samples were obtained on d 35. Results showed CE decreased the urease activity and inhibited the activity of *Escherichia coli*, Proteus vulgaris and Staphylococcus aureus. The concentration of UN in the mixture of urine and feces in CE-added treatment was higher ($P < 0.05$) than that in the control from 6 h to 168 h, but the concentration of H_2S was lower ($P < 0.05$). Compared with the control group, growth performance in CE group changed little ($P > 0.05$), whereas urease activity in feces decreased by 17.16% ($P < 0.05$). It was observed that the concentration of UN in the mixture of urine and feces in CE group was greater ($P < 0.05$) vs. the control, but the concentrations of NH_3 and H_2S were less ($P < 0.05$). Additionally, serum concentrations of UN and NH_3 decreased ($P < 0.05$) by 9.27% and 25.97%, respectively, by the CE treatment. These findings suggest that CE decreases urease activity and inhibits the activity of bacteria related to urease production to increased the retention of NH_3 and H_2S in pig slurry. It is an effective botanical deodorant in pig industry.

Key Words: cinnamon extract, piglet slurry, urease activity

596 The effects of environment-friendly feed on growth performance and excrements of piglets. N. Zhang* and C. Jiang, *Feed Research Institute, Chinese Academy of Agricultural Sciences, Beijing, China.*

The nutrient composition of swine excreta can be altered by manipulating the composition of diets. Environment-friendly feeds, which are formulated according to the feed's digestible amino acids, the ideal protein approach, available phosphorus, the addition of phytase and the addition of plant extracts instead of antibiotics, aid to maintain growth performance and lower nitrogen and phosphorus excretion in piglets. This study determined the effects of an environment-friendly feed on growth performance and nutrient excretion of piglets. One hundred and eighty weaned piglets were divided into 2 groups with 6 replicates (15 piglets per replicates), and fed either a basal diet (control) or an environment-friendly diet. All animals were fed ad libitum with free access to water. The experiment lasted for 42 d. The animals were weighed at the beginning and the end of experiment, and group feed intake of each replicates was recorded. The nutrient digestibility was measured by the indirect method using Cr_2O_3 as a digesta marker. Compared with the control, the average daily gain of piglets fed the environment-friendly diet was increased by 7.6% (465.0 vs 500.2 g/d, respectively, $P < 0.05$), the ratio of feed to gain was decreased by 8.9 % (2.13 vs 1.94, respectively, $P < 0.05$). The digestibility of DM, OM, CP and EE was improved numerically by the environment-friendly feed ($P > 0.05$). Compared with control, the daily excretion of fecal N, P, Cu and Zn in piglets receiving the environment-friendly feed were decreased by 10.6% (2.83 vs 2.53 g/d, respectively, $P < 0.05$), 55.6% (0.54 vs 0.30 g/d, respectively, $P < 0.05$), 84.3% (23.2 vs 3.64 mg/kg, respectively, $P < 0.05$), and 76.3% (22.0 vs 5.22 mg/kg, respectively, $P < 0.05$). The results suggested that the environment-friendly feed enhanced the growth performance of piglets and decreased the environment pollution by nutrients in swine production.

Key Words: piglets, environment-friendly feed, pollution of environment

597 Foliar uptake and utilization of phosphorus by grazing cattle as influenced by nitrogen fertilization regime. S. L. Dillard*, W. F. Owsley, C. W. Wood, B. H. Wood, C. J. Weissend, and R. B. Muntifering, *Auburn University, Auburn University, AL.*

Efficiency of nutrient utilization in grazed pasture may be increased by management practices that facilitate phytoextraction of nutrients from nutrient-enriched soils. A 2-yr experiment was conducted to determine the effect of N fertilization regime on foliar P uptake and utilization by cattle in pasture with high soil-test P. In October 2010 and 2011, 6 0.28-ha plots were overseeded with triticale (*Triticum secale*) and crimson clover (*Trifolium incarnatum*) into a tall fescue (*Lolium arundinacea*)/bermudagrass (*Cynodon dactylon*) sod and assigned to 1 of 3 treatments (trt) (n = 2): 100% of N recommendation for tall fescue in a split application, 50% of N recommendation and 0% of N recommendation. In January, 6 cattle were randomly assigned to graze plots

(1 animal/plot) until May. In June, plots were overseeded with cowpea (*Vigna unguiculata*) and maintained on the same N-fertilizer regimes, based on N recommendation for bermudagrass. In August, 6 steers were randomly assigned to graze plots until September. Forages were sampled biweekly, and intake and fecal excretion of P were determined twice in each season of both years using Cr dilution technique by reference to forage IVDMD. Data were analyzed as a completely randomized design using mixed-model procedures. Mean available DM mass was not different among trt or between yr, and was greater ($P < 0.05$) for cool-season (CS) than warm-season (WS) forage (3,628 vs. 2,612 kg DM/ha). Mean foliar P mass was not different among trt or between yr, but CS forage had greater ($P < 0.05$) available P than WS forage (8.0 vs. 6.2 kg P/ha). Intake of P by cattle was not different among trt or between seasons, but was greater ($P < 0.05$) in 2012 than 2011 (28.5 vs. 11.1 g P/d). Similarly, fecal P output was greater ($P < 0.05$) in 2012 than 2011 (22.0 vs. 12.6 g P/d) but was not different among trt or between seasons. Nitrogen-fertilization trt did not affect available forage DM or foliar P mass. Results are interpreted to mean that grazing season had a greater effect than N fertilization on foliar P dynamics, whereas year had the greater effect on P utilization by cattle.

Key Words: phosphorus, cattle, nitrogen

598 Forage allowance on reproductive response of primiparous cows submitted to suckling restriction and flushing grazing Campos native pastures. M. Claramunt[1], M. Carriquiry[2], G. Gil[1], and P. Soca*[3], [1]*Facultad de Veterinaria, Universidad de la Republica, Paysandu, Uruguay,* [2]*Facultad de Agronomia, Universidad de la Republica, Montevideo, Uruguay,* [3]*Facultad de Agronomia, Paysandu, Uruguay.*

Suckling restriction and flushing with energy supplement (S+F) is a tactical tool which enhances pregnancy in primiparous cows. Evaluation of any practice at grazing would be performed under 2 or more grazing intensities. The objective was to evaluate the effect of Forage allowance (FA) on BCS, probability of pregnancy and Calving conception interval (CI) of primiparous cows with S+F grazing Campos native pastures. The study took place in Facultad de Agronomía, Uruguay (31°S 57°W). Eighty spring calving primiparous cows were assigned in the previous autumn to a complete randomized experiment of 2 FA in spatial replication on 2 blocks during 2 years. The experiment started at autumn −150 d postpartum (dpp) and finished 190 dpp. Treatments consisted in annual average FA of 10 and 6 kg DM/100kg liveweight (LW)/d for high (H) and low (L) respectively. Grazing system was continuous. The LW and FM were determined monthly and used to adjust FA by "put and take" method. At 82 ± 12 dpp cows were exposed to bulls for 80 d. Calf suckling restriction with nose plate during 12 d and flushing offering 2 kg/cow d of whole rice middling were applied at 76 ± 12 dpp. Pregnancy diagnoses for early (EP) and total (TP) probability of pregnancy were performed 152 and 205 ± 12 dpp. Date of subsequent calving was recorded and CI was determined. The experimental unit was the group of cows grazing a plot. Effect of FA on EP, TP and CI were analyzed by generalized linear model with logit function and binomial distribution and effect of FA and FA*dpp on BCS by repeated measurements. FA increased BCS during prepartum but not at calving and after ($P = 0.03$). FA did not affect EP (0.6 ± 0.09 $P = 0.3$) but TP was superior in H than L cows ($P = 0.07$ 0.9 vs 0.6 ± 0.04). The CI was reduced 12 d in H ($P < 0.05$). Increase FA improved reproductive performance of primiparous cows. The lacks of differences in BCS at calving and postpartum reflect a long-term effect of FA on cow energy balance to improve reproduction.

Key Words: forage allowance, flushing, suckling restriction

599 Utilization of stockpiled perennial forages in winter feeding systems for beef cattle. D. G. R. S. Kulathunga*[1], H. A. Lardner[1,2], J. J. Schoenau[1], and G. B. Penner[1], [1]*University of Saskatchewan, Saskatoon, SK, Canada,* [2]*Western Beef Development Centre, Humboldt, SK, Canada.*

A study was conducted to determine the effects of grazing stockpiled forage as an extensive winter feeding system relative to feeding a similar quality baled hay in a dry lot setting on beef cow performance, reproductive efficiency, dry matter intake, forage utilization, forage yield and quality, and system costs. Winter feeding systems were (1) field grazing stockpiled perennial forage (SPF) consisting of a meadow bromegrass (*B. riparius*)-alfalfa (*M. sativa*) blend (TDN = 52.5%; CP = 11.2%) with (2) dry lot (DL) cows receiving a similar quality hay (TDN = 54.6%; CP = 10.2%). Sixty dry pregnant Angus cows (675 kg ± 51 kg), stratified by body weight (BW; corrected for conceptus gain), were allocated to either the SPF or DL systems (n = 3). Drylot and SPF cows were supplemented with rolled barley (TDN = 86.4%; CP = 12.4%) at 0.05 and 0.4% of BW, respectively. Cow body condition score (BCS), rib and rump fat were measured at start and end of study and BW was measured every 14 d during the trial. Dry matter intake (DMI) was estimated using the herbage weight disappearance method. Statistical analysis was conducted as a one way ANOVA using the Proc Mixed Model procedure of SAS. Forage yield before grazing was not different ($P = 0.52$) between DL and SPF systems (4413 ± 914 vs. 4130 ± 673 kg/ha, respectively) however, forage utilization was higher ($P = 0.001$) in DL (94.3%) than SPF (68.1%) system. Total DMI between DL and SPF systems was not different ($P = 0.29$), 10.4 vs. 11.2 kg/d, respectively. For DL and SPF systems, cow BW change (18.2 vs. 17.5 kg; ($P = 0.89$), average daily gain (0.34 vs. 0.33 kg/d; $P = 0.96$), rib fat change (2.6 vs. 3.1 mm; $P = 0.34$) and rump fat change (2.6 vs. 2.7 mm; $P = 0.76$) were not different. Calf birth weight (42 ± 14 vs. 41 ± 18 kg; ($P = 0.37$) and calving interval (363 ± 9 vs. 361 ± 2 d; ($P = 0.72$) did not differ between DL and SPF systems, respectively. Total costs were $1.71 and $1.55 cow/day for DL and SPF systems, respectively. These study results suggest it may be cost effective to manage beef cows in field, grazing stockpiled forage and that winter feeding system does not affect cow performance.

Key Words: stockpiled forage, beef cow

Ruminant Nutrition Symposium: Burk Dehority—Swimming in the Rumen with Protozoa

601 Burk Dehority: An introduction. S. Loerch*, *The Ohio State University, Wooster.*

Burk A. Dehority is recognized worldwide as a leader in the field of rumen microbiology. Early research focused on the isolation and identification of those species of rumen bacteria primarily responsible for degradation and utilization of the structural carbohydrates of forages. His classic 1961 paper reported the effect of forage particle size and lignin on cellulose digestion. This work was fundamental to his later discoveries on the synergism among microbial species for digestion of structural carbohydrates. In more than 15 papers, Burk published the most complete characterization of the microbial ecology and digestive capacity of newly-weaned calves after feedlot arrival. Other studies explored microbial digestion in the hindgut of both ruminant and non-ruminant animals (guinea pigs, sheep, capybara, horse, Blue Duiker, and turkey) and its contribution to overall diet digestibility. Burk has published more than 40 papers on the rumen protozoa, with special emphasis on protozoal taxonomy and the effects of ration composition on protozoal ecology and activity in the rumen. Dr. Dehority has studied environmental effects on rumen protozoal populations around the world, working with over 25 domesticated and non-domesticated animal species. His studies in Australia on microbial populations in the forestomach of marsupials led to his discovery of a new family of entodiniomorph protozoa with descriptions of a new genus and 5 new species. Two protozoa species have been named in his honor: *Dasytricha dehorityi* – a new species found in the eastern gray kangaroos by Australian scientists and *Eudiplodinium dehorityi* – a new species isolated from the rumens of cattle by Turkish scientists. Burk has developed novel methods for the cryopreservation of rumen ciliate cultures, ensuring that more detailed studies of rumen protozoology can be undertaken worldwide, with a genetically more stable line of organisms. Burk's research on the microbial population of the rumen has opened this "black box" to scientists worldwide. For these achievements, Burk Dehority is recognized as a world authority on protozoa that inhabit the mammalian digestive tract.

Key Words: rumen, protozoa, bacteria

602 Protozoa taxonomy and morphology. J. L. Firkins*, *Ohio State University, Columbus.*

Burk Dehority was an international expert on rumen ciliated protozoa because their taxonomy was based on their morphology. He characterized ciliates from >10 different species of herbivores. His artistic talent was evident in his 2003 textbook; his seminal 1994 paper on subsampling, fixing, and counting; and in handouts from ruminant microbiology courses across the world. Although multiple species of rumen protozoa primarily are classified within the families Isotrichidae and Ophryoloscolecidae, Burk characterized ranges in size and morphology both among and within species. One compelling intersection between the art and science of protozoal taxonomy is his 1994 characterization of the multiple lineages of *Entodinium dubardi* in the Blue Duiker. Clearly, morphology-based taxonomy must catch up with molecular systematics. For example, caudal projections are "morphotypes" (depend on environment), but what about skeletal plates, macronucleus shape and location, and other morphological features used for current speciation? Burk's scientific curiosity led him to cultivate various single or mixed species of ciliates in vitro and in situ (inside a meshed apparatus within the rumen) and to improve cryopreservation protocols. Although long-term cultivation of the isotrichids was elusive for him, he contributed seminal work on their migration and chemotaxis in vivo. He determined differing generation times and other features such as minimum pH values for species in several genera. He wasn't afraid to ask anti-dogmatic questions such as, do protozoa really have a role or are they successful inhabitants of the rumen just because they can be? He looked for the simplest explanation of an observation and branched from there. For example, he always considered the roles (prey vs competitors for substrate) of the bacterial and sometimes fungal co-inhabitants in cultures characterized as a single protozoan species. Thus, Burk characterized live versus killed bacteria to enhance protozoal growth. My colleague considers his legacy to motivate others to "love science and appreciate the thrill of discovery." He did and will—and not just because at least 2 species are named after him!

Key Words: protozoa, ciliate, rumen

603 The "ebb and flow" of cultivation based studies. R. I. Mackie*[1], I. K. Cann[1], and M. Morrison[2,3], [1]*University of Illinois, Urbana,* [2]*The Ohio State University, Columbus,* [3]*CSIRO Animal, Food and Health Sciences, St Lucia, QLD, Australia.*

This presentation seeks to describe and highlight Dehority's contributions to cultivation-based studies of rumen ecology. We also place these contributions in the context of modern molecular microbial ecology and cultivation-independent approaches to the study of microbial ecology and biology. Hungate was the first to propose that a complete ecological analysis of a natural habitat such as the rumen required answers to 3 questions. What kind and numbers of organisms are present (who's there)? What are their activities (who's active)? And, to what extent their activities are performed (what are they doing)? These principles featured prominently in Burk's research career spanning more than 50 years (1957–2012) and 172 peer reviewed journal publications; most of his research used cultivation-based approaches. His initial research focused on growth requirements of rumen bacteria and techniques for the study of mixed and pure culture fermentations. These studies translated into work that focused on optimizing rumen fermentation of dietary components of forages such as pectin, cellulose and hemicellulose. These studies were followed by isolation of fiber-degrading bacteria and description of ciliate protozoa in the rumen of cattle sheep, moose, musk ox, and other animal species. He is still one the few scientists to have studied the vitamin requirements of cellulolytic bacteria, essential to the formulation of chemically defined media. Cultivation based approaches have limitations and attempts to improve the proportion and diversity of bacteria in culture occupied Burk over the years. One of his innovations was the use of pre-incubated rumen fluid medium to reduce the non- specific background counts for functional groups of rumen bacteria. He made an important contribution to the study of interactions between rumen bacteria during degradation of plant biomass. Over the past 20 years, cultivation independent approaches have become well established and have become a requirement for publication. However, it is clear that this approach also has limitations and the best method is to combine cultivation based techniques with molecular approaches to advance the study of rumen biology.

Key Words: rumen bacteria, cultivation, Dehority

604 International efforts and collaborations, especially with exotic herbivores. A.-D. G. Wright*, *Department of Animal Science, University of Vermont, Burlington.*

Prof. Burk Dehority has studied the rumen/gut protozoa from a wide range of herbivores on 5 different continents, from Moose to Alaskan Dall sheep, to Zebu cattle and Blue and Black wildebeests, to capybara, llamas, and alpacas, to Cypriot domestic horses, to kangaroos and quokkas, just to name a paltry few. Burk spent many years patiently peering through a microscope at his beloved rumen ciliates, taking meticulous notes and measurements, and eloquently making detailed hand-drawings. This eventually led to his laboratory writings and line-drawings being published in 1993 as a 120-page "Laboratory Manual for Classification and Morphology of Rumen Ciliate Protozoa," which is still widely used today and a must for anyone venturing into the world of rumen protozoa. After all, Burk has identified no less than 21 new species of rumen microorganisms. This presentation seeks to highlight some of Burk's international efforts and collaborations, especially his work with exotic herbivores and their rumen ciliates. Even though Burk retired from The Ohio State University more than 5 years ago, he still continues to collaborate and publish today, thereby extending his research career to 56 years (1957–2013), and more than 170 peer reviewed journal publications. Burk credits his collaborations as a good way of keeping his research stimulated. Of course, collaborations are all the more stimulating when they involve travel, and his collaborative work took him several times to Australia and Brazil for a couple of months each as well as to Alaska, Ethiopia, and Kenya for shorter stays. I hope to capture his 3 visits to Australia, especially the last 2 visits (2004 and 2006) with me in Perth, West Australia.

ADSA Southern Section Symposium: Strategies for Managing Reproduction and Udder Health in Heat-Stressed Dairy Cows

605 Optimization of breeding decisions for dairy cattle subject to long periods of seasonal heat stress. A. De Vries*[1], F. Du[1], K. D. Gay[1], T. R. Bilby[2], J. Block[3], and P. J. Hansen[1], [1]*University of Florida, Gainesville,* [2]*Texas AgriLife Research and Extension, Stephenville,* [3]*OvaTech LLC, Gainesville, FL.*

Long periods of heat stress in the Southeast United States have persuaded many dairy producers to adopt a different breeding policy in the warm summer compared with the cooler winter. During heat stress, often cheaper semen is used or breeding is stopped altogether. Major reasons are difficulty in getting cows pregnant or the desire to avoid calving in the summer, and the availability of grass on pasture based farms. Policies are known to vary widely. The objectives of this project were (1) to develop an economic decision aid that can evaluate different seasonal breeding policies and find an optimum policy given dairy farm constraints, and (2) compare policies including the transfer of sexed female embryos (ET) to dairy cows in the summer, and (3) evaluate the use of sexed semen when it is available year round. A large Markov chain dairy herd simulation model combined with linear programming was developed. The model simulated heifers and cows from birth to the end of the ninth parity, using weekly steps. Seasonality was modeled as 52 periods per year. Heat stress was assumed to affect milk yield production, fat yield production, fertility, involuntary culling, and death risk. Decision variables were 3 types of breedings, culling, and which heifer calves to keep. Available constraints included the number of milking cows, total cows, a closed herd, and sale or purchase of pregnant heifers. The profitability of ET in the summer vs. conventional AI depended on the constraint imposed. In an open herd with all heifer calves sold, a total cow constraint, no delayed inseminations, and all breedings in the summer with ET, the ET policy resulted in a loss of $4 per milking cow per year. In a closed herd with optimal decision making regarding breeding type and a milking cow constraint, the value of the ET option was $88 per milking cow per year. The milking cow constraint also resulted in the use of more sexed semen in heifers during the summer and even in cows during the fall. In summary, optimal breeding decisions depended largely on dairy farm constraints, in addition to the effects of heat stress on animal performance.

Key Words: heat stress, breeding decision, dairy

606 Strategies to improve reproductive performance during heat stress in lactating dairy cows. T. R. Bilby*, *Merck Animal Health, De Soto, KS.*

Heat stress (HS) negatively affects all aspects of dairy cattle production. Decreased milk production and reproduction losses during the summer substantially affect the economic potential of dairy farms. The annual economic impact of HS on US animal agriculture has been estimated at $2 billion, with the dairy industry alone accounting for $900 million of this loss. Consequently, strategies should be initiated to lessen the severity of HS on both reproduction and milk production to improve cow performance and farm profitability. With the continued increase in milk production per cow, sensitivity of the dairy cow to elevated climatic conditions has increased. Higher milk production associated with an increase in dry matter intake enhances metabolic heat production which aggravates thermoregulatory competence of lactating dairy cattle. Several experiments have shown that milk production declines during summer months with a greater reduction in fertility. Intensive cooling of cattle still remains the superior strategy for improving reproduction. However, strategies in addition to proper cooling can be implemented to mitigate the negative effects of HS on reproduction dairy cattle. Increased demands for factors such as glucose and IGF-I during HS to sustain milk production may compromise early embryo development, in turn, increasing embryo loss. Recent research on manipulation of embryos in vitro with hormonal supplements has illustrated beneficial effects on fertility post transfer during summer. In addition, the percent of heifers born was increased due to the use of sexed semen for in vitro embryo production. The use of reproductive hormones to by-pass the low estrous detection, improve ovulation, and (or) increase progesterone concentration during summer has shown promise in negating summer fertility decline. Utilizing natural service sires during summer may reduce fertility due to the effects of HS on male fertility. In conclusion, different hormonal, managerial, and reproductive techniques can be employed to reduce the severity of HS in lactating dairy cows.

Key Words: dairy cattle, heat stress, fertility

607 Management and dietary manipulations during heat stress periods to improve lactation and reproduction. J. E. P. Santos* and C. R. Staples, *University of Florida, Gainesville.*

Dairy cows undergo hyperthermia during heat stress which causes a dramatic reduction in nutrient intake and absorption. Nevertheless, only half of the loss in production is attributed to reduced dry matter (DM) intake. Reduction in DM intake is thought to reduce heat production within the digestive tract, perhaps as a compensatory mechanism to reduce heat load in hyperthermic cows. Hyperthermia and reduced DM intake decreases rumen contractility and increases retention time of feeds, thereby increasing the risk of acid accumulation in the rumen. Cows exposed to high ambient temperatures have increased respiration rate, which can result in respiratory alkalosis and excessive loss of CO_2, thus reducing the amount of salivary buffers produced. Dairy cows exposed to heat stress also have depressed reproductive performance. In general, most dietary interventions during heat stress that have resulted in benefits to lactation have only had minor effects on reproductive performance. An often neglected area is the immediate prepartum period. Recent research at the University of Florida has demonstrated that cooling pregnant cows either during the entire nonlactating period or only during the last 4 weeks of gestation has long-lasting effects on the subsequent lactation. Providing evaporative cooling at temperature and humidity index >65 reduced body temperature approximately 0.3 to 0.4°C for 7 to 10 h during the afternoon which seems to be sufficient to elicit positive pre- and postpartum responses in cows. Cows cooled prepartum had increased mammary cell proliferation, which is thought to mediate some of the improvements in lactation performance. Increments in lactation performance due to evaporative cooling prepartum have ranged from 3 to 5 kg/d more milk during the first 15 to 40 wk postpartum. The same benefits from cooling dairy cows prepartum have not been observed for reproductive performance. Nevertheless, heifers born from cows receiving evaporative cooling prepartum had altered immune function and improved lactation.

Key Words: heat stress, nutrition, reproduction

608 Milk somatic cell counts in Southeast dairy herds. K. L. Anderson*[1], E. Wemple[1], K. Ingawa[2], M. Correa[1], R. Lyman[1], and K. Mullen[3], [1]*College of Veterinary Medicine, North Carolina State University, Raleigh,* [2]*Dairy Records Management Systems, Raleigh, NC,* [3]*College of Agriculture and Life Sciences, NC State University, Raleigh.*

The objectives of this study were to examine herd average milk SCC from Southeast (SE) dairies to assess potential compliance with the 400,000/mL European Union (EU) SCC standard and to determine if seasonal SCC patterns were present. Recent efforts to reduce US levels for maximal bulk milk SCC to 400,000/mL were not successful. However, beginning in early 2012, milk products shipped from the US to the European Union (EU) must come from milk documented to have an SCC ≤400,000/mL. The USDA National Animal Health Monitoring System has published data that indicate that dairies in the Central, Upper Mideast, Midwest and Southwest regions produce milk that averaged <400,000/mL SCC, with the presence of distinct seasonal increases during the summer and fall. Data from the Southeast (SE) US region were not available in the USDA study. Therefore, SCC records from dairies in 12 SE states were obtained from Dairy Records Management Systems (Raleigh, NC) for the period from March 2009 to February of 2011 and mean SCC by month were determined. Mean monthly SCC of dairy herds in several SE states were often >400,000/mL and exhibited a distinct seasonal pattern, with peak mean levels occurring from July to October. To determine associations between elevated SCC and individual mastitis pathogens, microbiology was completed on 4988 quarter milk samples from 1,247 cows from 14 North Carolina dairies with a range of low to high bulk milk SCC. Statistical associations between specific mastitis pathogens and elevated SCC were determined using either Chi-Square or Fisher's Exact test. *Staphylococcus aureus*, *Streptococcus* spp., and mixed major pathogens were significantly ($P < 0.0007$) associated with increased individual cow SCC (>400,000/mL). Dairies in the SE face challenges to lower SCC and will need to use strategies to control specific mastitis pathogens such as *Staphylococcus aureus* and environmental streptococci.

Key Words: milk, SCC, Southeast

609 Management practices to reduce heat stress, prevent mastitis, and lower somatic cell counts in dairy cows and heifers. S. C. Nickerson*, *University of Georgia, Athens.*

This presentation discusses various management practices for abating heat stress in dairy cattle to maximize cow comfort, reduce udder infections, lower SCC, and improve milk production. Hot and humid environmental conditions along with solar radiation, animal crowding, insect pests, and poor ventilation add to the stress already imposed on the productive capacity of the dairy cow. Collectively, these sources of stress are associated with an increased prevalence of mastitis, elevated SCC, lowered milk quality, and reduced yield. Methods to manage heat stress include a balanced diet, provision of adequate shade to alleviate solar radiation, and cow cooling in the forms of chilled drinking water, commercial coolers, corral manger misters, mechanical refrigeration, cooling ponds, and shower and fanning stations in the premilking preparation holding areas and exit lanes. Unfortunately, use of water is problematic because it is an excellent transport medium for mastitis-causing bacteria, especially those from environmental sources. In addition, warm, humid conditions are ideal for the growth of environmental streptococci and coliforms; thus, the environmental load with mastitis-causing organisms markedly increases. As such, proper management of bedding, alley ways, and premilking udder hygiene to minimize bacterial exposure to teats is critical during the summer months of the year to maintain milk quality. Strict monitoring of udder health, bedding management, and pre-milking cow prep through routine bulk milk and individual cow cultures and SCC, and recording of all clinical mastitis cases are essential. In addition, bred heifers, representing the future milking herd, should be managed to reduce the stress associated with horn flies during the hot summer months, which are instrumental in the spread of staphylococcal mastitis.

Key Words: heat stress, mastitis, somatic cell count

ADSA-ASAS Northeast Section Symposium: Optimal Land Use for Northeast Farms—Growing Crops and Feeding Animals

610 Whole-farm assessment of alternative cropping and feeding strategies. C. A. Rotz*, *USDA/ARS, University Park, PA.*

A change in cropping and feeding practices can affect the performance, economics and environmental impacts of a dairy farm. A whole farm assessment of all major effects can only be done through process level simulation of the production system. The Integrated Farm System Model provides a research and educational tool for this type of evaluation. A farm production system can be simulated through many years of weather to quantify the performance, economics and environmental effects under the assumed management. Then various changes in cropping and feeding practices can be simulated to determine their effects. Performance measures include crop yield and nutritive value, animal intake and production, machinery use and timeliness of operations, and the use of resources such as fertilizer, fuel, and labor. Production costs, income and net return are then calculated from the simulated performance. Predicted environmental impacts include emissions of ammonia, hydrogen sulfide and greenhouse gases, edge of farm losses of sediment and phosphorus, and leaching of nitrogen and phosphorus to groundwater. From the predicted performance and losses, carbon, energy, water and reactive nitrogen footprints are determined for each production practice. A life cycle assessment is used to determine these footprints, which includes both direct farm sources as well as those occurring in the production of resources used on the farm. This Windows-based software tool is available for research and educational use at https://www.ars.usda.gov/Main/docs.htm?docid = 8519. Information obtained through the simulation of various management practices will lead to the selection of more sustainable production systems for dairy production in the Northeast in response to changing climate and economic conditions.

Key Words: farm model, production economics, environmental footprint

611 The expanding role of alternative forages for dairy farms in the Northeast. G. W. Roth*, *Penn State University, University Park.*

There has been a dramatic increase in the interest in use of alternative crops for feed in the dairy industry in the Northeast. This has been driven by several factors: (1) the high cost of off farm purchased feed and forages, (2) periodic droughts which have affected corn production on some soils and (3) the high cost of corn production with high N and seed costs. Overall this has resulted in an intensification of crop production with some farms harvesting up to 3 crops in a year where only one may have been harvested in the past. This intensive cropping has been facilitated by the availability of good no-till equipment and custom planting and harvesting operators that can rapidly harvest and plant quickly to optimize potential yields. Fall oats, winter triticale, rye, wheat, and barley, ryegrass, sorghum-sudan, and forage sorghums are some of the most popular alternatives. Each crop has a unique fit in different soils and climates and role in dairy rations. When managed well, these crops can play an important role in the lactating cow rations. If management or weather conditions cause issues with the forage quality then they can often be utilized in rations for replacement animals, and often this is the key objective of alternative crop production. Two key management challenges are proper N fertilization and harvesting at the correct maturity. Under fertilizing with N can result in lower yields and low protein forages, while harvesting too late can result in high fiber and low energy forages. The fall and winter small grains have the potential to use the growing season between corn harvest and planting and in some regions and this can add an additional 3–4 tons/acre of dry matter to the forage production potential. Sorghum and sorghum sudan crops are more drought resistant than corn and have a special niche on droughty soils that result in poor corn yields or wet soils that are difficult to plant corn in on a timely basis. These systems are providing ways to manage crop production risks, protect soils from erosion, reduce runoff and leaching and improve the nutrient balance of dairy farms while increasing the forage production on the farm.

Key Words: forage, small grain, sorghum

612 Integrating land use and dairy cattle rations: Challenges and opportunities. L. E. Chase*, *Cornell University, Ithaca, NY.*

Dairy producers face formidable challenges integrating crop acres, cropping programs, animal feed requirements, rations, environmental considerations and economics. A case study approach was used on a New York dairy farm over a 5-year period to examine these interactions. At the intiation of the study, this farm had 435 tillable hectares that were divided into 43% as corn silage and 57% as alfalfa and grass mixed forages. The farm was milking 408 cows with an average mlk production of 30.9 kg/cow/day. Forty-three percent of the total ration consumed was home grown feeds. The land base was a mix of well-drained valley and moderate to poorly drained sloping soils. A whole farm planning process was implemented that encompassed changes in the cropping program, forage harvest procedures, forage storage, ration management and ration formulation. The key changes were increasing the hectares of grass forages grown on the hillside lands, improved bunker silo management, utilizing an electronic feed management system and adjusting rations using the CNCPS (Cornell Net Carbohydrate and Protein System) model. At the end of the study, there were 460 tillable hectares consisting of 38% in corn silage and 31% each in alfalfa and grass forages. Herd size had increased to 544 milking cows producing 33.6 kg/cow/day. The increase in herd size was mainly due to lower culling rates and some purchased animals. The rations fed contained 59% home grown feed. During this study, total milk sold per day incresased by 45% as a result of the changes in milk produced per cow and cow numbers. Daily purchased feed cost decreased by 24% while the feed cost/kg of milk produced was 52% lower. Imported nitrogen and phosphorus decreased by 37 and 40% due to utilizing more home produced feeds in the ration. Total herd nitrogen excretion was 17% lower at the end of the study while phosphorus excretion decreased by 28%. This project provides an example of the types of changes that can result from using a whole farm planning and implementation process on a commercial dairy farm.

Key Words: nutrient management, CNCPS, whole-farm planning

613 Measurement time required to detect sow lameness using an embedded microcomputer-based force plate system. B. M. McNeil*[1], C. E. Abell[1], J. D. Stock[1], S. T. Millman[2], A. K. Johnson[1], L. A. Karriker[2], and K. J. Stalder[1], [1]*Department of Animal Science, Iowa State University, Ames,* [2]*Swine Medicine Education Center, College of Veterinary Medicine, Iowa State University, Ames.*

Sow lameness is a key reason for sow removal from the breeding herd. Current sow lameness measures are subjective and therefore, biased. Efficient objective lameness measures are needed to improve diagnosis. It has been shown that an embedded microcomputer-based force plate system can detect lameness by measuring sow weight distribution. The objective of this study was to identify time required to adequately assess sow weight distribution on an embedded microcomputer-based force plate. Sound and lame states were examined to ensure that time requirements were the same for all lameness stages. Lameness was induced in 12 mature mixed parity sows on d 0 using a chemical synovitis model, applied to 1 of 2 randomized injection sites, left rear claws (LR) or right rear claws (RR) with 3 replicates per sow. There was a 2-wk time period between subsequent injections. A static force plate was used to measure the weight applied to each foot twice per second for 15 min on d −1, +1, +6 and +10 relative to lameness induction. Data were analyzed using a mixed model with time fitted as a fixed effect and a random sow effect. Results indicate mean and standard deviation force plate weight recordings after 5 min are not different ($P \geq 0.05$) when compared with those taken for 10 and 15 min, respectively. The maximum difference observed between the weight placed on each foot averaged over 5 and 15 min was 2.22 kg and 2.07 kg, for lame and sound sows, respectively. In conclusion, the force plate can discriminate weight distribution differences for sows when sound and acutely lame within 5 min. The results of this research can be used to improve the efficiency of using the force plate to objectively measure sow lameness by increasing the number of sows that can be measured within a given time period.

Key Words: sow, lameness, weight distribution

614 Embedded micro-computer based force plate as an objective tool to measure painful and non-painful hoof lameness states in multiparous sows. C. Mohling*[1], A. Johnson[1], C. Abell[1], H. Coetzee[2], S. Millman[3], L. Karriker[4], and K. Stalder[1], [1]*Animal Science, Iowa State University, Ames,* [2]*Cyclone Custom Analyte Detection Service, Iowa State University, Ames,* [3]*Veterinary Diagnostic and Animal Production Medicine, Iowa State University, Ames,* [4]*Swine Medicine Education Center, Iowa State University, Ames.*

Lameness diagnosis using subjective gait scoring may not be repeatable and reliable. Weight distribution is one tool that might provide objective measures to determine the severity of lameness. The objective of this study was to compare differences in weight placed on each limb from sows in painful and non-painful hoof lameness states. Twelve mixed parity sows weighing 228.51 ± 18.08 kg (mean BW ± SD) were individually housed. On d 0, lameness was induced on a randomized rear hoof using a chemical synovitis model. After completion of the first round, sows were given a 7d rest period and then the trial was repeated with lameness induced in the other rear hoof. Three treatment days were compared (1) sound (1 d before induction), (2) most lame (first day after induction of transient lameness) and (3) resolved (sixth day after induction). Sows stood individually on an embedded force plate for 15 min, and weight on each hoof was measured independently. Data were analyzed using the PROC MIXED procedure in SAS with sow as the experimental unit in a crossover design. Weight distributions were compared between sound, most lame and resolved days. On the most lame day, sows exhibited less weight bearing on the injected hoof compared with sound and resolved days ($P < 0.0001$). On the resolved days, sows placed less weight on the lame hoof compared with the sound day ($P < 0.0001$). Regardless of which hoof was injected, sow weight distribution did not vary between the injected hooves ($P = 0.62$) or between rounds ($P = 0.97$). In conclusion, the embedded microcomputer force plate was a sensitive tool detecting acute hoof lameness in mature sows.

Key Words: force plate, lameness, swine

615 Porcine reproductive and respiratory syndrome virus (PRRSV) causes neuroinflammation and cognitive impairment in neonatal piglets. M. Elmore[1], M. Burton[1], M. Conrad[1], J. Rytych[1], W. Van Alstine[2], and R. Johnson*[1], [1]*University of Illinois, Urbana,* [2]*Purdue University, West Lafayette, IN.*

Inflammatory cytokines produced during infection affect the developing brain. This is important to animal agriculture because developmental events may program behavioral and physiological systems that affect production and well-being. Unfortunately, little is known in agricultural animals about how neonatal infection affects brain development and behavior. To begin addressing this issue, piglets obtained 48 h after birth were placed in disease containment chambers where they received a nutritionally complete piglet milk replacer. At 7 d of age, piglets were inoculated with PRRSV or sterile PBS. Throughout the study, body weight, rectal temperature, and sickness behaviors were measured daily. At 2-wk of age, piglets were trained to locate a reward in a constant place and location using extra-maze visual cues in a T-maze. After behavioral testing, piglets were euthanized (~4 wks of age) for tissue collection. RT-PCR was used to assess expression of a panel of genes in the hippocampus that served as markers of inflammation, oxidative homeostasis, and synaptic plasticity. Microglia were isolated from the hippocampus and stained with antibodies to confirm cell type (CD11b and CD45) and indicate cell activation (MHC II). PRRSV piglets had a higher average daily temperature ($P < 0.0001$), were less likely to consume their first meal each day ($P < 0.0001$), and had lower average body weights at the end of the study ($P = 0.0022$) compared with control piglets. Maze performance was affected by treatment ($P = 0.003$), with PRRSV piglets taking longer to reach performance criterion than controls. PRRSV piglets had significantly higher levels of activated microglia (43.18 ± 5.91%) compared with controls (2.52 ± 6.93%; $P = 0.0003$). This was accompanied by a general increase in inflammatory gene expression. Overall, these data demonstrate that piglets infected with PRRSV exhibit cognitive impairment and a marked increase in activated microglia in the hippocampus. This heightened neuroinflammatory response likely explains the cognitive deficits observed following PRRSV infection.

Key Words: infection, microglia, swine

616 Automatic lameness detection by computer vision and behaviour and performance sensing. T. Van Hertem*[1,2], S. Viazzi[2], C. E. B. Romanini[2], C. Bahr[2], D. Berckmans[2], A. Schlageter-Tello[3], C. Lokhorst[3], D. Rozen[4], A. Antler[1], V. Alchanatis[1], E. Maltz[1], and I. Halachmi[1], [1]*Institute of Agricultural Engineering - Agricultural Research Organization (ARO) - the Volcani Center, Bet-Dagan, Israel,* [2]*Division M3-BIORES: Measure, Model & Manage Bioresponses, KU Leuven,*

Heverlee, Belgium, [3]WageningenUR Livestock Research, Lelystad, Netherlands, [4]Fellow in the EU BioBusiness project.

The objective was to develop a reliable automatic lameness detection method based on consecutive daily automatic measurements of cow's back posture, behavioral and performance variables. The experimental setup was located in a commercial Israeli dairy farm of 1,100 Israeli Holstein cows. All cows were housed in open, roofed cowsheds with dried manure bedding and no stalls. All cows were equipped with a commercial neck activity and ruminating time data logger. Milk yield was measured with a milk flow sensor. Cow gait recordings were made during 4 consecutive nighttime milking sessions with a depth image camera. From the videos, the "inverse radius" of the back posture contour and the "body movement pattern" were extracted. The reference in this study was a daily live locomotion score of the animals. A dataset of 186 cows with 4 video-based lameness scores and 4 live locomotion scores was built. A logistic regression model was built with the highest correlated behavioral and performance variables. Model validation was done with 10-fold cross-validation. The analysis of the video-based scores as independent observations lead to a correct classification rate of 53.0% and a misclassification rate of 9.8% on a 5-point level scale. A multinomial logistic regression model based on 4 consecutive "body movement pattern"-scores and "inverse radius"-scores obtained a correct classification rate of 60.8% and a misclassification rate of 9.1%. Binary classification to lame vs. not-lame categories reached 76.5% sensitivity, 97.8% specificity and 91.9% accuracy with a multinomial logistic regression model. The logistic regression model based on the behavioral and performance data reached a sensitivity of 89%, and a specificity of 85%. The use of consecutive video measurements improved the correct classification rate with 7.8% and misclassification rate with 0.7% compared to the independent analysis of the observations. The combination of image processing and behavioral monitoring is believed to further improve the lameness detection accuracy. This study is part of the Marie Curie Initial Training Network BioBusiness (FP7-PEOPLE-ITN-2008).

Key Words: lameness, computer vision, behavior and performance sensing

617 Effect of dystocia on daily activity patterns prior to parturition in Holstein dairy cows. M. Titler*, M. G. Maquivar, S. Bas, E. Gordon, P. J. Rajala-Schultz, K. McCullough, and G. M. Schuenemann, *Department of Veterinary Preventive Medicine, The Ohio State University, Columbus.*

Dystocia increases the risk for health disorders or mortality, and reduces performance of both the dam and calf. The objective of the present study was to assess the effect of dystocia on cow activity behavior 4 d before calving. A total of 147 Holstein cows (PRIM and MULT) housed in free-stall barns from 3 dairy herds were used. All cows were housed in similar facilities using a close-up pen 15 d before the expected calving date and a contiguous individual maternity pen for parturition. Electronic data loggers (IceQube, IceRobotics, Edinburgh, Scotland) were placed on the hind leg of periparturient dairy cows at 7 ± 3 d before the expected calving date and 14 ± 3 DIM. Calving ease (CE; scale 1–4), parity, calving date and time, and stillbirth (born dead or died within 24 h) were recorded. The number of steps, standing time (min), number of lying bouts (LB), and mean duration of LB (min) were recorded. Unassisted cows (n = 132; CE score of 1) were compared with assisted cows (n = 15; CE scores of 2–3). Data were analyzed using MIXED (activity patterns) and GLIMMIX (stillbirth) procedures of SAS. Activity patterns for assisted or unassisted cows were adjusted for the effect of herd, parity, and CE. Cows with assisted births spent more time standing (18.6%; ($P < 0.05$), had similar number of LB ($P > 0.05$), but LB of longer duration (42.6%; ($P < 0.05$) 24 h before birth compared with unassisted cows. These findings provided evidence that cows experiencing difficult births showed distinct activity behavior 1 d before calving. Recognizing early warning signs (restless activity) of dystocia before birth may help identify those cows most at risk and preplan a triage as opposed to waiting for the usual signs of intervention. Monitoring cow activity along with proactive management practices around the time of calving should improve the overall survival and welfare of both the dam and calf.

Key Words: dystocia, stillbirth, dairy cow welfare

618 Rumination and feeding behavior before calving can identify cows at risk for metritis and subclinical ketosis after calving. K. Schirmann*[1,2], N. Chapinal[1], W. Heuwieser[2], D. M. Weary[1], and M. A. G. von Keyserlingk[1], [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.*

The objective of this study was to investigate differences in rumination and feeding activity between healthy and sick animals in the transition period. Cows were monitored from 10 d before to 21 d after calving. Daily rumination and feeding activity were recorded electronically and cows were subject to daily health checks. Twice a week cows were examined for vaginal discharge, and 3 times a week blood was sampled for β-hydroxybutyric acid concentration (BHBA). Cows were diagnosed as metritic when they had purulent (>50% pus visible) or fetid, watery discharge. Subclinical ketosis (SCK) was classified at a BHBA concentration of ≥1.0 mmol/L during the week after calving or ≥1.4 mmol/L during the following week. Cows with BHBA >3.0 mmol/L at any time throughout the study were classified as ketotic. Cows that were healthy (n = 19) were compared with those that had metritis (n = 16), SCK (n = 9), or both metritis and SCK (n = 10) using mixed models in SAS, including health status as a fixed effect. The contrast statement was used to test for differences between the LSM. Compared with healthy cows, those with SCK or metritis and SCK spent less time ruminating in the prepartum period (−88.3 ± 27.0 min/d; and −42.2 ± 25.3 min/d, respectively). There were no differences between healthy and any of the sick groups in time spent ruminating after calving. Dry matter intake before calving was lower for all 3 classes of sick animals (metritic: −0.8 ± 1.1 kg/d; SCK: −2.5 ± 1.2 kg/d; metritic and SCK: −3.1 ± 1.2 kg/d) relative to healthy cows; theses differences were no longer evident after calving. Cows with SCK spent less time feeding than healthy cows before calving (SCK: −60.0 ± 18.8 min/d) and after calving (−30.8 ± 14.8 min/d), but there was no difference between healthy cows and those with metritis or metritis and SCK in either period. In conclusion, electronic recordings of rumination and feeding behavior before calving show promise in identifying cows at risk for metritis and SCK after calving.

Key Words: welfare, rumination, postpartum disease

619 Detecting post-calving ketosis by sensors and models. M. Steensels*[1,2], E. Maltz[1], C. Bahr[2], D. Berckmans[2], A. Antler[1], and I. Halachmi[1], [1]*Institute of Agricultural Engineering - Agricultural Research Organization (ARO) - the Volcani Center, Bet-Dagan, Israel,* [2]*Division M3-BIORES: Measure, Model & Manage Bioresponses, KU Leuven, Heverlee, Belgium.*

The aims were to analyze behavior (lying time, lying bouts, rumination time, activity) and performance (milk yield and composition) variables

of multiparous cows in early lactation in relation to post-calving ketosis and to develop a model to detect post-calving ketosis based on these variables. Every cow between 5 to 12 days after calving was examined for ketosis. A cow with a Ketostix test result higher than 1,470 µmol AcAc/L was considered as ketotic.Six commerical Israeli dairy farms contributed to the research. Two were equipped with behavior sensors that recorded maximal number of steps per hour, lying bouts and lying time. In the analysis, 39 ketotic and 118 healthy cows were used. Four were equipped with rumination and neck activity sensors. In the analysis, 203 ketotic and 503 healthy cows were used. Daily behavior and performance data for the first three weeks after calving were analyzed using a repeated measures procedure and then, a logistic regression model was developed for post-calving ketosis detection. Lying time was higher in ketotic (546 ± 4 min/d; mean ± standard error) than in healthy (503 ± 2 min/d) cows. Maximal number of steps per hour was not different in ketotic and healthy cows. Rumination time was lower in ketotic (36.3 ± 0.6 min/2 hour) than in healthy (39.1 ± 0.4 min/2 hour) cows. Neck activity was lower in ketotic (27.9 ± 0.5 units/2 hour) than in healthy (30.0 ± 0.3 units/2 hour) cows. Milk yield was lower in ketotic (34.4 ± 1.0 kg/d) than in healthy (38.9 ± 0.6 kg/d) cows. For post-calving ketosis detection, the best model results were obtained when calibration and validation were performed on data from the same farm: sensitivity ranged from 78% to 90% and specificity ranged from 71% to 74%. It was concluded that behavior and performance variables in early lactation (rumination time, activity and milk yield) can be used to detect post-calving ketosis. Other diseases might show similar patterns. Between-farm differences can affect model robustness and it is suggested that including more variables from other sensors into the model could improve model quality.

Key Words: ketosis, behavior and performance sensing, logistic regression model

620 Effect of metritis on daily activity patterns in lactating Holstein dairy cows. M. Titler*, M. G. Maquivar, S. Bas, E. Gordon, P. J. Rajala-Schultz, K. McCullough, and G. M. Schuenemann, *Department of Veterinary Preventive Medicine, The Ohio State University, Columbus.*

Metritis increases the risk for mortality and reduces milk yield and reproductive performance of lactating dairy cows. The objective of the present study was to assess the effect of metritis on activity behavior 3 d before and after diagnosis. A total of 15 lactating Holstein cows diagnosed with metritis (MET) were matched with 15 non-MET lactating Holstein cows. All cows were housed in free-stall barns and calved during the same week. Electronic data loggers (IceQube, IceRobotics, Edinburgh, UK) were placed on the hind leg of periparturient dairy cows at approximately 7 ± 3 d before the expected calving date and remained until 14 ± 3 DIM. Metritis was defined as a fetid red-brown watery vaginal discharge with systemic signs of illness within 14 DIM. Calving ease (CE; scale 1–4) of cows, parity, and stillbirth (born dead or died within 24 h) were recorded. The number of steps, standing time (min), number of lying bouts (LB), and mean duration of LB (min) were recorded. Activity patterns of MET cows were compared with non-MET cows. Data were analyzed using MIXED procedures of SAS. Activity patterns for MET or non-MET cows were adjusted for the effect of herd, parity, and CE. MET cows spent more time standing (4–28%), had fewer steps (12–35%) and LB (23%), and LB of longer duration (22–28%) 1–3 d before and after diagnosis compared with non-MET cows ($P < 0.05$). These findings provided evidence that cows experiencing MET showed distinct behavioral activity patterns 1–3 d before diagnosis. Although proactive management practices to prevention MET should be a top priority for dairy herds, monitoring transition cow activity may help identify those cows at risk of MET before developing the clinical signs and improve the overall survival and welfare of MET cows.

Key Words: transition cow management, metritis, dairy herd welfare

621 Cow activity around diagnosis of naturally occurring clinical mastitis. P. J. Rajala-Schultz*, K. E. McCullough, P. N. Gott, G. M. Schuenemann, and M. Titler, *Department of Veterinary Preventive Medicine, The Ohio State University, Columbus.*

As the most common disease of dairy cows worldwide, mastitis causes considerable economic losses in dairy herds and it is also an animal welfare issue. Early diagnosis and treatment could mitigate these negative effects. Dairy cows display classic sickness behavior after experimentally induced mastitis, but behavioral changes in naturally occurring cases of clinical mastitis (CM) have rarely been reported. The objective of this study was to describe sickness behavior in cows with naturally occurring CM. Activity monitors (IceQube, IceRobotics, Edinburgh, UK) were placed on a hind leg of 80 pregnant dairy cows about a week before expected calving and kept for 14–21 d after freshening in 2 Ohio dairy herds during July and August of 2011 and of 2012. CM cases were diagnosed by farm personnel according their standard operating procedures. The monitors measured number of steps taken and lying bouts, and lying and standing time. Data were analyzed with PROC MIXED in SAS (SAS Institute Inc., Cary, NC). Daily summaries of the different activity parameters were used as outcomes and days with respect to CM diagnosis was the main variable of interest. Day 5 before diagnosis was used as the baseline level in the analysis. Days in milk at CM diagnosis, herd and parity were tested in the models as potential confounders. During the study periods, 12 cows were diagnosed with CM only (no other diseases) and were included in statistical analysis. Preliminary results indicate that an average length of a lying bout was significantly shorter 3 and 2 d before CM diagnosis (by 34 min, $P = 0.0063$ and 37 min, $P = 0.0048$, respectively). Also, overall standing time was 2.2 h longer ($P = 0.0293$) 2 d earlier compared with the day of CM diagnosis. These preliminary results suggest that cow activity is altered around CM occurrence and before herd personnel is able to make a diagnosis of CM. As this type of technology becomes more readily available on farms, monitoring of behavioral changes could assist in early diagnosis of CM and alert herd personnel to more careful examination of high risk cows.

Key Words: cow activity, clinical mastitis, sickness behavior

622 Use of accelerometers for early detection of hoof lesions and lameness in dairy cows. J. H. Higginson Cutler*[1], S. T. Millman[2], G. Cramer[1,3], K. E. Leslie[1], A. M. B. de Passille[4], T. F. Duffield[1], and D. F. Kelton[1], [1]*University of Guelph, Guelph, ON, Canada,* [2]*Iowa State University, Ames,* [3]*Cramer Mobile Bovine Veterinary Services, Stratford, ON, Canada,* [4]*Agriculture and Agri-Food Canada, Agassiz, BC, Canada.*

Lameness is considered one of the primary welfare concerns in the dairy industry. Early identification of lameness has been suggested as one method for decreasing the prevalence of lameness. The objective of this research was to determine differences in activity and lying behavior in lame and sound cows as well during development of hoof lesions could be observed with accelerometers. All cows on a research farm (n = 234) were fitted with Afikim Pedometer Plus accelerometers. All cows had their hooves examined every 3–4 mo at which time lesions were identified, video of gait was taken for locomotion scoring, and trimming was performed if necessary. Cows with a locomotion score

of 3 or above on a 5-point scale were considered lame. To determine if activity and lying differed between lame and sound cows, linear mixed models were built. To determine if changes could be observed within cow but comparing periods of time where individual cows were sound and lame, a generalized linear mixed model was used to assess change between the 2 time periods (approximately 3–4 mo apart). Eleven cows with ulcers, one cow with digital dermatitis, and 3 cows with both ulcers and digital dermatitis were observed lame and included in analysis. Lame cows were significantly less active ($P = 0.01$) and had greater lying duration ($P = 0.04$) compared with sound cows. When comparing data for cows in periods where they were sound and periods where painful lesions were present, data was available for 22 cases of ulcers, 10 cases of digital dermatitis, and 8 cows with both ulcers and digital dermatitis. Lying duration differed between the 2 time periods, with cows lying for 55 min more when a painful ulcer was present compared with when they did not have a painful lesion ($P = 0.03$). This accelerometer can be used to detect changes both between lame and sound cows and within cow when comparing periods of time when cows were sound to periods when a painful lesion was present. Early detection could allow for timely treatment and decrease the prevalence of lameness in dairy cattle.

Key Words: lameness, accelerometer, hoof lesion

623 Pheromone/Interomone effects of behavior of foals after weaning. K. A. Guay*, M. D. May, and J. J. McGlone, *Texas Tech University, Lubbock.*

Weaning can be stressful to both the mother and offspring. This was a preliminary study to determine if calming pheromones had an effect on foal behavior immediately after the weaning process. After weaning, foals vocalize, pace, increase aggression and show increased activity. The pig pheromone (androstenone) was shown in our laboratory to reduce head-shy behavior of horses. The rabbit maternal pheromone (2-methylbut-2-enal) was shown to reduce anxious behaviors in dogs. Both the pig and rabbit pheromones act as interomones on other species. Ten foals were selected and randomly assigned to a treatment group. Twelve foals (6 to 8 mo of age) from a large commercial ranch in West Texas were weaned on a single day. All subjects were stock type ranch horses (Quarter Horse). Foals were randomly assigned a treatment, n = 4 (pig pheromone; PP, rabbit pheromone; RP, or Control; CON). Treatments were administered as a gel to the nose of the animal and then separated into non-adjacent, group pens. Stress behavior such as vocalizations, pawing, fighting, headshaking, defecation, pacing and sweating were recorded for 15 min post weaning. Analysis was done by 2 × 2 Chi-squared. The CON group paced more ($P < 0.01$) than RP or PP groups (70.8, 15.7, 13.4%, respectively). The RP-treated foals vocalized more ($P < 0.01$) compared with CON (52.0 vs. 30.0%) and CON vocalized more than PP-treated foals (30.0, 18.0%, respectively). The CON group displayed more ($P < 0.001$) aggressive/fighting behavior than RP and PP (59.3, 7.3, 33.33%, respectively), and PP fought more than RP (33.33 vs. 7.3%, respectively). Our findings suggest pheromones/interomones may reduce some negative behavioral effects observed at weaning. The RP and PP may calm weaned horses. More research is needed to describe behavioral and physiological influences of interomones on horses in stressful situations.

Key Words: horse, pheromone, interomone

624 Relationships of temperament, exit velocity and rectal temperature of crossbred steers challenged with bovine viral diarrhea virus. X. Fang*[1], E. Downey[1], C. A. Runyan[1], J. E. Sawyer[2], T. B. Hairgrove[1], J. F. Ridpath[3], W. Mwangi[1], C. A. Gill[1], and A. D. Herring[1], [1]*Texs A&M University, College Station,* [2]*Texas Agrilife Extension, College Station,* [3]*USDA-ARS, Ames, IA.*

The objective of this study was to investigate genetic influences of temperament that may affect health-related measures in cattle. Angus-Nelore F_2 and F_3 yearling steers born in 2009–2011 were stratified by breed composition and sire across bovine respiratory disease vaccine strategies of killed (2009 n = 28, 2010 n = 32, 2011 n = 35), modified live (MLV) (2009 n = 25, 2010 n = 36, 2011 n = 35) or no vaccine (2009 n = 25, 2010 n = 36, 2011 n = 36). Prior to vaccination, temperament score (TS) was assessed through a 1-to-9 scoring of system shortly after weaning (approximately 8 mo age) by 4 evaluators. Following vaccination (25 to 35 d), with killed booster or single MLV, steers were challenged intranasally with a strain of type 1b bovine viral diarrhea virus (BVDV). Exit velocity (EV, m/s) and rectal temperature (RT) were collected on vaccination days, BVDV challenge day (d 0), and d 3, 7, 10, 14, 28, and 42 d following challenge. Pearson correlations among TS, EV and RT were evaluated. Mean TS was 4.2, 5.9 and 4.5 in 2009, 2010 and 2011-born steers, respectively; some sires were only represented in one year. Correlations (0.17 to 0.37, $P < 0.05$) between TS and EV were observed after first vaccination day. Correlations (0.19 to 0.31, $P < 0.005$) between TS and RT were observed. Correlations (−0.12 to −0.28, $P < 0.005$) between EV and RT on the same day were observed after 7 d following challenge. Mixed model analyses of EV and RT as repeated measures incorporated fixed effects of year (YR), vaccine group (VAC), sire nested within YR, pen nested within YR, and day, along with potential interactions involving YR, VAC and day. Sire, YR and day were significant influences on EV and RT. VAC × day influenced RT, but not EV. The interaction of YR × VAC × day influenced both EV and RT, but without obvious patterns. In these cattle it appears temperament may be a primary influence on rectal temperature. Interpretation of rectal temperature for cattle health is complex and should perhaps involve assessment of temperament score and/or exit velocity, at least in some circumstances.

Key Words: temperament, exit velocity, BVDV challenge

625 Analysis of immune-relevant genes expressed in spleen of *Capra hircus* kids fed with Cr-Met supplement. M. J. Najafpanah* and M. Sadeghi, *University of Tehran, Tehran, Iran.*

Various metals are responsible for many immunological activities of the body as micronutrients. Chromium has a significant role in altering the immune response by immunostimulatory or immunosuppressive processes. Our objective is to survey the effect of Chromium (Cr^{3+}) on expression of B2M, MHCII-DRA, MHCII-DRB and RAP2A genes in spleen that it houses immune cells such as T and B cells. Here, we investigated the effect of Chromium on genes expression in goat that treated with Chromium as chromium-methionine (Cr-Met) supplement. Twenty-four, male kids of Mahabadi goat were used and randomly allocated to 1 of the 4 dietary treatments according to live weight. They were individually penned for 90-d feeding period. The treatments were included 3 levels of 0.5, 1 and 1.5 mg/day of chromium plus standard control diet and the fourth treatment was standard control diet without Cr-Met supplement. After feeding, the kids were slaughtered and samples taken from the spleen. Total RNA was extracted and first-strand cDNA synthesis was performed. Real-time PCR was performed on iQ5 Bio-Rad system using HSP-90 as a reference gene. The results showed that expression of each 4 genes affected by chromium have increased significantly compared with the control treatment ($P < 0.05$). The highest and the lowest level of expression was related to the treatment containing 1.5 and 0.5 mg/day of chromium, respectively. Consequently, it may be concluded that supplemental chromium has some beneficial effects on the health status and it may lead to the increased susceptibility of animals to resist certain diseases such as bacterial infection or parasitic illness.

Key Words: chromium, Mahabadi goat, MHC gene

626 Prenatal transportation alters the acute phase response (APR) of bull calves exposed to a lipopolysaccharide (LPS) challenge. N. C. Burdick Sanchez*[1], J. A. Carroll[1], D. M. Price[2,4], B. P. Littlejohn[2,4], M. C. Roberts[2,4], R. C. Vann[3], T. H. Welsh Jr.[4], H. D. Hughes[5], J. T. Richeson[5], and R. D. Randel[2], [1]*Livestock Issues Research Unit, USDA-ARS, Lubbock, TX,* [2]*Texas A&M AgriLife Research, Texas A&M University System, Overton,* [3]*MAFES-Brown Loam, Mississippi State University, Raymond,* [4]*Texas A&M AgriLife Research, Texas A&M University System, College Station* [5]*Department of Agricultural Sciences, West Texas A&M University, Canyon.*

This study was designed to determine if prenatal transportation influences the APR to a postnatal LPS challenge. Pregnant Brahman cows (n = 96) matched by age and parity were separated into transported (TRANS; n = 48; transported for 2 h on gestational d 60, 80, 100, 120 and 140) and non-transported control groups (CONT; n = 48). From these cows, bull calves (n = 16 per TRT) were identified at weaning (176 ± 2 d of age) to subsequently receive a LPS challenge. We previously reported an effect of TRANS on temperament (TEMP); therefore bulls were also grouped based on TEMP score [Calm (C); Intermediate (I), or Temperamental (T)]. On d −3 bulls were fitted with rectal temperature (RT) probes and were transported from Overton to Lubbock, TX on d −2. On d −1 bulls were fitted with jugular cannulas and placed in individual stanchions. On d 0 blood samples and sickness behavior scores (SBS) were collected at 0.5-h intervals from −2 to 8 h and again at 24 h relative to LPS challenge (0.5 μg/kg BW). Serum was analyzed for cortisol, interferon-γ (IFNγ), tumor necrosis factor-α (TNFα), and interleukin-6 (IL6) concentration. All variables increased following LPS ($P < 0.01$). Both pre- and post-LPS TRANS bulls had greater RT than CONT bulls ($P < 0.01$), and T bulls had greater RT than C and I bulls ($P < 0.01$). The SBS was greatest in the C TRANS bulls post-LPS and post-LPS cortisol was lowest in the T bulls ($P < 0.01$). Pre- and post-LPS TNFα was greater in TRANS than CONT bulls ($P = 0.03$ and < 0.01). Post-LPS TNFα was greatest in the T TRANS bulls ($P < 0.01$). Pre-LPS IL6 was greater in TRANS than CONT bulls ($P = 0.02$), yet was greater in CONT than TRANS bulls post-LPS ($P = 0.04$). Pre-LPS, IFNγ was greater in CONT than TRANS bulls ($P < 0.01$), yet was greater in TRANS than CONT bulls ($P < 0.01$) post-LPS. Post-LPS IFNγ was greatest in the I TRANS bulls ($P < 0.01$). Prenatal transportation influenced the physiological and APR before and after LPS, and altered the response within temperament groups. These data demonstrate that prenatal transportation can alter the acute phase response to LPS, and may affect subsequent health and performance of these calves.

Key Words: cattle, immune, transportation

627 Circulating immune cell subpopulations in pestivirus persistently infected calves and non-infected calves varying in immune status. S. M. Falkenberg*, J. Ridpath, and F. V. Bauermann, *USDA-ARS-National Animal Disease Center, Ruminant Immunology Group, Ames, IA.*

The circulating immune cell subpopulations in cattle representing varying stages of immune status categorized as; colostrum deprived (CD), receiving colostrum (COL), colostrum plus vaccination (VAC) and persistently infected with a pestivirus (PI) were compared. The PI calves were infected with a HoBi-like virus, which is a member of the Pestivirus genus and similar to bovine viral diarrhea virus. All calves in the PI group tested positive for viral protein using a commercial ELISA test, all other calves tested negative. Calves in the CD and COL group averaged 60 d of age (DOA), VAC averaged 150 DOA and PI 24 DOA. Blood samples were collected and analyzed by flow cytometry within 2 h after collection. The leukocyte (LEUK) and granulocyte populations were identified using forward and side scatter plots. Primary antibodies were used for identification of the cell markers CD4, CD8, B cell, Gamma-delta (GDTCR) and CD14. Comparisons between immune status groups for total circulating cell populations (cell/mL) revealed differences ($P < 0.0001$) for total LEUK, CD8, B cell, GDTCR and CD14 with the PI group having the lowest total numbers of cells in circulation. While no differences were observed for the absolute number of circulating CD4 among the groups, the proportion of CD4 within total LEUK populations was significantly different ($P < 0.0001$). Significant differences ($P < 0.002$) were also observed in the CD8, B cell, GDTCR and CD14 populations. The PI group had a greater proportion of CD4 cells and the VAC group had the greatest proportion of CD8, while the COL group had the greatest B cell, GDTCR and CD14. No differences ($P > 0.05$) in the absolute number or proportion of circulating cells identified as granulocytes. These results suggest immune cell populations vary between immune status groups with the greatest differences observed for the PI calves. Defining differences associated with different immune statuses could provide insight into immune function.

Key Words: cattle, immune, pestivirus

628 Ontogenetic changes of ochratoxin A on growth performance, serum biochemistry and nephrotoxic damages in cherry valley male ducks. W. Wang[1], L. Zhong[1], H. Ye[1], H. Zhang[2], and L. Yang*[1], [1]*College of Animal Science, South China Agricultural University, Guangzhou, China,* [2]*China National Key Laboratory of Animal Nutrition, Beijing Animal and Veterinary Science Institute, Chinese Agricultural Academy, Beijing, China.*

The objective of this study was to investigate the ontogenetic changes of ochratoxin A (OTA) on growth performance, serum biochemistry and nephrotoxic damages in cherry valley male ducks. Eight hundred one-day-old ducks were assigned to 5 treatment groups with 8 replicates of 20 birds each. The experiment was conducted across 2 periods. Period 1 was d 1 to 21; group I (control group) was fed with commercial diet I free of OTA. Groups II to IV were fed diets containing 2.11, 4.22, 6.33, 8.44 μg/g OTA, respectively. In period 2, all 5 groups were fed with commercial diet II from 22 to 45 d. Our results showed that OTA-contaminated feed reduced ADG and mean intakes significantly, but F/G was not different across treatments in Period 1. In Period 2, ADG of ducks fed 6.33 μg/g diet OTA were decreased. There were no significances of ADFI and F/G in 5 groups. The relative kidney damage in groups D and E from 9 to 35 d was remarkable higher than that in control groups ($P < 0.05$). As to the relative liver weights, group E had the higher damage index compared with the control group after 21 d ($P < 0.05$). Mean blood urea nitrogen, and albumin levels in toxic groups were higher than in control group, especially at second period ($P < 0.05$). No significant difference was observed of TP between toxic groups and control group, but Alb in toxic groups was increased after 21 d. Nephritic glutamic pyruvic transaminase in toxic groups were decreased from 9 to 21 d, and nephritic glutamicoxaloacetic transaminase levels were decreased from 9 to 45 d respectivelyacross periods. Obvious pathomorphological damage in renal tissues of the toxic groups were seen at 3, 9, 15, 21, 35, 45 d. Hyperaemia and granular degeneration in renal tubular epithelial cells were increasingly severe with the higher OTA concentration. These results showed that OTA-contamined feed reduces growth performance and induces nephrotoxic damage in cherry valley male ducks. The damage was not improved even after OTA was eliminated from the feed.

Key Words: ochratoxin A, growth performance, nephrotoxic damage

629 Anamnestic antibody response to BVDV 1b challenge in Angus-Nelore steers. E. D. Downey*[1], X. Fang[1], C. A. Runyan[1], J. E. Sawyer[4], T. B. Hairgrove[3], J. F. Ridpath[2], and A. D. Herring[1], [1]*Texas A&M University, College Station,* [2]*National Animal Disease Center, USDA-ARS, Ames, IA,* [3]*Texas AgriLife Extension, College Station,* [4]*Texas AgriLife Research, College Station.*

Bos taurus-Bos indicus F_2 and F_3 steers were examined over 3 years (2010–2012) for differences in anamnestic antibody responses to a BVDV 1b challenge following a standard vaccine protocol. Angus-Nelore F_2 (n = 122) and F_3 (n = 156) yearling steers were randomly allocated to 1 of 3 vaccine treatments: non-vaccinated (n = 94), a 2-shot killed vaccine (n = 91), or a single-immunization modified-live vaccine (MLV; n = 94). Steers were vaccinated against 5 viral pathogens, BRSV, IBR, PI_3, BVDV 1a and 2, approximately 21d pre-challenge. Serum samples were collected at challenge (d0) through d42 at 14-d intervals. The anamnestic response was measured as the $\log_2$ titer of the area under the curve (AUC) for 42 dpi, calculated using the trapezoid rule for each of the 4 viral responses (IBR, BVDV 1a, 1b, and 2). The measured anamnestic response appeared lowest for IBR and greatest for BVDV 1b, with the largest range in antibody response to BVDV 1b. Factors influencing AUC for the 4 viral pathogens were investigated using mixed model analyses with fixed effects of vaccine treatment, year, composition (F2 or F3), and sire nested within composition along with covariates of d0 titer ($\log_2$), weaning temperament score and d0 weight; pen nested within year was a random effect. The 4 antibody responses were affected ($P < 0.05$) by vaccine treatment and d0 titer. Animals vaccinated with the killed vaccine had significantly higher BDVD 1b AUC responses to the challenge than MLV or non-vaccinated animals (values of 405.6, 256.2, and 183.3, respectfully). Similar trends were seen for the other viruses. A 1-point $\log_2$ increase in titer at time of challenge increased the anamnestic response (AUC) by 15.7, 17.9, 17.4, and 26.5 for BVDV 1b, 1a, 2 and IBR, respectively. Sire nested within composition affected ($P < 0.05$) for BVDV 1a and b and approaching significance for BVDV2 ($P = 0.08$), however no trends across sires were apparent. These results indicate that both genetic and environmental factors affect the anamnestic antibody response mounted to a BVDV challenge and that the d0 titer from the vaccine treatment pre-challenge has significant influence on the response.

Key Words: antibody response, BVDV challenge, cattle

630 Increasing the dietary ratio of n-3 to n-6 fatty acids increases the n-3 concentration of peripheral blood mononuclear cells in Holstein calves. L. C. Nagengast*, A. L. Lock, S. N. Woodruff, C. M. Ylioja, N. A. Martinec, C. V. Vanderson, C. L. Preseault, N. L. Trottier, M. J. VandeHaar, and E. L. Karcher, *Michigan State University, East Lansing.*

Our objective was to test if increasing the ratio of n-3 to n-6 fatty acids (FA) in diets for weaned calves alters growth, the n-3 FA content of peripheral blood mononuclear cells (PBMC), or inflammatory response. Twenty-seven Holstein calves (16–20 wks-old) were housed individually and fed 1 of 3 diets (9 calves/treatment). Diets were total mixed rations of alfalfa silage, corn grain, and soybean meal supplemented with (1) 4% Ca-salts of soybean FA (N6) containing 50% 18:2 n-6; (2) 4% Ca-salts of flaxseed FA (N3) containing 35% 18:3 n-3; or (3) a 50:50 mix of N6 and N3 (MIX). Blood was sampled on d 1 and 28 to determine FA composition of PBMCs. Blood from d 28 was incubated with endotoxin (LPS) for 2 h, and gene expression of tumor necrosis factor (TNF)-α, interleukin (IL)-1β, IL-8 and osteopontin determined. On d 28, calves were challenged with Pasteurella vaccine and rectal temperatures measured for 48 h. Treatment did not alter body weight or average daily gain. As a percent of total FA, PBMC of N6 calves had 30% total n-6, 11% 18:2 n-6, 15% 20:4 n-6, 6% total n-3, 0.6% 18:3 n-3, 0.4% 20:5 n-3, and 1.0% 22:6 n-3. Compared with N6, N3 resulted in 22% less total n-6 FA, 15% less 18:2, 17% less 20:4, 39% more total n-3 FA, 93% more 18:3, 213% more 20:5, and 11% more 22:6 (all $P < 0.01$, with MIX intermediate). Compared with N6, MIX (but not N3) decreased expression of osteopontin mRNA in PBMC ($P < 0.05$). Compared with N6, N3 tended to decrease expression of IL-1β mRNA in PBMC ($P = 0.08$). Treatment did not alter expression of IL-8 or TNF-α ($P > 0.12$) and had no effect on expression of genes after LPS-stimulation ($P > 0.13$). Treatment did not alter change in rectal temperature following vaccination. We conclude that increasing the dietary ratio of n-3 to n-6 FA for 28-d resulted in corresponding changes in the FA profile of PBMC in postweaned Holstein calves. However, these changes in FA profile of PBMC were not associated with changes in growth or health of calves during the study.

Key Words: dairy calf, immune response, n-3 fatty acid

631 Epigenetic mechanisms control over cytokine gene expression of biased immune response dairy cattle. M. Paibomesai* and B. Mallard, *University of Guelph, Guelph, ON, Canada.*

The adaptive immune response is composed of 2 branches: (1) the antibody-mediated immune response (AMIR; high IFN-γ production), which responds primarily to extracellular pathogens; and (2) the cell-mediated immune response (CMIR; high IL-4 production), which responds primarily to intracellular pathogens. These immune processes are both genetically and epigentically controlled. Epigenetics is defined as modification to DNA which control gene expression without changes to the DNA sequence (ex. DNA methylation). Epigenetics provides the link between environment and genetics, defining the potential that a gene has to be expressed. T- helper cells (CD4+) are the mediators of AMIR and CMIR, producing cytokines that help direct other cell types to an appropriate response to an invading pathogen. Biased immune responder cattle were used to investigate mechanisms of immune response variation and the role of epigenetics in controlling T-helper cell cytokine production in cattle. Biased immune responder cattle respond strongly with either a high AMIR or CMIR to test antigens (H-AMIR/L-CMIR n = 10 and H-CMIR/L-AMIR n = 11). Isolated T-helper cells (CD4+) from H-CMIR/L-AMIR and H-AMIR/L-CMIR cows were stimulated with a T-cell mitogen (ConA) and cell culture supernatant was harvested at the 24 h time point to quantify IFNγ and IL-4 by ELISA. Simultaneously, DNA was extracted from unstimulated and stimulated cells and DNA methylation status of the promoter regions for both IFNγ and IL-4 was determined by bisulfite pyrosequencing. Previously it was shown that H-CMIR/L-AMIR produced significantly more cytokine than the H-AMIR/L-CMIR cows for both IL-4 and IFN-γ when sampled 21 d into lactation. Increased IFN-γ secretion was associated with decreased methylation status both in the promoter region and at specific CpG sites proximal to the transcription start site, but requires more individuals to be confirmed. Increased DNA methylation at the IL-4 promoter did not associate with IL-4 secretion. These preliminary results suggest that immune response variation in cattle is partially controlled by DNA methylation at gene promoter regions.

Key Words: epigenetics, immune response

632 The effect of feeding endophyte-infected fescue on the metabolic response to a provocative immune challenge in beef heifers. A. W. Altman*[1], N. C. Burdick Sanchez[2], J. A. Carroll[2], T. B. Schmidt[3], E. S. Vanzant[1], and K. R. McLeod[1], [1]*Department of Animal and Food Sciences, University of Kentucky, Lexington,* [2]*Livestock Issues Research Unit, USDA-ARS, Lubbock, TX,* [3]*Department of Animal Science, University of Nebraska-Lincoln, Lincoln.*

To determine the effect of endophyte-infected fescue on the metabolic response of beef heifers to a lipopolysaccharide (LPS) challenge, Angus heifers (n = 22; 292 ± 9.0 kg BW) were paired by body weight and randomly placed on either an endophyte-infected (E+) or endophyte-free (E−) diet for 10 d. Heifers were fed at 1.8 × NEm. Diets contained 20% fescue seed, 30% cottonseed hulls, 36% cracked corn, 10% supplement, and 4% molasses, and were balanced to meet protein and mineral requirements. On d −1, heifers were fitted with indwelling jugular cannulas. On the day of challenge, blood samples were collected and serum isolated from heifers at 0.5-h intervals from −2 to 8 h, and again at 24 h relative to LPS administration (0.5 μg/kg BW at time 0 h). Serum was analyzed for glucose, insulin, nonesterified fatty acids (NEFA), blood urea nitrogen (BUN), creatinine, and β-hydroxybutyrate (β-HB). Data were analyzed separately within pre- and post-challenge periods with the Mixed Procedure of SAS, using repeated measures in a completely randomized design. Within period, no treatment by time interactions were detected ($P > 0.10$). Insulin was decreased both pre-and post-LPS in E+ heifers ($P < 0.10$; 0.50 vs 0.46 ng/mL for pre- and 1.17 vs. 1.02 ng/mL post-LPS). Glucose was unaffected ($P = 0.87$) by endophyte status pre-LPS, and was decreased ($P < 0.01$) for E+heifers post-LPS (78.1 vs 71.2 mg/dL). Concentrations of NEFA were decreased ($P = 0.06$) in E+ heifers pre-LPS (0.11 vs 0.08 m*M*) but were unaffected ($P = 0.85$) by endophyte status post-challenge. Both BUN and creatinine differed ($P < 0.01$) between E+ and E− during both periods, BUN was decreased in E+ heifers (1.10 vs 1.04 mg/dL pre-LPS and 1.17 vs 1.04 mg/dL post-LPS) whereas creatinine was increased in E+ heifers (1.31 vs 1.41 mg/dL pre-LPS and 1.16 vs 1.29 mg/dL post-LPS). Concentrations of β-HB were not different ($P = 0.47$) pre-LPS, and were decreased ($P < 0.01$) in E+ heifers post-LPS (1.06 vs 0.97 n*M*). These results indicate that exposure to fescue endophyte alters the metabolic response of heifers during a provocative immune challenge.

Key Words: endophyte, metabolism, LPS

633 Gut microbiome profile of early weaned piglets in response to crowding stress, *Escherichia coli* K88$^+$ challenge, and anti-*E. coli* K88 probiotics. P. M. Munyaka*[1], R. J. Hartmann[1], J. C. Rodriguez-Lecompte[2], J.-E. Ghia[1], D. O. Krause[1], and E. Khafipour[1], [1]*University of Manitoba, Winnipeg, MB, Canada,* [2]*University of Prince Edward Island, Charlotte, PEI, Canada.*

Post-weaning diarrhea (PWD) in pigs is usually caused by enterotoxigenic *Escherichia coli* K88 (ETEC).The current study was conducted to determine the effect of stress and anti- *E. coli* K88$^+$ probiotics on the gut microbiome of early weaned piglets challenged with *Escherichia coli* K88$^+$. To model stress, 2 floor spaces were used; Standard floor allowance (SFA) or half standard floor allowance (HSFA). Ninety 6 male piglets weaned at 21 ± 1 d and fed a basal mash diet were allocated in to 6 experimental treatments: 1) SFA, 2) HSFA, 3) SFA + *E. coli* K88$^+$ (ESFA), 4) HSFA + *E. coli* K88 (ESHFA), 5) ESFA + probiotic *E. coli* UM2 and *E. coli* UM7 (PSFA), 6) EHSFA + probiotics *E. coli* UM2 and *E. coli* UM7 (PHSFA). DNA was extracted from ileal digesta samples and the V1-V3 regions of bacterial 16S rRNA genes amplified and sequenced using Roche 454 pyrosequencing. Sequences were analyzed using mothur software package comparing to the Silva 16S rRNA bacterial database. Data was evaluated using partial least squared determinant analysis and SAS 9.2 to identify significant taxa associated with each treatment. *Paraprevotella* spp., *Dorea* spp., and *Roseburia* spp. were significantly associated with non-stress treatments. Contrary, *Bacteroidales*, *Lachnospiraceae*, *Proteobacteria*, *Achromobacter* spp., *Stenotrophomonas* spp., *Sporobacter* spp., *Delftia* spp., *Papillibacter* spp., *Finegoldia* spp., and *Sporacetigenium* spp. were associated with stress treatment. *Actinobacteria*, *Bacteroidetes*, *Firmicutes*, and *Proteobacteria* contributed to approximately 97% of all phyla within the treatments. Probiotics *E. coli* UM2 and UM7 helped to maintain the gut microbiome similar to that of non-infected pigs; however, stress reduced the population of *Firmicutes* ($P = 0.006$) but increased *Proteobacteria* ($P < 0.0001$) and *Actinobacteria* ($P = 0.01$). Data suggest that stress induces notable changes in the bacterial composition of the gut. The use of anti-ETEC probiotics could effectively reduce negative effects of ETEC in a piglet challenge model; however, probiotics alone may not attenuate the effects of stress.

Key Words: microbiome, probiotic, stress

634 Breed susceptibility to pathogenic enterotoxigenic *Escherichia coli* strains in piglets from South Africa. N. S. Chaora*[1], F. C. Muchadeyi[2], E. Madoroba[2], E. F. Dzomba[1], and M. Chimonyo[1], [1]*University of KwaZulu Natal, Pietermaritzburg, South Africa,* [2]*Agricultural Research Council, Pretoria, South Africa.*

Escherichia coli is an important cause of diarrhea in piglets. It is responsible for economic losses through mortality, morbidity, decreased growth rate and cost of medication. The increase in *E. coli* strains' resistance to various antibiotics and the increase in incidences of post weaning diarrhea have necessitated the exploration of alternative methods for control. The pathogenesis of *E. coli* involves the production of fimbriae that adhere to specific receptors present on the intestinal epithelium and enterotoxins which release water and electrolytes into the gut lumen. Earlier reports show that *E. coli* causing post weaning diarrhea usually carry the F4ab/ac and F18 fimbrial strains. Molecular studies have positioned the receptor(s) for F4ab/ac located on pig chromosome 13 and for F18 on chromosome 6. To date, the causative mutations for these receptor(s) remain unknown. After fine mapping the loci for F4ab/ac receptor(s), the region of interest was mapped between markers SW207 and S0075, where candidate genes such as MUC4, MUC13, MU20 and TRFC surfaced. A recent study investigating collibacillosis in South African pigs observed absence of F4ab/ac and F18 fimbrial adhesins carried out in 263 piglets aged between 9 and 136 d of age. However, non-fimbrial adhesins such as, AIDA-1, PAA and EAST-1 were detected in 14.5, 17.9 and 20.15% of the piglets respectively. Such findings necessitate further investigations into the South African pig populations to these new and prevalent *E. coli* strains. An in vitro adhesion test will identify receptors in the intestinal tissues of the local pigs to which the fimbrial and non-fimbrial adhesins attach to during infection. Analysis of these receptors will help identify genes conferring resistance/susceptibility to *E. coli* infections in South African pigs. The presence of resistant pigs to these newly found strains could help in developing a resistant population through marker assisted selection methods.

Key Words: adhesion, *Escherichia coli*, susceptibility

Breeding and Genetics: Genomic Selection Methods II

635 Mating programs including genomic relationships. C. Sun*[1] and P. VanRaden[2], [1]*National Association of Animal Breeders, Columbia, MO,* [2]*Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD.*

Computer mating programs have helped breeders minimize pedigree inbreeding and avoid recessive defects by mating animals with parents that have fewer common ancestors. With genomic selection, breed associations, AI organizations, and on-farm software providers could use new programs to minimize genomic inbreeding by comparing genotypes of potential mates. Relationships could be computed between (1) only requested males and females via a web query, or (2) all genotyped females with only the marketed males (e.g., >200,000 females and >1,500 bulls), because (3) relationships between all >300,000 genotyped animals are difficult to store and transfer. To compare mating strategies, 50 marketed bulls in each of breed (Jersey and Holstein) were selected for top genomic Lifetime Net Merit (LNM), top traditional LNM, or randomly selected. The 500 youngest genotyped females in the largest herd were assigned mates of the same breed with limits of 10 females per bull and 1 bull per cow (for Brown Swiss, only 79 females and 8 bulls were included). Linear programming, a simpler method that assigned least related mates sequentially, and random mating were compared. For each method, calf value was the average of parents' genomic LNM plus the inbreeding loss times average of parents' expected future inbreeding, minus inbreeding loss time parents' genomic or pedigree relationship. A value of $23.11/1% was assumed for inbreeding loss for all mating methods. Compared with random mating, assigning mates using pedigree inbreeding gave only about 60% of the advantage of using genomic inbreeding for Holsteins, and the simpler mating strategy gave about 90% of the linear programming advantage. The economic value of a mating strategy that uses linear programming and genomic instead of pedigree inbreeding is already >$2 million per year for Holsteins and will grow as more females are genotyped. Eventually, dominance effects could also be included in mating programs to estimate inbreeding losses more precisely. Software to estimate dominance variance and to estimate the dominance effect for each SNP could allow mating plans to include both dominance effects and genomic inbreeding.

Key Words: linear program, dominance, inbreeding

636 Random regression and reaction norm extensions of whole genome prediction models accounting for genotype by environment interaction. W. Yang*, C. Chen, and R. J. Tempelman, *Michigan State University, East Lansing.*

Whole genome prediction (WGP) improves accuracy of the breeding values (BV) in livestock. However, these accuracies can be badly compromised when genotype by environment interaction (G × E) presents but is not accounted for. Reaction norm (RN) and random regression (RR) models have been proven to be useful in accounting for G × E by modeling BV as linear functions of environmental covariates. We extended these RR/RN models to infer upon SNP-specific intercepts and linear effects of environmental covariates. We considered several alternative specifications for modeling the distribution of the 2 × 2 variance-covariance matrices (VCV) of the SNP effects in WGP models: (1) independent inverted Wishart (IW) densities and (2) independent conjugate densities on the square root free Cholesky decomposition (CD) of the VCV. Three common extensions being specified were all SNP-specific VCV (BayesA-like), a mixture with a point-mass at zero (BayesB-like) and all SNPs having the same VCV (BayesC-like). Here we considered 5 of the 6 possible RR/RN models: IW-BayesC/IW-BayesA/IW-BayesB/CD-BayesA/CD-BayesB, and compare them to a conventional BayesA model. Based on 20 replicates, each involving around 2200 SNP markers and 2000 individuals in an RN simulation study, 3 scenarios based on an average genetic correlation between SNP-specific intercept and slope effects of 0, 0.5 and 0.8 were studied. In general, IW-BayesA had the highest accuracy under 3 scenarios although all 5 RN/RR based-methods demonstrated better performance in predicting BV than the conventional BayesA ($P < 0.0001$). In an RR application of a Duroc × Pietrain resource population at MSU, 2000 randomly chosen SNP markers and 324 F2 animals were analyzed for back fat thickness at wk 10, 13, 16, 19 and 20. RR-based methods have a 2.4% greater cross-validation accuracy ($P < 0.0001$) for predicting phenotypes compared with the conventional BayesA. We believe that when G × E presents, RR/RN extensions to WGP models are useful for improving accuracy of predicting genetic merit compared with current conventional approaches.

Key Words: whole-genome prediction, genotype by environment interaction

637 Exploring alternative specifications for whole genome prediction bivariate trait models. W. Yang*, C. Chen, and R. J. Tempelman, *Michigan State University, East Lansing.*

Multiple trait (MT) whole genome prediction (WGP) using high density single nucleotide polymorphism (SNP) marker panels may reap benefits for improving accuracy of selection and generation intervals. One current approach is based on specifying independent inverted Wishart prior densities (IW-BayesA) on SNP-specific variance-covariance matrices (VCV). We propose an alternative bivariate WGP model based on a modified Cholesky decomposition (CD) of the VCV as it potentially allows greater flexibility for modeling bivariate heterogeneity of genetic effects across SNP. We consider such a specification across all SNP (BayesA-like) and a specification that allows some SNP have null effects for either or both traits (BayesB-like). We refer to these 2 specifications as CD-BayesA and CD-BayesB. Univariate BayesA/B on Trait 1, univariate BayesA/B on Trait 2, and bivariate IW-BayesA, CD-BayesA and CD-BayesB on both traits, were compared using 20 replicates of simulated data derived from 2000 SNP markers and 500 animals and an average genetic correlation between the 2 traits of 0.5. Furthermore, QTL effects were generated from heterogeneous bivariate gamma densities based on 10 QTL for Trait 1 only, 10 QTL for Trait 2 only and 10 QTL for both traits. Heritabilities for Traits 1 and 2 were specified to be 0.5 and 0.1, respectively. For Trait 2, we found that bivariate WGP models had generally the highest average accuracy of breeding value compared with the univariate models. In particular, CD-BayesA had 8% greater accuracy than univariate BayesA for Trait 2 ($P < 0.0001$), and 5% higher accuracy than univariate BayesB ($P = 0.0145$). For Trait 1, IW-BayesA had a 2% lower accuracy ($P < 0.0001$) compared with univariate BayesA/BayesB, CD-BayesA and CD-BayesB, reflecting somewhat the inflexibility of the IW-BayesA approach. We applied these models to various phenotypes from the Wellcome Trust mice database, using 1787 animals and 1900 randomly selected SNP markers. Based on a cross-validation study, differences in predictive abilities between the competing models were rather heterogeneous depending on the magnitude of the genetic correlations.

Key Words: pleitropy, multiple trait, genetic correlation

638 Prediction of direct genomic values by using a restricted pool of SNP selected by maximum difference analysis. M. Cellesi[1], N. P. P. Macciotta[1], G. Gaspa[1], D. Vicario[2], P. Ajmone-Marsan[3], A. Stella[4], and C. Dimauro*[1], [1]*Dipartimento di Agraria, Sezione Scienze Zootecniche Universita' di Sassari, Sassari, Italy,* [2]*Associazione Nazionale Allevatori Razza Pezzata Rossa Italiana (ANAPRI), Udine, Italy,* [3]*Istituto di Zootecnica, Universita' Cattolica del Sacro Cuore, Piacenza, Italy,* [4]*CNR IBBA, Lodi, Italy.*

In the present research, a new technique able to select SNP-markers significantly associated with a particular trait (T) is proposed. Genotypes of 2,093 Italian Holstein and of 1,310 Simmental bulls were generated with the Illumina's 50K BeadChip. Phenotypes used were deregressed proofs for milk, fat and protein yield. Animals were ranked according to T. Then, the best 100/80 (B) and the worst 100/80 (W) were selected for Holstein and Simmental, respectively. For each SNP, frequency of the 3 genotypes (2 homozygote and one heterozygote) were calculated. Finally the genotype with the highest frequency in B animals (f(B)) was found and compared with the frequency of the same genotype in W (f(W)). The difference f(B)-f(W) represented the measure that gives the name of the method, maximum difference analysis (MDA). A bootstrap procedure was implemented to derive a posterior probability distribution used to declare a SNP positively associated with T. Markers negatively associated with T (i.e., with the maximum genotypic frequency in W) were also detected. Direct genomic values (DGV) were predicted with a BLUP procedure using both MDA-selected or all SNP available (40,780 and 49,870 for Simmental and Holstein, respectively). DGV accuracies were higher with the MDA selected SNP than with all original markers (in parentheses), particularly for Simmental (around 15% on average) (Table 1). These results suggest that a customized assay containing only the MDA selected SNPs could be developed to genotype animals thus reducing costs and computational resources.

Table 1. Number of MDA selected SNP and DGV accuracies obtained with the selected SNP and with all original markers (in parentheses)

	Holstein			Simmental		
	Milk	Fat	Protein	Milk	Fat	Protein
MDA selected SNP	763	557	823	155	177	217
DGV accuracies	0.45 (0.43)	0.51 (0.41)	0.38 (0.39)	0.35 (0.20)	0.39 (0.27)	0.41 (0.24)

Key Words: genomic selection, SNP selection

639 Using identifiability of genetic causal effects as a criterion for covariate choice in genome-enabled selection models. B. D. Valente*, G. J. M. Rosa, D. Gianola, and K. A. Weigel, *University of Wisconsin-Madison, Madison.*

In applications of genome-enabled selection models to study relationships between genome-wide markers genotypes and a trait, it is common to use other phenotypic traits as model covariates. In this study, we demonstrate that in the context of animal breeding, the choice of model covariates is not a purely statistical problem, and that poor decisions in this regard may result in misleading interpretation of inferences. As an example, consider a scenario where trait A is affected by variable G representing genome-wide genotypes. Suppose that A is also affected by a trait B that is not heritable (i.e., G does not affect B). This scenario may be represented by a causal model structured as G→A←B, which suggests that although B is independent of G, conditioning on A renders them associated to each other. Therefore, if one proposes a genome-enabled selection model to study the trait B as a function of genome-wide markers genotypes but decides to use A as a covariate, inferences would indicate a relationship between G and B, even though B is not heritable. Although still allowing genome-enabled predictions of phenotypes, the application of these for selection purposes would be misleading, as B could not be modified by selection. In selection, phenotypes are expected to change as a result of interventions on genotypes, so that the relevant information in this context is not just the statistical association between genotypes and phenotypes, but the causal relationship between them. However, inferences provided by the analysis described above are not relevant for breeding purposes because the expressed association between G and B does not reflect a causal relationship. We review requirements for identifying causal information from data. Considering different scenarios, we demonstrate that ignoring causal assumptions for the identifiability of genetic causal effects may lead to proposing models that may be useful for phenotypic predictions but not for selection. The use of graph criteria for identifying causal effects is suggested for the construction of genome-enabled selection models applied for breeding.

Key Words: genetic effect, genome-enabled prediction, selection

640 Assessing statistical properties of cSNP discovery and genotyping using RNAseq and genotyping chip data. P. D. Reeb*, C. W. Ernst, N. Raney, L. Preeyanon, T. Brown, R. O. Bates, and J. P. Steibel, *Michigan State University, East Lansing.*

A first step in allelic specific expression (ASE) testing using RNaseq data consists of discovering coding SNP (cSNP) and calling genotypes. In this work, we used genotypes from Illumina PorcineSNP60 Beadchip (SNP60) to estimate properties of cSNP calling and genotyping from RNaseq of skeletal muscle samples. Total RNA was extracted from longissimus muscle of 24 pigs genotyped with the SNP60. Individual RNA was reverse transcribed into cDNA, fragmented and labeled into barcoded libraries, sequenced on Illumina HiSeq 2000 (100 bp, paired-end reads). Reads were aligned to reference genome using TopHat. Total and allele-specific read counts at each SNP in the SNP60 set was obtained with mpileup of SAMTools. SNP60 positions to which a minimum number of reads (Rmin) were aligned were used to call cSNP with the VarScan program. Each genomic position from the SNP60 was classified as polymorphic or monomorphic in the sample. Monomorphic sites were used to estimate cSNP false discovery rate (FDR) and polymorphic sites allowed estimating sensitivity (proportion of segregating SNP called as cSNP). For cSNP discovery (Table), sensitivity increased (67% to 96%) with Rmin (20 to 500). In contrast, FDR was constant (2%). Accuracy of estimated MAF also increased with Rmin, but the increase was explained by the genotype call rate (not shown in table). Contrastingly, calling heterozygous genotypes with low FDR required much larger coverage (Rmin > 200). Error in calling heterozygotes will have the greatest impact on estimation of ASE. These results emphasize the importance of studying properties of cSNP calling and genotyping for future eQTL applications.

Table 1.

						Heterozygous genotype rates	
Rmin	#SNP	Sensitivity	cSNP FDR	Genotype call rate	MAF	Sensitivity	FDR
20	3485	0.67	0.020	0.53	0.39	0.37	0.56
50	2312	0.79	0.019	0.68	0.53	0.48	0.31
100	1745	0.86	0.016	0.80	0.70	0.60	0.16
200	1318	0.93	0.016	0.90	0.82	0.72	0.05
500	951	0.96	0.018	0.97	0.94	0.87	0.01

Key Words: RNAseq, cSNP, pig

641 A robust Bayesian regression model for whole-genome analyses. K. Kizilkaya*[1,2], R. L. Fernando[1], and D. Garrick[1], [1]*Iowa State University, Ames,* [2]*Adnan Menderes University, Aydin, Turkey.*

Following the groundbreaking paper of Meuwissen et al. (2001) establishing BayesA and BayesB methods, Habier et al. (2011) extended these to BayesCpi and BayesDpi. The relationships among these models are established using 3 parameters; pi, scale and degrees of freedom. We propose an overarching model for whole-genome analysis, where pi, scale and degrees of freedom are treated as unknown. The models were compared using a simulation study carried out to examine the estimability of these parameters, and by applying them to de-regressed milk, fat, and protein yields, and somatic cell scores. A trait with heritability of 50% was simulated for 5,000 animals based on 50, 500 or 5,000 QTL randomly sampled from real SNPs from the 50k panel. The QTL substitution effects were sampled from t-distributions with 4 or 100 degrees of freedom. Phenotypic values of animals were generated for 5 reps by adding residuals from normal distribution to the sum of the QTL effects. Two sets of SNP genotypes were used for genome-wide analyses: only QTL genotypes (Set1) or all 50k marker except QTL (Set2). Estimates of degrees of freedom from Set1 and 2 converged to the true values within QTL scenarios. Estimates of pi from Set1 approached zero, indicating a BayesA model with low degrees of freedom, or BLUP model with high degrees of freedom. Estimates of pi from Set2 approached the true values, indicating a BayesB model with low degrees of freedom. Accuracies of genomic estimated breeding values from the robust model showed good agreement with those from BayesA, BayesB, BayesCpi or BayesDpi models.

Key Words: robust model, degrees of freedom, pi

642 Genome-wide analysis of case-control data using logit, probit and robit models. K. Kizilkaya*[1,2], R. L. Fernando[1], S. Kachman[3], and D. Garrick[1], [1]*Iowa State University, Ames,* [2]*Adnan Menderes University, Aydin, Turkey,* [3]*University of Nebraska, Lincoln.*

The threshold model using the probit link, is the most commonly used model for genetic evaluation of categorical traits. It has been recently extended to genome-wide analysis. However, the alternative logit and t (robit) links are preferred for many statistical applications. The logit or robit model can be computed by augmenting the joint posterior density with Logistic or t-distributed rather than normally distributed underlying variables. A simulation study was conducted to quantify accuracy of genomic prediction assuming probit, logit and robit models. A binary trait (full data) determined by 50 QTL with heritability 10, 25 or 50% was generated based on incidence rates of 0.01, 0.02, 0.05 or 0.10 using 2,250 purebred training animals. QTL were simulated by randomly selecting loci from 50k SNPs and assigning effects from a normal distribution. Underlying variables of 2,250 animals were generated by summing 50 QTL effects and by adding simulated Normal, Logistic or t distributed residuals. Case-control data were generated by selecting matching controls for every case. Simulations were replicated 10 times. SNP effects were estimated by BayesC with pi = 0.995 assuming Normal, Logistic or t distributed residuals. Accuracies of genomic estimated breeding values were calculated by correlating true and estimated genotypic values of animals. There was no substantial difference among accuracies from the logit, probit or robit models in analyses of either full or case-control data sets. However, case-control data resulted in about half the accuracies of full data. Accuracies increased as incidence rate and heritability increased.

Key Words: case-control, probit, logit

643 A structural model for genetic similarity in genomic selection of admixed populations. E. Hay*, S. Smith, and R. Rekaya, *University of Georgia, Athens.*

Current approaches for dealing with admixed and crossbred populations in genomic selection rely on using different groups of animals in training and validation sets. These approaches gain from increased power as results of increasing the size of the training set. However, they fail at different degrees depending on the genetic similarity between the sub-populations of the admixed population. Our proposed multi-compartment model where the effect of an SNP could be different between breeds and parameterized as a function of its effect on one of the breeds in admixed population through a one to one mapping function, was able to remediate some problems of the pooled data approaches but still suffer from the high dimensionality of the unknown parameters to estimate. To overcome this problem, we propose not to estimate a mapping parameter α for each SNPi rather to build a model for α as a function of information already available in the genotype data via a hierarchical structural model. In this study, α was modeled as a function of the change in minor allele frequencies across lines and potential change in linkage phase. An admixed population consisting of 2 breeds was simulated. Each breed consisted of 2000 individuals genotyped for 50K SNPs and measured for a quantitative trait with 0.40 heritability. Genetic dissimilarity was simulated mainly by changing SNP minor allele frequencies between the 2 breeds. Three analyses were conducted: 1) classical pooled data (M1); 2) pooled data using the multi-compartment model and α for each SNP (M2); and 3) pooled data using multi-compartment model and our structural model for α (M3). For M1, accuracy (correlation between EBVs and GEBVs) was 0.54. The accuracy increased to 0.66 using M2 very likely due to a better accounting for the genetic dissimilarity between the 2 breeds. When a structural model was assumed (M3) the accuracy dropped to 0.63. This small decrease compared with M2 indicates that it is possible to model α as a function of the information already available in the genotype data with little impact in accuracy but with a substantial reduction in the number of parameters to estimate.

Key Words: genomic selection, admixed population

644 Use of plasma, hydrolyzed wheat gluten, or the combination in dairy calf milk replacers. T. M. Hill*, H. G. Bateman III, J. M. Aldrich, J. D. Quigley, and R. L. Schlotterbeck, *Nurture Research Center, Provimi North America, Brookville, OH.*

Plasma and hydrolyzed wheat gluten are relatively well accepted alternatives to milk ingredients in the US. Five milk replacer powders that were: all milk protein control (M), 6% plasma (P), 6% hydrolyzed wheat gluten (W), 3% plasma and 3% hydrolyzed wheat gluten (LOPW), and 6% plasma and 6% hydrolyzed wheat gluten (HIPW). The MR were 27% CP, 17% fat, equalized in amino acids to published optimum concentrations using synthetic sources, and fed at 0.66 kg DM/calf daily until weaning at d 28. Post-weaning measurements were made until d 56. A textured 20% CP starter and water were fed free-choice all 56 d. Calves (20/treatment) were 2 to 3 d old Holstein male calves (46 ± 1.2 kg BW) sourced from a single farm and housed in individual 1.2 by 1.4 m pens within a naturally ventilated nursery. The nursery temperature averaged 14°C ranging from −4 to 30°C based on hourly measurements. Data were analyzed as a completely randomized block design using repeated measures with means separated using pre-planned contrasts (M vs. others, M vs. P, M vs. W, LOPW vs. HIPW). Starter intake, ADG, and change in hip width were greatest for calves fed M ($P < 0.05$, M vs. others, M vs. P, M vs. W). Pre-weaning ADG was 0.440, 0.408, 0.395, 0.376, and 0.366 kg/d (SEM = 0.024 kg/d) for M, P, W, LOPW, and HIPW, respectively. Overall 56 d ADG was 0.560, 0.494, 0.473, 0.519 0.468 kg/d (SEM = 0.034 kg/d) for M, P, W, LOPW, and HIPW, respectively. Overall 56 d hip width change was 3.7, 3.3, 3.3, 3.4, 3.2 cm (SEM = 0.2 cm) for M, P, W, LOPW, and HIPW, respectively. Medical treatments were low and not different among treatments. Depending upon the feed ingredient market, it was estimated that the milk replacers with alternative proteins would need to be 10 to 20% less expensive than M to equalize the feed cost per unit ADG. Under the conditions of this trial, replacing ≥18% of the milk protein with plasma or hydrolyzed wheat gluten alone or in combination was not advantageous.

Key Words: milk replacer, plasma, hydrolyzed wheat gluten

645 Standing time of dairy calves within a naturally ventilated, unheated nursery over different seasons of the year, fed different amounts of milk replacer, and housed individually or in groups. . T. M. Hill*, H. G. Bateman III, J. M. Aldrich, J. D. Quigley, and R. L. Schlotterbeck, *Nurture Research Center, Provimi North America, Brookville, OH.*

Holstein calves (2 to 5 d of age initially) from a single dairy farm were transported 3.5 h to the Nurture Research Center in southwest OH in 6 different 56-d periods. Standing and lying behavior was measured using an electronic data logger attached to the medial side of the right rear leg of calves. Data were analyzed as completely randomized designs using repeated measures with calf being the experimental unit. Period, time of day, and/or treatment (MR program or housing) were factors in the model. In the first 4 periods, calves were housed in 1.2 by 2.4 m individual pens with wire mesh sides within a curtain sidewall barn with no added heat. Pens were bedded with long straw. Calves were fed 0.66 kg DM of milk replacer (MR) powder in 2 equal meals at 0615 and 1600 h. Starter and water were offered free-choice. Calves were weaned at 42 d. The first 4 periods were seasons of the year and there were 10 calves/period combined in the analysis. Standing time did not differ among periods and averaged 303 ± 52.8 min/d. Standing time differed ($P < 0.05$) throughout the day and was greatest during AM and PM feeding, intermediate during midday and evening, and least at night. There was no interaction of period of year by time of day. In period 5, standing time was measured for calves (10/treatment) fed ad libitum MR or the fixed amount of 0.66 kg DM/d. In period 6, standing time was measured for calves (6/treatment) fed ad libitum MR in groups of 3 calves, individually, or fed 0.66 kg DM/d in individual housing. In periods 5 and 6, total time standing/d or throughout the day did not differ by feeding rate or grouping. In summary, calves averaged approximately 300 min/d standing to approximately 2 mo of age independent of season of the year, feeding rate of MR, or housing as individuals or groups of calves.

Key Words: standing time, behavior, season

646 Replacing 10 and 20% of dairy calf milk replacer with whey cream yields similar starter intake, growth, and health performance during the nursery phase. R. J. LaBerge*[1], R. S. Younker[2], and N. B. Litherland[1], [1]*University of Minnesota, St. Paul,* [2]*Milk Specialties Global, Eden Prairie, MN.*

Whey cream (WC) is a byproduct of whey protein concentrate production and contains milk nutrients and potentially healthful functional food compounds. Our objective was to determine if replacing a proportion of all milk protein calf milk replacer (CMR) with increasing amounts (0, 10, and 20%) of WC affects calf growth and health. Seventy-two male (n = 33) and female (n = 37) Holstein and Holstein-cross dairy calves were raised in hutches from October to January and randomly assigned to 1 of 3 nonmedicated CMRs formulated to provide 22% protein and 20% fat; (1) 0% WC (0WC); (2) 10% WC (10WC); (3) 20% WC (20WC). CMR was fed at 1.5% of birth body weight (BBW) and reconstituted to 13% solids. BBW and serum total protein concentration averaged 40.4 ± 0.7kg and 6.3 ± 0.07mg/dL, respectively. Calves were fed CMR twice daily (0630, 1700 h) d 1 to 41, once daily d 42 to 48, weaned d 49, and removed from trial d 56. Starter (19.9% CP, DM basis) and drinking water were provided ad libitum. Daily starter intake, thrice weekly fecal score, and weekly growth [body weight (BW), wither height (WH), hip height (HH), hip width (HW), body length (BL), heart girth (HG)] were measured. Data were analyzed using PROC MIXED in SAS as a randomized block design. Starter consumed through d 56 averaged 1.0, 1.1, and 1.1 ± 0.08 kg ($P < 0.22$), and ADG averaged 0.83, 0.91, 0.84 ± 0.05 kg ($P < 0.13$), and gain:feed through d 56 averaged 0.55, 0.58, 0.53 ± 0.03 ($P < 0.18$), for 0WC, 10WC, and 20WC, respectively. 20WC calves tended ($P < 0.08$) to consume more starter than 0WC by d 49, and 10WC calves consumed 500 g/d of starter 2.3 ± 1.8 d before 0WC ($P < 0.03$). WH, HH, HW, BL, and days treated for illness were similar among treatments. Calves fed 0WC had greater HG gain over 20WC and 10WC ($P < 0.05$). Days scouring were similar but average fecal score tended to be less for 10WC over 0WC calves ($P < 0.09$). Results indicate that replacing CMR with up to 20% WC successfully resulted in some tendencies for calf growth and health.

Key Words: nursery calf, whey cream, milk replacer

647 Feeding dairy calves once or twice a day: Effects on solid feed intake and ruminal physico-chemical parameters from birth to weaning. C. Julien*[1,2], F. Enjalbert[1,2], and C. Bayourthe[1,2], [1]*INRA, UMR1289 TANDEM, Tissus Animaux Nutrition Digestion Ecosystème et Métabolisme, Castanet-Tolosan, France,* [2]*Université de Toulouse,*

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The experiment tested a simplified feeding program for dairy calves (Technique Once a Day, Bonilait-Protéines, France). Sixteen male Holstein calves from birth (d 1) to weaning (d 63) were reared in individual pens. Two feeding programs were tested. Each was based on a milk replacer (MR) with the same chemical composition: 20% CP and 18% fat, on DM basis. Calves were divided into 2 groups at 4-d of age: (1) OAD (n = 8): calves received MR once a day (200 g/L of MR), (2) TAD (n = 8): calves received MR (125 g/L) twice a day; volume distributed per calf and per meal varied with age but did not differ between groups. The week before weaning, all calves received MR once a day. All calves received water, wheat straw and a starter concentrate (16.6% CP) ad libitum. Individual straw and concentrate intake were recorded daily. Ruminal samples were taken through a stomach tube at birth and thereafter at a 7-d interval. The pH and oxidation-reduction potential (ORP) of ruminal content were measured after a 20 min-stabilization period. Data were analyzed as a mixed model with repeated measures using R.14.1 software with calf as random effect, age and treatment as fixed effects. Body weight of calves and straw intake did not differ ($P > 0.10$) from birth to weaning between treatments. Ruminal pH averaged 6.25 and did not differ with age and treatment. From d 42 to d 56, calves fed OAD presented a more acidic ruminal content than TAD calves (5.94 and 6.65 on average for OAD and TAD, respectively, $P = 0.05$) which could originate from a nonsignificant but numerically higher intake of starter by OAD calves: +14% on average from d49 to d56. Ruminal ORP tended to be higher with OAD than TAD from birth to weaning ($P = 0.08$) and differed between groups from d 42 to d 56 ($P = 0.007$): −131 and −172 mV for OAD and TAD calves, respectively. These differing physico-chemical ruminal conditions observed before weaning could suggest that the feeding program altered ruminal microbiota composition and richness, which needs further investigations for confirmation.

Key Words: calf, rumen, ORP

648 Effect of altering the ratio of dietary n-6 to n-3 fatty acids on lactational performance and acute phase response to an intramammary lipopolysaccharide challenge. L. F. Greco*[1], J. T. Neves Neto[1], A. Pedrico[1], R. Ferrazza[1], F. S. Lima[1], R. S. Bisinotto[1], N. Martinez[1], E. S. Ribeiro[1], M. Garcia[1], G. C. Gomes[1], M. A. Ballou[2], W. W. Thatcher[1], C. R. Staples[1], and J. E. P. Santos[1], [1]*University of Florida, Gainesville,* [2]*Texas Tech University, Lubbock.*

Objectives were to evaluate the effects of altering the dietary ratio of n-6/n-3 fatty acids (FA) on lactation performance and acute phase response of cows after a challenge with *Escherichia coli* lipopolysaccharide (LPS). Diets were supplemented (1.43% of dietary DM) with a mixture of Ca salts of fish, safflower, and palm oils (Virtus Nutrition, Corcoran, CA) to create different ratios of n-6/n-3 FA; 4, 5 and 6 parts of n-6 to 1 part of n-3 FA (R4; R5; R6). Multiparous (45) Holsteins were blocked by milk yield between 6 and 10 DIM, and assigned randomly to the 3 treatments at 15 DIM, in a randomized complete block design. Blood was sampled and analyzed weekly for the first 5 wk in the study. At 75 DIM, cows underwent a LPS challenge 3h after the morning milking. Ten μg of LPS in PBS solution was infused via teat canal of one quarter. Body temperature and concentrations of acute phase proteins and cytokines in plasma were measured every 2 h up to 14 h, and then at 24 and 48 h relative to the challenge. Milk was sampled separately from each quarter at the same time points as blood and at 72 and 96 h post challenge. Milk somatic cell count was measured from the infused quarter and from the 3 mammary quarters pooled. Data were analyzed using PROC GLIMMIX of SAS for repeated measures with orthogonal polynomials. Lactation performance improved with decreasing ratio of n-6 to n-3 FA in the diet (Table). Based on IL-6 response, cows fed the R4 diet had an attenuated inflammatory response to the LPS challenge (Table). Overall, decreasing the dietary ratio of n-6 to n-3 FA improved performance of dairy cows.

Table 1.

	Diet				*P*-value	
	R4	R5	R6	SE	Linear	Quadratic
DMI, kg/d	26.1	24.6	24.7	0.5	0.05	0.17
FCM, kg/d	48.0	45.4	43.4	0.8	0.01	0.73
FCM/DMI	1.86	1.87	1.78	0.03	0.07	0.21
Milk fat, kg/d	1.71	1.60	1.53	0.03	0.01	0.73
Milk protein, kg/d	1.32	1.28	1.24	0.02	0.01	0.94
BW, Kg	621	632	627	5.6	0.44	0.28
Energy balance, Mcal/d	−1.22	−0.79	1.03	0.69	0.03	0.41
NEFA, mM	0.31	0.26	0.25	0.02	0.06	0.46
LPS Challenge						
Body temperature, °C	39.1	39.3	39.1	0.08	0.62	0.09
IL-6, pg/mL	113.5	353.4	365.1	86.6	0.04	0.28
IFN-γ, pg/mL	10.3	29.9	17.9	9.0	0.51	0.17
Milk SCC × 10^6/mL	3.68	4.33	3.58	0.25	0.78	0.03

Key Words: dairy cow, fatty acid

649 Comparison of two supplemental fat sources differing in saturated fatty acid content on the production response of lactating dairy cows. J. K. Bernard* and N. A. Mullis, *University of Georgia, Tifton.*

Thirty-two lactating Holstein cows were used in a 10 wk study to evaluate the production response to supplemental fat sources differing in linoleic acid concentration. Diets included distiller's grains with solubles and whole cottonseed plus supplemental fat provided by a blend of tallow (86.1%) and soybean oil (13.9%) containing 15% linoleic acid (CON) or a prilled saturated fatty acid blend (SFA, EB-Select, Milk Specialties Global Animal Nutrition). Diets contained 6.57 and 6.53% fat (DM) for CON and SFA, respectively. Cows were fed CON for 2 wk, then blocked by parity and DIM and randomly assigned to fat supplements within block for the following 8 wk. No differences were observed in DMI among treatments. Yield of milk, fat, lactose, solids-not-fat, and ECM and milk fat percentage were lower ($P < 0.05$) and tended to decrease ($P < 0.05$) throughout the study for cows fed CON compared with SFA. Efficiency (ECM/DMI) was higher ($P < 0.01$) for SFA compared with CON. Milk urea nitrogen concentrations were lower for CON compared with SFA. Cows fed CON gained more ($P < 0.01$) BW than cows fed SFA during the study. Concentrations of most short and medium chain fatty acids in milk were lower ($P < 0.05$) for CON compared with SFA, whereas concentrations of C14:1, C16:1 and C18:1n9t were higher ($P < 0.05$) for CON compared with SFA. Results of this study are consistent with previous research in which feeding high linoleic acid supplements resulted in the formation of *trans* fatty acids that have been associated with depressed milk fat. These results suggest that feeding 15% linoleic acid negatively affects milk yield and composition.

Table 1. Effect of supplemental fat on DMI and performance

	Treatment			*P*-value	
	CON	SFA	SE	TRT	TRT × Week
DMI, kg/d	27.5	26.6	1.2	0.2909	0.0357
Milk, kg/d	40.6	43.2	0.5	0.0124	0.0005
Fat, %	3.08	3.58	0.12	0.0004	0.0467
Fat, kg/d	1.25	1.55	0.06	0.0013	0.0009
Protein, %	2.91	2.86	0.07	0.2475	<0.0001
Protein, kg/d	1.18	1.23	0.02	0.1851	0.5408
ECM, kg/d	38.5	43.6	1.04	0.0004	0.0010
Efficiency	1.40	1.64	0.04	0.0016	0.0149
MUN, mg/dL	9.43	12.60	0.49	0.0027	0.0005

Key Words: fatty acid supplementation, milk yield, milk fatty acid

650 Incorporation of n-6 and n-3 fatty acids into plasma lipid fractions of lactating cows: Chronic effect of abomasal infusion of linoleic and linolenic acids. C. L. Preseault, L. C. Nagengast, J. C. Ploetz, C. M. Klein, and A. L. Lock*, *Michigan State University, East Lansing.*

Six rumen-fistulated Holstein cows (252 ± 33 DIM and 44 ± 6 kg milk/d) were randomly assigned to one of 2 treatments in a repeated measures design to examine the effect of abomasal infusions of linoleic (18:2) and linolenic (18:3) acids on the incorporation of n-6 and n-3 fatty acids (FA) in plasma lipid fractions. Treatments were abomasal infusions (67 g/d total FA) of (1) n-6 FA blend (N6) providing 43 g/d 18:2 and 8 g/d of 18:3; or (2) n-3 FA blend (N3) providing 43 g/d 18:3 and 8 g/d 18:2. FA were provided every 6 h for 20 d. Blood was collected d −2, d −1, and 0 h before the first infusion and d 2, 4, 8, 12, 16, and 20. Blood was also collected 18 and 20 d following termination of infusions. FA concentrations of plasma phospholipids (PL), cholesterol esters (CE), triglycerides (TG), and NEFA were determined. Data were analyzed using PROC MIXED in SAS with day as the repeated measure. Concentration of total FA in each lipid fraction was not affected by treatment ($P > 0.37$). N3 increased the

concentration of 18:3 and total n-3 FA in all lipid fractions ($P < 0.002$). Increases became evident between d 2 to 4 and by d 20 the concentration of 18:3 was increased 127, 224, 270, and 317% compared with N6 for NEFA, TG, CE, and PL, respectively ($P < 0.001$). N6 increased the concentration of 18:2 and total n-6 FA in CE and PL ($P < 0.04$); by d 20 the concentration of 18:2 was increased 19 and 9% compared with N3, respectively. In NEFA, N6 increased the concentration of 18:2 ($P < 0.04$) but not total omega-6 FA ($P = 0.11$); 18:2 and total n-6 FA were not different in TG ($P > 0.78$). Pre vs. post infusion results indicated that 18 to 20 d following termination of infusions the concentration of individual FA in CE, PL, and TG had returned to pre-infusion levels ($P > 0.13$); 18:3 and total n-3 FA remained slightly higher in NEFA for N6 ($P < 0.03$). Abomasal infusions of 18:2 and 18:3 increased the concentration of n-6 and n-3 FA in plasma lipids, respectively, although relative increases in n-3 FA were much greater than that for n-6 FA.

Key Words: dairy cow, plasma lipid, polyunsaturated fatty acid

651 Milk yield and milk fat responses to increasing levels of palmitic acid supplementation of dairy cows receiving low and high-fat diets. J. E. Rico*, M. S. Allen, and A. L. Lock, *Michigan State University, East Lansing.*

Dose-dependent effects of a palmitic acid-enriched fat supplement on feed intake and production responses of dairy cows were evaluated. Basal dietary fat concentration (2.7% or 4.2% ether extract) was used as a split-plot to determine relationships between basal dietary fat concentration and fat supplement dose. A covariate period with a common diet (3.5% ether extract) was included to evaluate treatment interactions. Sixteen Holstein cows (149 ± 56 DIM) were assigned randomly to treatment sequence within basal fat group (n = 8 cows/group). Palmitic acid-enriched fat (PA; Bergafat F100; 87% C16:0) was supplemented at 0, 0.75, 1.50, or 2.25% of ration DM in a 4x4 Latin Square design within each basal fat group. Periods were 14 d with the final 4 d used for data collection. Corn silage and alfalfa silage-based diets were formulated to contain 30% NDF and 16.5% CP. The statistical model included the random effect of cow and the fixed effects of basal group, PA dose, period, and their interactions. 3.5% FCM was used as a covariate in the model to account for initial milk and fat effects. The PA dose increased milk fat concentration (3.78, 3.88, 4.01, and 4.03%, $P = 0.004$), fat yield (1.62, 1.68, 1.78, and 1.70 kg/d, $P = 0.003$), and 3.5% FCM yield (45.3, 46.1, 47.9, and 45.8 kg/d; $P = 0.02$) for 0, 0.75, 1.50, and 2.25% PA, respectively. PA dose had no effect on milk protein and lactose concentration, DMI, BW, or BCS ($P > 0.32$), but tended to increase yields of milk ($P = 0.06$), milk protein ($P = 0.08$), and milk lactose ($P = 0.08$). There were no main effects of basal fat group on the yield of milk or milk components ($P > 0.17$), but feed efficiency (3.5% FCM/DMI) was higher for the high-fat relative to the low-fat basal group (1.74 vs. 1.51; $P = 0.04$). There was an interaction of basal fat group with PA dose for yields of milk ($P = 0.09$) and milk protein ($P = 0.10$), and a trend for yields of milk fat ($P = 0.15$) and 3.5% FCM ($P = 0.13$). Results demonstrate that response to PA varies with dose, and under the dietary conditions tested, the yield of 3.5% FCM and milk fat were optimal when PA was fed at 1.5% of ration DM.

Key Words: fat supplementation, milk fat, palmitic acid

652 Effect of dietary NDF and PUFA concentration on recovery from diet induced milk fat depression (MFD) in monensin-supplemented dairy cows. D. E. Rico*[1], A. W. Holloway[2], and K. J. Harvatine[1], [1]*The Pennsylvania State University, University Park,* [2]*Elanco Animal Health, Greenfield, IN.*

Eight ruminally cannulated and 9 non-cannulated Holstein cows were arranged in a 3x3 Latin Square design. Each period was divided into a 10 d MFD induction and an 18 d recovery phase. Milk fat depression was induced by feeding a low fiber and high oil diet. Treatments during the recovery phase were (1) High forage, low PUFA diet (control; 31.8% NDF, no added oil), (2) Low forage, low PUFA diet (LF; 28.4% NDF, no added oil), and (3) High forage, high PUFA diet (HO; 31.5% NDF, 1.5% soybean oil and 7.8% whole soybeans). All cows were supplemented with monensin (Rumensin 90, Elanco animal health) at 450 mg/d. Milk and milk component yield and milk FA profile were measured every 3 d during the recovery phase. Data were analyzed as repeated measures using Proc Mixed (SAS institute). Time was the repeated variable and cow by treatment was the subject. The model included treatment, time, and their interaction as fixed effects. The preplanned contrasts were control vs HO and control vs LF at each time point. Milk yield decreased progressively for the HO and control diets, whereas it was maintained in the LF diet and was higher ($P < 0.01$) than control on d 15. Milk fat concentration increased progressively during recovery in all treatments, but LF was lower than in control from d 12 to 18 (9%; $P < 0.05$). Milk fat yield increased progressively in all treatments and was not different between control and LF at any time point, but was lower in HO compared with control on d 15. Similar to milk fat yield, yield of de novo synthesized and 16 carbons FA increased progressively and were not different between control and LF, but did not recover in HO. Conversely, yield of preformed FA was not different between LF and control, but was increased by HO compared with control on d 9 and 18 (16 and 12%; $P < 0.05$). Milk trans-10 C18:1 concentration decreased progressively in all treatments, but was higher in both HO and LF compared with control from d 3 to 18 and d 9 to 18, respectively (236 and 67%; $P < 0.01$). Correcting dietary PUFA concentration is the predominant factor affecting the rate of recovery from MFD.

Key Words: dairy cow, milk fat depression, monensin

653 Saturated fat supplementation interacts with dietary forage concentration during the immediate postpartum and carryover periods in Holstein cows. P. Piantoni*, A. L. Lock, and M. S. Allen, *Michigan State University, East Lansing.*

Forty-eight multiparous cows were used in a randomized complete block design experiment with a 2 × 2 factorial arrangement of treatments. Treatment diets were offered from 1 to 29 d postpartum (postpartum period; PP) and contained 20% or 26% forage NDF (fNDF; 50:50 corn silage:alfalfa, DM basis) and 0% or 2% saturated free fatty acid supplement (Energy Booster 100; FAT). From 30 to 71 d postpartum (carryover period; CoP), a common diet (~23% fNDF, 0% FAT) was offered to all cows. During PP, high fNDF decreased DMI by 2 kg/d ($P < 0.01$), while FAT increased it by 1.4 kg/d ($P = 0.05$). In addition, high fNDF with no FAT decreased DMI compared with other diets and this difference increased throughout PP ($P < 0.01$). During CoP, FAT increased DMI for the high fNDF diet but decreased it for the low fNDF diet ($P = 0.10$) and differences among treatments tended to decrease over time ($P = 0.13$). Treatment did not affect 3.5% FCM yield during PP. During CoP, FAT decreased 3.5% FCM yield for the low fNDF diet (51.1 vs. 58.7 kg/d) but not for the high fNDF diet (58.5 vs. 58.0 kg/d; interaction $P = 0.10$). Low fNDF and FAT increased BCS during PP (both 3.0 vs. 2.7; $P = 0.02$) and treatment differences increased over time for fNDF during PP ($P = 0.02$) and CoP ($P = 0.08$). Effects on BCS were sustained through CoP: BCS was increased by FAT (2.62 vs. 2.26; $P = 0.02$) and low fNDF (2.70 vs. 2.18; $P < 0.01$). During PP, low fNDF and FAT decreased feed efficiency (FE; 3.5% FCM/DMI) by 0.31 and 0.23 units, respectively (both $P \leq 0.05$). Early in PP, low fNDF with FAT decreased FE greatly compared with other diets, but this difference decreased over time ($P =$

0.09). Low fNDF reduced FE during CoP (1.82 vs. 1.98; $P = 0.03$), but FAT did not. Supplementation of FAT in PP favored energy partitioning to body reserves and limited DMI depression and BCS loss for the high fNDF diet, which might allow higher fNDF diets to be fed to cows in PP. However, FAT had deleterious effects on production for the low fNDF diet. Diet fNDF and FAT interacted affecting performance not only during the treatment period, but also when cows were fed a common diet.

Key Words: body condition, postpartum, prilled fat

654 Milk production responses to dietary stearic acid vary by production level in dairy cattle. P. Piantoni*, A. L. Lock, and M. S. Allen, *Michigan State University, East Lansing.*

Effects of stearic acid supplementation on feed intake and metabolic and production responses of dairy cows with a wide range of milk production (32.2 to 64.4 kg/d) were evaluated in a crossover design experiment with a covariate period. Thirty-two multiparous Holstein cows (142 ± 55 DIM) were assigned randomly within level of milk yield to treatment sequence. Treatments were diets supplemented (2% of diet DM) with stearic acid (SA, 98% C18:0) or control (CONT, soyhulls). The corn silage and alfalfa based diets contained 24.5% forage NDF, 25.1% starch and 17.3% CP. Treatment periods were 21 d with the final 4 d used for data and sample collection. Compared with CONT, SA increased DMI (26.1 vs. 25.2 kg/d, $P = 0.008$) and milk yield (40.2 vs. 38.5 kg/d, $P = 0.02$). Stearic acid had no effect on the concentration of milk components, but increased yields of fat (1.42 vs. 1.35 kg/d, $P = 0.002$), protein (1.19 vs. 1.14 kg/d, $P = 0.02$), and lactose (1.96 vs. 1.87 kg/d; $P = 0.02$). Stearic acid increased 3.5% fat-corrected milk (FCM, 40.5 vs. 38.6 kg/d, $P = 0.005$), but did not affect feed efficiency (3.5% FCM/DMI, 1.55 vs. 1.53, $P = 0.38$), body weight, or body condition score compared with CONT. Period by treatment interactions ($P \leq 0.15$) were detected for yields of milk and milk components indicating that period 2 was responsible for these treatment effects. The cause of the interactions could not be determined and requires further investigation. Linear interactions between treatment and level of milk yield during the covariate period ($P < 0.10$) were detected for DMI and yields of milk, fat, protein, lactose, and 3.5% FCM; responses to SA were positively related to milk yield of cows. Treatment did not affect plasma insulin, glucagon, glucose, and NEFA concentrations. Results show that stearic acid has the potential to increase DMI and yields of milk and milk components, without affecting conversion of feed to milk, body condition score, or body weight. Moreover, effects on DMI and yields of milk and milk components were more pronounced for higher yielding cows than for lower yielding cows.

Key Words: feed intake, milk fat, stearic acid

655 Effects of rumen-protected conjugated linoleic acid (CLA) on expression of genes involved in hepatic gluconeogenesis and insulin sensitivity in dairy cows. A. Kinoshita[1], L. Locher[1], K. Huber[2], U. Meyer[3], S. Daenicke[3], and J. Rehage*[1], [1]*Clinic for Cattle, University of Veterinary Medicine Hannover, Hannover, Germany,* [2]*Dep. of Physiology, University of Veterinary Medicine Hannover, Hannover, Germany,* [3]*Dep. of Animal Nutrition, Friedrich-Loeffler-Institute, Braunschweig, Germany.*

The aim of this study was to investigate the effects of long-term dietary CLA supplementation on expression of hepatic genes related to insulin signaling, gluconeogenesis and systemic insulin sensitivity in dairy cows. Twenty-one pluriparous German Holstein cows were divided in 2 groups (CLA; n = 11 and control; n = 10), studied from 21 d ante partum (ap) to 224 d postpartum (pp). Cows were fed a diet including 37% concentrate and 63% silage (60% maize silage and 40% grass silage based on dry matter content) ad libitum. From 1 d pp to 182 d pp each group received 4 kg concentrate additionally with 100 g/d of fat supplement (10% C16:0, > 80% C18 fatty acids) including either CLA (Lutrell pure, BASF SE, Germany; 50% C18:0, 10% each C18:1, t10c12-CLA, c9t11-CLA) or not (>80% C18:0). Blood and hepatic biopsy samples were taken at 21 d ap, 1, 21, 105, 182, and 224 d pp. In blood samples concentrations of glucose, NEFA, insulin, β-hydroxybutyrate (BHB) were analyzed and the revised quantitative insulin sensitivity check index (RQUICKI) was calculated. Expression of hepatic mRNA for gluconeogenic enzymes (pyruvate carboxylase; PC, phosphoenol pyruvate carboxykinase; PEPCK isotype 1and 2, glucose-6-phosphatase; G6P), glucose transporters (SLC2A1 and SLC2A2) and insulin receptors (INSRA and INSRB) were measured with real-time RT-PCR using UXT, RPS15 and RPS9 as reference genes. Data was analyzed by SAS PROC MIXED for repeated measures with group and day as fixed effects. CLA supplements did not affect transcription of any investigated genes in liver and the levels of BHB and NEFA in blood. However, CLA cows showed increased mean glucose and insulin levels in blood and decreased RQUICKI compared with controls after d 105 (time and group effects: $P < 0.001$). Hepatic mRNA expression of gluconeogenic enzymes and insulin receptors was not affected by long-term CLA supplementation although systemic insulin sensitivity appeared reduced. Thus, the physiological relevance of observed CLA induced changes in insulin sensitivity remains unclear.

Key Words: fat, herd health, insulin

656 Interaction between rumen unsaturated fatty acid load and forage:concentrate ratio on the formation of biohydrogenation intermediates in continuous culture. Y. Sun*[1], T. C. Jenkins[2], and A. L. Lock[1], [1]*Michigan State University, East Lansing,* [2]*Clemson University, Clemson, SC.*

Three dual-flow continuous fermenter studies examined the interaction between rumen unsaturated fatty acid load (RUFAL) and forage:concentrate ratio (FCR) on the formation of biohydrogenation intermediates (BHI). Cultures (4/treatment) were fed basal diet plus respective fat treatments for 10 d with the last 3 d for sample collection. Study 1 determined if canola (high 18:1) vs. corn oil (high 18:2) at 0, 1, 2, and 3% of diet DM resulted in differences in the formation of BHI. Increased RUFAL caused a nonlinear increase ($P < 0.05$) in daily production of *trans*-10, *cis*-12 18:2 (CLA), which was lower for canola (3.0, 3.7, 3.3, and 6.0 mg/d) vs. corn oil (3.5, 4.3, 8.6, and 18.5 mg/d) for the 0, 1, 2, and 3% treatments, respectively. Total *trans* 18:1 and *trans*-10 18:1 production also increased ($P < 0.05$) nonlinearly with increased RUFAL and was lower ($P < 0.05$) for canola vs. corn oil. Study 2 examined the relationship between FCR (60:40 vs. 40:60) and soy oil (high 18:2) at 0, 1, 2, and 3% of the diet DM on the production of BHI. FCR had no effect on types or amount of BHI. Increasing soy oil linearly increased ($P < 0.05$) production of total *trans* 18:1 and CLA. Study 3 examined the relationship between FCR (60:40 vs. 40:60) and canola oil (high 18:1) at 0, 1, 2, and 3% of the diet DM on the production of BHI. FCR had no effect on types or amount of BHI. Increasing canola oil linearly increased ($P < 0.05$) production of total *trans* 18:1 and CLA, with a nonlinear effect for *trans*-10 18:1 ($P < 0.05$). In all studies, increasing RUFAL increased extent of biohydrogenation of dietary fatty acids ($P < 0.05$). Grinding of forages might have negated FCR effects on BHI. Overall, the relationship between CLA production and fatty acid intake was curvilinear with a significant increase in production when fatty acid intake exceeded 40 g/kg DMI. In conclusion, increasing RUFAL via increased dietary 18:1 or 18:2 led to an increase in the production of BHI, which increased most rapidly when added supplemental fat exceeded 2% of diet DM, reaching higher levels for 18:2 than for 18:1 addition.

Key Words: biohydrogenation, continuous culture, fatty acid

657 Effect of abomasal infusions of *trans* octadecenoic fatty acids on plasma lipids and milk fat synthesis in dairy cows. C. M. Klein* and A. L. Lock, *Michigan State University, East Lansing.*

Four rumen-fistulated Holstein cows (211 ± 12 DIM) were used in a 4 × 4 Latin square experiment to examine the effect of *trans* 18:1 fatty acids (TFA) on plasma lipid fractions and milk fat synthesis. Treatments were abomasal infusions of (1) ethanol (control), (2) conjugated linoleic acid supplement (CLA; positive control), (3) partially hydrogenated safflower fatty acid supplement (SAF), and (4) partially hydrogenated sunflower fatty acid supplement (SUN). CLA provided 5.0 g/d of *trans*-10, *cis*-12 18:2 and SAF and SUN supplied 119 g/d of total TFA. SUN contained more *trans*-4 to *trans*-10 18:1 (57% of total TFA) compared with SAF, which contained more *trans*-11 to *trans*-16 18:1 (53% of total TFA). Treatment periods were 5 d in length with a 7 d washout interval. Daily dose was provided by infusion at 6 h intervals. Data were analyzed using the fit model procedure of JMP. Total fatty acid concentration in plasma lipid fractions was not affected by treatment ($P > 0.18$). Compared with control, SAF and SUN increased the concentration of total TFA in plasma triglycerides 44 and 27% and in phospholipids by 24 and 26%, respectively ($P < 0.01$). Treatments did not affect total TFA in plasma cholesterol esters and NEFA ($P > 0.26$). DMI and the yields of milk, milk protein, and milk lactose were unaffected by treatment ($P > 0.15$). Compared with control, SAF and SUN had no effect on milk fat synthesis ($P > 0.40$), whereas CLA resulted in a 24 and 20% reduction in milk fat concentration and yield, respectively ($P < 0.01$). There were no milk production differences between SAF and SUN ($P > 0.1$). The transfer efficiency for abomasally infused *trans*-10, *cis*-12 18:2 into milk fat was 28% from the CLA treatment. Transfer efficiency of TFA from SAF and SUN was 14 and 16%, respectively. Transfer of individual TFA ranged from ~10 to 30%. *Trans*-10 18:1 transfer was 20 and 22% for SAF and SUN, respectively. In conclusion, TFA had no effect on milk fat synthesis when abomasally infused at 119 g/d, although they were incorporated into plasma triglycerides, taken up by the mammary gland, and incorporated into milk fat.

Key Words: milk fat depression, plasma lipid, *trans* fatty acid

658 Impact of unsaturated free fatty acids and triglycerides on milk fat synthesis in dairy cattle. J. C. Ploetz* and A. L. Lock, *Michigan State University, East Lansing.*

This study determined if altering the amount of unsaturated fatty acids (FA) in the diet as triglycerides or free FA affected feed intake, yield of milk and milk components, and feed efficiency. Eighteen Holstein cows (132 ± 75 DIM) were used in a 3 × 3 Latin Square design. Treatments were diets supplemented (2% of diet DM) with soybean oil (TAG), soybean free FA (FFA), or control (CON, soyhulls). Treatment periods were 21 d with the final 4 d used for sample and data collection. The corn silage and alfalfa haylage-based diets contained 23% forage NDF and 17% CP. Total dietary FA were 2.6, 4.3, and 4.2% DM for CON, TAG, and FFA, respectively. Data were analyzed using the fit model procedure of JMP. Compared with CON, fat treatments decreased DMI (1.0 kg/d; $P < 0.05$) but increased milk yield (2.2 kg/d; $P < 0.01$) and milk lactose concentration and yield ($P < 0.01$). Fat supplements reduced milk fat concentration ($P < 0.05$), averaging 3.30, 3.18, and 3.11% for CON, FFA, and TAG, respectively. Yield of milk fat, milk protein, and 3.5% FCM ($P > 0.17$) remained unchanged. There were no differences in the yield of milk or milk components between FFA and TAG ($P > 0.22$). Fat treatments increased feed efficiency (3.5% FCM/DMI), averaging 1.42, 1.53, and 1.48 for CON, FFA, and TAG, respectively ($P < 0.01$). Although milk fat yield was not affected, fat treatments decreased the yield of de novo (<16-carbon) FA (40 g/d; $P < 0.001$) and increased preformed (>16-carbon) FA (134 g/d; $P < 0.001$). Yield of FA from both sources (16-carbon FA) was reduced by fat treatments ($P < 0.001$) but to a different extent for FFA vs. TAG (72 vs. 100 g/d; $P < 0.05$). Total *trans* 18:1 FA concentration and yield increased with fat treatments ($P < 0.001$) but was higher for TAG vs. FFA ($P < 0.01$). While the ratio of t10 18:1 to t11 18:1 was not affected by treatment ($P = 0.21$) there was a trend for t10c12 18:2 concentration and yield to be higher for fat treatments ($P = 0.06$). In conclusion, FA supplemented at 2% diet DM as either FFA or TAG increased milk yield but did not effectively cause MFD with preformed FA replacing de novo synthesized FA in milk fat.

Key Words: biohydrogenation, milk fat, unsaturated fatty acid

659 Effects of ruminally inert essential fatty acids on postpartum immune-related functions and productivity in lactating dairy cattle. J. Pankowski*[1], J. Noble[2], P. Brennan[3], G. Jarrett[4], and E. Block[1], [1]*Arm & Hammer Animal Nutrition, Princeton, NJ,* [2]*Linwood Management,LLC, Linwood, NY,* [3]*Purina Animal Nutrition LLC, Caledonia, NY,* [4]*Cows Come First LLC, Batavia, NY.*

This prospective field study tested the effects of increasing intestinally available essential FFA (EFA) on production, immune and reproduction parameters in 2 large commercial dairies. A commercially available FFA prilled supplement was replaced with commercially available calcium salts of FA containing both linoleic and linolenic acids at rate of 114 g/cow/d in the 21-d prepartum ration and 340 g/cow/d in the postpartum ration fed until 100 DIM. Measurements, descriptions, and results are in Table1. The effects of treatment on primary response variables were quantified using linear regression analysis. A total of 1909 cows were used to evaluate the base case and 2219 cows were used to evaluate the EFA case. Economics showed a favorable profitability for the use of the EFA supplement. Results from this and other cited trials present evidence that EFA supplementation of pre- and postpartum dairy cattle has positive roles both biologically and economically.

Table 1. Production, reproduction and immune responses to inclusion of intestinally available EFA in pre- and postpartum diets for dairy cows[1,2]

Parameter	Baseline	EFA	$P > F$
Milk (kg/d)	33.5	36.3	<0.001
FCM 3.5% (kg/d)	34.4	36.3	<0.001
Fat (kg/d)	1.23	1.27	0.006
Protein (kg/d)	1.03	1.07	0.003
BHBA (mg/dL)	5.05	2.82	<0.001
Start up milk yield (kg/d)[3]	15.8	16.6	0.005
First SCC linear score	3.09	2.73	<0.001
Monthly EED (n)[4]	7.6	2.5	<0.001
FSCR (%)[5]	35.4	39.4	0.082
Heat detection rate (%)	66.7	67.7	0.318
Conception rate (%)	35.6	38.2	0.035
Preganancy rate (%)	23.8	25.9	0.034

[1]Baseline: 1 December 2010 through 30 August 2011. EFA: 1 December 2011 through 30 August 2012.
[2]EFA supplement as calcium salts replaced same quantity of saturated fatty acid prills fed during baseline period.
[3]Statistical model corrected for parity and DIM at first DHI test. Average actual milk volumes for baseline and EFA periods were 35.5 and 37.3 kg/d, respectively, with DIM at first DHI test ranging 1 to 39 d and parity ranging 1 to 8.
[4]Average monthly number of early embryonic death defined as animals returning to service at 35 days post insemination following a diagnosis of pregnancy.
[5]First service conception rate.

Key Words: EFA, immune function, reproduction

660 Effect of organic grain supplementation on production, body weight, body condition score, and profitability of organic dairy cows. B. J. Heins*[1,3], J. C. Paulson[2], M. I. Endres[3], and R. D. Moon[3], [1]*University of Minnesota, West Central Research and Outreach Center, Morris,* [2]*University of Minnesota Extension, Willmar,* [3]*University of Minnesota, Saint Paul.*

Organic cows (n = 96) were used to evaluate grain supplementation levels during the grazing season (May to September 2012) on production, body weight, body condition score (BCS), and profitability of organic dairy cows. Cows were assigned to one of 3 replicate supplementation groups, 1) no grain supplementation (100% pasture, GRS, n = 32), 2) low grain (2.72 kg/head/day, LOW, n = 32), and 3) high grain (5.44 kg/head/day, HI, n = 32), and calved at the University of Minnesota West Central Research and Outreach Center, Morris, Minnesota from October to December 2011 and March to May 2012. Supplement (organic corn and minerals) was fed with a total mixed ration of corn silage and alfalfa haylage, and at least 30% of diet dry matter intake for LOW and HI cows consisted of organic pasture. Milk production, from daily milk weights, was averaged weekly for cows, and body weight and BCS were recorded bi-weekly. Analysis was with PROC MIXED of SAS, and independent variables for statistical analysis were fixed effects of season of calving (fall or spring), parity (1,2,3+), supplementation group, breed group nested within supplementation group, and week nested with supplementation group, with replicate and cow nested within supplementation group and breed group as a random effect. The GRS (14.6 kg/d) cows had significantly ($P < 0.05$) lower energy-corrected milk than LOW (16.9 kg/d) and HI (16.5 kg/d) cows; however, the LOW and HI cows were not significantly different from each other. The GRS, LOW, and HI cows were not significantly different for body weight across the grazing season; however, GRS (2.98) cows had significantly ($P < 0.05$) lower BCS than HI (3.15) cows. Milk urea nitrogen was significantly ($P < 0.05$) higher for GRS (14.3 mg/dl) than LOW (10.1 mg/dl) and HI (7.3 mg/dl) cows. Income over feed costs was significantly higher ($P < 0.05$) for the GRS ($3.61/cow/day) cows compared with the LOW ($2.20/cow/day) and HI ($0.38/cow/day) cows. Organic dairy cows that consume 100% pasture had lower production, but were more profitable because of higher feed costs for supplemented cows.

Key Words: organic, profitability, pasture

661 Effect of organic grain supplementation on pasture and total mixed ration dry matter intake and fatty acid profiles of organic dairy cows. B. J. Heins[1,3], J. C. Paulson*[2], M. I. Endres[3], and R. D. Moon[3], [1]*University of Minnesota, West Central Research and Outreach Center, Morris,* [2]*University of Minnesota Extension, Willmar,* [3]*University of Minnesota, Saint Paul.*

Organic cows (n = 96) were used to evaluate grain supplementation levels during the grazing season (May to September 2012) on pasture herbage mass and milk fatty acid profiles of organic dairy cows. Cows were assigned to one of 3 replicate supplementation groups, (1) no grain supplementation (100% pasture, GRS), (2) low grain (2.72 kg/head/day, LOW), and (3) high grain (5.44 kg/head/day, HI), and calved at the University of Minnesota West Central Research and Outreach Center, Morris, Minnesota from October to December 2011 and March to May 2012. Supplement (organic corn and minerals) was fed with a total mixed ration of corn silage and alfalfa haylage, and at least 30% of diet dry matter intake for LOW and HI cows consisted of organic pasture. Pasture herbage mass was assessed for each replicated group for pre- and post-grazing measurements with an electronic rising plate meter. Milk for fatty acid analyses was collected monthly and analyzed at R-Tech Analytical Laboratory (Arden Hills, MN). Analysis was with PROC MIXED of SAS, and independent variables were fixed effects of supplementation group and date of sample was a random effect. The group of GRS (255 kg/d) cows consumed significantly ($P < 0.05$) more dry matter intake per acre from pasture than LOW (211 kg/d) and HI (214 kg/d) cows. Neutral detergent fiber digestibility of cool-season pasture grasses were highest in June (69.7%) 2012 and lowest in September 2012 (51.3%). Oleic (C18:1) and linolenic (C18:3) acids were higher ($P < 0.05$) in milk of GRS (24.5%, 0.9%) cows compared with milk from LOW (21.6%, 0.7%) and HI (21.6%, 0.7%) cows, respectively. Furthermore, n-3 fatty acid was significantly higher ($P < 0.05$) for the GRS (0.05%) cows compared with the LOW (0.04%) and HI (0.03%) cows; however, the GRS (0.37%) cows had significantly ($P < 0.05$) higher levels of trans fat than LOW (0.21%) and HI (0.22%) cows, respectively. Results indicate that milk from cows that consume 100% pasture compared with pasture and TMR have fatty acid profiles that may provide human health benefits.

Key Words: organic, n-3 fat, herbage mass

662 Cost of corn silage in dairy farms in Viçosa, state of Minas Gerais, Brazil. G. A. Freitas, M. I. Marcondes*, O. G. Pereira, F. L. Araujo, and R. L. Albino, *Universidade Federal de Vicosa, Vicosa, Minas Gerais, Brasil.*

The costs of corn destined to silage production were evaluated according to the soil preparation system: conventional tillage or no-tillage systems, with or without previous plantation of common beans. Data and samples from 18 dairy farms registered in the Program for the Development of Dairy Farming of the region of Viçosa, state of Minas Gerais, Brazil, were analyzed. All data were collected from September 2009 to April 2010. The farms were assigned to a completely randomized design in a 2 × 2 factorial arrangement. The GLM of the software SAS was utilized to run the analysis using 0.10 as significance level. The pH, concentration of dry matter, crude protein, neutral detergent fiber, in vitro dry matter digestibility, wet yield and dry matter production were evaluated. The economic aspects studied were gross income, effective operating costs, total operating costs, gross margin, net margin, natural matter cost and dry matter cost. Higher level of crude protein was observed in the corn silage produced in the no-tillage system ($P < 0.10$). No effects of plantation systems were observed for any of the other characteristics evaluated ($P > 0.10$). The difference in the corn silage protein observed might be explained by the additional increment of nitrogen in the no-tillage system. There is a higher rate of nitrogen release from residues under conventional tillage during the first 4 weeks, compared with no-tillage, and it can be attributed to the effect of tillage systems on incorporation and physical fractioning of residues. Thus, it is inferred that there was a greater loss of nitrogen to the environment under conventional tillage, which may explain the lower concentration of crude protein in corn silage under this system. The costs of corn silage produced without previous plantation of bean was higher than that with it ($P < 0.10$). However, no differences were observed for their gross margin and net margin because there was a higher production of corn silage without previous plantation compared with corn silage with previous plantations of beans which offset its higher cost.

Key Words: no-tillage, production cost, silage

663 Changes in alfalfa silage fermentation products during aerobic exposure and its impact on dry matter intake by goats. K. Gerlach*, Y. Liao, and K.-H. Südekum, *University of Bonn, Bonn, Germany.*

Third-cut alfalfa (*Medicago sativa* L.) was harvested at late-bud stage and, after field-wilting, ensiled either untreated (CON) or treated (TRE) with a chemical additive containing sodium nitrite and hexamine (Kofasil liquid, Addcon Europe, Bonn, Germany; 3.5 l/t). Each treatment was ensiled in a separate round bale, at DM contents (g/kg) of 401 and 385, and at densities of 127 and 133 kg DM/m^3 for CON and TRE, respectively. After 5 mo, both round bales were opened, each silage homogenized and exposed to air for 8 d. In 2-d intervals, silages were sampled for chemical and microbiological analyses and stored anaerobically in vacuum-sealed polyethylene bags for use in feeding trials. For both silages, one preference trial was done with Saanen-type wethers (n = 5, body weight 91 ± 12.3 kg), each one lasting 15 d. During the experimental phase, each possible combination of 2 silages (n = 10) was offered to the goats as free choice for 3 h. Data were analyzed using the SAS procedure multidimensional scaling (MDS), ANOVA, and correlation analysis between silage characteristics and DM intake (DMI). At opening, concentrations of lactic, acetic, and butyric acids were 39, 25, and 3 g/kg DM in CON, and 31, 12, and <0.02 g/kg DM in TRE silages. During aerobic exposure, mold counts in CON increased, but silage temperature remained stable. TRE heated (>3.0 °C above ambient) at d 8, possibly due to higher amounts of water-soluble carbohydrates and increasing yeast counts. In both trials, goats showed a strong avoidance for aerobically exposed silages. The 3-h DMI (n = 20) for d 0-silage was 700 g (TRE) and 670 g (CON), it decreased at d 2 (TRE) and d 4 (CON) of aerobic exposure ($P < 0.001$). At d 8, there was a decline ($P < 0.001$) in DMI of 67% (CON) and 58% (TRE) compared to d 0-silages. Concentrations of ethanol and methanol were positively correlated to DMI (r = 0.78 and 0.76, $P < 0.05$). Aerobic exposure of alfalfa silage strongly influenced preference and short-time DMI by goats, although silage temperature, fermentation products and microbiological variables changed only slightly.

Key Words: aerobic deterioration, preference trial, ruminant

664 Effects of stocking rate and monensin supplementation on forage characteristics and performance of beef heifers receiving warm-season grasses. J. M. B. Vendramini*[1], J. D. Sanchez[1], W. L. da Silva[1], R. F. Cooke[2], P. Moriel[1], and G. Caputti[1], [1]*University of Florida, Ona,* [2]*Oregon State University, Burns.*

The objective of this study was to evaluate the effects of stocking rates and monensin supplementation on forage characteristics and performance of beef heifers (Bos sp.) receiving warm-season grasses. The experiments were conducted in Ona, FL from June to October 2012. In experiment 1, treatments were the factorial combination of 2 stocking rates [1.2 and 1.7 AU (500 kg LW)/ha] and supplementation with monensin (200 mg/d) or control (no monensin) distributed in a complete randomized design with 3 replicates. The heifers received 0.4 kg of a concentrate supplement (14% CP and 78% TDN) daily. Twelve bahiagrass (Paspalum notatum) pastures (1.2 ha) were used as experimental units. Herbage mass (HM) and nutritive value were estimated every 14 d and the heifers were weighed at d 0, 43, and 86. Pastures grazed with greater stocking rates had significant ($P < 0.05$) lesser HM (2,300 vs. 2,800 kg/ha) and herbage allowance (HA, 1.0 vs. 1.8 kg DM/kg LW), however, there was no effect of stocking rates on forage CP (8.5%) and in vitro digestible organic matter (IVDOM, 49.7%). Pastures grazed by heifers receiving monensin or control had similar ($P > 0.10$) HM, HA, CP, and IVDOM. Average daily gain was not affected by stocking rate ($P = 0.63$) or monensin supplementation ($P = 0.94$, mean = 0.44 kg/d). In experiment 2, 20 4 heifers (380 ± 18 kg BW) were distributed in 8 drylot pens for forage DM intake and total DM intake measurements. Treatments were supplementation with monensin (200 mg/d) or control (no monensin) in a completely randomized design with 4 replicates. The adaptation period was 10 d followed by 7 d collection. All animals received 0.4 kg of concentrate supplement daily. Ground stargrass (*Cynodon nlemfuensis*) hay (11% CP, 51% IVDOM) was offered and adjusted to allow 10% refusals. There was no difference in total DM intake ($P = 0.64$, mean = 2.1% BW) or forage DM intake ($P = 0.61$, mean = 2.0% BW) between treatments. Monensin supplementation may not improve performance of beef heifers with limited energy intake grazing warm-season grass pastures.

Key Words: monensin, stocking rate, warm-season grass

665 Evaluation of different dietary supplements for cattle consuming ryegrass baleage. L. V. Durst*, B. J. Rude, and S. H. Ward, *Animal and Dairy Sciences, Mississippi State University, Starkville.*

The objectives of this study were to evaluate the digestibility and CP retention of ryegrass baleage supplemented with hay or soybean hull pellets. Crossbred steers (n = 12, BW 247 ± 20.8 kg) were halter broken, and allowed to adapt to ryegrass baleage for a period of 14 d. Following the adaptation period, the steers were placed in individual metabolism crates for a total of 10 d. All 12 steers had ad libitum access to ryegrass baleage (DM = 51%; CP = 16%, DM basis) and were allotted to 3 treatments: (1) no supplement (NS); (2) hay (H; CP = 13%, DM basis); (3) soybean hull pellets (SH; CP = 7%, DM basis), with 4 steers per treatment group. Sample collections were for 7 d following a 3-d adaptation to crates. Data was analyzed using the GLM procedures of SAS with steer as the experimental unit. Dry matter intake was different ($P = 0.0465$) with steers fed NS (4.49 kg/d) and H (4.60 kg/d) consuming less than those fed SH (5.39 kg/d). However, DMI was not different ($P = 0.4146$) when BW was accounted for ranging between 1.7 and 2.1% BW/d. Apparent digestibility of DM was not different ($P = 0.9222$) and ranged between 73 and 74%. There was no difference for apparent OM digestibility ($P = 0.9266$) which ranged from 74 to 76%. Apparent CP digestibility did not differ ($P = 0.3679$) and ranged from 60 to 65%. No difference was found for apparent NDF digestibility ($P = 0.9087$) with a range from 78 to 79%. Apparent hemicellulose digestibility did not differ ($P = 0.5982$) and ranged from 78 to 81%. Apparent fat digestibility was not different ($P = 0.9936$) with a range between 84 and 85%. Amount of protein retained was not different ($P = 0.7322$) and ranged between 11 and 20 g/d. The data collected indicated there was no effect of supplementing a fiber source to cattle consuming ryegrass baleage. This may be attributed to ryegrass being more mature when harvested for baleage.

Key Words: ryegrass baleage, digestibility, beef cattle

666 Using weekly pasture cover measurements to monitor growth and utilization. J. R. Seymour and T. W. Downing*, *Oregon State University, Corvallis.*

Managing pastures on grazing dairies is a continuous challenge because pasture quality, quantity and growth rate are changing daily. Using weekly pasture cover measurements have been demonstrated in New Zealand and Ireland to provide useful information to manage pastures allowing managers to estimate daily growth rates, feed inventories and feed budgeting. The objectives of this project were to document weekly pasture growth, forage quality and utilization and to understand how to

use this information to make management decisions on US dairies. Two dairies were studied for a year. Pastures were measured and mapped and total standing dry matter was estimated weekly in all 65 pastures using a calibrated rising plate meter. Measurements started with the grazing season in the spring in March and continued until the end of November. Weekly grazing wedges were developed and printed for each farm and were used to make grazing decisions that week. Paddocks grazed and residual pasture covers were recorded daily and forage cover measurements were measured weekly and entered into management software. Paddock grazing and residual heights were also included in the electronic recordkeeping. Dry matter yields ranged from 12671 to 22066 ± 2902 kg/ha. Daily growth rates ranged from 5 to 137 kg/ha a day throughout the season and averaged 83.1 ± 32.3 for Farm 1 and 53.7 ± 27.6 for Farm 2. Weekly pasture quality samples were taken and analyzed with season long energy values averaging 12.15 ± 0.822 mJ/kg for Farm 1 and 12.58 ± 0.77 mJ/kg for Farm 2. Monitoring weekly growth and cover provides valuable information for the grazing dairy. Pasture quality and productivity in Oregon is comparable to some of the most productive pastures reported from around the world.

Key Words: rising plate meter, pasture cover, pasture energy values

667 In vitro NDF digestibility and its correlation with chemical components of tropical grasses under intensive rotational grazing strategies. J. C. Lopes*[1], R. B. Reis[2], and D. K. Combs[1], [1]*Department of Dairy Science, University of Wisconsin-Madison, Madison,* [2]*Escola de Veterinária, Universidade Federal de Minas Gerais, Belo Horizonte, MG, Brazil.*

This study was conducted to determine the in vitro NDF digestibility (IvNDFD) and its correlation with chemical components of the main tropical grasses produced under intensive rotational grazing practices in Brazil. One-hundred six samples of *Brachiaria brizantha* (n = 22); *Brachiaria hibrida* (n = 6); *Cynodon dactylon* (n = 13); *Cynodon nlemfuensis* (n = 4); *Panicum maximum* (n = 31) and *Pennisetum purpureum* (n = 30) were collected from research paddocks from the Southeast region of Brazil. All grasses were grown on highly fertilized soils and managed with intensive rotational grazing practices. Grasses were hand-clipped at the cutting height of 95% of sward canopy light interception. Samples were shipped to the University of Wisconsin-Madison, and analyzed sequentially for NDF, ADF and lignin. In vitro NDF digestibility was analyzed for 24-, 30-, and 48-h. Data were analyzed as a split-plot in time using a mixed procedure of SAS. Pearson correlation coefficients were used to describe relationships between IvNDFD and NDF and lignin. Average NDF content ranged from 60 to 63% of DM across grass species. Mean IvNDFD differed due to time of incubation ($P < 0.0001$) and were 37 ± 13, 45 ± 13 and 61 ± 13% of NDF at 24-, 30- and 48-h, respectively, across forages species. Comparison of mean IvNDFD estimates indicated that *C. dactylon* and *C. nlemfuensis* had high IvNDFD; *B. hibrida* and *P. maximum* were intermediate in IvNDFD; and *P. purpureum* and *B. brizantha* had lowest NDF digestibility estimates. Lignin was not significantly correlated to IvNDFD of tropical grasses. A negative relationship between IvNDFD and NDF content was only observed for *C. dactylon*. Our findings indicate that fertilized tropical forages with short defoliation intervals can be relatively high in fiber digestibility. Forage species had a significant effect on IvNDFD. These data also suggest that NDF digestibility in tropical grasses may not be correlated to the same chemical components related to digestibility in temperate grasses and it possibly differs within species of tropical grasses.

Key Words: tropical grass, NDF digestion, in vitro

668 Days of rest affects forage mass and quality in a rotational stocking system. J. C. Emenheiser*[1], B. F. Tracy[1], A. E. Tanner[1], D. Fiske[2], W. S. Swecker, Jr.[3], W. M. Clapham[4], and R. M. Lewis[1], [1]*Virginia Polytechic Institute and State University, Blacksburg,* [2]*Shenandoah Valley Agricultural Research and Extension Center, Steeles Tavern, VA,* [3]*Virginia-Maryland Regional College of Veterinary Medicine, Blacksburg,* [4]*USDA-ARS Appalachian Farming Systems Research Center, Beaver, WV.*

Forage growth is a key dynamic in rotational stocking systems. We evaluated effects of stockpiling and rest on forage mass and quality in rotational stocking. Twelve 6.47-ha fescue-clover pastures (block) were stocked with equivalent beef cattle units between March and November in 2008 to 2011. Each block consisted of 8 paddocks with variable rest durations. Each year, an alternating half of the paddocks were stockpiled from August to November and stocked in winter. Forage samples were collected mid-monthly; May to November samples were used (7 periods). Average daily temperature (TEMP, °C) and precipitation (PREC, cm) were obtained by period. Days since last grazed (REST) were calculated for paddocks. Dry matter mass (MASS; kg) and CP and ADF contents (g/kg MASS) were measured. A linear mixed-model with block, period, stock, and period by stock interaction as fixed effects was fitted. Covariates were REST, TEMP and PREC; their interactions with period and stock, singly and together, also were fitted. Year nested within block and residual were random effects. Block only defined variation in CP ($P < 0.02$). The REST ranged from 1 to 110 d and was right-skewed with mean 28.8 (±26.0) d. The TEMP was parabolic with a low of 9.3 (November) and high of 22.2°C (August). The PREC ranged from 0.19 (August) to 0.36 cm (May), and varied across periods and years. Mean MASS was 7573 ± 5261 kg/ha. Means for CP and ADF were 132 ± 4 and 338 ± 6 g/kg, respectively. For MASS, REST corresponded with an increase of 49 ± 19 kg/ha per d ($P < 0.001$); there was no interaction of REST with period ($P = 0.18$), stock ($P = 0.05$), or their combination ($P = 0.49$). For CP and ADF, such interactions were evident ($P < 0.04$). The CP content (g/kg of MASS) also was affected by REST ($P < 0.001$). In May to July, CP content in non-stockpiled (0.63 ± 0.51) and stockpiled (0.17 ± 0.43) paddocks increased with REST. In August to November, CP content increased 0.46 ± 0.52 in non-stockpiled, but decreased 0.12 ± 0.45 in stockpiled, paddocks with REST. Forage mass accumulated at a similar rate irrespective of period or stockpiling, likely reflecting influences of weather patterns across a grazing season.

Key Words: rotational stocking

669 Effects of pasture management and energy supplement on ingestive behavior of grazing cattle. J. R. R. Dorea[1], L. R. D. Agostinho Neto[1], V. N. Gouvea[1], D. F. A. Costa*[1], A. V. Pires[1], L. G. R. Pereira[2], and F. A. P. Santos[1], [1]*University of Sao Paulo, Piracicaba, Sao Paulo, Brazil,* [2]*Empresa Brasileira de Pesquisa Agropecuaria, Juiz de Fora, Minas Gerais, Brazil.*

The objective of this trial was to evaluate the effect of 2 pre-grazing canopy heights and 2 levels of energy supplementation on ingestive behavior of Nellore steers grazing a well-managed tropical grass during the rainy season. Treatments consisted of control (mineral supplement only) and a medium level of energy supplemention (0.6% of BW of fine ground corn) combined with 2 pre-grazing heights (25 and 35 cm), using a common stubble height of 15 cm. Eight 48-mo-old rumen-cannulated steers (300 kg BW ± 7.40) were assigned to 2 4x4 Latin squares and allocated to 2 ha of *Brachiaria brizantha* pasture. Ingestive behavior was evaluated in a 24h observation period in which grazing, rumination and resting activities were monitored every 5 min. Bite and ingestion rates were also evaluated. Grazing time decreased when 25 cm

canopy height and energy supplementation were used (44.5 and 71.0 min, respectively). The rumination time was not affected by energy supplementation and pre-grazing canopy height. However, there was an increase in resting time when the pre-grazing canopy height was 25 cm. This could decrease energy expenditure for maintenance resulting in an increased animal performance. The ingestion rate was greater for 25 cm pre-grazing height suggesting a higher harvest efficiency; however no effects were observed for energy supplementation. The bite rate was also higher on 25 cm pre-grazing height and, as for ingestion rate, it could result in an increased harvest efficiency consequently resulting in greater dry matter intake. The use of the pre-grazing canopy height of 25 cm and of a medium level of energy supplementation resulted in improvements on harvest efficiency.

Table 1. Effects of pasture management (M) and supplementation (S) on grazing, rumination and resting times, ingestion and bite rates

	M, cm		S, % BW		*P*-value			
	25	35	0	0.6	M	S	M× S	SEM
Grazing time, min	390	434	447	376	*	*	*	29.23
Rumination time, min	392	441	401	431	NS	NS	NS	36.43
Resting time, min	607	502	543	566	*	NS	NS	35.05
Ingestion DM rate, g of DM/min	15.15	8.38	12.24	11.29	*	NS	NS	3.03
Bite rate, bites/min	29.72	19.59	23.41	25.90	*	NS	NS	3.69

*$P < 0.05$.

Key Words: pasture management, energy supplement

670 The use of logistic and cumulative normal distributions to model ruminal temperature and pH by radiofrequency rumen boluses under different conditions in goats. A. Castro-Costa[1], J. Torrent*[2], A. A. K. Salama[1], M. Creus[3], and G. Caja[1], [1]*Ruminant Research Group (G2R), Universitat Autonoma de Barcelona, Bellaterra, Spain,* [2]*Oligo Basics USA LLC, Wilmington, DE,* [3]*Nutcat, Lleida, Spain.*

The objective of this study was to investigate the relationship between ruminal temperature and pH to develop a predictive model under different feeding and environmental conditions using either logistic regressions or cumulative normal distributions (CND). Eight open and dry Murciano-Granadina goats (43.6 ± 1.4 kg BW) were randomly allocated to treatments according to a 2 × 2 factorial (control or functional oil diets, thermoneutral or heat stress temperatures) to assess whether these factors affected the relationship. The experiment consisted of 2 consecutive periods of 3 wk (adaptation, 2 wk; data collection, 1 wk) during which ruminal pH and temperature were continuously recorded every 30 min. Diet consisted of a TMR (concentrate:forage, 30:70) the functional oil being added to concentrate (1 g/goat and day). Data were collected using radiofrequency (433.92 MHz) rumen boluses (KB1000, Khane Auckland, NZ) and a receiver (KR2002). Mean pH and temperature values and ranges were 6.446 ± 0.013 (5.68 to 7.37) and 39.875 ± 0.020°C (38.91 to 40.82). Although logistic regressions predicted slightly more accurately pH and temperature kinetics (r^2 from 0.96 to 0.99; RSD from 0.037 to 0.169; $P < 0.001$) than CND ($r^2 = 0.95$ to 0.99; RSD from 0.035 to 0.174; $P < 0.001$), no significant relationship was found between the coefficients of rumen pH and those of rumen temperature. The SD of rumen temperature was more accurate predicting pH nadir and average pH than any other estimated parameter. Supplementation of functional oil increased ($P = 0.002$) and heat stress tended ($P = 0.086$) to decrease ruminal nadir pH independently of rumen temperature. In conclusion, the use of logistic regressions only marginally improved the accuracy of ruminal pH predictions over the CND. The SD of the temperature was the best predictor of nadir pH, and factors that affect ruminal pH and temperature decrease the accuracy of pH predictions that use either the rumen temperature or its SD as a predictor.

Key Words: logistic regression, ruminal pH, ruminal temperature

671 Biomarkers for bovine rumen acidosis. A. M. Danscher[1], S. C. Li*[2], P. H. Andersen[3], E. Khafipour[2], N. B. Kristensen[4], and J. C. Plaizier[2], [1]*University of Copenhagen, Copenhagen, Denmark,* [2]*University of Manitoba, Winnipeg, MB, Canada,* [3]*Swedish University of Agricultural Sciences, Uppsala, Sweden,* [4]*Danish Agricultural Advisory Service, Aarhus, Denmark.*

Prevalence of ruminal acidosis in dairy production is allegedly high with large effects on production and welfare. Field diagnosis still relies on rumen pH measurements, which are insensitive, invasive or require expensive equipment. Previous attempts to identify new candidate markers for ruminal acidosis have shown conflicting results. Here, we evaluated several blood, urine and feces parameters as potential biomarkers of this disease. Eight Danish Holstein dry cows were fed a conventional total mixed ration (TMR) with forage-to-concentrate ratio of 78:22 on a DM basis. Acidosis challenge was conducted in 4 animals for 2 d by substituting up to 45% of TMR DM with pellets containing 50% wheat and 50% barley. Rumen pH was measured continuously (eCow). Daily mean, minimum and maximum rumen pH and duration and areas below pH 6.0, 5.8, 5.6, and 5.2 were calculated. Samples of blood, urine and feces were collected at 15:00 and 21:00 on 2 acidosis days. Blood samples were analyzed for pCO_2, pO_2, pH, electrolytes, lactate, glucose, packed cell volume and total plasma protein concentration. pH was measured in urine and feces. Acidosis challenge decreased mean daily rumen pH from 6.6 to 5.8 and minimum daily rumen pH from 6.1 to 5.2, and increased the duration of pH below pH 5.8 (from 3 to 662 min/d), 5.6 (0 to 493 min/d), 5.2 (0 to 304 min/d) ($P < 0.05$). Also areas below pH 6.0, 5.8, and 5.6 were increased ($P < 0.05$). Acidosis increased blood lactate from 0.35 to 0.46 mM ($P < 0.05$). Blood pH on the first day of challenge was similar to control but tended to decline on the second day ($P < 0.10$). Acidosis also decreased urinary pH from 8.3 to 7.3 and fecal pH from 6.7 to 5.9 and both measurements were lower on the second day of challenge ($P < 0.05$). Fecal pH was lower at 21:00 relative to 15:00 ($P < 0.05$). Other parameters were not affected. Despite low rumen pH (average minimum pH = 5.2), only minor changes in blood lactate and pH were observed and no other blood parameters were altered. Blood lactate and pH in blood, urine and feces may be used as markers of ruminal acidosis especially when serial measurements are made, but changes were small and diurnal variation was observed in fecal pH.

Key Words: cow, biomarker, rumen acidosis

672 Liver mitochondrial efficiency of two lineages of Angus bulls with high and low residual feed intake (RFI). G. Acetoze*[1], K. L. Weber[1], A. L. Van Eenennaam[1], J. J. Ramsey[2], and H. A. Rossow[3], [1]*University of California, Department of Animal Science, Davis,* [2]*University of California, School of Veterinary Medicine, Davis,* [3]*University of California, School of Veterinary Medicine, Tulare.*

Significant differences in mitochondrial oxygen consumption are observed in steers with high and low RFI (Keisler et al., 2006). Data suggest that mitochondrial function is a maternally inherited trait, however important proteins such as intermembrane space and matrix proteins are encoded in the cell nuclei and therefore, could be inherited by both the sire and the dams (Lymbery et al., 2001). It is still unknown if there's any correlation between lineage of sires and mitochondrial oxygen consumption. The objective of this experiment is to analyze mitochondrial efficiency for 2 sires with high and low RFI. Two popular Angus bulls were selected based on the HD 50K MVP genetic test (Pfizer Animal Genetics) and were used as sires at the Sierra Foothill Research and Extension Center. Eight offspring (10–11mo) from each sire were selected based on body weight and shipped to the UC Davis feedlot. Following a diet adaptation period of 14 d, steers were housed in individual pens to allow individual measurements of feed intake for 70–105 d and fed a typical feedlot finishing diet with 63% rolled corn and 17% dry distilled grains (DDG) 4 times a day. Slaughter criteria were 11mm of backfat using ultrasound (SONOVET 2000). Statistical model $Yij = \mu + xij\beta + \tau i + \varepsilon ij$ will be analyzed using ANOVA. Respiratory control ratio (RCR) is the ratio of oxygen consumption in State 3 and State 4 respiration and provides an indication of mitochondrial coupling and efficiency. State 3 (maximum ATP stimulated respiration) and State 4 (leak-dependent oxygen consumption) did not differ between the 2 group of animals ($P = 0.87$) and ($P = 0.99$), respectively. Also, no differences in RCR (±SD) were found with averages of 2.98 (0.45) and 3.03 (0.39) for low and high RFI steers, respectively ($P = 0.85$). These results differ from Keisler et al. (2006) in which low RFI steers had greater RCR values. Therefore even though there were differences

in RFI between the 2 groups, their liver mitochondria did not present differences in maximum oxygen consumption, proton leak dependent respiration or uncoupling.

Key Words: mitochondria, RFI, steer

673 Effect of lipid source on fatty acid profile in the rumen of cattle fed a tropical hay. D. F. A. Costa*[1], P. Isherwood[1], S. Quigley[1], S. R. McLennan[2], J. De Souza[3], J. Gibbs[5], X. Sun[4], and D. P. Poppi[1], [1]*The University of Queensland, Gatton, QLD, Australia,* [2]*The University of Queensland, Brisbane, QLD, Australia,* [3]*University of Sao Paulo, Piracicaba, Sao Paulo, Brazil,* [4]*College of Animal Science and Technology, Northwest A&F University, Yangling, Shaanxi, China,* [5]*Lincoln University, Lincoln, Canterbury, New Zealand.*

The objective of this study was to examine the fatty acid (FA) profile in the rumen fluid (RF) of steers fed a low crude protein tropical grass (Chloris gayana hay, 38g CP, 17g crude lipid and 752g NDF kg DM^{-1}) supplemented with various lipids. Five rumen cannulated steers (799 ± 15kg LW) were allocated to a 5 × 5 Latin square design. Hay ad libitum intake was determined over 7d and fixed at this level. The treatments were Control, hay only, or the addition of 3g kg hay DM^{-1} of lipid sources: Coconut (high lauric acid), cottonseed and soybean (high linoleic acid) or fish oil (high long chain FA (LCFA)). The experiment consisted of 5 runs of 18d feeding followed by 3d collection. Retention time (RT) was estimated on d 19 using CrEDTA. FA profile of RF collected at 0, 4, 8, 12 and 16h was determined by gas chromatography. Statistical analyses were done on proc GLM and LSD test for multiple comparisons. RT decreased with addition of soybean oil (14h) but no differences between other treatments (mean 17h). Coconut oil increased lauric and myristic acids in RF. No changes in total saturated FA (TSFA) in RF, with exception of a lower concentration for fish oil treatment. Addition of fish oil also decreased the concentration in RF of stearic and linolenic acid, but no differences to coconut and cottonseed treatments for linolenic acid. Fish oil also resulted in higher LCFA, linoleic and total unsaturated FA (TUFA), but no differences to soybean oil for the latter 2 acids. CLA was only different in RF between cottonseed and fish oil treatments. Differences in FA profile of oils were only partially translated into the FA profile in RF of steers fed a tropical hay.

Table 1. FA profile in RF of cattle fed a tropical hay

FA% of total FA	Control	Coconut	Cottonseed	Fish	Soybean	SEM
C12:0	1.9^{a}	8.5^{b}	1.5^{a}	0.9^{a}	1.9^{a}	1.03
C14:0	5.9^{b}	14.2^{c}	5.5^{ab}	3.9^{a}	4.7^{ab}	1.34
C18:0	8.2^{b}	6.7^{b}	8.2^{b}	3.9^{a}	8.3^{b}	1.25
C18:2n-6	9.4^{a}	4.5^{a}	10.2^{a}	19.9^{b}	18.3^{b}	9.90
C18:3n-3	2.5^{bc}	1.5^{a}	1.8^{ab}	1.3^{a}	3.0^{c}	0.60
CLAc9,t11	0.1^{ab}	0.2^{ab}	0.4^{b}	0.1^{a}	0.3^{ab}	0.19
LCFA	2.1^{a}	2.4^{a}	2.1^{a}	4.7^{b}	1.9^{a}	1.27
TSFA	66.1^{b}	64.2^{b}	62.5^{b}	43.7^{a}	53.9^{ab}	9.73
TUFA	27.6^{ab}	20.5^{a}	31.6^{ab}	47.8^{c}	40.8^{bc}	11.07

$^{a–c}$Different superscripts across rows indicate significant differences ($P < 0.05$).

Key Words: C4 grass, fatty acid, rumen fluid

674 Effect of dietary glucogenic precursors and linseed oil on growth performance, rumen fermentation and intramuscular fatty acids of lambs. R. J. B. Bessa*[1], J. M. Pestana[1,3], A. S. H. Costa[1], E. Jeronimo[2], S. P. Alves[1,2], J. Santos-Silva[2], and J. A. M. Prates[1], [1]*CIISA, Faculdade de Medicina Veterinária, Lisbon, Portugal,* [2]*UIPA, Instituto Nacional de Investigacao Agrária e Veterinária, Santarem, Portugal,* [3]*GIRM, Grupo de Investigação em Recursos Marinhos, Instituto Politécnico de Leiria, Peniche, Portugal.*

This experiment was conducted to test the hypothesis that adding glucogenic precursors (propylene glycol and calcium propionate mix) to a high-forage and high-oil diet would enrich lamb meat in *cis*-9,*trans*-11 18:2 (rumenic acid), through both the maintenance of high level of *trans*-11 18:1 in rumen outflow and an increase in its endogenous conversion to rumenic acid. To test this hypothesis, the effect of inclusion of a propylene glycol and calcium propionate mix (PP) (0 g/kg vs.50 g/kg dry matter, DM) and linseed oil supplementation (0 g/kg vs. 60 g/kg DM) in diets was evaluated, during 6 weeks, on 36 Merino Branco lambs with initial live weights of 27.3 ± 3.52 kg (randomized 2 × 2 factorial design). PP did not affect DM intake, average daily gain and carcass traits, except for an increase ($P < 0.05$) of subcutaneous fat proportion of chump and shoulders. Serum insulin concentration was not affected by treatments, although PP tended ($P = 0.09$) to decrease serum glucose concentration. Linseed oil supplementation increased 18:3n-3 as most of the C18 biohydrogenation intermediates, including trans-11 18:1 and rumenic acid. PP attenuated the strong increase of *trans*-11 18:1 induced by linseed oil supplementation and tended to reduced ($P = 0.054$) the *trans*-11/*trans*-10 18:1 ratio in meat. The stearoyl CoA desaturase activity, estimated by the ratio of catalyzed FA, was depressed by oil supplementation but not by PP, except for the *cis*-9 16:1/(*cis*-9 16:1+16:0) index. Contrarily to our working hypothesis, the PP reduced the rumenic acid concentration.

Key Words: glucogenic precursor, linseed oil, biohydrogenation intermediate

675 The interference of time interval and number of samples on the parameter estimates of GnG1 nonlinear models for passage rate data. L. F. L. Cavalcanti*[2,1] and L. O. Tedeschi[1], [1]*Texas A&M University, College Station,* [2]*Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil.*

The use of GnG1 nonlinear models to estimate fractional passage rate (kp) of grazing animals has frequently been used because its parameters are readily correlated to biological phenomena of scientific interest. The use of marker concentration to determine passage rate is laborious and occasionally expensive. Therefore, the reduction of number of samples is of interest, but how many samples are necessary without interfering with the parameter estimates has not been clearly set. This study aimed to evaluate the influence of sample size (SS) and time interval (TI) on the parameter estimates of GnG1 model using a synthetic database obtained via simulation. Ten curves for each of 3 different fibers (bermudagrass, solka floc, and wood chips) were simulated using a normal pseudo-randomization approach over 240 h of observation, using parameters' means and standard deviations obtained in the literature. The 240-h period was divided into 5 parts of 48 h each. The sample sizes were 30, 25, 20, 15, or 10 data points, and for each of them 5 different time intervals were used, with the following % distributions: 20, 20, 20, 20, 20; 30, 20, 20, 20, 10; 30, 30, 20, 10, 10; 40, 30, 20, 5, 5; or 40, 40, 10, 5, 5% of total samples within each of the 48 h interval. The 25 curves for each of the 30 initial curves (750 curves) were converged by a nonlinear least squares method using the Gauss-Newton algorithm, fitting the GnG1 model (n = 1–5). The Akaike Information Criterion was used to select the best fitted model (G1G1, G2G1, G3G1, G4G1, or G5G1). The observed kp were compared with a paired *t*-test ($\alpha = 0.05$). The estimated kp was influenced by both factors (SS and TI; $P < 0.05$) for the bermudagrass and solka floc, but not for wood chips, which had the lowest kp. The kp differences were observed more often for sample sizes lower than 20 and

in the 4th distribution interval studied. The models with less samples had better fit for more compartment GnG1 models (n > 2), differently of the original one with 2 compartments. The SS and TI may influence the interpretation regarding kp when GnG1 models are used.

Key Words: kinetics, modeling, simulation

676 Effect of increasing concentrations of DHA-Gold in concentrate diets fed to Canadian Arcott lambs on the fatty acid profiles of adipose tissue and skeletal muscle. S. J. Meale*[1,2], S. Ding[1,2], M. L. He[2], A. V. Chaves[1], and T. A. McAllister[2], [1]*1Faculty of Veterinary Science, University of Sydney, Sydney, NSW, Australia,* [2]*2Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, Alberta, Canada.*

Lamb is often characterized by high saturated fatty acid concentrations, such that the saturated: polyunsaturated FA ratio (SFA: PUFA) is high, an attribute considered to be a risk factor for coronary heart disease (CHD). Increasing consumption of PUFA, especially n-3 PUFA, such as EPA (C20:5) and DHA (C22:6) is considered to reduce the risk of CHD. The primary source of DHA in human diets is fish, however, fish consumption is considered to have peaked, yet intakes of DHA and EPA are still well below recommend levels of 500 mg/d. As such, this trial aimed to investigate the effects of supplementing a commercial algal meal (DHA-Gold, Schizochytrium sp.), high in DHA, in the diet of Canadian Arcott lambs, on the FA profiles of subcutaneous (SAT) and visceral adipose tissues (VAT) and skeletal muscle (diaphragm; SM). Forty-four lambs were randomly assigned to dietary treatments by LW, where flax oil was replaced with 0, 1, 2 or 3% DM DHA-Gold in a barley-based finishing diet. Adipose tissues and SM samples were taken at slaughter and analyzed for FA profiles (% total FA). Data were analyzed using the mixed procedure of SAS with orthogonal contrasts testing linear or quadratic contrasts when $P \leq 0.05$ for treatment effects. Total SFA content of SAT and VAT was not affected (50.79 ± 0.98; $P > 0.05$), but a linear decline was observed in SM ($P = 0.01$). In comparison, VAT was the only tissue to exhibit changes in PUFA content, linearly increasing ($P = 0.003$) with additional DHA-Gold (47.47, 48.09, 48.27 ± 0.39 for 1, 2 and 3% DM, respectively). Consequently, the SFA:PUFA ratio was linearly reduced ($P = 0.01$) in VAT. The content of EPA linearly increased ($P < 0.01$) in both SM and VAT. Percentage of DHA linearly increased ($P \leq 0.01$) in both adipose tissues, but was not affected ($P > 0.05$) in SM. Supplementing DHA-Gold decreased ($P \leq 0.03$) the n-6/n-3 ratio in all tissue types. These results indicate supplementing DHA-Gold can beneficially alter the FA profiles of adipose tissues and diaphragm muscle in growing lambs.

Key Words: adipose tissue, Canadian Arcott lamb, fatty acid

677 Small intestinal digestion of raw cornstarch in cattle is increased by duodenal infusion of glutamate. D. W. Brake*, E. C. Titgemeyer, and D. E. Anderson, *Kansas State University, Manhattan.*

Previous research demonstrated that small intestinal starch digestion (SISD) in cattle is increased by postruminal infusion of casein or of crystalline non-essential AA (NEAA). Our objective was to determine if these improvements in SISD could be replicated by supplementation of Glu or of a mixture of some essential AA. Five duodenally and ileally cannulated steers (initial BW = 361 kg) were used in a 5 × 5 Latin square with 6-d periods. All cattle were fed 4.8 kg DM/d of a soybean hull-based diet and received continuous duodenal infusions of raw cornstarch (1.6 kg/d) and Cr-EDTA in 12.6 L/d volumes. Treatments were duodenal infusions of 1) 436 g/d casein, 2) negative control, 3) 133 g/d Glu, 4) a mixture of 30.4 g/d Phe, 6.5 g/d Trp, and 17.5 g/d Met (PTM), and 5) a combination of Glu and PTM. On d 6 of each period, 6 spot samples of ileal digesta and feces were composited and subsequently analyzed. Effects of treatments were evaluated using contrasts for a 2 (Glu) × 2 (PTM) + 1 (casein) treatment structure. Casein reduced ($P = 0.02$) ileal starch flows and increased SISD ($P = 0.02$), but increased ileal flow of ethanol-soluble oligosaccharides (ESO; $P = 0.06$). Duodenal infusion of Glu decreased ($P < 0.01$) ileal starch flow and increased ($P \leq 0.01$) SISD, whereas PTM did not. Neither Glu alone nor PTM alone increased ileal flow of ESO, although Glu and PTM provided together tended to increase ileal flows of ESO (interaction, $P = 0.07$). Ileal flows of glucose averaged 16.5 g/d and were not affected by treatment. Infusion of casein tended ($P = 0.08$) to decrease fecal flow of starch and of ESO, and Glu decreased ($P = 0.02$) fecal flow of glucose. However, large intestinal starch digestion was not different among treatments ($P \geq 0.37$). Postruminal digestion of starch averaged 91% and tended to be greater for casein than for control ($P = 0.07$). Data suggest that Glu alone can increase SISD in cattle similarly to casein, but increases in SISD in response to Glu were not associated with increases in ileal flows of ESO as was observed for casein.

Key Words: cattle, glutamate, small intestinal starch digestion

678 Importance of yeast viability for reducing the effects of ruminal acidosis in beef heifers during and following an imposed acidosis challenge. D. Vyas*[1], A. Uwijeye[1], W. Z. Yang[1], K. A. Beauchemin[1], and N. Walker[2], [1]*Agriculture and Agri-Food Canada, Lethbridge, AB, Canada,* [2]*AB Vista, Marlborough, Wiltshire, UK.*

The study was aimed at determining the importance of yeast (*Saccharomyces cerevisiae*) viability for reducing the severity of ruminal acidosis in cattle during and following an imposed acidosis challenge. Six ruminally cannulated beef heifers (680 ± 50 kg BW) were used in a replicated 3 × 3 Latin square design and fed a diet consisting of 40% barley silage, 10% chopped grass hay, and 50% barley grain based concentrate (DM basis). Treatments were: 1) control (no yeast); 2) active dried yeast (ADY; 4 g providing 10^{10} cfu/g; AB Vista, UK); and 3) killed dried yeast (KDY; 4 g autoclaved ADY). The treatments were directly dosed via the rumen cannula daily at the time of feeding. The periods consisted of 2 wk of adaptation (d1–14), wk 3 of baseline measurements (d15–20) and wk 4 of acidosis challenge (d21–28). The acidosis challenge was imposed by restricting consumption of the TMR to 50% of ad libitum intake for 24 h (d21) followed by adding barley grain (amount equivalent to 25% of DMI) directly to the rumen before feeding the TMR (d22). The acidosis challenge reduced mean ruminal pH from 6.20 to 5.75 and nadir pH from 5.47 to 4.77. The DMI on d1 post challenge was reduced by 5 and 15% for control and KDY respectively, while for ADY DMI was maintained similar to that during the pre-challenge baseline period. No treatment effects were observed for mean, nadir and maximum ruminal pH on d1 post challenge (0–24 h). However, ADY tended to increase mean ruminal pH ($P = 0.13$) and lower area under curve below pH 5.8 ($P = 0.11$). Ruminal lactate and VFA profile on d1 post-challenge were similar for all treatments. During the recovery phase (d24–28), both yeast treatments improved minimum ruminal pH ($P = 0.04$) and reduced bout frequency (pH <5.8; $P = 0.05$) irrespective of yeast viability. In conclusion, yeast supplementation did not elevate rumen pH during a severe acidosis challenge, but viable ADY helped stabilize DMI and elevate rumen pH during recovery. This study demonstrates the importance of yeast viability in stabilizing rumen fermentation during conditions that predispose cattle to ruminal acidosis.

Key Words: acidosis, rumen pH, yeast

679 Molecular weight of legume condensed tannins does not correlate with biological activity. H. D. Naumann*[1,2], J. P. Muir[2], L. O. Tedeschi[1], B. D. Lambert[2,3], and A. E. Hagerman[4], [1]*Texas A&M University, College Station,* [2]*Texas A&M AgriLife Research, Stephenville,* [3]*Tarleton State University, Stephenville, TX,* [4]*Miami University, Oxford, OH.*

Condensed tannins (CT) are polyphenols that sometimes demonstrate biological activities in ruminants including suppression of ruminal CH_4 and protein binding (PB). Some evaluations of limited numbers of highly purified compounds have resulted in positive correlations between CT molecular weight (CTMW) and biological activity, while others have failed to show a correlation. The objectives of this study were to determine if MW of CT from a variety of rangeland legumes could predict biological activity relative to in vitro ruminal CH_4 suppression and PB. Condensed tannin MW, in vitro CH_4 and in vitro PB were determined for 9 species of rangeland legumes. Methane was assayed using an in vitro gas production technique. A randomized-incomplete block design was used. Two fermentation chambers were concurrently run in 2 separate events where each fermentation chamber was a block, individual fermentation flasks within each chamber were random factors, and CH_4 was a dependent variable. Protein binding ability was determined using a completely random design where 3 separate in vitro protein-precipitable phenolic assays were conducted for each species and nitrogen analysis of the protein-phenolic precipitates was conducted. Molecular weights of CT were determined by size-exclusion chromatography. The GLIMMIX procedure of SAS was used to estimate LS-means. A value of $P \leq 0.05$ was considered significant. Molecular weights ranged from 552 Da for *L. stuevei* to 1483 Da for *L. cuneata*. Fermentation of *L. retusa* resulted in the greatest amount of CH_4 (40.7 g/kg DM) whereas that of *A. angustissima* var. *hirta* resulted in the least (0.6 g/kg DM). Condensed tannins from *L. stuevei* bound the greatest amount of protein (74.8 g/kg DM), whereas *L. retusa* only bound 4.4 g/kg DM. In vitro CH_4 regressed on CT MW resulted in a R^2 of 0.0009 ($P = 0.80$). There was also no correlation between CT MW and PB (R^2 0.08; $P = 0.23$). The results from our study strongly suggested that CT MW does not explain the biological activities of enteric CH_4 suppression or PB by CT from the forage legumes surveyed.

Key Words: bypass protein, condensed tannin, ruminal methane

680 Total body fat and subcutaneous fat distribution in beef steers. M. J. McPhee*[1], B. J. Walmsley[1], J. P. Siddel[2], J. F. Wilkins[3], V. H. Oddy[1], and P. L. Greenwood[1], [1]*Beef Industry Centre of Excellence, Armidale, NSW, Australia,* [2]*Glen Innes Research Station, Glen Innes, NSW, Australia,* [3]*Wagga Wagga Institue, Wagga Wagga, NSW, Australia.*

A serial slaughter study (5 time points) was undertaken to elucidate some factors influencing fat development in beef cattle. Relationships between the following factors were evaluated from weaning to slaughter: (1) total body fat (TBF; kg) and EBW; and (2) the contribution (proportion) of subcutaneous fat (SUB; kg) to TBF (SUB/TBF; SUBPROP) across BREED (Angus, A; Hereford, H; and Wagyu × Angus, W×A) (n = 135). Breeds were chosen to represent high intramuscular fat (IMF) plus high SUB (A), low IMF plus high SUB (H) and high IMF plus lower SUB (W×A). From weaning, steers were backgrounded and fed pasture (P) or pasture plus high energy pellets (12.3 MJME/kgDM, 110g CP/kgDM) at 1% BW (Supplementation; S) with 2 replicates per treatment for 168d. Base-line steers (n = 15, 6 mo) were slaughtered at weaning, and groups were slaughtered at the end of nutritional treatments (n = 30, 12 mo), before feedlot entry (n = 30, 18 mo), and after short (n = 30, 21 mo) and long (n = 30, 26 mo) grain finishing. Ommental, mesenteric, and channel (visceral) fat were collected and weighed at the abattoir. All primal cuts from the left carcass side were scanned using a Picker Ultra Z Spiral Computer-aided Tomography (CT) scanner (Philips Medical Imaging Australia, Sydney NSW). Total fat and lean in each primal cut was calculated using image analysis software. Boundaries for fat and lean were set at 10 to 128 and 129 to 210 gray scale units, respectively, with an image diameter of 487mm. TBF was calculated as the sum of fat in the primal cuts plus visceral fat. To estimate SUB fat, intermuscular and IMF were removed from the image of each slice using an elliptical tool in ImageJ (http://rsb.info.nih.gov/ij/). The following curves were fitted: (1) TBF = A + B*(CEBW); and (2) SUBPROP = A + (B + C*TBF)*(DTBF) where A, B, C, and D are parameter values. For the relationship between TBF vs. EBW (1) (Variance = 94.8%; SE = 13.7) EBW, BREED and BREED × EBW were significant ($P < 0.01$) for both P and S. For the relationship between SUBPROP vs. TBF (2) (Variance = 69.29%; SE = 0.026) TBF and BREED were significant ($P < 0.01$) and ($P < 0.05$) for P and S, respectively. Replicates within treatments were not significant.

Key Words: depot, deposition, development

681 Development of target growth charts for Ayrshire, Brown Swiss, Holstein and Jersey heifers. D. E. Santschi, R. Lacroix, and D. M. Lefebvre*, *Valacta, Ste-Anne-de-Bellevue, QC, Canada.*

The objective was to establish heifer growth charts for body weight (BW), wither (WH) and hip height (HH) for 4 breeds of Canadian dairy cattle, Ayrshire (AY), Brown Swiss (BS), Holstein (HO) and Jersey (JE), to monitor growth and establish targets to reach calving at 24 mo of age at a desired BW and height. Body measurements were obtained for approximately 1000 heifers for each breed and the resulting data set was used to develop target growth curves. For BW, the procedure consisted of determining: 1) BW at birth; 2) target BW at 24-mo; and 3) variation of standard deviation (SD) of weight as a function of age. BW at birth was analyzed using regression analysis and final values were established based on literature and the results of data analyses. The target BW at 24-mo was made equal to the average, 75th and 90th percentile for BW of primiparous cows within 30 d in milk plus 11.1%, assuming a BW loss of 10% at calving. A linear equation was derived from BW at birth and at 24-mo assuming constant growth rate. This equation was used to generate target weights at the 50th percentile. Target BW curves for 75th and 90th percentiles were generated from the SD at each age, assuming normal distribution at each age and that the 75th and 90th percentile values were respectively at 0.662 and 1.297 SD from the 50th percentile. Cubic polynomial produced the best fit for both HH and WH. Differences between WH and HH were constant for all ages ($P \geq 0.22$) within a breed except for HO with significant slope of −0.01 cm/month ($P = 0.001$).

Table 1.

	AY	BS	HO	JE
BW parameters (kg)				
Intercept	51	49.5	54	38
Slope	21.38	23.60	25.25	16.75
ADG (50th percentile) (kg/d)	0.703	0.776	0.830	0.551
ADG (90th percentile) (kg/d)	0.799	0.848	0.897	0.682
WH parameters (cm)				
Intercept	76.52	78.62	78.08	69.55
A1	5.44	5.52	6.72	6.12
A2	−0.18	−0.19	−0.26	−0.26
A3	0.002	0.002	0.004	0.004
HH parameters (cm)				
Intercept	80.55	83.69	81.58	72.00
A1	5.69	5.59	7.02	6.33
A2	−0.20	−0.19	−0.28	−0.27
A3	0.003	0.002	0.004	0.004
WH-HH (cm)	−4.7	−5.4	−4.4	−3.4

Key Words: dairy heifer, growth chart, equation

682 Mammary gland development in heifers under different metabolizable protein and metabolizable energy ratios. R. L. Albino[1], M. I. Marcondes*[1], A. C. F. Rocha[1], A. S. Trece[1], A. S. Castro[1], and B. C. Gomes[2], [1]*Universidade Federal de Vicosa, Vicosa, Minas Gerais, Brazil,* [2]*Empresa Brasileira de Pesquisa Agropecuaria, Juiz de Fora, Minas Gerais, Brazil.*

This experiment was designed to evaluate dry matter intake, performance and mammary gland development in Holstein heifers under different metabolizable protein and metabolizable energy ratios (MPMER) in diets. The experiment was conducted at the Universidade Federal de Viçosa, Brazil, throughout from 4 mo. Twenty-five heifers with age between 3 and 12 mo were divided into 5 treatments. The treatments were composed to 5 MPMER in diets, being 33, 38, 43, 48, or 53 g of metabolizable protein per Mcal of metabolizable energy (ME) for each treatment. All diets were formulated to permit an average gain daily (ADG) around 1 kg/d, being all diets isoenergetics (2,3 Mcal of ME/kg of dry matter). The dry matter intake (DMI) was adjusted daily, and it was permitted at maximum 5% of orts. Ultrasounds were performed in all quarters of each heifer at the end of each month to evaluate the mammary gland development. Images were taken, positioning the probe sloped 45° toward cranial caudal while the animals were standing. The software ImageJ® (NIH, United States) was used to analyze the average pixels taken in 6 points within each image. Then, it was used

the average pixels to analyze the variation on the density of the image. The DMI and ADG were analyzed in randomized block design. The mammary gland data were analyzed in a split plot design with repeated measures. Analysis were done using the software SAS. The MPMER did not affect DMI (P = 0.736) and ADG (P = 0.090). These results were expected, once all diets showed the same energy. The mammary gland was affected significantly for treatment (P = 0.0001), period (P = 0.06) and period-treatment interaction (P = 0.01). Throughout the experiment, the heifers fed diets with high protein (48 and 53) showed a reduction in pixel value. However the heifers fed with low protein (33 and 38) showed an increase of pixel value. The MPMER show has influence on the density of mammary gland image. It is inferred that the images generated with high pixel value can be associated with a higher fat accumulation in the mammary gland due to higher reflection of fat over the ultrasound waves. Supported by CNPq/INCT-CA.

Key Words: mammary gland

683 Relationships between pre- and postweaning growth on estrus behavior and reproductive parameters of Holstein heifers. B. F. Silper*[1], A. M. L. Madureira[1], T. A. Burnett[1], A. M. de Passillé[2], J. Rushen[2], and R. L. A. Cerri[1], [1]*University of British Columbia, Vancouver, BC, Canada,* [2]*Agriculture and Agri-Food Canada, Agassiz, BC, Canada.*

The relationships between weight gain in the first year of life and age at puberty, ovarian activity, and estrus expression were evaluated. Holstein heifers (n = 43) were group housed as calves and then in a free stall barn in groups of 7 to 12 animals from 6 to 12 mo old. Milk allowance was 12 kg/d until weaning when the milk allowance was reduced according to the heifer's starter intake. From 6 to 12 mo of age the heifers were weighed weekly and body size was measured monthly. Ovarian ultrasonography was performed twice a week from 7 mo old on. Physical activity and lying bouts were monitored by data loggers. Continuous data was analyzed by ANOVA using the proc MIXED of SAS. Heifers with high preweaning weight gain (PrWG) (0.92 ± 0.03 kg/d) were heavier than those with low PrWG (0.63 ± 0.03 kg/d) from 7 to 12 mo old (P < 0.05). However, PrWG did not influence withers height at 9 and 10 mo old (P > 0.05). Puberty onset was at 9.5 ± 1.1 mo of age. Age and weight at puberty were influenced by rate of weight gain from 8 to 10 mo of age (WG810) (P < 0.01). Heifers with high rate of weight gain from 8 to 10 mo of age (1.15 ± 0.03 kg/d) were heavier and older at puberty onset (331.3 ± 8.3 kg and 298.1 ± 7.8 d old). Heifers with low WG810 (0.85 ± 0.03 kg/d) weighed 304.8 ± 7.6 kg and were 266.9 ± 7.1 d old and at puberty onset. Weight gain from birth to puberty influenced preovulatory follicle size (P = 0.006). Heifers that gained less than 0.9 kg/d had preovulatory follicle of 11.1 ± 0.8 mm, whereas those with weight gain of 0.9 kg/d or more had preovulatory follicle of 14.6 ± 0.6 mm. Preovulatory follicle diameter, and estrus duration and intensity were not influenced by WG810 (P > 0.05). Estrus episodes lasted 14.9 ± 3.5 h and had 374 ± 133% increase in number of steps when compared with baseline days. Estrus cycle length was 19.9 ± 2.2 d. Preweaning weight gain is correlated with postweaning weight gain, but not with skeletal growth. Heifers with the highest post-weaning growth rates appear to reach puberty at a later age.

Key Words: body weight, estrus, puberty

684 Partial substitution of conventional milk replacer with whey cream drives starter intake, gastrointestinal development, and growth of dairy calves. R. J. LaBerge*[1], J. Schefers[1], R. S. Younkers[2], and N. B. Litherland[1], [1]*University of Minnesota, St. Paul,* [2]*Milk Specialties Global, Eden Prairie, MN.*

Whey cream (WC) contains nutrients and potentially functional food compounds such milk fatty acids and milk fat membrane. Our objective was to determine if replacing 0, 10, and 20% of all milk protein milk replacer (MR) with WC affects calf gastrointestinal development. Holstein and Holstein-cross dairy calves (n = 70) raised in hutches were randomly assigned to 1 of 3 isonitrogenous and isocaloric MRs which provided 22% protein and 22% fat; (1) 0% WC (0WC); (2) 10% WC (10WC); (3) 20% WC (20WC). MR was fed at 13% solids and 1.5% of birth body weight (BBW). BBW and total protein (TP) averaged 40.4 ± 0.7 kg and 6.3 ± 0.07 mg/dL. Calves were fed MR twice daily (0630, 1700) d 1 to 41, daily d 42 to 48, weaned d 49, and removed from trial d 56. Starter (19.9% CP) and water were provided ad libitum. Six male calves from each treatment (n = 18) representing average BBW, TP, and breed were harvested for gastrointestinal measurement on d 56. Data were analyzed using PROC MIXED and Pearson's coefficient of SAS. The 20WC harvested calves tended (P < 0.07) to have greater total d 49 and d 56 starter intake (SI). 20WC tended (P < 0.09) to consume 500 g/d of starter earlier, and had earlier (P < 0.04) SI consumption of 1000 g/d, than 0WC calves. Day 56 gain did not differ (P < 0.14). Reticulorumen weight (RR), abomasum weight, small intestine (SMI) length, and cecum length were similar between treatments. Omasum weight tended to be greater (P < 0.07) for 20WC over 10WC. SMI weight alone and as percent of BW of 10WC and 20WC was greater (P < 0.05) than 0WC. 20WC had a greater cecum weight alone or as a percent of BW (P < 0.02) than 0WC. Days to reach 250 g/d of SI was inversely correlated to SMI length (r = –0.71, P < 0.001) and days to 500, 1000, and 2000 g/d of SI (r = 0.69, P < 0.002). Days to SI of 500, 1000, and 2000 g/d was inversely correlated (r = 0.68, P < 0.001) to d 49 and 56 gain and RR weight as a percent of d 56 BW (r = –0.46, P < 0.05). Earlier SI of WC calves drove development of the gastrointestinal tract to provide greater tissue mass and surface area for potential nutrient absorption, allowing greater growth.

Key Words: nursery calf, gastrointestinal development, whey cream

685 Dietary reduction from early gestation in obese/overnourished ewes reduced adiposity and serum lipids and increased liver glycogen in late gestation fetuses. J. F. Odhiambo*[1], T. Nurmamat[1], P. W. Nathanielsz[2], and S. P. Ford[1], [1]*Center for the Study of Fetal Programming, Department of Animal Science, University of Wyoming, Laramie,* [2]*Center for Pregnancy and Newborn Research, Department of Obstetrics and Gynecology, University of Texas Health Sciences Center, San Antonio.*

As previously reported, pre-pregnancy maternal obesity and overnutrition in the ewe increases fetal plasma glucose, insulin and adiposity, predisposing offspring to metabolic syndrome (Ford et al., 2009; Am J Physiol Reg Integ Comp Physiol 297:835). In this study we evaluated the effects of reducing maternal nutrient intake of obese ewes to requirements from early gestation on fetal growth, adiposity and lipid profiles in late gestation. Sixty days before conception ewes were assigned to control [CON, 100% of National Research Council (NRC) recommendations; n = 5], obese [OB, 150% NRC; n = 5] or obese intervention [OBI, 150% NRC to d 28 of gestation then 100% NRC thereafter, n = 5] diets until necropsy on d 135 of gestation. Maternal body fat % was quantitated by DEXA, and fetal kidney-pelvic fat depots by weighing. Serum triglycerides (TG) and cholesterol (CHOL) were determined by commercial assay kits. Liver TG and glycogen were extracted by chemical methods and then quantified by colorimetric kits. PEPCK and Glucose-6-phosphatase (G6Pase) protein expression were determined

by Western blotting. Data were analyzed by mixed procedures of SAS. Maternal BW and % body fat were greatest in OB, intermediate in OBI and lowest in CON ewes ($P < 0.05$), while fetal BW were similar. Kidney-pelvic fat weight was greater ($P < 0.05$) in OB than OBI and CON fetuses, averaging 31.4 ± 1.4 vs. 21.8 ± 1.0, and 24.2 ± 1.3g, respectively. Further, serum TG and CHOL were elevated ($P < 0.01$) in fetuses of OB ewes compared with those of CON and OBI ewes (23.1 ± 1.9 vs. 16.0 ± 2.0, and 16.2 ± 2.0 mg/dL and 36.3 ± 2.2 vs. 22.9 ± 2.3, and 22.6 ± 2.3 mg/dL, respectively). PEPCK expression was elevated ($P < 0.01$) and glycogen was reduced ($P < 0.01$) in fetal livers from OB versus OBI and CON ewes, while liver G6Pase and TG content were similar. The increased serum lipids, and liver PEPCK expression as well as decreased liver glycogen in late gestation fetuses might contribute to the observed elevation in plasma glucose and adiposity, predisposing OB fetuses to metabolic syndrome in postnatal life.

Key Words: obesity, fetal lipid, glycogen

686 Effect of feeding 25-hydroxycholecalciferol on vitamin D status and skeletal muscle growth and development in broiler chickens. K. C. Hutton[1], J. D. Starkey*[1], M. A. Vaughn[1], B. J. Turner[2], and G. Litta[2], [1]*Texas Tech University, Lubbock,* [2]*DSM Nutritional Products, Basel, Switzerland.*

Increases in breast meat yield have been observed in broiler chickens fed 25-hydroxycholecalciferol ($25OHD_3$; Rovimix Hy-D, DSM Nutritional Products), but it is unclear whether this effect is satellite cell-mediated. Our objective was to determine the effect of feeding $25OHD_3$ on skeletal muscle satellite cell function in both fast-twitch (pectoralis major; PM) and slow-twitch (biceps femoris; BF) muscles. Day-old male Ross 708 broiler chickens (n = 150) were obtained from a commercial hatchery and fed one of 2 corn/ soybean meal-based diets for 49 d. The control diet (CTL) was formulated to contain 5,000 IU D_3/kg of diet, while the experimental diet ($25OHD_3$) contained 2,240 IU vitamin D_3/kg diet + 69 µg $25OHD_3$/kg diet. Ten birds per treatment were harvested every 7 d. Two hours before harvest, birds were injected intraperitoneally with 5′-bromo-2'deoxyuridine (BrdU) to facilitate labeling of mitotically active cells. Blood was collected from each bird at harvest to determine vitamin D status. The PM and BF muscles were weighed and processed for cryohistological determination of skeletal muscle fiber cross-sectional area, enumeration of Myf-5+ and Pax7+ satellite cells, and mitotically active satellite cells using immunofluorescence microscopy. Circulating $25OHD_3$ concentrations were greater in $25OHD_3$-fed birds on d 7, 14, 21, 28, 35, 42, and 49 when compared with CTL ($P < 0.001$). PM and BF muscle mass were not different among treatments. Feeding $25OHD_3$ increased the number of mitotically active (Pax7+; BrdU+) satellite cells ($P = 0.01$) and the density of Pax7+ cells ($P = 0.07$) in the PM muscle on d 21 and 35, respectively. In addition, broiler chickens fed $25OHD_3$ tended to have greater PM Myf-5+ satellite cell density ($P = 0.09$) on d 14, greater total PM nuclear density ($P = 0.05$) on d 28, and greater PM muscle fiber cross-sectional area ($P = 0.09$) on d 49 compared with their CTL counterparts. Combined, these results suggest that feeding $25OHD_3$ affects broiler chicken vitamin D status and stimulates a classic satellite cell-mediated muscle hypertrophy response in fast-twitch skeletal muscle.

Key Words: vitamin D, skeletal muscle, broiler chicken

687 Effect of fluted pumpkin (*Telfaria occidentalis*) leaf extract on growth performance, serum chemistry, and carcass yield of cockerel chickens. A. O. Ladokun*, N. O. Adewale, M. K. Adeoye, and J. A. Abiona, *Federal University of Agriculture, Abeokuta, Ogun, Nigeria.*

A total of 120 2-week-old cockerel chicks of the Yaffa strain were used for the experiment to determine the effect of fluted pumpkin (*Telfaria occidentalis*) leaf extract (FPLE) administered orally on growth performance characteristics-weight gain, feed intake and feed efficiency; blood chemistry-hematology and serum chemistry; carcass yield-relative organ weights and cut-out parts for a 16 week period. The birds were randomly assigned to 4 treatment groups: control group with no FPLE; 30 mL FPLE/liter of drinking water; 60 mL FPLE; and 90 mL FPLE respectively at 3-d intervals. Weighing of birds was done weekly to obtain weight gain, Feed was given ad libitum. Blood sampling was carried out at the sixteenth week of experiment. The data obtained were subjected to one-way ANOVA; i.e., a completely randomized design (CRD) of SAS (2001), the only factor being FPLE. The results show that FPLE significantly ($P < 0.05$) increased feed intake and weight gain with birds in group with 90 mL FPLE/L water having higher values than other groups. For haematology, packed cell volume (PCV), red blood cell count (RBC) and white blood cell count was not affected by FPLE. However for serum chemistry, serum total protein, albumin, creatinine and cholesterol were significantly ($P < 0.05$) increased by FPLE. For urea there was no significant change, while globulin was significanly ($P < 0.05$) reduced by FPLE addition. FPLE has been proven to be a haematinic in rats and broiler chickens; this present result further strengthens this assertion. The values obtained for the organ-gizzard were significantly influenced by FPLE with size decreasing with increase in FPLE without compromise in final live weight of the birds. This result suggests that FPLE as used in this study contains certain substances that makes it convenient for birds to "grind" their feed without corresponding big size gizzard. It can therefore be concluded that up to 90 mL FPLE/L of drinking water can be tolerated by cockerel chickens from chick phase to growing-finishing phase.

Key Words: fluted pumpkin leaf, serum chemistry, carcass yield

828 ASAS Early Career Award: Proteome basis of muscle- and species-specificity in meat color stability. S. P. Suman*, *University of Kentucky, Lexington.*

At the point-of-sale, meat color is an important quality governing the consumers' purchase decisions. Maintaining consumer-desirable cherry-red color of fresh meat is critical to retailing, and discoloration-induced quality deterioration in fresh meat leads to more than $1 billion annual revenue loss to the United States livestock industry. The chemistry of myoglobin and its interactions with other biomolecules in post-mortem skeletal muscles are the major factors influencing meat color stability. Characterizing the molecular basis of these interactions is critical to developing novel strategies to improve meat color. High-throughput analytical tools in proteomics offer valuable means to examine the fundamental mechanisms of meat color biochemistry. In this perspective, proteomics has been successfully employed to characterize the molecular basis of muscle- and species-specificity in meat discoloration. Beef muscles in a carcass demonstrate variations in color stability, based on which they are categorized as color-stable and color-labile. Two-dimensional gel electrophoresis and mass spectrometry were employed to characterize the sarcoplasmic proteomes of beef color-stable (Longissimus lumborum) and color-labile (Psoas major) muscles and to correlate the differential abundance of proteomes to color stability. Proteome analyses identified 16 differentially abundant proteins, including antioxidant proteins and chaperones, in beef muscles. Proteins demonstrating positive correlation with color stability were over-abundant in Longissimus. The results suggested that the color stability of beef Longissimus could be attributed to the over-abundance of antioxidant proteins and chaperones, which minimizes myoglobin oxidation. Dietary vitamin E improves color and lipid stabilities in beef; however, in pork, while lipid oxidation is minimized by vitamin E supplementation, a color-stabilizing effect is not observed. Mass spectrometric analyses revealed that pork myoglobin is inherently less susceptible to lipid oxidation-induced oxidation than its beef counterpart, due to the differences in the primary structure and the number of nucleophilic histidines. This finding offers an explanation for why dietary vitamin E supplementation has only limited effect on pork color.

Key Words: meat color, longissimus, vitamin E

688 Effects of myogenin on muscle fiber types and muscle oxidative metabolism. L. N. Zhu*, Y. Ren, J. Q. Chen, and Y. Z. Wang, *Institute of Feed Science, Zhejiang University, The Key Laboratory of Molecular Animal Nutrition, Ministry of Education, Zhejiang Provincial Laboratory of Feed and Animal Nutrition,, Hangzhou, Zhejiang, China.*

Skeletal muscle fiber type composition is one of the important factors influencing muscle growth and meat quality. As a member of myogenic transcription factors, myogenin (MyoG) is required for embryonic myoblast differentiation, but expression continues in mature muscle tissue of adult animals, especially in oxidative metabolic muscle, suggesting that it may play a more extended role. Therefore, using MyoG geng tranfer mice and C2C12 myoblasts as models in vivo and in vitro respectively, we elected to study the role of MyoG on muscle fiber types and oxidative metabolism by using overexpression and siRNA suppression strategies. Overexpression of MyoG by DNA electroporation in mouse gastrocnemius muscle had no significant effect on fiber type composition, but upregulated the mRNA expression ($P < 0.01$) and enzyme activity ($P < 0.05$) of oxidative succinic dehydrogenase (SDH). In addition, downregulations of glycolytic enzyme lactate dehydrogenase (LDH, $P < 0.05$) and pyruvate dehydrogenase (PK, $P < 0.05$) activities were found in geng tranfer mice. In vitro experiments verified the results obtained in mice that stable MyoG transfected differentiating C2C12 cells showed higher mRNA expression levels of myosin heavy chain (MyHC) isoform IIX ($P < 0.01$) and SDH ($P < 0.05$), while the LDH mRNA attenuated. Enzyme activities of SDH ($P < 0.01$) and LDH ($P < 0.05$) were similarly altered as the mRNA levels. When MyoG was knocked-down in C2C12 cells, MyHC IIX expression ($P < 0.05$) was decreased but the mRNA level ($P < 0.05$) and enzyme activity ($P < 0.05$) of SDH were increased. Downregulating MyoG also increased glycolytic enzyme PK ($P < 0.05$) and hexokinase (HK, $P < 0.05$) activities. Based on those results, we concluded that MyoG does not change the major MyHC fiber isoforms (MyHC I / MyHC IIB), but probably influence the shift toward oxidative metabolism in muscle. These results contribute to further understanding the role of MyoG in skeletal muscle energy metabolism, and also help to explore the key genes regulating meat quality.

Key Words: myogenin, muscle fiber type, oxidative metabolism

689 FNDC5 transcript variants and protein detection in skeletal muscle and plasma of cattle. K. Komolka[1], E. Albrecht[1], J. Brenmoehl[2], A. Hoeflich[2], and S. Maak*[1], [1]*Institute for Muscle Biology and Growth, Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany,* [2]*Institute for Genome Biology, Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany.*

Fibronectin type III domain containing 5 (FNDC5) encodes a type I transmembrane protein located in peroxisomes. Physical activity leads to cleavage and release of a part of this protein. This processed protein, called irisin, induces "browning" of white adipocytes and thermogenesis in mice. Irisin is related to body composition in mice and human and thus, may be a candidate for variation in carcass composition in cattle. Bovine FNDC5 was automatically annotated on chromosome 2 but information on the locus is incomplete and contains errors. We therefore characterized FNDC5 transcripts in bovine skeletal muscle by cDNA sequencing. Two groups of Charolais × Holstein F_2-bulls with different intramuscular fat content (1.9%, n = 10 vs. 6.8%, n = 10; $P < 0.001$) were investigated. Total FNDC5 mRNA abundance, measured with RT-qPCR, was not different between both groups ($P > 0.05$). However, sequence analyses revealed the existence of 3 and 5 alternative exons in the 5′- and 3′-region of the gene, respectively. One transcript was present in muscle samples of all animals in both groups, whereas 2 further variants were more frequently detected in bulls with high IMF. This suggests that total FNDC5 mRNA in skeletal muscle of individual bulls may be composed of different transcripts. All observed transcript variants would result in different length and amino acid composition of the N- and C-terminal regions of the bovine FNDC5 protein, respectively. The irisin domain remained unaffected in all cases. In accordance with the observed transcript variability at this locus, 3 specific bands for FNDC5 protein were detected in bovine skeletal muscle by Western blot. Immuno-histochemical staining of FNDC5 revealed signals at the plasma membrane and in the cytosol of muscle fibers. In bovine plasma, specific bands for a single FNDC5 protein and irisin were detectable. This suggests release of a soluble FNDC5 form and of irisin from skeletal muscle into circulation as described for mice and human. Our results

provide the first experimental data on the FNDC5 locus in a farm animal species and a basis for functional investigations.

Key Words: FNDC5, irisin, cattle

690 Effect of aging on muscle color from Nellore beef cattle. L. R. Simonetti, J. F. Lage*, E. E. Dallantonia, E. San Vito, E. A. Oliveira, M. Machado, G. M. Delamagna, M. O. Santana, A. L. Esper, and T. T. Berchielli, *Universidade Estadual Paulista, Jaboticabal, Sao Paulo, Brasil.*

This objective of this study was to evaluate the effects of aging on color of 5 muscles: biceps femoris (BF), gluteus medius (GM), longissimus dorsi (LD), Ssemitendinosus (ST) and trapezius thoracis (TT) from young bulls fed in feedlot. Fourteen young bulls (Nellore), with 15 mo of age were confined to individual stalls with feeders and drinkers. The diet was consisted of 40% corn silage and 60% of concentrate. After 60 d of feed, the animals were harvest and the carcasses were chilled at 0°C for 24 h. The muscles were removed, cut into 2.54 cm steaks and individually vaccum packaged and chilled at 0°C for 1, 7 and 14 d post mortem. The color reading was conducted on the surface, using the CIE L*a*b* system, collected using a Minolta on the first posterior steak of each muscle. The experiment was conducted according to a completely randomized design in a factorial arrangement 3 × 5 (3 aging days x 5 muscles) with 14 replicates. Data were analyzed by the GLM procedure of SAS, and the Tukey test used considering 5% probability. The interaction between aging days and muscles was significant (P = 0.02) for redness (a*). The lightness (L*) from beef evaluated in 1 d was lower (41.30; P = 0.01) than beef evaluated in 7 (42.90) or 14 d (43.33). The beef evaluated in 14 d had greater b* (P < 0.01). The ST muscle had greater L* (49.52; P < 0.01) compared with the other muscles: BF (39.90), GM (41.19), LD (41.28) and TT (40.63). The ST muscle had lower a* (14.60; P < 0.01) than those muscles evaluated: BF (15.70), GM (15.93), LD (15.95) and TT (16.35). The BF muscle had lower b* (13.65; P < 0.01) than GM muscle (15.01). The ST muscle had greater value of b* (17.50; P < 0.01) than those muscles evaluated. The predominant fiber types within muscles, as white fibers are characterized by less myoglobin and a lighter appearance. Muscles with lower myoglobin content were less color stable because their myoglobin was oxidized at a greater frequency to maintain normal cellular respiration. The aging for 14 d had a greater L*, a* and b* of beef. The ST muscle had lower a*, greater L* and b* than BF, GM, LD, and TT muscles.

Key Words: biceps femoris, lightness, longissimus

691 Comparison of histochemical characteristics and meat quality of longissimus dorsi muscle between commercial pig breeds (Yorkshire × Landrace × Duroc vs. Yorkshire × Berkshire × Duroc crossbred pigs). G. D. Kim*[1], K. B. Kwon[2], E. Y. Jung[3], H. W. Seo[3], H. J. Lim[3], J. Y. Jeong[3], H. S. Yang[3], and S. T. Joo[3], [1]*Division of Animal Biotechnology, College of Applied Life Sciences, Jeju National University, 66 Jejudaehakro, Jeju, South Korea,* [2]*Darby Genetics Inc., Anseong, Gyeonggi-do, South Korea,* [3]*Department of Animal Science, Institute of Agriculture & Life Science, Gyeongsang National University, Jinju, Gyeongnam, South Korea.*

The traditional 3-way crossbred Yorkshire × Landrace × Duroc (YLD) pigs have been commonly produced in South Korea. Recently, Berkshire breed was introduced for improving the meat quality of 3-way crossbred pigs. Because Berkshire breed is good in muscle fiber characteristics and in meat quality compared with Landrace breed. The objective of this study was to compare the histochemical characteristics and meat quality of commercial pig breed, YLD to Yorkshire × Berkshire × Duroc (YBD). A total of 27 YLD (female: 16, castrated male: 11) and 30 YBD (female, n = 17; castrated male, n = 13) were selected and their longissimus dorsi muscles were used to investigate the histochemical characteristics including fiber density, fiber type composition and cross-sectional area, and meat quality such as color, cooking loss, drip loss and Warner-Bratzler shear force (WBSF). All traits of histochemical characteristics showed that YBD had higher values in muscle fiber types I and IIA than YLD (P < 0.05). However, YLD had higher density, fiber number and fiber area compositions in muscle fiber type IIB than YBD (P < 0.05). There were breed × sex interactions of fiber number and area compositions in type IIA (P < 0.01) and IIB (P < 0.05), respectively. The female of YBD had the highest compositions of type IIA (10.96% of number composition and 7.71% of area composition, respectively), whereas the female of YLD had the highest compositions of type IIB (89.46% of number composition and 93.78% area composition, respectively). In the result of meat quality analysis, lightness (L*), yellowness (b*) and drip loss showed the significances between breeds (P < 0.05). YBD had higher L* value than YLD (P < 0.05), whereas b* value and drip loss were lower in YBD than in YLD (P < 0.05). However, there were no significances in redness, cooking loss and WBSF between breeds (P > 0.05). Therefore, Berkshire breed could be used for improving the composition and size of muscle fiber types I and IIA, and meat color and drip loss in 3-way crossbred pig production.

Key Words: meat quality, muscle fiber, pig

692 Effect of vitamin A on early intramuscular adipogenesis: a model for improving marbling in beef. S. M. Harris[1,2], J. L. Schneider*[2], C. Trost[2], A. M. Gibson[2], C. J. Rogers[1], J. R. Busboom[1], M. V. Dodson[1], J. B. Lamb[1], and M. Du[1], [1]*Washington State University, Pullman,* [2]*Brigham Young University-Idaho, Rexburg, ID.*

Marbling is consistently identified as one of the top beef quality problems. Marbling, or intramuscular fat, is vital for the perceived flavor, juiciness, and tenderness in beef. While intramuscular fat in beef can be improved through genetic selection, prenatal and postnatal factors have a profound effect on intramuscular fat development. Vitamin A deficiencies in cattle during late pregnancy and early lactation are not uncommon. While the effect of vitamin A or retinoic acid (RA) on late intramuscular adipogenesis and lipid accumulation has been well characterized, its effect on early adipogenic differentiation has not been characterized in beef cattle. The objective of this study was to evaluate the effect of vitamin A on early adipogenesis. Stromal vascular (SV) cells were obtained from Angus muscle, which were sorted based on their expression of platelet derived growth factor receptor (PDGFR)α. These cells were then exposed to 4 different treatments, with or without RA and with or without adipogenic media. Cells treated with adipogenic media in addition to RA had the greatest proliferation rate (P < 0.05), while there were no differences among other treatments. mRNA expression of peroxisome proliferator-activated receptor (PPAR)γ tended to be higher for both treatments containing RA after 2 d of treatment (P < 0.1), while treatment with both adipogenic media and RA enhanced Zfp423 mRNA expression (P < 0.05). After 6 d of treatment, Zfp423 expression was the greatest when treated with both adipogenic media and RA (P < 0.05). Our results suggest that RA has a stimulatory effect on Zfp423 expression and early adipogenic differentiation of cattle SV cells. These data imply that supplementation of vitamin A to pregnant cattle, especially during late gestation and early lactation, may be an effective method to enhance intramuscular adipogenesis and marbling in beef cattle.

Key Words: marbling, Angus, retinoic acid

693 Enzymes activities in the muscle and subcutaneous fat of steers finished at feedlot fed with lipid sources. G. Fiorentini*[1,2], I. P. C. Carvalho[1,2], J. F. Lage[1,2], L. G. Rossi[1], Y. T. G. Salcedo[1,2], C. S. Ribeiro Junior[1,2], and T. T. Berchielli[1,3], [1]*University of São Paulo State, Jaboticabal, SP, Brazil,* [2]*São Paulo Research Foundation, São Paulo, SP, Brazil,* [3]*National Institute of Science and Technology in Animal Science, Brasília, DF, Brazil.*

The objective of the experiment was to evaluate the effect of lipid sources on the activity of enzymes related to the fatty acid metabolism of feedlot steers. Forty-five Nellore steers (BW = 419 ± 11 kg; 15 ± 2 mo) were utilized. The steers were feed on 60% corn silage and 40% concentrate. Five concentrates were formulated: without additional lipid source (WL); with linseed oil (LO); with palm oil (PO); with soybeans (SB) and with a commercial protected fat (PF; Lactoplus). The diets LO and PO contain 4.5% of oil, the SB diet contain 13.8% of soybeans and PF diet contain 5.1% of Lactoplus on DM basis, resulting in diets with 4.2% of additional ether extract. The concentrates were composed of corn and soybean meal and diets were isonitrogenous (16.0% CP). The experiment was set up as a completely randomized design with 5 treatments and 9 replications and lasted 90 d. After slaughter, samples were taken from the longissimus muscle and subcutaneous fat (between the 12th and 13th rib) for evaluation of the activity of the enzymes. The means were compared by the Tukey test at 5%. The action of Δ^9-desaturase C18 in the longissimus muscle and subcutaneous fat increased in steers fed with the WL diet and decreased in animals fed with PO and PF ($P = 0.001$). Δ^9-desaturase C16 had a higher activity in the longissimus muscle of steers fed with WL diet (11.2%) than in those fed with PF (7.53%; $P = 0.01$). In addition, Δ^9-desaturase C16 activity in subcutaneous fat increased in the diet with LO (15.8%) as compared with steers fed PF (11.3%; $P = 0.02$). The greater elongase activity was detected in steers fed with LO and SB (68.0 in the muscle and 70.1 in the fat), as compared with those fed with PO, WL and PF (64.4 in the muscle and 64.3 in the fat; $P = 0.001$). LO decreased atherogenicity indices (0.69 in the muscle and 0.76 in the fat) in relation to PO (0.85 in the muscle and 1.01 in the fat; $P = 0.001$). Diets with LO and WL increase activity of the Δ^9-desaturase and thus there is a potential to increase the amount of unsaturated fatty acids in the tissues. Also LO provides less atherogenicity indices.

Key Words: meat quality, protected fat, soybean

694 Comparison of real-time ultrasound measurements for body composition traits to carcass and camera data in feedlot steers. A. J. Thompson*, F. R. B. Ribeiro, S. N. Aragon, A. H. Hosford, J. E. Hergenreder, M. A. Jennings, and B. J. Johnson, *Texas Tech University, Lubbock.*

The objective of this study was to compare measurements of real-time ultrasound (RTU), carcass and camera data to determine body composition in feedlot steers (n = 72). The RTU, camera and carcass data were collected on 72 crossbred feedlot steers within a 76-h period. Measurements of RTU were taken by a certified ultrasound technician approximately 24 h before slaughter using an Aloka 500-V instrument with a 17-cm 3.5-MHz transducer. Hair was clipped to less than 0.64 cm and vegetable oil was applied to enhance image quality. The RTU measured traits consisted of 12–13th rib backfat thickness (uBF, mean = 1.04 cm), 12–13th LM area (uREA, mean = 102.7 cm^2), and marbling score (uMARB, mean = 4.6). Intramuscular fat was converted to uMARB by using the equation: uMARB = ((769.7 + (56.69 × uIMF))/100) – 5. Overall means for 48 h chill carcass data were 12–13th rib backfat thickness (cBF, 0.97 cm), 12–13th LM area (cREA, 103.5 cm^2), and marbling score (cMARB, 5.0). Marbling scores were converted to a numeric cMARB ($Slight^{00} = 4$, $Small^{00} = 5$, and $Modest^{00} = 6$). Carcass camera data consisted of 12–13th rib backfat thickness (camBF, 0.99 cm), 12–13th LM area (camREA, 103.8 cm^2), and marbling score (camMARB, 4.5). Data were analyzed using the PROC REG, MEANS and CORR procedures of SAS. Results show that all 3 methods were highly correlated to each other. Correlations ranged from 0.79 to 0.82, 0.68 to 0.95 and 0.57 to 0.87 for BF, REA, and MARB, respectively. The largest differences between the means (bias) across all 3 methods were 0.07 cm, 0.78 cm^2 and 0.48 for BF, REA and MARB. Carcass BF and camBF were over predicted by RTU (0.07 and 0.06 cm, respectively), however, REA was under predicted by RTU when compared with cREA and camREA (−0.78 and −1.13 cm^2, respectively). Camera MARB was over predicted by uMARB (0.17) and cMARB was under predicted (−0.32). These results show that linear measurements of carcass traits can be more accurately predicted when compared with a non-linear measurement (MARB).The results also show that RTU can be used to accurately predict carcass traits immediately before slaughter.

Key Words: ultrasound, carcass, camera

695 Influence of graded levels of Tetracin on physico-chemical properties of broiler meat. A. O. Akinwumi*, A. A. Odunsi, A. B. Omojola, and T. O. Akande, *Ladoke Akintola University of Technology, Ogbomoso, Oyo, Nigeria.*

Veterinary antibiotic Tetracin was administered in feed to broilers at varying levels to study its effect on physical and chemical qualities of poultry meat. Tetracin was administered at 0, 50, 100, 150, and 200 mg/kg of feed for broilers for a period of 6 wk while withdrawal period of 2 weeks was observed as recommended by the manufacturer before slaughter to make an 8 –week feeding trial. Breast meat was analyzed for physico-chemical properties. Cooking and thermal losses were expressed as percentage changes in weight and length during cooking respectively, while water-holding capacity (WHC) was determined by the filter press method. Warner-Brazter shear force (WBSF) determination was performed on broiler meat for shear force determination. The results showed that cooking loss, thermal loss and crude protein increased ($P < 0.05$) while WHC and ether extract decreased ($P < 0.05$) with increase in the inclusion level of Tetracin. However, drip loss, chilling loss, shear force, ash and moisture contents of broiler meat showed no significant ($P > 0.05$) differences across the treatment groups. Conclusively, the inclusion of Tetracin improved the chemical properties of broiler meat but the physical properties (cooking loss and WHC) were compromised especially when administered above 100 mg/kg of feed.

Key Words: Tetracin, physical and chemical properties, broiler

696 Nutrient profile and in vitro vs. in vivo energy digestibility of wheat co-products from flour milling in growing pigs. R. Jha*[1,2], P. R. Regmi[1], L. F. Wang[1], A. Pharazyn[3], and R. T. Zijlstra[1], [1]*University of Alberta, Edmonton, AB, Canada,* [2]*University of Hawaii at Manoa, Honolulu,* [3]*Nutreco Canada, Guelph, ON, Canada.*

Wheat flour milling generates co-products (WFM) such as wheat shorts, millrun, middlings, and bran that are classified based on fiber content. These WFM can serve as alternative feedstuffs for conventional energy sources in swine diets to reduce feed cost, a major challenge of swine industry; however, information is scarce about their digestible nutrient content that limits their use in swine diets. Nutrients of 9 WFM (2 shorts, Shorts A and B; 5 millrun, Millrun A, B, C, D, and E; Middlings; and Bran) were profiled. In vitro energy digestibility was determined using 3-step assay. In a 30-d digestibility study (a 10-d acclimation to a standard pre-grower diet, followed by 2 consecutive 10-d experimental periods), 20 growing pigs (BW, 37.5 kg) were fed at 3 × maintenance requirement with 1 of 10 diets (9 WFM added at 40% to corn; and corn as control). Feces were collected by grab sampling and apparent total tract digestibility (ATTD) of wheat co-products was calculated using the indicator method. The CP content of WFM ranged from 15.9 (Bran) to 27.8% (Shorts A) and crude fiber from 5.2 (Shorts B) to 12.0% (Bran). Diet DE content was highest ($P < 0.05$) for Shorts B and lowest for Bran (3.56 vs. 3.21 Mcal/kg DM), corn had 3.46 Mcal DE/kg. The ATTD of energy of WFM diets ranged from 74.4 in Bran to 82.5 in Shorts A, and was 82.9% in the corn diet. The in vivo energy digestibility was highest ($P < 0.01$) in Short B (81.9) and lowest in Bran (62.6%). In vitro energy digestibility was highest ($P < 0.05$) in Short B (69.1) and Middlings (68.0) and lowest in Millrun B (51.6%). In vitro energy digestibility was strongly related ($R^2 = 0.80$) with ATTD of energy of the WFM. Among nutrients, NDF was the best predictor for in vitro ($R^2 = 0.74$) and in vivo DE ($R^2 = 0.81$). In conclusion, nutrient profiles and digestibility of WFM vary widely but some WFM (Short A and B; Millrun A, B and D; and Middlings) have a DE content comparable to corn. Thus, type and composition of wheat co-products should be considered for swine feed formulation. Finally, the existing in vitro technique predicts ATTD of energy in WFM accurately.

Key Words: energy, pig, wheat co-product

697 Nutrient profile and in vitro vs. in vivo energy digestibility of grain legumes in growing pigs. R. Jha*[1,2], L. F. Wang[1], P. R. Regmi[1], A. Pharazyn[3], and R. T. Zijlstra[1], [1]*University of Alberta, Edmonton, AB, Canada,* [2]*University of Hawaii at Manoa, Honolulu,* [3]*Nutreco Canada, Guelph, ON, Canada.*

Grain legumes contain protein and energy and can serve as alternative feedstuffs to mitigate rising swine feed cost. However, their nutrient content and digestibility are poorly understood. Nutrients of 8 grain legumes and fractions (3 field pea, Pea A, B, C; Lentil; Maple bean; Roasted bean; Pea protein; and Pea starch) were profiled. In vitro digestibility of samples was determined following 3-step assay. In a 30-d digestibility study (10-d acclimation to standard pre-grower diet followed by 2 consecutive 10-d experiments), 18 growing pigs (BW 43.5 kg) were fed 1 of 9 diets (8 legumes and corn as control) at 3 × maintenance requirement for 4 observations per diet. Feces were collected by grab sampling. Apparent total tract digestibility (ATTD) of energy was measured with the indicator method. The CP content ranged from 6.4 (Pea starch) to 55.3% (Pea protein) and crude fiber from 1.8 (Pea starch) to 6.9% (Roasted bean). The GE content was higher in Pea protein (4.78) and Lentil (4.54) than Corn (4.45 Mcal/kg DM). Diet DE content was highest ($P < 0.05$) for Pea protein and lowest for Maple bean (3.30 vs. 3.07 Mcal/kg DM, respectively), DE of corn diet was 3.18 Mcal/kg. The ATTD of energy of diet was highest in Pea starch (91.0) and lowest in Roasted bean (76.4%) while Corn diet was 84.4%. In vitro energy digestibility was highest ($P < 0.05$) in Pea protein (88.8) and lowest for Maple and Roasted bean (79.0 and 79.8%, respectively). In vitro energy digestibility was moderately related to ATTD of energy for legume samples ($R^2 = 0.44$; linear) although in vitro DE and in vivo DE were related tighter ($R^2 = 0.57$). Among nutrients, ADF was the best predictor ($R^2 = 0.67$) for in vivo DE. In conclusion, some grain legumes provide more DE with higher ATTD of energy than corn; thus, can serve as alternative feed ingredient for growing pigs. However, variation due to type and composition of grain legume should be considered for swine pig diet formulation. Finally, the current in vitro digestibility technique needs improvements to better predict the ATTD of energy in grain legumes in swine.

Key Words: energy, legume, pig

698 Digestible and metabolizable energy concentration in canola meal, 00-rapeseed meal, and 00-rapeseed expellers fed to growing pigs. T. Maison* and H. H. Stein, *University of Illinois at Urbana-Champaign, Urbana.*

This experiment was conducted to measure DE and ME in canola meal, 00-rapeseed meal, and 00-rapeseed expellers fed to growing pigs. Twenty 3 barrows (initial BW: 27.7 ± 2.92 kg) were allotted to an 8 × 23 Youden square design with 8 periods and 23 animals. Twenty-three diets were prepared. One diet was a corn based basal diet; 6 diets were based on corn and each of 6 samples of canola meal from solvent-extraction crushing plants in North America (average of 4,218 kcal GE/kg, 38.0% CP, and 3.82% crude fat); 11 diets were based on corn and each of 11 samples of 00-rapeseed meal from solvent-extraction crushing plants in Europe (average of 4,210 kcal GE/kg, 36.2% CP, and 3.87% crude fat); and 5 diets were based on corn and each of 5 samples of 00-rapeseed expellers from mechanical-press crushing plants in Europe (average of 4,721 kcal GE/kg, 35.6% CP, and 11.5% crude fat). Pigs were fed at 3 times their estimated energy requirement for maintenance, and were placed in metabolism cages that allowed for the total, but separate, collection of feces and urine. The concentration of DE and ME in corn was calculated from the basal diet and the contribution of DE and ME from corn to the remaining diets was then calculated, and the DE and ME of each source of canola meal, 00-rapeseed meal, and 00-rapeseed expellers were calculated by difference. Results of the experiment indicate that the apparent total tract digestibility in 00-rapeseed expellers (78.32%) was greater ($P < 0.01$) than in 00-rapeseed meal (70.63%), but no difference between 00-rapeseed meal and canola meal (69.82%) was observed. The concentration of DE and ME in canola meal (3,378 and 3,127 kcal/kg DM) were not different from DE and ME in 00-rapeseed meal (3,461 and 3,168 kcal/kg DM), but 00-rapeseed expellers had greater ($P < 0.01$) DE and ME (4,005 and 3,691 kcal/kg DM) than 00-rapeseed meal. In conclusion, the concentration of DE and ME is not different between canola meal and 00-rapeseed meal, but 00-rapeseed expellers contain more DE and ME than 00-rapeseed meal.

Key Words: canola meal, rapeseed product, pig

699 Determination of true phosphorus digestibility in *Brassica napus* black and *Brassica juncea* yellow fed to growing pigs using regression analysis. P. A. Adhikari*, J. M. Heo, and C. M. Nyachoti, *University of Manitoba, Winnipeg, MB, Canada.*

Diet formulation on the basis of apparent phosphorus (P) digestibility values can vary within a single feed ingredient that leads to P over-feeding and excessive P excretion in pigs. The determination of true digestibility values in feed ingredients helps to address this issue. The objectives of this study were to determine the apparent (ATTD) and true (TTTD) total tract digestibility of P in canola meals (CM) from *Brassica napus* black and *Brassica juncea* yellow fed to growing pigs using the regression analysis technique. Forty-eight barrows (initial BW = 19.9 ± 0.22 kg mean ± SD) housed individually in metabolic crates were allotted to 8 dietary treatments in a completely randomized design to give 6 observations per treatment. Eight isocaloric cornstarch-based diets (4 diets per cultivar) were formulated to contain 0.8, 1.6, 2.4 and 3.3 g/kg DM from either *B. napus* black or *B. juncea* yellow. Canola meal (*B. napus* black or *B. juncea* yellow) was the sole source of P and limestone was added to maintain Ca:total P ratio of 1.2:1. The daily quantity of feed provided per pig was calculated as 2.6 times the maintenance energy requirement of the pigs and divided into 2 equal meals at 0800 and 1600 h. Pigs were adapted to dietary treatments for 9 d followed by the total collection of feces for 5 d. The ATTD values of P increased from 17.9 to 29.4% for *B. napus* black and from 16.6 to 27.2% for *B. juncea* yellow as the dietary P content increased from 0.8 to 3.3 g/kg DM. The endogenous fecal outputs of P were not different between the CM cultivars and averaged 0.667 g/kg DMI. There was no difference ($P > 0.05$) in TTTD of P (33.3 vs. 31.9%) in *B. napus* black and *B. juncea* yellow when determined with the regression method. In this study, estimates of endogenous P loss were higher than previous studies which can be due to various factors including diet type, age or metabolic state of animal.

Key Words: digestibility, endogenous loss, phosphorus

700 Physiological effects of L-methionine compared with DLDL-methionine fed to nursery pigs. Y. B. Shen* and S. W. Kim, *North Carolina State University, Raleigh.*

D-Methionine is slowly transported to intestinal cell and need to be converted to L-Met (LM) in the liver for biological functions. Thus, we hypothesized dietary LM as a direct source of Met will have beneficial effects on gut development and growth of pigs compared with the use of DL-Met (DLM). Twenty individually housed crossbred pigs (8.40 ± 0.25 kg BW) were randomly allotted to 2 treatments at 26 d of age: (1) basal diet (0.16% endogenous Met) + 0.145% DLM; or (2) basal diet + 0.145% LM. Both diets had Met meeting 95% the NRC requirement. Pigs were fed assigned diets for 20 d. During the entire period, pigs fed a diet supplemented with LM tended to have 7.4% greater gain:feed ratio (0.62 vs. 0.58; $P = 0.064$) compared with pigs fed a diet supplemented with DLM. On d 20, pigs fed a diet supplemented with LM had 15.4% and 7.4% greater villus height (709 vs. 614, μm; $P = 0.047$) and width (159 vs. 148 μm; $P = 0.036$) in duodenum compared with pigs with DLM. Pigs fed a diet supplemented with LM tended to have 17.5% greater villus height:crypt depth ratio (1.54 vs. 1.31; $P = 0.075$) in duodenum compared with pigs with DLM. Pigs fed a diet supplemented with LM tended to have 19.9% lower concentration of malonedialdehyde (MDA) in plasma (7.45 vs. 9.30 μM; $P = 0.069$) and 52.6% lower concentration of MDA in ileum mucosa (0.55 vs. 1.16, umol/g protein; $P = 0.081$) compared with pigs with DLM. Concentrations of protein carbonyl in duodenum mucosa of pigs fed a diet supplemented with LM was 12.0% lower (3.00 vs. 3.41, umol/g protein; $P = 0.023$) than pigs with DLM. However, concentrations of glutathione in duodenum and liver were not affected by dietary treatments ($P = 0.123$). Collectively, compared with DLM, use of LM as a source of dietary Met supplementation in nursery pig diets improved gut development by enhancing villus development associated with reducing oxidative stress in nursery pigs.

Key Words: DL-methionine, gut development, L-methionine

701 Predicting digestible energy (DE) and net energy (NE) of dried distillers grains with solubles from its oil content. S. Nitikanchana*, A. B. Graham, R. D. Goodband, M. D. Tokach, S. S. Dritz, and J. M. DeRouchey, *Kansas State University, Manhattan.*

The energy content of dried distillers grains with solubles (DDGS) is a concern as more oil content is being extracted during the ethanol production process. The objective of this study was to determine the DE and NE value of DDGS varying in oil content. To determine the DE of DDGS, a total of 12 pigs in metabolism cages were fed a corn-based diet and corn-50% DDGS diets from 5 sources of DDGS that had various oil contents (5.35, 7.63, 9.38, 9.57, and 12.10%; as-fed basis).The same 5 sources of DDGS were also used in 3 growth studies to determine the NE of the DDGS sources from the G:F responses. Four of the DDGS sources were tested at 20 and 40% of the diet. One DDGS source was tested at 15, 30, and 45%. The net energy efficiency (calories of NE intake (kcal) per kg of gain; NEE) of pigs fed the respective DDGS diet in each study was solved to equal the NEE of pigs fed the corn-soybean meal diet in the same study by adjusting the dietary NE of the DDGS diet. Corn and soybean meal were assumed to have a NE content of 2,672 and 2,087 kcal/kg, respectively. The dietary NE content that resulted in equal NEE was then used to calculate NE of DDGS according to the percentage of DDGS in that diet. From this method, NE of 5 sources of DDGS were determined. Then, DE from the digestibility study and NE from the growth studies for the 5 DDGS sources were used in a stepwise regression to establish the DE and NE prediction equations. The linear and quadratic term of oil (ether extract), crude protein, crude fiber, acid detergent fiber, neutral detergent fiber, particle size, bulk density, including the interaction terms were the variables in the regression analysis. Of these measures, oil content was the only significant variable. The equations to predict DE and NE as a function of oil content were: [DE (kcal/kg) = 62.347 × oil (%) + 3058.13 (n = 5, Adjusted $R^2 = 0.41$); NE (kcal/kg) = 115.011 × oil (%) + 1501.01 (n = 5, Adjusted $R^2 = 0.86$)]. These equations indicate changing the oil content 1% in DDGS will change the DE by 62 kcal/kg and NE by 115 kcal/kg.

Key Words: DE, dried distillers grains with solubles, NE

Production, Management and the Environment: Surveys and Models I

702 Expected value of beef cattle breeding strategies: Sexed versus non-sexed semen. E. D. Lord*[1], N. J. Olynk Widmar[1], B. Gloy[1], W. M. Hilton[2], and C. A. Wolf[3], [1]*Purdue University, Department of Agricultural Economics, West Lafayette, IN,* [2]*Purdue University, College of Veterinary Medicine, West Lafayette, IN,* [3]*Michigan State University, Department of Agricultural, Food, and Resource Economics, East Lansing.*

The US beef cattle herd is currently the smallest since 1952. Given current market conditions, what strategies should producers pursue to breed beef cattle and grow their herds? The objective of this research is to evaluate the expected value (EV) of artificial insemination (AI) beef breeding strategies. Sexed semen has only recently become a topic of interest for beef cattle. Producers may consider AI using non-sexed semen or sexed semen; a spreadsheet-based model was developed to calculate the EV of breeding a heifer and/or cow with non-sexed semen AI and sexed semen AI. Multiple scenarios were investigated to assess the differences in EV among breeding strategies. Sex ratios were assumed at 49.2% female for non-sexed AI and were investigated at assumptions of 75% and 90% of the desired sex for sexed AI. Both male and female sorted semen were analyzed as potential strategies. Sexed semen was assumed to yield a conception rate (CR) 75% to 85% of that of non-sexed semen. Costs per AI were held constant at $20.00/non-sexed AI and $30.00/AI for 90% bull-sorted sexed AI of approximately the same genetic value. A sample scenario was created in which bull and heifer calves were valued at $450 and $300, respectively. The value of the average calf increased by approximately $60 with 90% bull-sorted sexed semen. Assuming 90% bull-sorted sexed semen yielded 85% of non-sexed AI conception rate (61%) and simplifying with a 100% AI submission rate, 2 AI with sexed semen yielded an EV of approximately $20 higher than that of 2 AI with non-sexed semen. All else equal, in this scenario, to achieve an EV with 2 sexed semen AI equal to that with 2 non-sexed semen AI, the sexed semen must yield at least 78% of the conception rate of non-sexed semen. Ceteris paribus, 2 sexed semen AI yielded an equal EV to 2 non-sexed AI, as long as the bull calf value was at least $426. This model provides insight into key tradeoffs between beef breeding strategies. Other considerations in the model include the effects of carrying costs for open animals, changing AI costs, and varying reproductive performance to various breeding methods.

Key Words: sexed semen, beef reproduction, beef breeding

703 Meta-analysis of consumer willingness to pay for specialty attributes of beef. R. White*[1] and M. Brady[2], [1]*Department of Animal Sciences, Washington State University, Pullman,* [2]*School of Economic Sciences, Washington State University, Pullman.*

Improving sustainability of beef production systems will help ensure a long-term food supply. Sustainability of a system can be quantified via measures such as environmental impact (EI), economic viability and social acceptability. An accepted metric for social acceptability is consumer willingness to pay (WTP). The objective of this study was to perform a quantitative survey of consumer WTP for various attributes of beef to identify the consumer WTP for lowered EI. An Agricola database search for consumer WTP for beef from 2003 to 2012 returned 16 usable studies representing 44 treatments applied to over 11,000 consumers in 6 countries. Following a Hedonic approach, breaking goods into constituent parts, studies were categorized using 21 binary dummy variables to describe study location, methodology and beef attribute. For each variable, 95% confidence intervals were calculated to determine the expected mean and range of consumer WTP. A multi-variate regression was used to relate consumer WTP to location and methodological variables, 4 single-attribute variables (health, local, EI or quality) and 3 dual-attribute variables (health+local, health+EI, local+EI). Confidence intervals indicated consumer WTP for beef attributes related to quality (tenderness, yield) or personal health (safety, traceability, no GMO, no antibiotics/hormones, vegetarian diet, organic) was between a 35% and 104% premium (mean = 51%). The WTP for EI or local economic impact was a premium of 6% to 33% (mean = 20%). Results agree with existing literature that consumers are WTP more for private goods than public goods. The regression model was significant ($P = 0.0003$) and explained 67% of the variability in WTP. When location variables were used to predict WTP for US consumers, the model indicated WTP a 4% premium for environmental attributes. When products with environmental attributes also had local or health benefits, WTP increased to a 23% or 82% premium, respectively. Consumers show measurable WTP for non-quality attributes of beef including reduced EI; thus, WTP should be included in assessments of methods to improve sustainability of beef production.

Key Words: meta-analysis, environmental impact, willingness to pay

704 Environmental footprints of beef production at the U.S. Meat Animal Research Center. C. A. Rotz*[1], B. J. Isenberg[1], K. R. Stackhouse-Lawson[2], and E. J. Pollak[3], [1]*USDA/ARS, University Park, PA* [2]*National Cattlemen's Beef Association, Centennial, CO,* [3]*USDA/ARS, Clay Center, NE.*

Environmental footprints of beef produced at the US Meat Animal Research Center (MARC) in Clay Center, Nebraska were determined to quantify improvements achieved over the past 40 years. Relevant information for MARC operations was gathered and used to represent their production system with the Integrated Farm System Model. The MARC farm, cow calf and feedlot operations were each simulated over recent historical weather to evaluate performance, environmental impact and economics. The current farm operation included 840 ha of alfalfa and 1,160 ha of corn to produce feed predominately for the beef herd of 5,500 cows, 1,200 replacement heifers and the 3,724 cattle finished each year. Spring and fall cow calf herds were fed on 9,710 ha of pastureland supplemented with hay and silage produced by the farm operation. Feedlot cattle were backgrounded 3 mo on hay and silage and finished over 7 mo on a diet high in corn grain and purchased wet distiller's grain. Model simulated predictions for 2011 were within 1% of actual records for feed production and use, energy use, and production costs. A 25-year simulation of their current production system gave a carbon footprint of 10.9 kg of CO_2e/kg BW sold, and the energy required to produce that beef (energy footprint) was 26.5 MJ/kg BW. Total water use (water footprint) was 21,300 l/kg BW sold, and the water footprint excluding that obtained through precipitation was 2,800 l/kg BW. Simulation of the production practices of 2005 indicate that the use of distiller's grain in animal diets has had a relatively small impact on environmental footprints except that reactive nitrogen loss has increased 10%. Compared with 1970, the carbon footprint of the beef produced has decreased 6% with no change in the energy footprint and a 3% reduction in the reactive nitrogen footprint. The water footprint, excluding precipitation, has increased 42% due to greater use of irrigated corn production. These results support that progress has been made in reducing some environmental impacts of beef produced at MARC.

Key Words: beef, environment, carbon footprint

705 Environmental, social, and economic footprints of current and past beef production systems. K. R. Stackhouse-Lawson*[1], C. A. Rotz[2], B. J. Isenberg[2], E. J. Pollak[3], T. Battagliese[4], B. Ulhman[4], C. Barcan[4], I. Schulze[5], J. Silva[5], and J. O. Reagan[1], [1]*National Cattlemen's Beef Association, Centennial, CO,* [2]*USDA-ARS, Pasture Systems and Watershed Management Research Unit, University Park, PA,* [3]*USDA-ARS-NPA, Roman L. Hruska U.S. Meat Animal Research Center, Clay Center, NE,* [4]*BASF Corporation, Nutrition and Health, Florham Park, NJ,* [5]*BASF Corporation, Fundação Espaço ECO, Sao Bernardo do Campo, Brazil.*

The beef industry has defined sustainability as meeting the growing demand for beef by balancing environmental responsibility, economic opportunity and social diligence. Accurately measuring sustainability is challenging, as the beef supply chain is one of the most complex food systems in the world. As the first and largest research project of this kind, this study represents an innovative approach toward creating a more sustainable beef product. Our objective is to establish a sustainability baseline (including environmental, economic, and social footprints) for the US beef industry by quantifying life cycle inputs and outputs for beef production over time. Our approach is to use a combination of models. The USDA-ARS Integrated Farm System Model (IFSM) is used to simulate the environmental and economic footprints from cradle to farm-gate. The socio-eco-efficiency tool (SEEBALANCE) extends this analysis by determining the environmental, economic, and social impacts of beef from cradle to grave providing a comprehensive assessment of sustainability. As an initial step, the environmental impacts and economics of beef production at the US Meat Animal Research Center were determined through simulation with the IFSM. These results were combined with primary data from the packer, case ready, retail, and consumer segments of the beef value chain for 2005 and 2011 using SEEBALANCE. This approach quantified sustainability considering economic, social and ecological impacts along all segments of the beef value chain expressed in 0.45 kg of minimally processed boneless edible consumed beef. Environmental impacts included solid waste contributions, greenhouse gas emissions, ozone depleting potential, photochemical ozone creation potential, acidification potential, emissions to water, resource consumption, land use and energy consumption. Social impacts were measured using toxicity potential, occupation illnesses and accidents, and risk. Economics for the full chain were expressed in consumer price. Overall, the sustainability of the US beef industry, given the present assumptions, has improved by 9% in 6 yr.

Key Words: beef, sustainability, life cycle assessment

706 Life cycle assessment of the production of one kilogram of milk in six buffalo farms. G. Pirlo*[1], S. Carè[1], V. Fantin[2], F. Falconi[3], P. Buttol[2], C. Pacelli[4], G. Terzano[1], and P. Masoni[2], [1]*Consiglio per la ricerca e sperimentazione in agricoltura (CRA), Cremona, Italy,* [2]*ENEA, Italian National Agency for New Technologies, Energy and Sustainable Economic Development, Bologna, Italy,* [3]*LCA-lab SRL, Bologna, Italy,* [4]*Dipartimento di Scienze delle Produzioni Animali, Università della Basilicata, Potenz, Italy.*

The purpose of this study was to quantify the environmental impacts of the production of milk of Italian Mediterranean buffaloes. For this purpose, life cycle assessment (LCA) was used in a sample of 6 farms. The functional unit was 1 kg of normalized buffalo milk (LBN), with a reference milk fat and protein contents of 8.3 and 4.73% respectively. The system boundaries included the agricultural phase of buffalo milk chain from cradle to farm gate. Impact categories were: global warming (GW), abiotic depletion (AD), photochemical oxidation (PO), acidification (AC), and eutrophication (EU). Refernce units were kg of CO_2eq for GW, kg of Sbeq for AD, kg of C_2H_4eq for PO, kg of SO_2eq for AC, and kg of PO_4^{3-}eq for EU. Farm activities were (1) on-farm energy consumption (EC); (2) manure management (MM); (3) manure application (MA); (4) on-farm feed production (ONFP, comprising production and application of chemical fertilizers and pesticides); (5) off-farm feed production (OFFP); (6) enteric fermentation (EF); (7) transports of off-farm feeds, chemical fertilizers and pesticides from suppliers to farms (TR). Farms were characterized by a herd size of 361 ± 40.6 buffaloes and a production of 2,069 kg/head/year of LBN. LCA was performed with the support of SimaPro 7.3.3. software. The average environmental impacts associated with 1 kg of LBN were: GW 5.02 (±1.14) kg of CO_2eq; AD 5.08 E-1 (±2.04 E-1) kg of Sbeq; PO 6.72 E-4 (±2.00 E-4) kg of C_2H_4eq; AC 6.52 E-2 (±1.98 E-2) kg of SO_2eq; EU 3.28 E-2 (±1.21 E-2). kg of PO_4^{3-}eq. Activities with major effects on GW were EF (37% ± 7.78) and MA (19.3% ± 3.0); on AD were EC (31.4% ± 12.6) and ONFP (32.6 ± 9.7); on PO was EF (37% ± 7.8); on AC were MM (53.6% ± 7.9) and MA (26.3% ± 4..5); on EU were MM (23.7% ± 5.9), MA (36.8% ± 12.1) and OFFP (26.6% ± 13.9). Normalization analysis showed that the major contributions to the environmental impact of LBN production come from GW, AC and EU; whereas those of AD and PO are negligible.

Key Words: life cycle assessment, buffalo milk

707 Assessment of culling risk and economic outcomes in dairy herds. G. M. Schuenemann*[1] and K. N. Galvão[2], [1]*Department of Veterinary Preventive Medicine, The Ohio State University, Columbus,* [2]*Large Animal Clinical Sciences, University of Florida, Gainesville.*

It is common to observe large among-herd variation in culling risk while having similar reproductive performance. The objective was to assess the effect of 2 culling risks (28% vs 38%) on the economic outcomes of dairy herds with the same reproductive performance using an individual cow-based stochastic model. For the simulation, 2 culling risks (28% vs 38%) were compared using the same reproductive program and performance. Cows were enrolled in an Ovsynch (OV) preceded by Presynch with 2 injections of PGF 14 d apart, and OV for resynchronization of open cows at 32 d after AI. Also, cows undergo estrous detection (ED) and AI after first AI, and cows diagnosed open 32 d after AI are resynchronized using OV. Cows were not inseminated after 365 DIM and open cows were culled after 450 DIM. Culled cows were immediately replaced with a primiparous cow. Herd was maintained at 1,000 cows. Mortality was set at 6% and abortion at 11.3%. The dry period and VWP was 60 d. Conception rate to first service was set to 32% (decreased by 2.5% for every subsequent service), and ED was set to 60%. Accuracy of ED and COM with each injection were set at 95%. Net daily value was calculated by subtracting the costs with replacement heifers ($1,600/heifer), feeding costs ($0.25/kg of lactating cow diet; $0.15/kg of dry cow diet), breeding costs ($0.15/cow/d for ED; $2.65/dose PGF; $2.4/dose GnRH; $0.25/injection administration), and other costs ($2.5/d) from the daily income with milk sales ($0.44/kg milk), cow sales ($2/kg live weight), and calf sales ($200/calf). Simulation was performed until steady-state was reached (4000 d), then average daily values for the subsequent 1000 d was used to calculate profit ($/yr). According to the model (same herd size, synchronization program and reproductive performance), the annual profit was $23687 higher for 28% compared with 38% culling risk. Culling affects the bottom line of dairy operations and the underlying causes should be investigated to develop preventive procedures to ensure optimum level of culling risk by considering both welfare and profitability.

Key Words: culling risk, economics, dairy herd

708 Effect of milking personnel performance and turnover on milk losses in dairy herds. G. M. Schuenemann*, M. G. Maquivar, S. Bas, and J. D. Workman, *Department of Veterinary Preventive Medicine, The Ohio State University, Columbus.*

It is common to observe large within-herd variation in milking personnel performance (MPP) and turnover (TO) over time. Assessing team performance, resolution of conflicts, and comprehensive training of dairy personnel are critical tasks to achieve consistent performance of dairy herds. The objective was to assess the effect of MPP (95% vs 85%) and TO of personnel (5% vs 30%) on milk losses of dairy herds. For the simulation, the performance of each milker (compliance with milking routine protocol) was set to 85% or 95%. Milk losses were set at 1 kg/cow/d due to lack of udder stimulation. An adjustment period of 14 d with a 66.5% performance was estimated for each new personnel. The overall risk performance (%; RP) was estimated taking into account the team milking performance and TO. The number of cows at risk (n/d) was estimated based on the RP (10 milkers) and herd size (2000 cows). Milk price was set at $0.41/kg. Costs for herd audit were set at $1000 and training program at $1000 (for 4 sessions per yr). Milk losses ($/yr/herd) and return on investment (ROI) were estimated. For a 2000-cow herd, the overall effect of TO (5% vs 30%) on milk losses was $6744 while the overall effect of RP (85% vs 95%) on milk losses was $27920. Cows at risk and milk losses were higher ($14 per cow/yr) for RP 85% with 30% TO (342 cows/d) compared with RP 95% with 5% TO (110 cows/d). The ROI for high performance teams (RP 95% and 5% TO) was $18 for every $1 invested (herd audit and training). The estimated ROI assumes that facilities are adequate, participants are willing to learn and apply the newly learned concepts, and the herd audit correctly identifies the needs and the training program correctly addresses them. Both TO and RP affect the bottom line of dairy herds. Frequent assessment of performance, educational needs, and training of dairy personnel should be top priorities for dairy operations to achieve a consistent and efficient herd performance over time.

Key Words: human resources, milk loss, dairy herd

709 Retention pay-off prediction using machine learning algorithms. S. Shahinfar*, A. S. Kalantari, V. Cabrera, and K. Weigel, *Department of Dairy Science, University of Wisconsin-Madison, Madison.*

Culling decisions have a major effect on dairy farm profitability. Dynamic programming (DP) has been widely used for finding the optimal replacement policies in dairy cattle. However, DP models are computationally intensive and might not be practical for daily decision making. Hence, the ability of machine learning to provide fast and accurate predictions of non-linear and inter-correlated variables makes it an ideal methodology. Milk class (1–5), lactation number (1–9), month in milk (1–20), and pregnancy status (0–9) were used to describe a cow in the DP model. Twenty-seven scenarios based on all combinations of 3 levels of milk production, milk price, and replacement cost were solved with the DP model, resulting in a data set of 122,716 records, each with a calculated retention pay-off. Then, a machine learning model tree algorithm was used to mimic the evaluated RPO in DP. The correlation coefficient factor was used to observe the concordance of RPO evaluated by DP and RPO predicted by the model tree. The obtained correlation coefficient was 0.991 with corresponding value of 0.11 relative absolute error. At least 100 instances were required per model constraint, and resulting in 204 total models. When these model s were used for binary classifications of positive and negative RPOs, error rate were %1 false negatives and %9 false positives. Applying this trained model from simulated data for prediction of retention pay-off for 102 actual culling records from UW-Madison dairy herd resulted in a 0.994 correlation with 0.10 relative absolute error rate.

Key Words: machine learning, retention pay-off, prediction

710 Model selection, estimation and cross validation of methane emissions prediction equations. L. E. Moraes*[1], E. Kebreab[1], A. B. Strathe[2], J. G. Fadel[1], and D. P. Casper[3], [1]*University of California, Davis,* [2]*University of Copenhagen, Copenhagen, Denmark,* [3]*South Dakota State University, Brookings.*

The quantification of methane emissions from livestock is essential in the development of national greenhouse gas inventories and in the assessment of mitigation strategies. Various prediction models have been developed over the past decade but predictive ability remains poor. The objective of this study was to develop methane prediction equations, using 1,111 methane emission records from 298 lactating cows, through the use of robust statistical techniques. Measurements were conducted through indirect calorimetry at the former USDA Energy Metabolism Unit at Beltsville, Maryland. Three model complexity levels (i.e., GE, Dietary and Animal levels) were specified for which the dimension of parameter space increased sequentially. A Bayesian approach was adopted in which statistical inference was based on Markov chain Monte Carlo methods. Key covariates to predict methane emissions at each model complexity level were identified through a Reversible Jump Markov Chain Monte Carlo sampler. The most probable model, conditional on the observed data, at each complexity level was estimated with a Bayesian hierarchical model. Residuals were modeled with a student-t distribution providing robust inference. Equations were evaluated through a K-fold cross validation procedure. Model selection was based on achieving high posterior probabilities ($P > 0.74$) across all complexity levels. Models fitted at GE (1), dietary (2) and animal (3) levels were: (1) CH_4 (MJ/d) = 3.25 (0.42) + 0.043 (0.001) × GEI (MJ/d); (2) CH_4 (MJ/d) = 0.2242 (0.71) + 0.042 (0.001) × GEI (MJ/d) + 0.124 (0.01) × NDF (% DM) − 0.329 (0.09) × EE (% DM); (3) CH_4 (MJ/d) = −9.317 (1.06) + 0.042 (0.001) × GEI (MJ/d) + 0.094 (0.01) × NDF (% DM) - 0.381 (0.09) × EE (% DM) + 0.008 (0.001) × BW (kg) + 1.622 (0.11) × Milk Fat (%). Mean square prediction error for the GE, dietary and animal complexity levels, expressed as a proportion of CH_4 emissions means were 18.1, 17.9 and 15.6%. Equations developed here outperformed current models from the literature and will improve the accuracy in the prediction of methane emissions in national greenhouse gas inventories.

Key Words: methane emission, prediction, lactating cow

Reproduction Symposium: External Influences on Reproductive Neuroendocrinology

711 While the grass may be greener in the other field, is it better for you or your baby? Hidden risks of environmental pollutants. N. P. Evans*[1], M. Bellingham[1], C. Cotinot[2], S. M. Rhind[3], R. Sharpe[4], and P. A. Fowler[5], [1]*University of Glasgow, College of Medical Veterinary and Life Sciences, Institute of Biodiversity Animal Health & Comparative Medicine, Glasgow, UK,* [2]*INRA, UMR 1198 Biologie du Developpment et Reproduction, Jouy en Josas, France,* [3]*James Hutton Institute, Aberdeen, UK,* [4]*University of Edinburgh, Queens Medical Research Institute, MRC Centre for Reproductive Health, Edinburgh, UK,* [5]*Institute of Medical Sciences, Division Applied Medicine, University of Aberdeen, Aberdeen, UK.*

Processed human sewage sludge, which contains low individual concentrations of an array of contaminants including heavy metals and organic pollutants e.g., PAHs, PCBs and PCDD/Fs is used as an agricultural fertiliser within the EU. Investigation of the physiological effects on grazing sheep on such treated pastures provides a model to investigate effects of exposure to mixtures of environmentally relevant concentrations of pollutants. Pasture treatment results in non-significant increases in environmental chemical (EC) concentrations in soil, and some tissues of ewes and their fetuses. Tissue EC concentrations were variable and low and deemed to pose little risk to consumer health. Investigation of the effects of gestational EC exposure on fetal development has highlighted several issues. The results indicate that gestational EC exposure can adversely affect gonadal development (males and females) and that these effects can affect testicular morphology and ovarian follicle numbers/health and proteo/transcriptomes in adult animals. In addition, EC exposure can be associated with altered expression of GnRH, GnRH receptor, galanin receptor and kisspeptin mRNA within the hypothalamus and pituitary gland, gonadotroph populations within the pituitary gland and regional aberrations in thyroid morphology. In most cases, these anatomical/functional differences do not result in altered peripheral hormone concentrations or reproductive function e.g., lambing rate, suggesting physiological compensation under the conditions tested. Physiological compensation is also suggested by studies which indicate that EC effects may be greater when exposure occurs either before or during gestation, compared with EC exposure throughout life. With regard to human/animal health, this body of work questions the concept of safe individual concentration of ECs when EC exposure typically occurs as complex mixtures. It suggests that developmental EC exposure may affect many different physiological systems, with some sex-specific differences in EC sensitivity and that EC effects may be masked under favorable physiological conditions. [Wellcome Trust grant 080338].

Key Words: environmental pollutant, fetal development, environmental chemical

712 E-Screen—Potential tool for assessment of relative serum estrogenicity. N. W. Shappell*[1], S. A. Hiablie[2], J. D. Magolski[3], K. A. Vonnahme[3], E. P. Berg[3], and L. O. Billey[1], [1]*Biosciences Research Laboratory, USDA-ARS, Fargo, ND,* [2]*Penn State University, State College,* [3]*North Dakota State University, Fargo.*

The E-Screen bioassay was evaluated for its usefulness in the assessment of serum estrogenicity as a potential sentinel of endocrine disruption. Porcine, ovine, bovine, and piscine samples were evaluated. High concentrations of swine, cattle, and fish serum were toxic to the E-screen (human) cell line, which is routinely maintained in fetal bovine serum. In contrast, high concentrations of sheep serum altered cell morphology, a change that was not seen at lower serum concentrations. Ovarectomized sheep on basal diets had serum estradiol (E2) of 1.8 ± 0.79 pg/mL (SD, RIA) and 18 ± 10.7 pg/mL E2Eq (E2 equivalents ± SD, E-Screen). Acetonitrile extraction of porcine serum (ACN:serum 2:1 v/v) removed the toxicity to E-screen cells. Extracted serum E2Eq from peripubertal gilts increased at the onset of estrus in most animals with a maximum E2Eq of 20 pg/mL. Validation experiments were conducted by comparing E2Eq from serum fortified with E2 before extraction and E2Eq from unextracted serum, with or without E2 fortification. At high unextracted serum concentrations, E2 addition produced a synergistic proliferative response in cells, while the expected additive proliferation was found with extracted serum. Sex differences in serum E2Eq were clear in 2 different species of catfish. Mean E2Eqs (pg/mL) from male fish were 333 ± 281 (SD) in African catfish (Clarias gariepinus) and 244 ± 49 in channel catfish (Ictalurus punctatus), whereas mean E2Eqs from female fish were 1560 ± 1054 and 1157 ± 71 for the 2 species, respectively. Collectively, these results suggest that the E-Screen assay is useful for evaluating serum samples for total estrogenicity. When assessing in vivo effects of possible endocrine disruptor exposure, ELISAs provide specific concentrations for steroid hormones, such as estradiol, while the E-Screen assay evaluates the net effects of estrogen agonists and antagonists in serum.

Key Words: E-Screen, serum, estrogenicity

713 Developmental programming of reproductive and metabolic health. V. Padmanabhan*, *Department of Pediatrics, Obstetrics and Gynecology, Molecular and Integrative Physiology, and Environmental Health Sciences, University of Michigan, Ann Arbor.*

The inappropriate programming of the reproductive system by developmental exposure to excess steroid hormones is of concern, especially in the female. The sheep is well suited for investigating developmental origin of reproductive and metabolic disorders. The developmental time line of sheep (5 mo gestation and 7-mo to puberty) is ideal for conducting sequential studies of the progression of metabolic/reproductive disruption from the developmental insult to manifestation of adult consequences. Major benefits of using sheep include knowledge of established critical periods to target adult defects, a rich understanding of reproductive neuroendocrine regulation that parallel humans, availability of non-invasive approaches to monitor follicular dynamics, established surgical approaches to obtain hypophyseal portal blood for measurement of hypothalamic hormones, and the ability to perform studies in natural setting keeping behavioral interactions intact. Of importance is the ability to chronically instrument fetus and mother for determining early endocrine perturbations. Prenatal exposure of the female to excess testosterone (T) leads to an array of adult reproductive disorders that include LH excess, functional hyperandrogenism, neuroendocrine defects, multifollicular ovarian morphology, and corpus luteum dysfunction culminating in early reproductive failure. At the neuroendocrine level all 3 feedback systems (estradiol negative, estradiol positive and progesterone negative feedback) are compromised. Estradiol negative feedback deficits are programmed by androgenic actions and estradiol positive by both androgenic and estrogenic influences of T. At the pituitary level, LH sensitivity to GnRH is increased. Multifollicular ovaria morphology stems from persistence of follicles as well as enhanced follicular recruitment. Together these defects culminate in progressive loss of cyclicity and reduced fecundity. Prenatal T excess also leads to fetal growth retardation, an early marker of adult reproductive/metabolic diseases, insulin resistance, hypertension and behavioral deficits. Col-

lectively, the reproductive/metabolic deficits of prenatal T-treated sheep provides a model for understanding the developmental origin of fertility and metabolic disorders.

Key Words: reproductive health, fertility, testosterone

714 Effects of bovine somatotropin administration on growth, physiological, and reproductive responses of replacement beef heifers. R. F. Cooke*[1], D. W. Bohnert[1], C. L. Francisco[1,2], R. S. Marques[1], C. J. Mueller[3], and D. H. Keisler[4], [1]*Oregon State University - Eastern Oregon Agricultural Research Center, Burns,* [2]*UNESP - Faculdade de Medicina Veterinária e Zootecnia, Botucatu, São Paulo, Brazil,* [3]*Oregon State University - Eastern Oregon Agricultural Research Center, Union,* [4]*University of Missouri - Division of Animal Sciences, Columbia.*

This study compared growth, body composition, plasma IGF-I and leptin, and reproductive development of beef heifers receiving or not recombinant bovine ST (BST) beginning after weaning until the first breeding season. Fifty Angus × Hereford heifers, weaned at 6 mo of age (d −30), were assigned to the experiment (d 0 to 210). On d 0, heifers were ranked by initial BW and age, and assigned to (1) treatment with BST or (2) saline control. Heifers assigned to the BST treatment received s.c. injections containing 250 mg of sometribov zinc whereas control heifers received a 5-mL s.c. injection of 0.9% saline every 14 d. Treatments were initiated on d 14, and last administered on d 196. Heifer shrunk BW was collected on d 1 and 211 for ADG calculation. Blood samples were collected weekly from d 0 to 210 for determination of plasma IGF-I, leptin, and progesterone to estimate puberty attainment. On d 0, 63, 133, and 189, heifers were evaluated for intramuscular marbling, LM depth, and backfat thickness via ultrasonography. No treatment effects were detected ($P = 0.27$) for heifer ADG (0.49 vs. 0.51 kg/d for control and BST heifers, respectively; SEM = 0.02). Mean backfat thickness was lesser ($P < 0.01$) in BST heifers compared with control cohorts (3.56 vs. 3.92 mm, respectively; SEM = 0.08). Heifers receiving BST had greater plasma IGF-I concentrations compared with control cohorts 7 d after treatment administration (treatment × day interaction; $P < 0.01$). Mean plasma leptin concentrations were lesser ($P = 0.05$) in BST heifers compared with control cohorts (1.82 vs. 2.03 ng/mL, respectively; SEM = 0.07). Onset of puberty was hastened in BST heifers compared with control cohorts (treatment × day interaction; $P = 0.04$). In summary, a greater proportion of BST heifers reached puberty during the experiment compared with control cohorts, despite lesser plasma leptin concentrations, backfat thickness, and similar ADG. Hence, circulating IGF-I was positively associated with hastened puberty attainment independently of growth rate, circulating leptin concentrations, and body fat content of replacement beef heifers.

Key Words: beef heifer, somatotropin, puberty

715 Neuroendocrine programing of accelerated puberty in heifers. M. Amstalden*[1], B. R. C. Alves[1], and R. C. Cardoso[1,2], [1]*Texas A&M University, College Station,* [2]*Texas A&M AgriLife Research, Beeville.*

Neuroendocrine events that lead to the onset of puberty and first ovulation in females are characterized by the initiation of frequent episodic secretion of GnRH and its downstream regulation of pulsatile release of LH. Studies using animal models of accelerated body weight (BW) gain during the prepubertal period support the hypothesis that advanced onset of puberty occurs in response to an earlier escape from estradiol negative feedback and alterations in afferent inputs to GnRH neurons. Recent studies in our laboratories have indicated that elevated BW gain in early-weaned heifers fed high-concentrate diets alters the pattern of hypothalamic expression of genes involved in the control of key biological functions important for pubertal development, including response to hormones, metabolic factors and nutrients, synaptic transmission and feeding behavior. Changes in afferent neuronal projections to GnRH neurons are also evident and comprise major metabolic-sensing pathways such as neuropeptide Y and proopiomelanocortin neurons. Kisspeptin neurons, which have been implicated in mediating the estradiol feedback control of GnRH secretion and pubertal development, appear to be also involved in the process of nutritional acceleration of puberty in heifers. The role of kisspeptin neurons in the nutritional programing of puberty is less clear, but may include the integration between metabolic signaling pathways and functional changes in the sensitivity to estradiol-negative feedback that are permissive for pubertal development. Overall, the mechanisms that mediate the neuroendocrine programing of accelerated puberty in heifers are likely to involve a network of metabolic- and gonadal steroid hormone-sensing effector cells and pathways in the hypothalamus. Changes in expression of key regulatory genes, and in functional structures that control neuronal and glial cell communication, are critical for pubertal activation of frequent episodic release of GnRH. Elevated BW gain during early juvenile period appears to facilitate the progression of these events. Supported by USDA-NIFA-AFRI 2009–65203–05678.

Key Words: puberty, GnRH, LH

716 Use of a stair-step compensatory gain nutritional regimen to program the onset of puberty in beef heifers. R. C. Cardoso*[1,2], B. R. C. Alves[1], T. Moczygemba[1], L. D. Prezotto[1,2], J. F. Thorson[1,2], L. O. Tedeschi[1], D. H. Keisler[3], M. Amstalden[1], and G. L. Williams[1,2], [1]*Texas A&M University, College Station,* [2]*Texas A&M Agrilife Research, Beeville,* [3]*University of Missouri, Columbia.*

Increasing dietary energy intake of heifers during the juvenile period leads to early maturation of the reproductive neuroendocrine system. Developing strategies that can exploit this process, achieve puberty at 12 mo of age consistently, and avoid precocious puberty are needed. Herein, we tested the hypothesis that a stair-step nutritional regimen could achieve this goal. Forty crossbred heifers were weaned at 3.5 mo of age and assigned to: High-Control (HC); feed intake was controlled to promote BW gain of 1 kg/d from 4 to 14 mo of age; Stair-Step Compensatory (SS-1); period 1: ad libitum feed intake until 6.5 mo of age; period 2: restricted dry matter access to promote BW gain of 0.35 kg/d until 9 mo of age; period 3: ad libitum feed intake until 11.5 mo of age; period 4: restricted intake to promote BW gain of 0.35 kg/d until 14 mo of age; SS-2; reverse sequence of SS-1; Low-Control (LC); controlled feed intake to promote BW gain of 0.5 kg/d until 14 mo of age. Starting at 8.5 mo of age, blood samples were collected twice weekly to assess pubertal onset (at least 2 consecutive samples with concentrations of progesterone ≥1 ng/mL). Puberty data were plotted on Kaplan-Meier survival curves using the log-rank test with Prism5 (GraphPad, La Jolla, CA). Body weight gain followed a pattern similar to that proposed in our design. The percentage of heifers pubertal in the LC group was lower ($P < 0.06$) than all other groups. Although heifers in SS-1 were nutritionally restricted between 6.5 to 9 mo of age, the proportion pubertal by 12 mo of age did not differ from that of the HC group, with 80% and 70% pubertal in SS-1 and HC, respectively. In contrast, the proportion of heifers pubertal by 12 mo of age in SS-2 (40%) was lower ($P < 0.05$) than both HC and SS-1. However, by 14 mo of age, 90% of heifers in the SS-2 had also attained puberty compared with only 40% of the LC group. Results indicate that functional changes occurring in the brain during the early juvenile period can program puberty that occurs months later, allowing optimal timing of pubertal onset in beef heifers. Supported by USDA-NIFA-AFRI 2009–65203–05678.

Key Words: beef heifer, puberty, nutrition

Ruminant Nutrition: Beef: By-Products and Dietary Modifications

717 Effect of dietary fat concentration from corn coproducts, during the growing phase, on beef cattle performance, carcass traits, digestibility, and ruminal metabolism. J. R. Segers*, T. L. Felix, and D. W. Shike, *University of Illinois at Urbana-Champaign, Urbana.*

The objective of this research was to study the effect of fat concentration from corn coproducts, fed during the growing phase on DMI, gain, carcass traits, digestibility, and rumen metabolism of steers. Exp. 1: 40 steers (age = 140d; BW = 185 ± 11 kg) were randomly allotted to 1 of 5 dietary treatments: (1) corn-based control (CNT), (2) 0% corn distillers solubles (CDS), (3) 10% CDS, (4) 19% CDS, or (5) 27% CDS. Diets 2–5 included coproducts (corn gluten feed and soybean hulls) and were formulated to achieve fat concentrations of 3, 5, 7, and 9%, respectively. Diets were fed once daily for 106 d (growing phase, GP). All steers were fed a corn-based diet from d107 to 196 (finishing phase, FP). Contrasts were used to examine a) the difference between CNT and 10% CDS; b) linear and quadratic effects of CDS inclusion. During the GP, steers fed CNT had increased ($P \leq 0.03$) BW, G:F and ADG compared with those fed 10% CDS. Increasing CDS inclusion increased (linear; $P = 0.01$) ADG and G:F. At the conclusion of the GP, back fat thickness (BF) determined via ultrasound increased ($P = 0.05$) in CNT-fed calves compared with 10% CDS. There were no treatment differences ($P \geq 0.14$) in FP ADG, DMI, or G:F. Steers fed CNT had increased($P = 0.02$) overall ADG compared with steers fed 10% CDS, and increasing CDS inclusion increased (linear; $P = 0.05$) overall ADG. Final BW, and overall DMI and G:F were not different ($P \geq 0.06$). There were no effects ($P \geq 0.10$) of treatment on carcass traits. Exp. 2: steers (n = 5; BW = 345 ± 22 kg) were fed Exp.1 diets for ad libitum intakes in a 5x5 Latin square design. Apparent dry matter digestibility (DMD) increased (linear; $P = 0.02$) with increasing dietary CDS inclusion. Steers fed CNT had increased ($P = 0.01$) DMD compared with those fed 10% CDS. Fat digestibility increased (linear; $P < 0.01$) as CDS inclusion increased, but NDF digestibility was unaffected ($P \geq 0.17$). In conclusion, feeding a coproduct diet with 10% CDS during the GP decreased overall ADG compared with feeding corn; however, increasing CDS inclusion improved DM and fat digestibility as well as overall ADG.

Key Words: condensed distillers solubles, dietary fat, digestibility

718 Effects of partially replacing supplemental N with condensed distillers solubles on feedlot cattle performance and carcass characteristics. J. Simroth-Rodriguez*[1], M. S. Brown[1], J. Kawas[2], R. Butler[1], B. Coufal[1], H. Hughes[1], K. Kraich[1], B. Mendonca[1], and J. Wallace[1], [1]*West Texas A&M University, Canyon,* [2]*Universidad Autónoma de Nuevo León, Monterrey, Nuevo Leon, Mexico.*

Further assessment of the feeding value of condensed distillers solubles (CDS) is needed. Crossbred steers (initial BW = 376 ± 11 kg) previously adapted to a finishing diet were blocked by BW and randomly assigned to treatments in a 2 × 2 + 1. Diets contained equal fat. The control diet was based on steam-flaked corn, with urea and cottonseed meal (CSM) providing supplemental N. In remaining diets, N from CDS replaced urea N or CSM N, with CDS included at either 10 or 20% of DM (11 pens/treatment). Composite samples for each diet were assayed and contained 13.45, 13.65, 13.90, 14,55, and 14.60% CP for the control, 10% CDS replacing urea N, 10% CDS replacing CSM N, 20% CDS replacing urea N, and 20% CDS replacing CSM N, respectively. The effects of CDS concentration and source of N replaced did not interact for growth performance or carcass measures ($P > 0.12$). Steer DMI was 3.8% lower ($P = 0.07$) for the control than when CDS N replaced a portion of urea N. Steer DMI was 3.4% higher and ADG was 3.7% greater ($P < 0.06$) when CDS N replaced urea N than when CSM N was replaced. Steer DMI and ADG were not altered by CDS concentration. Steer ADG and gain efficiency were not different between the control and when CDS N replaced a portion of urea N nor when CDS N replaced urea or CSM N. However, gain efficiency was decreased 3.0% ($P = 0.02$) when 20% CDS was fed compared with 10% CDS. Carcass measures were not different between the control and when CDS N replaced a portion of urea N ($P > 0.49$). Hot carcass weight was lighter and LMA was larger ($P < 0.08$) when CDS N replaced CSM N. Fat thickness, average yield grade, and calculated empty body fat were also lower ($P < 0.03$) when CDS N replaced CSM N, whereas 20% CDS increased marbling score compared with 10% CDS ($P = 0.03$). Results suggest that CDS N is a more effective replacement of urea N than cottonseed meal N. Replacing CSM N reduced ADG and carcass weight, and produced leaner carcasses, whereas carcass quality was slightly improved when more CDS was fed.

Key Words: condensed solubles, growth, nitrogen degradability

719 Performance and metabolism of Holstein dairy calves receiving concentrate starter containing citrus pulp as a replacement for corn. C. E. Oltramari[1,2], J. T. Silva*[1,2], M. R. Paula[1,2], G. G. O. Napoles[1,3], M. C. Soares[1,3], M. P. C. Gallo[1,3], and C. M. M. Bittar[1,2], [1]*ESALQ/USP, Piracicaba, Sao Paulo, Brazil,* [2]*CNPq, Brasilia, DF, Brazil,* [3]*Fapesp, Sao Paulo, Sao Paulo, Brazil.*

The aim of this study was to evaluate the effect of replacing ground corn grain (C) with dried citrus pulp (CP) in the concentrate starter on performance and metabolism of dairy calves. Twenty-four newborns Holstein calves were housed in individual shelters and distributed into three treatments, according to the birth date and weight: (1) starter containing 64% C (0CP), (2) starter containing 32% C and 32% CP (50CP), and (3) starter containing 64% CP (100CP). Animals were fed 4 L/d of milk replacer (20:15), in two meals. Starter intake was monitored daily and body weight weekly. Blood samples were collected weekly to determine plasma glucose and β-hydroxybutyrate (BHBA). Ruminal fluid samples were collected at the 4th, 6th and 8th weeks of age for short-chain fatty acids determination. At eight week of age, animals were slaughtered to evaluate development of the upper digestive tract and rumen papillae. Performance was not affected by the replacement of corn by citrus pulp (Table 1). However, there were some positive effects of CP inclusion (50CP or 100CP) in concentrate starter to the development of the upper digestive tract. Supported by Fapesp.

Table 1. Least squares means of variables of dairy calves receiving 0% (0CP), 50% (50CP) or 100% (100PC) of CP replacing corn in the starter

	0CP	50CP	100CP	SEM	P <
Starter intake, g/d	353.7	467.1	384.0	114.5	0.72
Daily gain, g/d	322.4	370.2	411.3	81.4	0.77
Live weight at weaning, kg	53.3	57.0	56.4	1.36	0.51
Plasma glucose, mg/dL	85.9	95.1	92.5	5.98	0.35
Plasma βHBA, mmol/L	0.07	0.15	0.11	0.05	0.53
Rumen acetate, µmol/mL	53.2	60.2	57.9	2.38	0.18
Rumen propionate, µmol/mL	28.5	26.5	20.8	3.24	0.25
Rumen butyrate, µmol/mL	6.3[b]	10.9[a]	9.2[ab]	0.74	0.01
Total upper digestive tract, kg	1.07[b]	1.54[a]	1.41[a]	0.29	0.01
Rumen-reticulum, % total tract	55.4[b]	68.7[a]	70.3[a]	4.5	0.06
Omasum, % total tract	14.6	13.4	13.4	2.2	0.28
Abomasum, % total tract	30.0[a]	17.9[b]	16.3[b]	4.1	0.006
Papillae/cm^2	82.4	71.2	85.1	24.3	0.36
Papillae height, mm	1.28[b]	3.30[a]	1.97[b]	0.39	0.01
Papillae width, mm	0.97	1.29	1.10	0.32	0.33
Papillae area, mm^2	1.55[b]	3.93[a]	2.03[ab]	1.02	0.03

[a–c]Means with different superscripts differ ($P < 0.5$).

Key Words: butyrate, forestomach, pectin

720 Evaluation of nutrient composition and variability of wheat grain entering feedlots in western Canada using commercially available near-infrared reflectance spectroscopy. A. R. Harding*[1], C. F. O'Neill[1], M. L. May[2], L. O. Burciaga-Robles[2], and C. R. Krehbiel[1], [1]*Oklahoma State University, Stillwater,* [2]*Feedlot Health Management Services, Okotoks, AB, Canada.*

Near infrared reflectance spectroscopy (NIRS) has been used to accurately predict the nutrient composition of feedstuffs. Considerable variation is observed in nutrient profiles of wheat grain used as an energy source in beef cattle diets. The objective of this study was to investigate the accuracy of current commercially available NIRS prediction models for wheat and the variation in nutrient composition of wheat entering feedlots in western Canada. Wheat samples (n = 75) were selected from feedlots in western Canada from September, 2011 to April, 2012, representing a range in nutrient compositions as predicted by NIRS (InfraXact, FOSS North America, Eden Prairie, MN). Samples were selected for HIGH, MEDIUM, or LOW nutrient composition of CP, starch and DM. DM was determined by placing samples in a forced air oven at 55°C for 48 h and measuring moisture loss. CP and starch were determined using AOAC methods 992.23 and 996.11, respectively. Laboratory analysis of the samples was completed and lab values were correlated to the NIRS predictions for CP, starch and DM using PROC REG of SAS 9.3 (SAS Institute, Cary, N.C.). NIRS predictions and laboratory values for CP were correlated for all samples ($R^2 = 0.90$, $P < 0.05$) whereas there were poor correlations for lab values and NIRS predictions for starch and DM of all samples ($R^2 = 0.02$ and 0.17 respectively, $P < 0.05$). Regression analysis was conducted to evaluate NIRS predictions across the ranges (HIGH, MED or LOW) of each constituent, CP, starch and DM. Improved R^2 values for each parameter were observed [CP = 0.92 (n = 15, $P < 0.01$), starch = 0.27 (n = 15, $P \leq 0.05$), DM = 0.20, (n = 15, $P = 0.09$)] when samples only selected for that constituent from all ranges (HIGH, MED, LOW) were analyzed. NIRS technology is able to accurately predict CP of wheat samples in western Canada for a broad range of CP content. Current commercially available NIRS prediction models for wheat DM and starch require improvement.

Key Words: wheat, near infrared reflectance spectroscopy, nutrient

721 Effect of nutrient composition variability of barley grains on near infrared reflectance spectroscopy predictions using commercially available technology. C. F. O'Neill*[1], A. R. Harding[1], M. L. May[2], L. O. Burciaga-Robles[2], and C. R. Krehbiel[1], [1]*Department of Animal Science, Oklahoma State University, Stillwater,* [2]*Feedlot Health Management Services Ltd., Okotoks, AB, Canada.*

Near infrared reflectance spectroscopy (NIRS) has been used to accurately predict nutrient composition of feed commodities. Feeding feedlot cattle is challenged by large variation in nutrient composition of commodities entering operations. The objective of this study was to examine the variation in nutrient composition and calibration prediction accuracy of NIRS technology. Barley samples (n = 98) were selected from 5 feedlots in western Canada between April and August, 2012, representing a range in nutrient compositions as predicted by NIRS using commercially available NIRS prediction equations (InfraXact, FOSS North America, Eden Prairie, MN). Samples were selected for HIGH, MEDIUM, or LOW nutrient composition of starch, crude protein (CP) and dry matter (DM). Laboratory analysis was completed and correlated to the predicted NIRS values for starch, CP, and DM. Data were analyzed with PROC REG of SAS (SAS Institute, Cary, N.C.) to determine correlations between laboratory assayed and NIRS values. When comparing laboratory and NIRS predictions of DM and CP for all samples, there was a strong correlation ($R^2 = 0.61$ and 0.64, respectively, $P < 0.05$). Whereas for starch predictions, there was a poor correlation ($R^2 = 0.12$, $P < 0.05$) when comparing NIRS and starch analysis. Regression analysis was conducted to evaluate NIRS predictions across the range (HIGH, MED or LOW) of each constituent (starch, CP, and DM). Similar or improved R^2 values for all parameters were observed, [DM = 0.86 (n = 21), CP = 0.63 (n = 24), and starch = 0.17 (n = 23) ($P < 0.05$)] when predictions were tested across the range. The NIRS technology can adequately predict across a variable range of barley samples in western Canada for DM and CP. However, prediction accuracy decreases when variation exists in the population sampled. Accurate predictions can be obtained for DM and CP concentration of barley arriving to feedlots in western Canada using commercially available NIRS prediction equations; however, starch concentration is not accurately predicted with this current application.

Key Words: barley, near infrared reflectance spectroscopy, nutrients

722 Co-prilling flaxseed and dolomitic hydrate to decrease ruminal biohydrogenation of polyunsaturated fatty acids. C. Alvarado*[1], D. Sousa[1], K. Miller[1], C. van Bibber-Krueger[1], E. van Cleef[1], F. Scarpino[1], D. Klamfoth[2], and J. Drouillard[1], [1]*Kansas State University, Manhattan,* [2]*Lhoist North America, Fort Worth, TX.*

Two experiments were conducted to evaluate ruminal biohydrogenation of flaxseed embedded in matrices consisting of dolomitic lime hydrate or a blend of hydrate and dolomitic limestone. In Study 1, steers (n = 45, 252.5 ± 18.2 kg) were blocked by weight and randomly assigned to individual pens and dietary treatments (15 replicates). Steers were fed for 14 d with a basal diet consisting of 30% corn gluten feed, 25% wheat straw, 25% prairie hay, 12.8% steam-flaked corn, and 3% linseed meal with no flaxseed (C), with 2.79% ground flaxseed (F), or 8.13% of a flaxseed-dolomitic hydrate blend (H) to provide an amount of α-linolenic acid (ALA) equivalent to the F diet. Cattle were fed once daily ad libitum and DMI was determined each day. For study 2, heifers (n = 40, 274 ± 11 kg) were blocked by weight and allocated randomly to each of 4 diets (10 replicates). The basal diet consisted of 30% corn silage, 27% wet corn gluten feed, 22% steam-flaked corn, and 15% alfalfa hay with no flaxseed (C), 0.45 kg/d ground flaxseed (F), 0.45 kg/d of a 50:50 flaxseed:dolomitic hydrate blend; or 0.45 kg/d of a 50:25:25

flaxseed:dolomitic hydrate:dolomitic carbonate blend (HC). On d 0 and 14 of each study, whole blood was sample by jugular venipuncture, plasma was recovered by centrifugation, and concentrations of fatty acid methyl esters were determined by gas chromatography. Plasma ALA concentrations were not different among treatments on d 0 of either study, remained low in C after 14 d of feeding, but increased by d 14 for cattle fed all sources of flaxseed ($P < 0.01$). In study 1, plasma ALA was 2.9-fold greater for H than for F ($P < 0.01$) after 14 d (0, 30, and 87 μg/mL for C, F, and H, respectively). In study 2, embedding flaxseed in dolomitic hydrate-carbonate or dolomitic hydrate matrices resulted in 195 and 339% greater assimilation of ALA, respectively, compared with ground flaxseed (11, 93, 96, and 153 μg/mL for C, F, H, and HC, respectively; $P < 0.01$). These studies indicate that matrices consisting of dolomitic hydrate or dolomitic hydrate and carbonate are effective barriers to ruminal biohydrogenation of unsaturated fats.

Key Words: encapsulation, matrix, n-3 fatty acid

Nonruminant Nutrition: Nutritional Values II

723 Diurnal variation of amino acid digestibility in pigs. B. G. Kim*[1] and H. H. Stein[2], [1]*Konkuk University, Seoul, Republic of Korea,* [2]*University of Illinois, Urbana.*

The index method is widely used to avoid the quantitative collection of ileal digesta or feces in digestibility experiments. Diurnal variations of indigestible index and CP concentrations in ileal digesta samples have been reported. However, diurnal variations of ileal AA concentrations and ileal AA digestibility are unknown. Therefore, we determined the concentration of AA in ileal digesta and ileal digestibility of AA in various collection-time periods. Eight barrows with an initial BW of 34.6 kg (SD = 2.1) fitted with a T-cannula in the distal ileum were randomly allotted to a duplicated 4 × 4 Latin square design with 4 diets and 4 periods per square. Three diets contained corn, soybean meal, or distillers dried grains with solubles as the only source of AA in each diet. An N-free diet was also prepared. All diets contained 0.5% chromic oxide. Equal meals were provided at 0800 and 2000. Ileal samples were collected with 2-h intervals from 0800 to 2000 during the last 3 d of each 7-d period. The concentrations of Lys, Met, Thr, Ile, His, Leu, and Phe in ileal samples were affected ($P < 0.05$) by collection time in pigs fed non-N-free diets during the 12-h collection. The apparent ileal digestibility of all indispensable AA (IAA) exhibited a quadratic response ($P < 0.01$) that increased and then decreased by collection time in pigs fed non-N-free diets. The endogenous losses of all IAA except Trp and Arg decreased (linear and quadratic, $P < 0.05$) by collection time. The standardized ileal digestibility of all IAA except Arg was also affected (linear and quadratic, $P < 0.05$) by collection time. Standardized ileal digestibility of all IAA calculated from samples collected for 2 h from 6 h after feeding was comparable (less than 0.6 percentage unit deviation, $P > 0.64$) to the 12-h digestibility value calculated using chromium and AA concentrations of the 12-h collection: Concentration, % = Σ (concentration, % × sample, g) ÷ Σ sample, g. Overall, diurnal variations of AA concentration in ileal digesta and ileal AA digestibility exist, and we suggest that 2 h of ileal sample collection from 6 h after feeding may provide a fairly representative AA digestibility.

Key Words: collection period, ileal digestibility, index method

724 Effects of adjusting the standardized ileal digestible (SID) amino acids in heat damaged soybean meal (SBM) or distillers dried grains with solubles (DDGS) in diets on performance of weaned pigs. F. N. Almeida*[1], J. K. Htoo[2], J. Thomson[3], and H. H. Stein[1], [1]*University of Illinois, Urbana,* [2]*Evonik Industries, Hanau, Germany,* [3]*Evonik Degussa Corporation, Kennesaw, GA.*

Two experiments were conducted to determine if adjustments of the SID of AA in heat damaged (HD) SBM or HD DDGS in diet formulation ameliorates performance reduction by heat damage in weaned pigs. In Exp. 1, 4 corn-SBM diets were formulated. The positive control (PC) diet, containing conventional SBM (35.1%), was formulated on the basis of analyzed AA and published SID values. Diet 2, negative control (NC), was like the PC but conventional SBM was replaced (1:1) with HD SBM (autoclaved at 125°C; 60 min). Diet 3 contained HD SBM but was based on analyzed AA and published SID values. Diet 4 also contained HD SBM, but was formulated on analyzed AA and by adjusting the SID of AA for HD SBM based on values derived from a previous study. Pigs (160; 10.4 kg BW) were allotted to 4 diets with 8 replicate pens per diet. On wk 1, ADG of pigs fed diet 4 (0.33 kg) was better ($P < 0.05$) than diets 2 (0.23 kg) and 3 (0.30 kg), but not different from PC (0.35 kg). On wk 1–3, ADG and G:F was greater ($P < 0.05$) for pigs fed the PC diet than pigs fed the other diets, and pigs fed diet 4 had greater ($P < 0.05$) ADG and G:F than pigs fed the NC diet (0.44 vs. 0.35 kg and 0.48 vs. 0.44, respectively). In Exp. 2, 144 pigs (9.9 kg BW) were allotted to 4 diets with 8 replicate pens per diet. Diets (corn-SBM-DDGS based) were formulated using the concepts described for Exp. 1, except that HD DDGS (autoclaved at 130°C for 60 min; 22% inclusion) but not HD SBM was used in diets. On wk 1, G:F of pigs fed diet 4 (0.36) was better ($P < 0.05$) than diets 2 (0.28) and 3 (0.32), but not different from PC (0.38). On wk 1–3, ADG was not affected but G:F was greater ($P < 0.05$) for pigs fed the PC diet than pigs fed the other diets mainly attributed to a greater ADFI in pigs fed diets containing HD DDGS. In conclusion, negative effects of heat damage in SBM or DDGS on performance of weaned pigs can be ameliorated at least during wk 1 if the reduction in concentration and the digestibility of AA are adjusted for the impact of heat damage.

Key Words: distillers dried grains with solubles, soybean meal, weaned pig

725 Prediction of voluntary feed intake in finishing pigs using physicochemical properties of bulky feeds. S. P. Ndou*, A. G. Bakare, and M. Chimonyo, *Animal and Poultry Science, University of KwaZulu-Natal, Pietermaritzburg, South Africa.*

The objective of the present study was to determine the physicochemical properties that predict voluntary feed intake (VFI) of bulky diets in finishing pigs. A total of 84 pigs weighing 65 ± 1.37 kg body weight (BW) were given, ad libitum, each of the 21 diets containing a basal feed diluted with 80, 160, 240, 320 and 400 g/kg of alfalfa hay, corn cob, sawdust or sunflower husks. The basal feed contained 12.3 MJ digestible energy and 160 g of CP/kg DM. Physicochemical properties of the feeds measured were dry matter (DM), crude protein (CP; g/kg DM), ether extract (g/kg DM), ash (g/kg DM), water holding capacity (WHC; g water/g DM), bulk density (g DM/ml), crude fiber (CF; g/kg DM), neutral detergent fiber (NDF; g/kg DM) and acid detergent fiber (ADF; g/kg DM). Each of the 21 diets was given to 4 pigs, in individual pens, for 31 d, inclusive of a 10 d adaptation period. The feed intake and live BW were determined for each pig, every week.Mixed model procedures for repeated measures was used to analyze the data set (SAS, Version 9.1). Stepwise regression was used to identify significant physicochemical properties that affect SFI and relationships between measured parameters were determined by the response surface option of regression (SAS, Version 9.1). Neutral detergent fiber ($R^2 = 0.86$; $P < 0.05$), CF ($R^2 = 0.76$; $P < 0.05$), CP ($R^2 = 0.75$; $P < 0.001$) and WHC affected ($R^2 = 0.74$; $P < 0.01$) SFI. There was a quadratic relationship between SFI and NDF given by the function SFI = 82.0 (SEM 5.30) − 0.18 (SEM 0.03) NDF + 0.0002 (SEM 0.00004) NDF^2 ($P < 0.01$). The SFI was related to CF and CP by quadratic functions; SFI = 63.4 (SEM 2.22) − 0.16 (SEM 0.03) CF + 0.0003 (SEM 0.00007) CF^2 ($P < 0.001$) and SFI = 61.8 (SEM 9.68) − 0.39 (SEM 0.16) CP + 0.002 (SEM 0.0006) CP^2 ($P < 0.01$), respectively. The SFI was related to WHC by linear function; SFI = 77.3 (SEM 4.37) − 7.43 (SEM 1.77) WHC ($P < 0.001$). In conclusion, although threshold values were not identified, WHC, NDF and CF content provide relationships with SFI that can be used to predict voluntary feed intake in finishing pigs.

Key Words: dietary fiber, water-holding capacity, feed intake

726 Effects of reducing the particle size of corn on energy, phosphorus, and amino acid by growing pigs. O. J. Rojas* and H. H. Stein, *University of Illinois at Urbana-Champaign, Urbana.*

Two experiments were conducted to determine the concentration of DE and ME, the standardized total tract digestibility (STTD) of P, and the standardized ileal digestibility (SID) of CP and AA in corn ground to 4 different particle sizes (i.e., 339, 485, 677, and 865 µm). In Exp. 1, 40 growing barrows (initial BW 22.8 ± 2.1 kg) were placed in metabolism cages and allotted to a randomized complete block design with 4 diets and 10 replicate pigs per diet. One lot of corn was divided into 4 batches that were ground to the specified particle sizes and each batch was used in one diet that contained 97.7% corn (as-fed basis). Vitamins and minerals were included in the diets to meet the requirements for growing pigs with the exception that no inorganic P was used and all the P in the diets originated from corn. . The concentration of ME was 3,964, 3,895, 3,868, and 3,826 kcal/kg DM for corn ground to a mean particle size of 339, 485, 677, and 865 µm, respectively. The ME concentration decreased (linear and quadratic, $P < 0.01$) as the particle increased. The STTD of P was 37.8, 37.1, 37.3, and 37.4% for corn ground to a mean particle size of 339, 485, 677, and 865 µm, respectively, and these values were not different. In Exp. 2, 10 growing barrows (initial BW: 29.2 ± 1.35 kg) were surgically equipped with a T-cannula in the distal ileum and randomly allotted to a replicated 5 × 5 Latin square design with 5 diets and 5 periods in each square. Four of the diets contained each batch of corn ground to a different particle size (96.6%, as-fed basis) as the only source of AA. A N-free diet was used to determine endogenous losses of CP and AA. With the exception of Trp, there was no effect of corn particle size on the SID of CP or any indispensable AA. In conclusion, reduction of the particle size of corn from 865 to 339 µm linearly increased the concentration of ME in the corn, but the particle size of corn does not affect the STTD of P or the SID of indispensable AA and CP.

Key Words: corn, particle size, pig

727 Net energy value of field pea, Napus and Juncea canola meals, and wheat millrun fed to growing-finishing pigs. T. A. Woyengo*[1], S. Moehn[1], E. Beltranena[1,2], and R. T. Zijlstra[1], [1]*University of Alberta, Edmonton, AB, Canada,* [2]*Alberta Agriculture and Rural Development, Edmonton, AB, Canada.*

A study was conducted to determine NE value of field pea (FP), Napus canola meal (NCM) and Juncea canola meal (JCM), and wheat millrun (WM), which are available as alternative feedstuffs for pigs in Canada. Six ileal-cannulated barrows (38 kg) were fed 6 diets in 5 × 5 Latin square design with 1 added column to give 6 replicates per diet. Diets contained either SBM, FP, NCM, JCM, or WM and between 4.23 and 58% of a N-free mix (constant ratio mix of cornstarch, sugar, canola oil, and cellulose). Soybean meal (SBM) was included as a reference. Diets were formulated to contain at least 0.86% standardized ileal digestible Lys, and Met, Thr, and Trp based on ideal AA ratio. Energy digestibility, DE, ME, and NE values of the feedstuffs were calculated by difference from N-free mix using values of the N-free mix from our previous study. On DM basis, SBM, FP, NCM, JCM, and WM contained 51, 28, 41, 42 and 18% CP; and 8.5, 20, 29, 21, and 38% NDF, respectively. Apparent total tract GE digestibility values of SBM, FP, NCM, JCM, and WM were 84, 86, 69, 72, and 74%, respectively, and were different ($P < 0.05$) from each other. The DE, ME and NE values for SBM were 3.86, 3.62 and 2.56 Mcal/kg DM, respectively. The DE value of FP, and DE and ME values of NCM, JCM, and WM were lower ($P < 0.05$) than that of SBM. The SBM and FP did not differ in ME. The NE values of FP, JCM, and WM were 2.32, 2.21, and 2.57 Mcal/kg DM, respectively, and were not different from that of SBM. The NE value of NCM was, however, lower ($P < 0.05$) than that of SBM by 23%. The standard error of mean for DE, ME and NE data was 0.03, 0.12, and 0.24, respectively. In conclusion, the NE value of NCM was lower than that of SBM likely due to the lower energy digestibility, and the higher fiber content of the NCM than SBM. However, it is difficult to firmly conclude that NE values of FP, JCM, and WM were not different from that of SBM due to the higher variability of NE data than of DE or ME data.

Key Words: feedstuff, net energy, pig

728 A comparison of three animal welfare assessment programs on Canadian swine farms. A. N. Roberts*[1], P. Lawlis[2], R. Bergeron[3], and T. M. Widowski[1], *[1]University of Guelph, Guelph, Ontario, Canada, [2]Ontario Ministry of Agriculture and Food, Woodstock, Ontario, Canada, [3]University of Guelph Alfred, Alfred, Ontario, Canada.*

Standard measures used in animal welfare assessments include animal-based measures (ABM) obtained by observing animals (e.g., body condition score and health measures), resource-based measures (RBM) obtained by observing facilities (e.g., non-slip flooring in walkways), and management-based measures (MBM) obtained by interviewing farmers and checking records (e.g., written euthanasia plan). It is widely accepted that it is easy to train assessors to use RBMs and MBMs with good reliability, whereas ABMs are considered to be more direct measures of animal welfare but more difficult to achieve good agreement among assessors. However, few measures have been systematically tested. Our objectives were to investigate inter-observer reliability (IOR) of different measures used in 3 current pig welfare assessment programs [PQA Plus, USA; Canadian Animal Care Assessment (ACA); and European Welfare Quality (WQ)] and to determine the concordance of scores across the 3 assessments. Data were collected on 5 grow-finish farms using a group of 10 trained assessors who conducted assessments on the same farms simultaneously. Individual dichotomous MBMs used in the assessments were analyzed quantitatively for inter-observer reliability using the kappa statistic. The kappa values for the ACA and PQA were 0.882 and 0.808 ($P = 0.05$) respectively, showing a very high level of agreement for data from 4 assessors present on all 5 farms. Overall results (ACA and PQA = Pass/Fail, WQ = Excellent, Enhanced, Acceptable or Not Classified) on 20 individual farrow-to-finish farms done by 2 observers were compared qualitatively to determine concordance among the 3 assessment programs in scoring individual farms. For 4 sample farms WQ scores (using primarily ABMs) categorized the welfare of the pigs on those farms as "Enhanced" whereas ACA and PQA (using primarily record-keeping MBMs) resulted in Failing scores for those same farms. These results indicate that MBMs are, in fact, highly reliable, but may not be concordant with ABMs. Results of this study can be used to identify the best measures and revise training programs for on-farm animal welfare assessments.

Key Words: animal welfare assessment, swine

729 A role for serotonin in piglet preweaning mortality. R. L. Dennis*, K. A. McMunn, D. C. Lay Jr., and H. W. Cheng, *Livestock Behavior Research Unit, USDA-ARS, W. Lafayette, IN.*

Improving piglet survivability rates is of high priority for swine production as well as for piglet well-being. Dysfunction in the serotonin system has been associated with growth deficiencies, infant mortalities or failure to thrive (FTT) in human infants. The aim of this study was to examine the role of serotonin in infant mortality and FTT in piglets. Umbilical blood was collected at birth from a total of 60 piglets from 16 litters for analysis of serotonin (5-HT) and tryptophan (the amino acid precursor to 5-HT) concentrations. Piglets were then followed for 48 h to determine early survival. Brain samples were also taken at 8 h after birth from healthy and FTT piglets (n = 4). The raphe nucleus, the center for brain 5-HT biosynthesis, was dissected out and analyzed for 5-HT and 5-HIAA (a major metabolite of 5-HT) concentrations. Data were analyzed by ANOVA using SAS 9.2 software. Piglets that died within 48 h of birth (n = 14) had significantly lower umbilical blood 5-HT concentrations at the time of their birth compared with their healthy counterparts (n = 46; $P = 0.003$). However, no difference in tryptophan was detected ($P = 0.38$). In the raphe nucleus FTT piglets had a higher concentration of 5-HIAA ($P = 0.02$), and seemingly higher concentrations of 5-HT ($P = 0.07$), compared with healthy piglets. Our results show evidence of serotonergic dysfunction, at both the central and peripheral levels, accompanying early piglet mortalities. These data suggest a possible route for intervention, via the serotonin system, to improve piglet survivability. However, further research is required to validate this hypothesis.

Key Words: serotonin, preweaning mortality, swine

730 Effects of alternative farrowing systems on sow productivity and piglet growth, behavior, and mortality. L. A. Mack*[1], S. P. Rossini[1], S. J. Leventhal[2], and T. D. Parsons[1], *[1]University of Pennsylvania, School of Veterinary Medicine, Kennett Square, [2]University of Delaware, Newark.*

Throughout gestation and lactation, commercial sows are usually housed in crates that limit locomotion and natural behavior. Welfare concerns are motivating housing changes during gestation. In lactation, farrowing crates present similar welfare challenges as gestation crates for the sow; however lactational housing also affects piglet welfare. A better understanding of various farrowing systems could benefit both the sow and piglets. Sows and litters were housed in either: (1) a standard farrowing crate, 1.0 m^2/sow (n = 19); 2) a hinged crate that when opened 2 wk after parturition provided turn-around space for the sow, 1.6 m^2/sow (n = 19); or 3) a thinly bedded pen, 6.0 m^2/sow (n = 20). Performance data was collected through lactation. At 27.26 ± 0.59 d of age, 2 female piglets per litter from the standard crate and pen treatments were separately observed in a 3.24 m^2 open field arena containing a novel food, a strawberry-filled cookie. The following day, the same pigs were placed in the arena along with an unfamiliar sex-, age-, and treatment-matched pig for a 5 min social behavior test. Data were analyzed using PROC GLIMMIX (SAS 9.3) with treatment, sow parity, and their interactions as main effects. Neither gestation length nor litter size differed. At 12.8%, 9.1%, and 1.3%, the percentages of stillborn pigs and mummies did not statistically differ between standard crates, hinged crates, or pens, respectively. Litter birth weights were greater in standard crates than pens ($P = 0.05$). However, neither growth rates nor litter weaning weights differed. At 29.4%, penned litters had greater preweaning mortality than standard (10.3%, $P < 0.001$) or hinged (15.2%, $P = 0.005$) crated litters. Crated piglets ate/rooted at the cookie less ($P = 0.04$) and defecated more ($P = 0.04$) than penned piglets in the isolation test. In the social test, crated piglets attempted more escapes ($P = 0.04$) and were in physical contact with the other pig longer ($P = 0.02$) than penned piglets. Housing litters in pens increased piglet mortality, but decreased fearful behavior suggesting that with improvement pen housing may offer better sow and piglet welfare.

Key Words: swine, housing, welfare

731 Establishing boarding level requirements while transporting finishing pigs from farm to packing plant. A. Sapkota*[1], A. K. Johnson[2], and J. McGlone[1], *[1]Laboratory of Animal Behavior, Physiology and Welfare, Texas Tech University, Lubbock, [2]Department of Animal Science, Iowa State University, Ames.*

The Trucker Quality Assurance Handbook published by the National Pork Board suggests use of different boarding levels depending on outside air temperature. The objective of this study was to evaluate boarding levels over different outside air temperatures. Average air temperature was 8.8 ± 0.30°C (range: −0.6 to 23.3°C; n = 301). Outside RH was 71.7 ± 1.12% (range: 19 to 100%; n = 301). Outside temperature was divided into 3 bins: <5°C, 5 to 10°C, and >10°C and boarding levels were also divided into 3 bins low % (0–30%), medium (31–60%) and high (>61%). Measures included average wait time at plant, skin surface temperature on 10 randomly selected pigs in each trailer at the packing plant, number of dead on arrival (DOA), non-ambulatory non-injured (NANI), non-ambulatory injured (NAI), and total losses (TL). PROC GLM was conducted in SAS 9.3 and the statistical model included effect of boarding level using trailers as experimental unit, and outside air temperature and bedding level as covariates. Average wait time at the plant before unloading was 43.7 ± 1.74 min (range: 0 to 161 min; n = 234). Average DOA, NANI, NAI, and TL were 0.3 ± 0.04, 0.12 ± 0.02, 0.04 ± 0.01, and 0.46 ± 0.05%, respectively (n = 302). The DOA, NANI, and NAI were not affected by boarding level ($P > 0.05$) when outside air temperature and bedding levels were used as covariates. The TL was higher when boarding percentage was low compared with medium and high (0.92, 0.22 and 0.23, respectively; SEp = 0.18; $P < 0.05$) when temperature was <5°C. When air temperature was lower than 5 C, the low level of boarding increased transportation losses. However, variations in boarding level (medium and high boarding) from 5 to 10°C did not affect pig losses.

Key Words: pig, boarding, welfare

732 Bedding level on trailers during warm weather and effects on transport losses of market weight pigs. R. K. Kephart*[1], A. K. Johnson[1], K. J. Stalder[1], T. W. Huiatt[1], A. Sapkota[2], and J. J. McGlone[2], *[1]Iowa State University, Ames, [2]Texas Tech University, Lubbock.*

Bedding is provided on the trailer to reduce slips and falls, provide comfort, and absorb pig waste. However, during warm weather, incorrect bedding levels may result in heat stress. To determine the relationship between bedding levels on the trailer and transport losses in market weight pigs, 76 trailers (n = 19,599 pigs) were used in a randomized design. In June and July of 2011 in the Midwestern US, 3 or 6 bags of wood shavings/trailer (0.2 m^3/bale) were randomly assigned. Ten pigs/load had surface temperature (ST; average 32.6 ± 3.1°C) measured laterally near the midline with a dual laser infrared thermometer. During loading, ambient temperature (average 26.9 ± 5.7°C) and relative humidity (average 73.3 ± 19.1%) were measured using a mini thermo-anemometer. Temperature humidity index (THI) was then calculated using the following equation (NOAA, 1976): $T–\{[0.55–(0.0055 \times RH_{dec})](T–14.5)\}$. Pigs were transported (average 2.6 ± 0.7 h) to a commercial plant. Pigs/trailer (average 173 ± 3 pigs) and average weight of pigs on that trailer (average 121.8 ± 5.7 kg) were used to calculate density of pigs on the trailer (Fitzgerald, 2009): (pigs/trailer)(average weight)/(m^2 floor space in trailer). At the plant, the number of non-ambulatory (sum of fatigued and injured) and dead (sum of dead on arrival and euthanized on arrival) were recorded. Total losses (TL) were summed from dead and non-ambulatory pigs. Data were analyzed using PROC GLIMMIX of SAS; trailer of pigs was the experimental unit. The THI, transport time, ST, and density were used as covariates. Site was used as a random effect. There was no difference between bedding levels for non-ambulatory ($P = 0.12$), dead ($P = 0.94$), or TL ($P = 0.40$). Since bedding adds substantial costs to transport and there is no evidence of deleterious effects of decreased bedding level on the pig performance, less bedding may be used when transporting market weight pigs during warm weather in the Midwestern US.

Key Words: bedding, market-weight pig, transport losses

733 Measuring the efficacy of flunixin meglumine for lame sows using nociceptive threshold tests. M. D. Pairis-Garcia*[1], S. T. Millman[4], L. A. Karriker[2], K. J. Stalder[1], J. F. Coetzee[3], and A. K. Johnson[1], *[1]Animal Science, Iowa State University, Ames, [2]Swine Medicine Education Center, Iowa State University, Ames, [3]Cyclone Custom Analyte Detection Services (CYCADS), Iowa State University, Ames, [4]Veterinary Diagnostic and Production Animal Medicine, Iowa State University, Ames.*

Lameness in breeding swine has a large negative economic impact and is a welfare concern. In the US, flunixin meglumine (FM) is labeled for the control of pyrexia associated with swine respiratory disease. Although FM is not labeled for pain in pigs, it can be used to alleviate pain under AMDUCA. Pressure algometry and thermal tests are non-invasive methods to quantify pain sensitivity using nociceptive thresholds (NT) to provoke withdrawal responses of lame and sound limbs. The objective of this work was to determine the effects of FM on NTs in lame sows. Lameness was induced in 24 mature mixed parity sows (241.4 ± 15.5 kg) on Day 0 using a chemical synovitis model during 2 trials (T1, T2). Two treatments were compared: FM (2.2 mg/kg) and sterile saline (S; comparable volume to FM administered) with 12 sows receiving FM in T1 and 12 in T2. On D1 and D2 each sow was injected IM in the neck with FM or S. Data were collected at the following time points (TP): baseline (D0; TP0), 24 h post lameness induction (D1; TP1), 48 h post lameness (D2; TP4), 72 h post lameness (D3; TP7) and resolution (D7; TP8). On D1 and D2 data were collected one h after treatment (TP2, TP5) and 8 h after treatment (TP3; TP6). For each TP, pressure algometry was measured on sound and lame limbs with 3 replicates at 3 landmarks (cannon, medial claw, and lateral claw). Thermal tests were collected with 3 replicates using a radiant stimulus positioned 3 cm above the coronary band of the lateral claw. Data were analyzed using PROC MIXED of SAS. Flunixin meglumine increased pressure algometer NT at TP4, TP6 and TP7 ($P < 0.005$) but did not differ within the first 24 h of lameness compared with S. Thermal test NT was greater for FM treated sows at TP7 (TP7; $P = 0.01$). In conclusion, administration of FM increased NT of sows after lameness induction although complete resolution of pain sensitivity did not occur.

Key Words: flunixin meglumine, lameness, swine

734 Barrow approachability to a human when selected for feed efficiency. J. Colpoys*[1], N. Gabler[1], A. Keating[1], S. Millman[2], J. Siegford[3], and A. Johnson[1], *[1]Animal Science, Iowa State University, Ames, [2]Veterinary Diagnostics and Production Animal Medicine, Iowa State University, Ames, [3]Animal Science, Michigan State University, East Lansing.*

The objective of this study was to determine if divergent selection for residual feed intake (RFI) influenced barrows' approach to a novel human. Twenty low-RFI (high FE) and 20 high-RFI (low FE) barrows (BW 49 ± 9.2 kg) from 8th generation Yorkshire RFI selection lines were randomly selected and evaluated once over a 4-wk period using a human approach test (HAT). The HAT arena measured 4.9 m long × 2.4 m wide, with black corrugated plastic walls 1.2 m high. The arena floor was divided into 4 zones; zone 1 being the human while zone 4 was furthest from the human and was the point where the pig entered the arena. Between 1300 and 1700 h pigs were moved individually from

their home pen and into a weigh scale for 1 min. Pigs then entered the HAT arena and were video recorded for 10 min. Video was then continuously scored by one observer for latency, duration, and total number of escape attempts (defined as front 2 legs off the ground, may include a jump). Latency, duration, and total number of zone visits were also collected. Data were analyzed with PROC Glimmix and the experimental unit was the barrow. Latency to show the first escape attempt and total length of time attempting escape did not differ between selection lines ($P > 0.11$). However, low-RFI attempted escape fewer times compared with high-RFI barrows ($P = 0.0007$). Latency to enter zones: low-RFI barrows tended to take longer entering zone 3 ($P = 0.06$), took longer to enter zone 2 ($P = 0.004$), but did not differ entering zone 1 when compared with high-RFI ($P = 0.26$). Duration of time within a zone: low-RFI barrows spent more time in zone 1 compared with high-RFI barrows ($P = 0.03$). For all other zones there was no difference in time spent in the zones ($P > 0.23$). Number of visits: low-RFI barrows visited zone 3 less often over the testing period compared with high-RFI barrows ($P = 0.01$). For all other zones there was no difference in number of visits ($P > 0.10$). These data suggest that differences exist in the response to a novel stressful situation between barrows of different RFI lines. Therefore, the ability of livestock to recognize and cope with stress may be related to RFI and feed efficiency.

Key Words: human approach, residual feed intake, pig

735 Measuring the efficacy of meloxicam for lame sows using nociceptive threshold tests. M. D. Pairis-Garcia*[1], S. T. Millman[4], L. A. Karriker[2], K. J. Stalder[1], J. F. Coetzee[3], and A. K. Johnson[1], *[1]Animal Science, Iowa State University, Ames, [2]Swine Medicine Education Center, Iowa State University, Ames, [3]Cyclone Custom Analyte Detection Services (CYCADS), Iowa State University, Ames, [4]Veterinary Diagnostic and Production Animal Medicine, Iowa State University, Ames.*

Lameness in breeding swine has a negative economic impact and is a welfare concern. In the EU, meloxicam is labeled for use in non-infectious locomotor disorders in swine. Pressure algometry and thermal tests are non-invasive methods to quantify pain sensitivity using nociceptive thresholds (NT) to provoke withdrawal responses of lame and sound limbs. The objective of this work was to determine the effects of meloxicam on NTs in lame sows. Lameness was induced in 24 mature mixed parity sows 241.4 ± 15.5 (mean BW kg ± SD) on d0 using a chemical synovitis model and a repeated measures design comparing responses for each sow during baseline (d −1), most lame/treatment (d 1; d 2), recovery (d 3) and resolution days (d7). Two treatments were compared: meloxicam (1.0 mg/kg) and sterile saline (IM injection). Pressure algometry was measured on sound and lame limbs with 3 replicates at 3 landmarks (cannon, medial claw, and lateral claw). Thermal tests were collected on sound and lame limbs with 3 replicates using a radiant stimulus positioned 3 cm above the coronary band of the lateral claw. Data were analyzed using PROC MIXED of SAS with sow (group × trial) as the random effect, replicate (round × time point × leg injected) as a repeated measure and treatment, leg injected, round, time point and its interaction with treatment and leg injected as a fixed effect. Following 8h after initial treatment administration to 72 h after lameness induction, sows on the meloxicam treatment had higher pressure algometry NT compared with those on saline (0.83 ± 0.03 kgf; $P < 0.01$). Sows on the meloxicam treatment had higher thermal NT compared with those on saline (2.07 ± 0.11 s; $P < 0.01$) immediately following drug administration. In conclusion, meloxicam mitigated pain sensitivity between 8 to 72 h post lameness for sows induced lame using a chemical synovitis model when pain sensitivity was evaluated with pressure algometry. Thermal NT tests revealed differences between treatments immediately after meloxicam administration suggesting that this NT tool may not be as sensitive when compared with pressure algometry.

Key Words: meloxicam, lameness, swine

736 Use of a pelleted corn residue complete feed for receiving feedlot cattle. S. J. Peterson*, B. L. Nuttelman, D. B. Burken, J. C. MacDonald, M. K. Luebbe, and G. E. Erickson, *University of Nebraska-Lincoln, Lincoln.*

The effects of feeding a complete pelleted feed versus a high quality receiving diet on feedlot performance and health of newly received calves was evaluated. The complete feed was made from 35% corn residue and a blend of grain byproducts and minerals and was designed to replace a conventional grain and forage diet. The study utilized 2 locations, Panhandle Research Center (PHREC) near Scottsbluff, NE, and the Agricultural Research and Development Center (ARDC) near Mead, NE. The calves were received over 2 d at PHREC (n = 500; BW = 267 ± 1.94 kg) and 4 d at ARDC (n = 818; BW = 264 ± 1.20 kg). Within location, steers were blocked by source within date received and assigned randomly to pens based on processing order (25 and 30 pens/treatment at ARDC and PHREC respectively). Pens were assigned randomly to a control diet consisting of 32% distillers grains, 32% dry rolled corn, 32% alfalfa, and 4% supplement (DM basis; CON) or the complete pelleted feed (PelCR). The PelCR contained a combination of plant extracts (RumeNext, ADM, Quincy, IL) whereas CON contained 150 mg/hd/d of monensin. Both diets were formulated to contain 125 mg/hd/d decoquinate. Studies averaged 24 d at ARDC and 25 d at PHREC. Steers were fed ad libitum. A treatment by location interaction was observed for DMI ($P < 0.05$). At PHREC, no difference in DMI was observed (5.8 vs. 5.9 kg/day for CON and PelCR respectively; $P = 0.03$); however, DMI was greater for the pelleted diet at ARDC (6.7 vs. 7.0 kg/day for CON and PelCR respectively; $P < 0.05$). No treatment by location interaction was detected for ADG or G:F ($P > 0.15$). The pelleted feed decreased ADG (1.54 vs. 1.29 kg/day for CON and PelCR respectively; $P < 0.01$) and G:F (0.246 vs. 0.198 kg/kg for CON and PelCR respectively; $P < 0.01$) compared with CON. The number of calves treated for bovine respiratory disease was numerically less for steers fed PelCR (30.3% vs. 26.5% for CON and PelCR respectively; $P = 0.13$). Receiving calves on PelCR may have a positive effect on DMI, but a negative effect on ADG and G:F compared with a high-quality receiving diet. However, feeding PelCR appears to be a viable option for receiving feedlot cattle.

Key Words: corn residue, health, receiving

737 Growth and carcass characteristics of feed efficiency sorted cattle fed corn or roughage-based diets and finished with corn or byproduct-based diets. J. R. Russell*[1], E. L. Lundy[1], N. O. Minton[2], W. J. Sexten[2], M. S. Kerley[2], and S. L. Hansen[1], *[1]Iowa State University, Ames, [2]University of Missouri, Columbia.*

The objective was to determine effects of growing phase (GP) diet, GP feed efficiency (FE) ranking and finishing phase (FP) diet on FP growth and carcass characteristics of beef steers. Three groups (YR) of steers (439 hd) were fed whole shell corn (GPC) or roughage-based (GPR) diets during GP in GrowSafe bunks to facilitate individual FE determination and ranking [low (LFE), medium (MFE), high FE (HFE)]. Steers were blocked by GP diet and FE ranking to corn (FPC) or byproduct-based (FPB) diets during FP. Pen (6 steers/pen) served as FP experimental unit. The FP diets were fed to the first group (28 pens; 471 ± 10 kg) for 85 d, the second (14 pens; 402 ± 14 kg) for 115 d and the third (32 pens; 473 ± 16 kg) for 65 d. All diets included 200 mg ractopamine hydrochloride/steer/d (Optaflexx), for the final 28–30 d. PROC MIXED of SAS was used to compare means with a Tukey test and YR as a random effect. For carcass traits and pre-Optaflexx period (PRE) growth, FP initial BW was used as a covariate. For Optaflexx period (OPT) growth, PRE ending BW was used as a covariate. Across the entire FP, LFE pens tended to have greater ADG than MFE ($P < 0.09$). During PRE, FPB pens had greater ($P < 0.05$) ADG and DMI versus FPC however during OPT the pens fed FPC had greater ($P < 0.05$) ADG and DMI with a tendency for greater G:F ($P < 0.07$) than FPB. The FPB pens had greater ADG ($P < 0.05$) during PRE compared with OPT. There were no effects of FE rank ($P > 0.1$) on G:F or DMI during FP. The GPR-FPB and GPC-FPB pens had greater HCW ($P < 0.05$) compared with GPR-FPC, and the GPR-FPB pens also had greater HCW ($P < 0.05$) than GPC-FPC. The FPB pens tended to have greater KPH ($P < 0.06$) than FPC. Interestingly, within GPR pens LFE had greater ending BW and HCW ($P < 0.05$) versus MFE. The GPR-FPB pens had greater ($P < 0.05$) backfat (BF) and yield grade (YG) versus GPR-FPC. There were no differences ($P > 0.3$) in ribeye area or marbling. In this study, GP FE rank had minimal effects on FP growth and carcass traits though GPR-LFE outperformed GPR-MFE pens. Regardless of GP diet, FPB increased HCW, BF and YG.

Key Words: byproduct, corn, feed efficiency

738 Apparent total-tract digestibility of steers gradually adapted to a finishing diet or dosed with Lactipro and placed directly onto a finishing diets. K. A. Miller*[1], C. L. Van Bibber-Krueger[1], C. C. Aperce[2], C. A. Alvarado[1], and J. S. Drouillard[1], *[1]Kansas State University, Manhattan, [2]MS-Biotec, Wamego, KS.*

Effects of 2 diet adaptation strategies on apparent total tract digestibility were evaluated in feedlot steers during the first 24 d on feed. Ninety steers (BW 399 ± 2.31 kg) were placed into concrete-surfaced pens (6 pens/treatment; 7 or 8 steers/pen) and assigned to a traditional step-up regimen consisting of 3 step-up diets followed by a finishing diet fed for 6 d each (Control), or were given a 100-mL oral dose of Lactipro at processing and placed directly onto the finishing diet (Lactipro). Diets were based on steam-flaked corn, wet corn gluten feed with corn silage (CS) as the roughage source. Transition diets contained 40, 30, and 20% CS, and were followed by a finishing diet with 10% CS. Feces and orts were collected from each pen daily, weighed, homogenized, subsampled, and composited into 6-d periods. Control steers had greater DMI (8.9 vs. 7.7 kg; $P < 0.01$) and DM fecal output (2.3 vs. 1.7 kg; $P < 0.01$) compared with Lactipro steers. Regardless of treatment, DMI and fecal output increased over the 24-d study ($P < 0.01$). Apparent DM digestibility was greater for Lactipro steers during d 7 to 12 and d 13 to 18 ($P < 0.01$), increased over time ($P < 0.01$) for both treatments, but was not different ($P = 0.11$) between treatments over the entire 24 d. Apparent CP digestibility was greater for Lactipro steers during d 1 to 6 and d 7 to 12 ($P < 0.01$), peaked for both treatments during d 7 to 12 ($P < 0.01$), and was greater ($P = 0.05$) for Lactipro steers compared with Control steers over the entire 24 d. Apparent NDF digestibility was greater for Control steers during d 1 to 6 ($P < 0.01$) and during the entire 24-d study ($P < 0.01$) compared with Lactipro steers. Total forage consumption was less for Lactipro cattle (46.9 vs. 18.4 kg for Control and Lactipro, respectively; $P < 0.01$). Dosing Lactipro at processing is an effective strategy for decreasing reliance on roughages without compromising diet digestibility.

Key Words: Lactipro, diet adaptation, roughage

739 Effect of low-fat dried distillers grains inclusion in finishing diets on feedlot cattle total-tract digestibility and ruminal fermentation parameters. I. Ceconi*[1], M. Ruiz-Moreno[2], A. DiCostanzo[1], and G. I. Crawford[1], [1]*University of Minnesota, Saint Paul* [2]*University of Florida, Marianna.*

Excessive dietary fat can negatively affect growth of fiber-digesting ruminal microorganisms and consequently decrease OM total-tract digestibility (OMD), feed intake and overall performance in feedlot cattle. Compared with conventional dried distillers grains (DDG), the smaller fat and greater protein content of low-fat DDG (LF-DDG) may attenuate these effects. An experiment was conducted to evaluate the effect of LF-DDG inclusion in beef cattle finishing diets on OMD and ruminal fermentation. Six ruminally cannulated Holstein steers (317 ± 7 kg initial BW) were assigned randomly to a duplicated 3 × 3 Latin square design. Steers were fed ad libitum once daily 1 of 3 dietary treatments containing (DM basis) 84% dry-rolled corn (DRC), 10% ryegrass haylage, and 6% supplement (CON) or 53% DRC, 10% ryegrass haylage, 2% supplement, and 35% traditional DDG (TRAD) or LF-DDG (LF). Dietary CP and fat concentrations measured 12.1, 15.9, and 19.9% and 3.7, 6.7, and 4.5% for CON, TRAD, and LF, respectively. Steers were intra-ruminally dosed with chromic oxide and fecal grab samples collected to determine OMD. Ruminal fluid was collected to measure VFA and ammonia-N (NH_3-N) concentrations. Ruminal pH was continuously recorded by ruminal probes. Intake of OM was greater for TRAD (8.26 ± 0.04 kg) and LF (8.31 ± 0.04 kg) than CON (8.09 ± 0.04 kg; $P \leq 0.01$). Dietary treatment did not affect OMD ($P = 0.12$) or ruminal pH ($P = 0.64$; 69.7, 69.0, and 72.8 ± 1.2% and 5.78, 5.73 and 5.66 ± 0.09 for CON, TRAD and LF, respectively). Ruminal NH_3-N concentration was smaller and ruminal VFA was greater for CON (2.74 ± 1.14 mg/dL and 92.8 ± 5.8 m*M*) and LF (2.69 ± 1.14 mg/dL and 92.4 ± 5.8 m*M*) than TRAD (3.75 ± 1.15 mg/dL and 74.6 ± 5.8 m*M*; $P \leq 0.04$). Inclusion of LF-DDG resulted in smaller NH_3-N concentration and increased ruminal VFA compared with traditional DDG. Partial replacement of DRC by LF-DDG led to no change in ruminal NH_3-N and VFA concentration while that by conventional DDG led to increased NH_3-N concentration and decreased ruminal VFA.

Key Words: digestibility, low-fat dried distillers grains, volatile fatty acids

740 Effect of slow-release urea inclusion in diets containing wet distillers grains on total-tract digestibility and ruminal fermentation parameters in feedlot cattle. I. Ceconi*[1], M. Ruiz-Moreno[2], A. DiCostanzo[1], and G. I. Crawford[1], [1]*University of Minnesota, Saint Paul* [2]*University of Florida, Marianna.*

Inclusion of rumen degradable N in feedlot diets containing distillers grains (DG) may be beneficial, as degradability of CP in DG can be low. As opposed to the rapid ruminal N release of conventional urea, slow-release urea can provide a steady supply of ammonia-N (NH_3-N) which may allow for improved N utilization by ruminal microbes. An experiment was conducted to evaluate the effect of supplementing urea (46% N) or 2 slow-release urea forms (41% N; Optigen and Nitroshure) on OM total-tract digestibility (OMD) and ruminal fermentation parameters. Four ruminally cannulated Holstein steers (588 ± 8 kg initial BW) were assigned randomly to a 4 × 4 Latin square design. Steers were fed ad libitum once daily one of 4 dietary treatments containing (DM basis) 8% corn silage, 20% wet corn DG with solubles, 30% corn earlage, 4.5% supplement, dry-rolled corn, and 0% (CON) or 0.6% urea (U), or 0.67% Optigen (O) or Nitroshure (NT). Estimated RDP concentrations were 6.7% for CON and 8.4% for U, O, and NT. Steers were intra-ruminally dosed every 12 h with chromic oxide and fecal grab samples collected to determine OMD. Ruminal fluid was collected to measure VFA and NH_3-N concentrations. Ruminal pH was continuously recorded by ruminal probes. Organic matter intake (13.9 ± 0.3 kg), ruminal VFA (107.6 ± 2.9 m*M*), and ruminal pH (5.84 ± 0.02) were not affected by treatment ($P \geq 0.53$). Ruminal concentration of NH_3-N tended to be affected by treatment ($P = 0.06$), being higher for U and NT (9.7 ± 2.0 mg/dL) than CON and O (7.5 ± 2.0 mg/dL; $P \leq 0.01$). Digestibility of OM was similar among treatments (67.4, 67.9, 70.1 ± 2.5%, and 71.0 ± 2.9% for CON, O, NT, and U, respectively; $P = 0.67$). Supplementing RDP through inclusion of conventional or slow-release urea did not affect OMD and most ruminal fermentation parameters evaluated. More research is needed to evaluate the use of slow-release urea in diets containing highly digestible grains and dried DG, as highly fermentable carbohydrates and lower dietary RDP concentrations may result in RDP deficit.

Key Words: digestibility, distillers grains, slow-release urea

741 Effects of feeding treated corn stover and distillers grains to beef cattle on performance, carcass traits, digestibility, and ruminal metabolism. W. P. Chapple*[1], D. B. Faulkner[1], M. J. Cecava[2], P. H. Doane[2], A. H. Grusby[2], and T. L. Felix[1], [1]*University of Illinois, Urbana,* [2]*Archer Daniels Midland Company, Decatur, IL.*

The objectives were to determine the effects of feeding chemically treated and thermo-chemically treated (extruded) corn stover (CS) in diets containing corn and modified wet distillers grain with solubles (MWDGS) on DMI, gain, carcass traits, digestibility, and ruminal metabolism in beef cattle. Exp. 1: Crossbred yearlings (n = 60; initial BW = 383 ± 28 kg) were allotted to 1 of 5 dietary treatments: 1) 55% corn and 5% untreated-ground CS on DM basis (control), 2) 5% calcium oxide (CaO)-treated (bagged) CS, 3) 5% CaO extruded CS, 4) 4% CaO: 1% sodium hydroxide (NaOH) extruded CS, and 5) 3% CaO: 2% NaOH extruded CS. For bagged CS, CS was hydrated to 50% moisture before treatment with CaO in a mixer wagon. For extruded CS, CS was hydrated to 50% moisture before treatment with CaO or combinations of CaO and NaOH, then extruded using a dual-shafted, encased processor. Treated CS diets contained 20% CS, 40% MWDGS, 35% corn, and 5% vitamin/mineral supplement (DM basis). There was no effect ($P \geq 0.13$) of dietary treatment on ADG, G:F, marbling score, or LM area. However, cattle fed the control diet had increased ($P \leq 0.05$) yield grade, DMI, and back fat thickness compared with cattle fed the treated CS diets. Exp. 2: Using the Exp. 1 diets, crossbred steers (n = 5; initial BW = 417 ± 21 kg) were fed for 90% of ad libitum intake in a 5 × 5 Latin square design. Apparent digestibility of NDF and ADF increased ($P < 0.01$) for all cattle fed treated CS diets compared with cattle fed the control diet. Mean ruminal pH from 0 to 3 h post-feeding decreased ($P < 0.01$) for cattle fed the bagged, treated CS diet compared with cattle fed all other diets. Diets containing 5% CaO (bagged or extruded) had the greatest ($P < 0.01$) mean acetate concentrations, resulting in increased ($P = 0.01$) total VFA concentrations. These data suggest inclusion of treated CS may increase fiber digestibility in finishing cattle diets without reducing feedlot cattle gain, feed efficiency, marbling score, or LM area. Therefore, treated CS could partially replace corn in beef cattle diets.

Key Words: calcium oxide, corn stover, distillers grains

742 Effects of ractopamine hydrochloride on performance and carcass characteristics in finishing heifers: 16-trial summary. N. A. Pyatt*, G. J. Vogel, J. W. Homm, R. L. Botts, and C. D. Bokenkroger, *Elanco Animal Health, Greenfield, IN.*

A meta-analysis of published scientific data was conducted to quantify the effects of ractopamine hydrochloride (RAC; Optaflexx, Elanco Animal Health, Greenfield, IN) on growth performance and carcass characteristics in feedlot cattle. Selection criteria was pen-level studies evaluating a negative control and at least one (RAC) treatment, on-label dose (10–30 mg/kg DM basis and 70–430 mg/hd/d) and duration (28–42 d before slaughter), and incremental performance (last 28–42 d). This summary represents analysis of 16 feedlot heifer studies encompassing 12,342 feedlot cattle. All data were analyzed in SAS using mixed regression models with RAC intake (mg/hd/d) as the primary predictor. Within-trial variance was set equal to the squared inverse of the standard error, while a random intercept term accounted for between-trial differences. Cook's D statistics were used to identify influence on parameter estimates. Yield and quality grade distributions were evaluated using a random effects proportional odds cumulative logit model. Live weight, ADG and feed efficiency improved (linear; $P < 0.01$) with increasing dose of RAC supplementation compared with controls. Dry matter intake was not affected ($P = 0.97$) by RAC level. Increasing RAC level improved HCW (linear; $P < 0.01$) and dressing percent (linear; $P = 0.03$). Fat thickness, KPH fat, calculated yield grade, marbling score, conformation score, and lean or skeletal maturity were not affected ($P \geq 0.08$), while longissimus muscle area increased (linear; $P < 0.01$) with level of RAC. However, RAC shifted quality and yield grade distributions slightly lower (linear; $P < 0.05$). Feeding an elevated level of RAC improves beef production efficiency with expected outcomes of 2.7, 5.4, and 8.1 kg live weight and 2.1, 4.3, and 6.4 kg carcass weight improvements in heifers fed 100, 200 or 300 mg/hd/d (respectively) relative to controls.

Key Words: heifers, Optaflexx, ractopamine

743 Effects of feeding functional oils and high levels of glycerol in feedlot bull diets. F. Zawadzki[2], I. N. Prado[2], and J. Torrent*[1], *[1]Oligo Basics USA LLC, Wilmington, DE, [2]Department of Animal Science, Univ. Estadual de Maringa, PR, Brazil.*

A 2 × 2 factorial design was used to evaluate the effects of the supplementation of a commercial mixture of functional oils (Essential, Oligo Basics, PR, Brazil) and the effects of corn substitution by glycerol on animal performance and carcass and meat characteristics of Puruna bulls. A total of 32 8 mo old bulls (206.1 ± 2.5 kg BW) were divided into 4 treatments: control, functional oil supplementation (3 g/animal/day), corn substitution by glycerol and corn substitution by glycerol plus functional oil supplementation. Animals were fed during 252 d a diet with 47.7% ground corn, 42.0% corn silage and 10.3% soybean meal, or a diet with 42.0% corn silage, 20.3% glycerol and 15.0% soybean meal. All diets were kept isonitrogenous. Longissimus dorsi and perirenal and subcutaneous fat samples were taken at the time of slaughter and stored at −20°C for later analysis. Although no differences were seen in ADG, both functional oil supplementation and corn substitution by glycerol increased hot and cold carcass weight ($P < 0.01$) and dressing percentage ($P < 0.02$). Longissimus dorsi temperature and pH at 0 and 24 h, area, texture, marbling and color characteristics were not affected by treatment. Whereas corn substitution by glycerol increased 15:0 pentadecanoic acid ($P < 0.01$), 17:0 margaric acid ($P < 0.01$), 17:1 n-9, *cis*-10-heptadecanoic acid ($P < 0.02$) and 20:4 n-6, arachidonic acid ($P < 0.05$) and decreased 20:5 n-3 eicosapentaenoic acid ($P < 0.01$) in perirenal fat, functional oil supplementation tended to increase 18:1 n-11t, transvaccenic acid ($P = 0.09$). Also, functional oil supplementation tended to increase saturated ($P = 0.09$) and polyunsaturated fat ($P = 0.08$) and tended to decrease ($P = 0.07$) monounsaturated fat in the Longissimus dorsi. Summarizing, both the substitution of corn by 20% glycerol and the supplementation of functional oils improved carcass weight and dressing percent of the supplemented animals. Also, the substitution of 20% of the corn by glycerol changed some of fatty acids deposited in the carcass of the animals.

Key Words: carcass characteristic, functional oil, glycerol

744 Effects of propolis and functional oils on performance, digestibility and blood parameters of crossbred bulls. M. V. Valero[2], I. N. Prado[2], and J. Torrent*[1], *[1]Oligo Basics USA LLC, Wilmington, DE, [2]Department of Animal Science, Univ. Estadual de Maringa, PR, Brazil.*

Some natural products such as functional oils and propolis have been shown to stabilize rumen fermentation and improve beef cattle performance. The objectives of this study were to evaluate the effects of propolis and functional oils on performance, feed intake, apparent digestibility and blood parameters of crossbred bulls. Thirty 18-mo-old bulls (321 ± 27 kg) were randomly assigned to a control, a commercial functional oil mixture (Essential, Oligo Basics, Cascavel, PR, Brazil) group (3 g/d) and a propolis group (3 g/d). Diets were formulated to be isocaloric and isonitrogenous. The animals were fed an ad libitum diet with 41.5% sorghum silage, 33.3% ground corn, 15.3 glycerol, 8.1% soybean meal, 1.0% vitamin-mineral premix and 0.8 urea during the 49 d of the study. Intake was recorded daily and bull BW every 2 weeks. Fecal samples were collected during 5 d starting on the 40th day to obtain apparent digestibilities using the indigestible DM as a marker. Blood samples from each animal were collected by jugular venipuncture into EDTA-coated vacutainer tubes the first and the last day of the experiment. Data was analyzed with an ANOVA. Functional oil supplementation improved ADG (1.53, 1.26 and 1.32 kg/d for the functional oil, control and propolis group, respectively; $P < 0.05$) and G: F (0.147 for the control, 0.151 for the propolis and 0.172 for the functional oils group; $P < 0.05$) when compared with the control and propolis groups. Apparent digestibilities of DM, OM, CP, EE, NDF or ADF were not affected by treatment. Although red cell counts were higher ($P < 0.001$) and white cell counts ($P < 0.001$), platelet counts ($P < 0.001$) and plasma proteins ($P < 0.05$) were lower at the end of the experiment, supplementation with either propolis or functional oils did not affect any blood parameter. In conclusion, supplementation of beef bulls with propolis did not affect any performance, digestibility or blood parameter. The supplementation with functional oils improved ADG and G: F but did not affect any other performance, digestibility or blood parameter.

Key Words: propolis, functional oils, digestibility

745 Effect of urea inclusion in diets containing distillers grains on total-tract digestibility and ruminal fermentation in feedlot cattle. I. Ceconi*[1], M. Ruiz-Moreno[2], A. DiCostanzo[1], and G. I. Crawford[1], *[1]University of Minnesota, Saint Paul, [2]University of Florida, Marianna.*

A high proportion of CP in distillers grains (DG) is RUP. Therefore, addition of RDP to feedlot rations containing DG may be beneficial. An experiment was conducted to evaluate the effect of RDP supplementation in feedlot cattle finishing diets on total tract digestibility and ruminal fermentation. Four ruminally cannulated Holstein steers (347 ± 18 kg initial BW) were assigned randomly to a duplicated 2 × 2 Latin square design. Each period consisted of a 16-d adaptation and a 5-d collection phase. Steers were fed ad libitum once daily one of 2 dietary treatments containing (DM basis) 52% dry-rolled corn, 20%

dried corn DG with solubles, 12% high-moisture corn, 10% ryegrass haylage, mineral-vitamin supplement, and 0% (CON) or 0.6% (U) urea. Energy, CP, and RDP concentrations were 1.32 or 1.30 Mcal NEg/kg, 14 or 15.6%, and 6.4 or 8.0% for CON or U, respectively. Steers were intraruminally dosed with chromic oxide from d 11 to 21 to determine OM digestibility. Fecal grab samples were collected from d 17 to 21. Ruminal VFA and ammonia-N (NH_3-N) concentrations were measured in ruminal fluid samples collected on d 21 at multiple time points after feeding. Ruminal pH was continuously recorded by probes residing in the rumen for 5 d. Organic matter intake (9.9 ± 0.1 kg) and ruminal pH (5.86 ± 0.02) were not affected by treatment ($P \geq 0.13$). Ruminal VFA and NH_3-N concentration, and OM digestibility were higher for U than CON (119.1 and 89.3 ± 5.9 m*M*, 8.5 and 3.9 ± 1.1 mg/dL, and 72.3 and 69.1 ± 2.9% for U and CON, respectively; $P \leq 0.04$). Results from this experiment agree with those from a concurrent feedlot finishing experiment by these authors where ADG and feed efficiency were improved by 11% and 7%, respectively, for U compared with CON. Increasing RDP through the inclusion of urea to dry-rolled and high-moisture corn-based feedlot diets containing 20% dried DG resulted in increased OM digestibility and concentration of NH_3-N and total VFA without affecting feed intake and ruminal pH.

Key Words: dried distillers grains, urea, volatile fatty acids

746 Seed orientation and row direction alter maize grain yield and composition. T. D. Kaufman*[1], P. Walker[1], L. Brown[2], L. Nuzback[2], and F. N. Owens[2], *[1]Illinois State University, Normal, [2]DuPont Pioneer, Johnston, IA.*

By modifying interplant shading, the compass direction of maize rows and the orientation of planted maize seeds may alter grain yield. Effects of row direction and seed orientation were studied in central Illinois in 2 trials. In 2011 using a 2 × 2 × 2 factorial design, 2 Pioneer maize silage hybrids were planted in plots 12 rows (rows 76 cm apart) at 2 populations (69,000 and 84,000 plants/hectare) with seeds were planted at 3 orientations, either randomly (R) with a mechanical maize planter or manually with all kernel tips downward but with each kernel's germ facing either the other plants within the same row (W) or alternately toward plants in adjacent rows (A). R kernels were planted in rows oriented both in a North-South (NS) and an East-West (EW) direction. Based on GLM analysis of this factorial experiment, weight of shelled grain at maturity per hectare was greater ($P < 0.05$) for kernels planted in W rows than in A rows; both were greater than for R (13.0 versus 11.9 and 10.9 t/ha; $P < 0.05$) due to lighter kernel weights and fewer kernels per ear for R. Grain yields were 26% greater ($P < 0.01$) for NS than EW rows due to heavier kernels and more kernels per ear ($P < 0.01$). In 2012, using a 3 × 2 × 3 × 2 factorial design, 3 Pioneer silage hybrids were grown at 2 populations and these same 3 seed orientations in both NS and EW rows. Yields again were least ($P < 0.05$) for R rows (12.2, 12.1, and 10.5 t/ha for A, W, and R). Kernels from R rows had the lowest kernel density but the highest percentage of starch. Grain yields were greater for NS than EW rows (12.0 versus 11.6 t/ha; $P < 0.01$) due to 6.5% greater kernel weights ($P < 0.01$). The higher plant population increased grain yield per hectare but decreased kernels per ear ($P < 0.02$). Regressed across all samples, each 1% added starch displaced 0.38% oil and 0.44% protein. Grain yields were greater for kernels specifically oriented when planted and when grown in NS than in EW rows.

Key Words: maize grain, row direction, yield

747 Influence of fines on the feeding value of steam-flaked corn in finishing diets for feedlot cattle. M. Montano*[1], V. Gonzalez[1], O. Manriquez[1], D. May[1], J. Melendrez[1], A. Plascencia[1], J. Salinas-Chavira[2], and R. Zinn[3], *[1]UABC, Mexicali, BC, Mexico, [2]UAT, Cuidad Victoria, Tamaulipas, MX, [3]University of California, Davis.*

Two trials were conducted to evaluate the influence of fines on the feeding value of steam-flaked corn (SFC) in finishing diets for feedlot cattle. Three levels (0, 33.3 and 66.7%) of re-rolled SFC replaced standard SFC (0.31 kg/L) in a corn-based finishing diet (DM basis). Re-rolled SFC consisted of standard air-dry SFC that was passed through the rollers a second time. The intent of re-rolling was to simulate loss of flake integrity which can occur during feed-handling. In Trial 1, the influence of fines in SFC on growth performance was evaluated in 18 crossbred steers (294 ± 69 kg) in a replicated 3 × 3 Latin square design. Daily weight gain was similar ($P > 0.10$) among treatments, averaging 1.31 kg/d. Dry matter intake tended to be greater (4.7%; quadratic effect, $P = 0.06$) for diets containing re-rolled steam-flaked corn. Dry matter conversion and NE value of the diets were not influenced by dietary treatments ($P > 0.10$). In experiment 2, 6 Holstein steers (205 kg) with cannulas in the rumen and proximal duodenum were used in a replicated 3 × 3 Latin square design to evaluate treatment effects on digestion. Reductions in particle size of corn grain due to rerolling did not influence ($P > 0.10$) ruminal or total tract digestion of OM, NDF, N, or starch ($P > 0.10$). There were no treatment effects ($P > 0.10$) on ruminal microbial efficiency, ruminal pH and ruminal VFA molar proportions. It is concluded that the effect of flake disintegration during mixing and further handling on performance of feedlot cattle and characteristics of digestion will be marginal, if appreciable.

Key Words: cattle, corn, fines

748 Diet inclusion rate for leftover residual biomass in a beef heifer diet. J. A. Tucker*[1], H. W. Harpster[2], J. S. Moritz[3], M. E. Wilson[3], J. A. Carroll[4], and D. L. Smith[1], *[1]Eastern New Mexico University, Portales, [2]The Pennsylvania State University, University Park, [3]West Virginia University, Morgantown, [4]USDA ARS, Lubbock, TX.*

Leftover residual biomass algae have the potential to be used as a cattle feed. The objective of this experiment was to determine the amount of algae (CP 76.1; TDN 85.7; fat 6.1; and ash 9.6 as a percent of DM) that could be included in a beef heifer diet. Crossbred beef heifers (n = 16; 95 ± 5 kg) were randomly assigned to 1 of 4 treatments, control (C; n = 4); 5% algae inclusion (A5; n = 4), 10% algae inclusion (A10; n = 4), or 20% algae inclusion (A20; n = 4). The animals were individually housed in 1.5 × 3 m pens in a climate-controlled facility maintained at 21°C. The diets were constructed using a commercially produced cattle grower ration (Purina Growena) as a base feed. Either 0, 5, 10, or 20% algae was added to the base feed and commercially pelleted to prevent feed separation. Heifers had ad libitum access to treatments and water during the 6-d experiment. In addition, each animal was fed 10 percent of their total diet in alfalfa hay. Feed intakes were calculated from weigh-backs before the addition of treatments before the a.m. and p.m. feeding. Data were analyzed by ANOVA utilizing the general linear model (GLM) procedure of SAS. Means were considered different if p-values were less than 0.05. The C group showed an average daily feed intake of 1,235 g per d. Average daily feed intakes of treatments A5, A10, A20 were 1,773.48, 1,770.68, and 1,283.88 g per d, respectively. These data suggest an inclusion of 5, 10, or 20% algae can be fed in a cattle ration. Further, the A5 and A10 treatments increased consumption ($P < 0.05$) over the C and A20 treatments. Our current research in the laboratory is to determine ADG and FE utilizing a ration containing 10% algae over a 30-d feeding period.

749 Rumensin in dairy cows diets containing high and low levels of linoleic acid from corn distillers grains and high and low fractions of physically effective fiber. M. L. Smith*[1], K. F. Kalscheur[1], J. L. Anderson[1], D. P. Casper[1], and D. L. Prentice[2], [1]*South Dakota State University, Brookings,* [2]*Elanco Animal Health, Greenfield, IN.*

The objective of this study was to determine production responses of dairy cows fed diets containing low (LoLA) or high (HiLA) concentrations of linoleic acid from dried distillers grains and low (Lpef) or high (Hpef) physically effective fiber from alfalfa (chopped hay or pellets made from the same lot of hay) with or without the addition of Rumensin (Rum) in the diet. Sixty-four lactating Holstein dairy cows (65-250 DIM) were used in a 12-wk randomized complete block design consisting of a Covariate Period (wk 1-3), Period 1 (wk 4-7), and Period 2 (wk 8-12). During the Covariate Period, all cows received a common diet. Cows were blocked according to parity, milk yield, and DIM, and were randomly assigned to one of four diets in a 2×2 factorial arrangement of treatments: (1) LoLA-Hpef; (2) LoLA-Lpef; (3) HiLA-Hpef; and (4) HiLA-Lpef. In Period 2, half of the cows on each diet in Period 1 were randomly assigned to be fed Rum resulting in a 2 × 2 × 2 factorial arrangement of treatments. Diets in Period 2 containing Rum were formulated to contain 22 g/ton. Diets were formulated for a 50:50 forage to concentrate ratio. Average DMI was not affected by diet in either Period 1 or 2. Milk yield was not affected by diet in Period 1, but in Period 2 cows fed LoLA tended to produce less than cows fed HiLA (34.33 vs. 36.34 kg/d; $P = 0.09$). In Period 1, cows fed LoLA vs. HiLA had greater fat % (3.70 vs. 3.35%; $P = 0.01$) and yield (1.32 vs. 1.21 kg/d; $P = 0.05$), respectively. FCM FE was greater for cows fed LoLA compared to HiLA (1.33 vs. 1.24; $P = 0.04$). In Period 2, cows fed LoLA vs. HiLA had greater fat % (3.80 vs. 3.23%; $P = 0.001$) and yield (1.28 vs. 1.17 kg/d; $P = 0.07$). In addition, cows fed Hpef vs. Lpef had greater fat % (3.76 vs. 3.27%; P=0.003) and yield (1.30 vs. 1.15 kg/d; $P = 0.01$). Cows fed Hpef vs. Lpef tended to have greater FCM FE (1.29 vs. 1.19; $P = 0.09$). The addition of Rum had no effect on intake, milk yield or milk composition with the exception of a lower lactose %. No interactions of main effects ($P > 0.05$) occurred during the study.

Key Words: physically effective fiber, linoleic acid, Rumensin

750 Effect of *Saccharomyces cerevisiae* CNCM I-1077 (Levucell SC) on rumen pH and milk production during heat stress. M. Fustini[1], A. Palmonari[1], H. Durand[2], A. Formigoni[1], and E. Grilli*[1], [1]*DIMEVET, University of Bologna, Ozzano Emilia, BO, Italy,* [2]*Lallemand Animal Nutrition, Blagnac, France.*

The aim of the study was to evaluate the effect of a live yeast (*Saccharomyces cerevisiae* CNCM I-1077, Levucell SC) on milk production and rumen pH of high-producing dairy cows challenged with a highly acidogenic diet during summer (temperature humidity index >68). Forty Holstein dairy cows were divided in 2 groups homogeneous for milk yield, milk fat and proteins, DIM, and parity. Twelve cows per group were then randomly selected and given a bolus with a continuous monitor indwelling pH meter. After 7 d adaptation during which cows were fed a basal TMR (57:43 concentrate:forage ratio), the treated group was given 2×10^{10} cfu *S. cerevisiae*/head/day through a premix in the TMR for 42 d. Individual daily milk production was monitored through Afilab and 5 milk samples per group were also collected at d 0, 9, 21, 27, and 40 of the study to perform chemical analyses. At 0, 21, and 42 d blood samples were collected to perform biochemistry and hematological analyses. Milk yield and quality, and blood data and mean daily pH were analyzed with ANOVA repeated measures, whereas ruminal pH fluctuation were grouped in discrete intervals (minutes/day at pH <5.8) and analyzed with a t-student test. Cows fed with *S. cerevisiae* had a numerically higher milk yield (+1.2 kg over an average of 34 kg/head/d at 180 DIM; $P = 0.2$) and a higher fat content than control cows (+3.6%; $P < 0.05$). As a result, the treated group resulted in a higher fat-corrected milk yield (+1.7 kg/head/day, $P < 0.05$) whereas protein and lactose contents were not affected. Moreover, treated animals had a longer interval of time during which the rumen pH remained above the critical value of 5.8 (+48 min/day; $P < 0.05$), while the average daily pH was unaffected. Blood parameters were not affected by the treatment. The results suggest that while the cows maintained a general good health status despite the stressful environment, *S. cerevisiae* CNCM I-1077 had the potential to prevent the development of rumen sub-acidosis, by probably improving fiber utilization, in cows that must be fed high energy diets to maintain highly efficient performance.

Key Words: dairy cow, rumen pH, *S. cerevisiae*

751 Production responses to increasing MP lysine supply in lactating Holstein cows. A. M. Schuler*[1], K. F. Kalscheur[1], F. Diaz-Royon[1], S. E. Boucher[2], and F. R. Valdez[2], [1]*South Dakota State University, Brookings,* [2]*Kemin Industries Inc., Des Moines, IA.*

The objective of this research was to determine production responses of high-producing dairy cows fed increasing concentrations of rumen-protected (RP) Lysine (Lys) (LysiPEARL; Kemin Industries Inc., Des Moines, IA) while maintaining a constant supply (g/d) of metabolizable protein (MP) and methionine (Met). Twelve multiparous and 4 primiparous Holstein cows were used in a 4 × 4 Latin square design with 3-wk periods. Four dietary treatments were formulated based on predicted MP Lys supply: (1) Negative control (NC) formulated to supply 186.3 g of MP Lys without the addition of Lys; (2) Positive Control using blood meal (PCBM)to supply 205.3 g of MP Lys; (3) Ruminally protected Met and Lys (RPML) using LysiPEARL (0.32%) to supply 205.2 g of MP Lys; (4) High Lys (Lys25) formulated to supply 229.8 g of MP Lys using LysiPEARL (0.74%). Diets were formulated to be similar in MP Met supply using rumen-protected Met (MetiPEARL). Basal diets contained 40.8% corn silage, 13.0% alfalfa hay, and 46.2% concentrate mix. Dry matter intake (DMI) was not affected by increasing MP Lys supply ($P > 0.05$). Cows responded to increasing MP Lys linearly for protein yield, energy corrected milk (ECM), and ECM feed efficiency (ECMFE) and in quadratic fashion for protein and total solids (TS) % ($P < 0.05$). Linear trends were observed for yields of milk, fat, and TS. Quadratic trends ($P < 0.10$) were observed for fat % and MUN ($P < 0.10$). Cows fed BM tended to increase in DMI compared with cows fed RPML ($P < 0.10$). Overall, cows increased milk protein yield and ECMFE when balancing rations for MP Lys using LysiPEARL.

Table 1.

Item	Treatment				SEM	*P*-value[1]
	NC	PCBM	RPML	Lys25		
DMI, kg/d	24.7	24.7	23.7	24.1	0.80	BT
Milk, kg/d	36.2	37.6	36.6	37.7	0.95	LT
Fat, %	3.96	3.84	3.86	3.92	0.107	QT
Protein, %	3.19	3.13	3.17	3.20	0.065	Q
TS, %	12.9	12.7	12.8	12.9	0.17	Q
MUN, mg/dL	13.1	12.5	12.7	13.0	0.29	QT
Fat, kg/d	1.42	1.44	1.39	1.47	0.043	LT
Protein, kg/d	1.15	1.18	1.15	1.20	0.033	L
TS, kg/d	4.66	4.78	4.66	4.84	0.120	LT
ECM	38.4	39.4	38.3	40.0	0.96	L
ECMFE	1.57	1.61	1.63	1.67	0.045	L

[1]L = linear response ($P < 0.05$); Q = quadratic response ($P < 0.05$); BT = trend for blood meal vs. RPML ($P < 0.10$); LT = linear trend ($P < 0.10$); QT = quadratic trend ($P < 0.10$).

Key Words: dairy cow, rumen-protected Lys

752 Feed intake, ruminal fill and pH of calcium oxide pretreated corn stover diets fed to lactating cows. D. E. Cook*[1], M. J. Cecava[2], P. H. Doane[2], M. B. Hall[3], and D. K. Combs[1], *[1]University of Wisconsin-Madison, Madison, [2]ADM Research, Decatur, IL, [3]USDA-ARS, US Dairy Forage Research Center, Madison, WI.*

Corn stover was pretreated with calcium oxide (50 g CaO kg^{-1} stover DM in 500 g H_2O kg^{-1} stover DM) at ambient conditions and fed to 8 ruminally cannulated Holstein dairy cows in a 4 × 4 Latin square design with 21-d periods. The treatments were 0, 40, 80, and 120 g stover DM kg^{-1} TMR DM, with treated stover replacing corn grain on a DM basis. Rumen sampling occurred on d 15, fecal sampling for pH on d 17, and rumen evacuations 2 h postfeeding on d 21. Ruminal pH was measured hourly from the time of feeding to 6 h postfeeding. Cows were 108 ± 58 DIM and produced 34.4 ± 2.1 kg milk d^{-1} on 23.6 ± 0.6 kg DMI. DMI decreased ($P < 0.01$) linearly with increasing levels of stover inclusion, from 25.3 to 21.9 kg DM d^{-1} (1.1 kg SE). Ruminal pH nadir and fecal pH increased linearly ($P < 0.05$) with stover inclusion level (Table 1). Rumen DM turnover rate (DMI·rumen digesta DM^{-1}) decreased linearly ($P < 0.01$) with stover inclusion. Rumen digesta measures were 93.1 kg wet matter, 14.3 kg DM, 12.5 kg OM, and 7.4 kg NDF, with no difference among treatments ($P > 0.2$). DMI was likely limited by stover inclusion because rumen digesta mass did not change, but the rumen DM retention time increased.

Table 1.

	Stover inclusion (g stover DM kg^{-1} TMR DM)				SEM
	0	40	80	120	
Rumen pH (nadir)	5.83	5.83	5.93	5.94	0.07
Fecal pH	6.33	6.39	6.45	6.47	0.05
Rumen DM turnover rate	1.86	1.65	1.62	1.51	0.06

Key Words: calcium oxide, stover, treated stover

753 Determining the optimal level of zinc amino acid complex in lactating dairy cows. A. Nayeri*[1], N. C. Upah[1], E. Sucu[1,2], M. V. Sanz-Fernandez[1], J. M. DeFrain[3], and L. H. Baumgard[1], *[1]Iowa State University, Ames, [2]Uludag University, Bursa, Turkey, [3]Zinpro Corporation, Eden Prairie, MN.*

Multiparous (n = 79) and primiparous (n = 68) Holstein cows were blocked by parity and previous 305 ME milk yield, and assigned to one of 3 dietary treatments: (1) 75 mg/kg DM supplemental Zn as $ZnSO_4$ (Control), (2) Control except 33 mg Zn/kg in the close up and 16 mg Zn/kg in the lactation diet from $ZnSO_4$ were replaced by Zn amino acid complex (Availa-Zn, Zinpro Corporation; 16 Availa-Zn), and (3) Control except 67 mg Zn/kg in the close up and 40 mg Zn/kg in the lactation diet from $ZnSO_4$ were replaced by Availa-Zn (40 Availa-Zn). Supplemental Mn, Cu, Co, Se and I levels and sources were the same among all treatments. Cows were housed at the ISU Dairy farm and individually fed a TMR containing dietary treatments beginning 28 ± 15 d before expected calving date and continued until 250 DIM. Relative to Control, multiparous cows (but not heifers) fed 16 Availa-Zn or 40 Availa-Zn had increased (20%) colostrum IgG. Prepartum DMI decreased with Availa-Zn supplementation ($P \leq 0.05$) and tended to decrease quadratically with increasing Availa-Zn level ($P \leq 0.15$), being lower for cows fed 16 Availa-Zn. Postpartum DMI decreased in cows fed Availa-Zn ($P < 0.05$) and decreased with increasing Availa-Zn level (Linear and Quadratic, $P \leq 0.05$), while milk yield (MY) increased (Linear and Quadratic, $P \leq 0.05$) with increasing Availa-Zn supplementation. Feeding Availa-Zn improved feed efficiency linearly ($P \leq 0.01$) when measured as MY/DMI, 3.5% fat-corrected MY/DMI and solids-corrected MY/DMI. Feeding a higher Availa-Zn level resulted in a linear decrease in services per conception (3.1, 2.0 and 2.6 for Control, 16 Availa-Zn and 40 Availa-Zn, respectively; $P \leq 0.10$). Feeding Availa-Zn decreased milk fat, lactose and total solids content ($P \leq 0.10$) and increased MUN ($P \leq 0.01$). Milk LnSCC tended to decrease with increasing Availa-Zn level (Linear; $P \leq 0.15$). Effects of treatment on plasma metabolites were minimal although Availa-Zn tended ($P \leq 0.05$) to increase NEFA concentration. Feeding increasing Availa-Zn levels improves fertility and increases production efficiency by reducing feed intake without affecting overall milk energy output.

Key Words: zinc, lactation

754 Temporal effect of feeding potassium carbonate sesquihydrate on milk fat. G. Ma*[1], J. H. Harrison[1], E. Block[2], T. C. Jenkins[3], and T. D. Nennich[4], *[1]Washington State University, Puyallup, [2]Church and Dwight Animal Nutrition, Princeton, NJ, [3]Clemson University, Clemson, SC, [4]Purdue University, Lafayette, IN.*

Our research team has previously demonstrated that supplementation of potassium carbonate sesquihydrate supplementation can increase milk fat test and is suggested to be in part mediated as a result of changing the biohydrogenation pathways in the rumen (J. Dairy Sci. 95:3919–3925). Previous experimental design has only allowed us to determine that potassium carbonate sesquihydrate supplementation can increase milk fat after a week of feeding. In this study, 10 multiparous dairy cows in early lactation were used to evaluate how quickly milk fat % would change when cows were supplemented with potassium carbonate sesquihydrate. Cows were fed individually via Calan headgates. In period 1, cows were fed a diet formulated to contain a DCAD of 288 mEq/kg of DM (1.48% K of total DM), 5.7% long-chain fatty acids (LCFA) (%DM), and 0.40 kg/d SBM oil for a 7 d adaptation and covariate period. In period 2, d 8 to 28, 5 cows remained on the same diet (Control) and 5 cows were switched abruptly to a diet containing potassium carbonate sesquihydrate to provide a DCAD of 431 mEq/kg of DM (2.05% K of total DM) with added SBM oil. A daily AM-PM composite of milk was obtained for each cow and analyzed for composition. Milk data were analyzed using Proc Mixed of SAS using a model that included treatment,

day, treatment × day. Milk fat from period 1 was used as a covariate. In period 1, milk fat % was 4.01 and 4.23 for cows that subsequently were on high versus low K, respectively. In period 2, addition of potassium carbonate sesquihydrate had no significant effect on milk production. There was an immediate (within 48 h) and significant increase ($P < 0.01$) in milk fat % for cows fed potassium carbonate sesquihydrate as compared with the control diet, milk fat of 4.28 and 4.06 (high versus low K, respectively) in period 2. In cows with normal milk fat test, the abrupt addition of potassium carbonate sesquihydrate was effective in immediately increasing milk fat %.

Key Words: dairy cow, milk fat, potassium carbonate sesquihydrate

755 Effects of supplemental amino acids and chromium propionate on plasma amino acids, energy digestibility, and productivity of peak lactation dairy cattle. C. F. Vargas*, K. Yuan, C. Titgemeyer, L. K. Mamedova, and B. J. Bradford, *Kansas State University, Manhattan.*

Chromium (Cr) feeding in early lactation increased peak milk production in some studies, but feeding Cr during peak lactation has not been studied. Furthermore, interactions of AA and Cr have not been evaluated. Our objective was to evaluate responses to CrPr (KemTRACE brand chromium propionate 0.04%, Kemin Industries Inc.), rumen-protected Lys (LysiPEARL, Kemin Industries Inc.) and Met (MetiPEARL, Kemin Industries Inc.), and their interaction in peak lactation cows. Forty-eight individually fed Holstein cows (21 primiparous, 27 multiparous, 38 ± 15 DIM) were stratified by calving date in 12 blocks and randomly assigned to 1 of 4 treatments within block. Treatments were control, CrPr (8 mg/d Cr), RPLM (10 g/d Lys and 5 g/d Met, intestinally available), or CrPr plus RPLM. Treatments were premixed with ground corn and top-dressed at 200 g/d for 35 d. Diets included corn silage, alfalfa hay, and concentrates, providing approximately 17% CP, 31% NDF, and 40% NFC. Data were analyzed as a complete block design with a factorial arrangement of treatments and week as a repeated measure using ProcMIXED in SAS. Intake (21.8 ± 4.7 kg/d) and milk yield (43.0 ± 7.0 kg/d) were not affected ($P > 0.10$) by treatments or interactions. Protein content was decreased by RPLM (2.64 vs. 2.72 ± 0.041%, $P = 0.05$) versus control, but protein yield was not altered. A CrPr by week interaction ($P < 0.05$) was detected for lactose content, which was increased by CrPr during wk 1 only (4.99 vs. 4.88 ± 0.036%) versus control. Total AA concentration in blood on d 35 tended to be decreased by RPLM (2.27 vs. 2.44 ± 0.098 m*M*, $P = 0.06$). As a proportion of total AA, only threonine was affected by treatment ($P < 0.05$), with a lower proportion for RPLM. Digestible energy intake and gross energy digestibility, measured by bomb calorimetry, were not affected ($P > 0.10$) by treatments. There were no treatment effects on feed efficiency, and change in body weight or body condition score ($P > 0.10$). In summary, feeding CrPr, RPLM, or both to dairy cows for 5 wk near peak lactation had few effects on energetics or production outcomes.

Key Words: lysine, methionine, chromium

756 Effects of feed additives during a starch and fructose challenge. H. M. Golder*[1,2], A. R. Rabiee[1,2], P. Celi[2,3], and I. J. Lean[1,2], *[1]SBScibus, Camden, New South Wales, Australia, [2]University of Sydney, Faculty of Veterinary Science, Camden, New South Wales, Australia, [3]Melbourne School of Land and Environment, The University of Melbourne, Parkville, Victoria, Australia.*

We hypothesized that feed additive(s) would reduce acidosis risk during a non-life threatening but substantial challenge with starch and fructose. Holstein heifers (n = 40) were allocated to 5 groups: (1) control (no additives); (2) virginiamycin (10 g/hd/d:VM); (3) monensin (2.2 g/hd/d) + tylosin (0.44 g/hd/d:MT); (4) monensin (2.5 g/hd/d) + yeast (Levucell SC Direct 25 g/hd/d:MY); (5) sodium bicarbonate (200 g/hd/d) + magnesium oxide (30 g/hd/d:BUF). Heifers were fed twice daily 62% forage 38% concentrate TMR at 1.25% of BW DM/d for a 20-d adaptation period with their additive(s). Fructose (0.1% of BW/d) was in the ration for the last 10 d of adaptation. On d-21 heifers were challenged with a 1.0% of BW DM wheat and 0.2% of BW fructose ration plus their additive(s). Ruminal samples were collected using stomach tube 5 times over 4 h after consumption of the challenge ration. Data were analyzed using a linear mixed model. There was a large amount of within and between group variation in response to challenge. Clinical acidosis occurred in 1 control heifer. VM and BUF maintained consistently high DMI over the 20-d adaptation ($P < 0.01$). Acetate concentration increased in the BUF and control groups. Butyrate concentration was lower in the MY and MT groups compared with other groups. The VM and BUF, and MY, VM, and BUF groups had the numerically lowest valerate and lactate concentrations, respectively. Ammonia concentration was lowest in the MY group. Mean total lactate was >10 mM for each group throughout challenge sampling. Rumen pH, propionate and total lactate were not influenced by feed additives on challenge day (Table 1). Despite large animal variation VM and BUF had DMI and rumen profiles indicating reduced acidosis risk.

Table 1. Effects and predicted means (±SEM).

	Group						*P*-value[1]	
Item	Control	VM	MT	MY	BUF	SEM	Group (G)	Time (T)
Acetate, mM	67.3^{b}	59.6^{a}	58.8^{a}	60.7^{a}	75.1^{c}	3.0	<0.01	<0.01
Propionate, mM	24.3	19.3	24.6	24.9	22.5	2.3	0.34	<0.01
Butyrate, mM	20.6^{bc}	23.8^{c}	15.9^{a}	15.3^{a}	19.9^{b}	1.9	0.02	0.03
Valerate, mM	2.1^{ab}	1.5^{a}	3.0^{b}	2.7^{b}	1.5^{a}	0.6	0.04	<0.01
Total lactate, mM	34.4	21.6	37.5	19.5	21.0	9.3	0.53	0.64
Ammonia, mM	4.3^{d}	3.6^{cd}	1.4^{ab}	0.6^{a}	2.4^{bc}	0.6	<0.01	0.04
Histamine, ng/mL	151^{bc}	210^{d}	116^{b}	47^{a}	173^{cd}	26	<0.01	0.90
pH	5.7	6.1	5.8	6.1	6.1	0.1	0.16	<0.01

[1]G × T was NS.

Key Words: acidosis, feed additive

757 Effects of addition of *Aspergillus oryzae* culture and 2-hydroxyl-4-methylthio butanoic acid on milk production and rumen fermentation in lactation dairy cows. H. Sun[1], Y. M. Wang*[2], K. J. Zhu[1], Y. B. Zhou[1], B. C. Zheng[1], C. Wang[3], Y. M. Wu[1], and J. X. Liu[1], *[1]Institute of Dairy Science, Zhejiang University, Hangzhou, China, [2]Novus International Trading (Shanghai) Co. Ltd., Shanghai, China, [3]Zhejiang A&F University, Hangzhou, China.*

The objective of the study was to evaluate the effects of *Aspergillus oryzae* culture (AOC) and 2-hydroxy-4-methylthio butanoic acid (HMB) on lactation performance and rumen fermentation in dairy cows. Sixty-four mid-lactation Holstein dairy cows (136 ± 5.0 DIM) were randomly allocated to 4 dietary treatments in a 2 × 2 factorial design: control diet, control diet top-dressed AOC at 5 g/d, control diet top-dressed HMB at 25 g/d, control diet top-dressed AOC at 5 g/d and HMB at 25 g/d. The experiment lasted 8 weeks including 2 weeks for adaptation. Data were analyzed using PROC MIXED of SAS with AOC and HMB as the main factors. Dry matter intake was not significantly affected by AOC or HMB supplementation ($P > 0.05$), while 3.5% FCM tended to increase by HMB ($P = 0.08$). Supplementation of HMB tended to increase the

contents of milk protein ($P = 0.05$) and milk fat ($P = 0.09$), while no significant effect of AOC was found for milk protein and milk fat. Either AOC or HMB supplementation significantly increased concentrations of rumen microbial protein and total volatile fatty acids ($P < 0.01$). However, AOC did not affect the VFA profile, while HMB significantly increased the molar proportion of acetate at the expense of propionate ($P < 0.01$). Both AOC and HMB significantly increased the populations of rumen *Fibrobacter succinogenes*, *Ruminococcus flavefaciens*, and fungi relative to total bacterial 16S rDNA ($P < 0.01$) without changing the protozoa and *R. albus*. It is inferred that addition of AOC and HMB can improve rumen microbial protein and volatile fatty acids by stimulating rumen microbes, resulting in numerical improvement in milk yield. Addition of HMB tended to increases milk fat and milk protein.

Key Words: *Aspergillus oryzae* culture, 2-hydroxy-4-(methylthio) butanoic acid, milk performance

758 Performance of Nili-Ravi buffaloes as influenced by feeding wheat straw fermented with rumen digesta treated without or with fibrolytic enzymes. M. Nisa*, A. Rehman, M. Sarwar, M. A. Shazad, and O. A. Khan, *Institute of Animal Nutrition and Feed Technology, University of Agriculture, Faisalabad, Punjab, Pakistan.*

An experiment using 12 mid-lactating multiparous Nili-Ravi buffaloes (weight 575 ± 17 Kg, 105 ± 15 d in milk) in a randomized complete block design was conducted to examine the influence of feeding wheat straw fermented with rumen digesta (RD) treated without or with fibrolytic enzymes on nutrient intake, digestibility, and milk production and composition. Fermented wheat straw was prepared by blending 70 kg wheat straw, 20 kg RD, 4 kg urea and 6 kg molasses on a dry matter (DM) basis. The 50% moisture concentration of this blend was maintained by adding water at the time of ensiling. Four iso-nitrogenous and iso-caloric diets were formulated. The diets containing unfermented wheat straw without or with enzymes were designated as $UFWS^-$ and $UFWS^+$. The diets containing fermented wheat straw without or with enzymes were designated as FWS^- and FWS^+. Dry matter, crude protein (CP) and neutral detergent fiber (NDF) intakes were the highest ($P < 0.05$) in buffaloes fed FWS^+ diet and were the lowest in animals fed $UFWS^-$ diet. A linear increase ($P < 0.05$) in DM and NDF digestibility were noticed in buffaloes fed FWS^+ diet than those fed FWS^-, $UFWS^-$ and $UFWS^+$diets. All animals were in positive nitrogen balance but the highest ($P < 0.05$) nitrogen balance was observed in animals fed FWS^+ and FWS^- diets. Blood urea nitrogen remained unaltered ($P > 0.05$) across all diets. Milk production, milk lactose, solids not fat and total solids remained unaltered ($P > 0.05$) across all diets. Results indicated that intake and digestibility of nutrients were higher ($P < 0.05$) in animals fed FWS^+ diet than those fed $UFWS^+$ diet.

Key Words: fibrolytic enzyme, fermented wheat straw, rumen digesta

759 Do dried distillers grains with solubles affect the occurrence of *Salmonella enterica* colonization in pigs? M. H. Rostagno*[1], B. T. Richert[2], L. V. C. Girao[2], G. M. Preis[2], L. J. Lara[2], A. F. Amaral[2], A. D. B. Melo[2], and A. Jones[2], *[1]USDA-ARS, West Lafayette, IN, [2]Purdue University, West Lafayette, IN.*

As an alternative to counteract the increased feed costs, dried distillers grains with solubles (DDGS) have been increasingly included in pig diets. Much research has been conducted recently to evaluate growth performance and carcass characteristics associated with feeding DDGS to pigs. However, little is known about the effect of DDGS on the intestinal microbiota, and on the susceptibility to infection or colonization with pathogens. Therefore, 2 experiments were conducted to determine if inclusion of DDGS in the diet of grow-finish pigs affects their susceptibility to or the intestinal levels and shedding of *Salmonella*. In experiment 1, 36 pigs (12 pigs/treatment) were assigned to 3 treatments: Control diet with no DDGS, diet with 20% DDGS, or diet with 40% DDGS. After an adaptation period of 2 wk, each pig was inoculated with *Salmonella* Typhimurium (10^4 cfu) and euthanized after 6 h to determine their susceptibility to the challenge. In experiment 2, 40 pigs (20 pigs/treatment) were assigned to 2 treatments: Control diet with no DDGS or diet with 30% DDGS. After 2 wk, each pig was inoculated with *Salmonella* Typhimurium (10^4 cfu); individual fecal samples were collected during 5 weeks, and pigs were euthanized at 3 and 5 weeks post-challenge to determine intestinal colonization. In experiment 1, no differences among treatments were observed on the susceptibility to *Salmonella* infection. In experiment 2, most pigs shed *Salmonella* at one of the fecal samplings during the study period, with control pigs having a significantly higher cumulative shedding frequency ($P < 0.05$) than pigs receiving the diet with 30% DDGS (80% versus 50%). The overall average shedding level was 2.2 $\log_{10}$ cfu/g of feces, with no difference between treatments ($P > 0.10$). Also, no difference between treatments was found on the frequency or levels of Salmonella in intestinal samples collected at 3 or 5 weeks post-challenge. In conclusion, dietary inclusion of DDGS does not alter the susceptibility to or colonization with *Salmonella* of grow-finishing pigs.

Key Words: DDGS, *Salmonella*, pig

760 Characterization of phage-resistant *Escherichia coli* O157:H7. Y. Hong*, J. Zhang, Y. Pan, and P. Ebner, *Purdue University, West Lafayette, IN.*

Phage therapy has great potential as an antimicrobial intervention in both the pre- and post-harvest stages of meat production. However, similar to other antimicrobial therapies, the application of phage therapy can result in rapid development of phage-resistance in targeted bacteria, which could lead to reduction in the efficacy of any phage-based products. Therefore, basic understanding of phage-resistance development in pathogens is critical to evaluate the effect of resistance on phage therapy application and assist in developing efficient and durable phage products. In this study, we isolated 2 phage-resistant strains (PR1, PR2) of *E. coli* O157:H7 after an 18 h co-incubation. Phage resistance was maintained throughout a 4-d subculture period (8 passes), indicating that resistance is stable in vitro in the absence of selection pressure from the phage. While other groups have reported a fitness cost associated with resistance development, no significant growth impairment was observed in resistant strains. The susceptible parent *E. coli* O157:H7 strain and 2 resistant strains had generation times of 20.9 ± 1.47 min, 19.8 ± 2.04 min (PR1) and 19.9 ± 1.21 min (PR2) and stationary concentrations of 4.30×10^8 cfu/mL, 4.49×10^8 cfu/mL (PR1), and 4.52×10^8 cfu/mL (PR2). Phage resistance in PR1 was, at least in part, the result of adsorption prevention. After a 10-min incubation, 82.1% of inoculating phages failed to adhere to PR1 while only 2.8% of inoculating phages failed to adhere to the susceptible parent strain. In PR2, adsorption did not appear altered, however, there was no phage proliferation indicating a second mechanism for resistance. Phage resistance did not affect adhesion to Caco-2 cells as the parent and resistant strains had recovered adhesion percentages of 2.94%, 2.75% (PR1) and 2.75% (PR2), respectively. These results indicate that the acquisition of resistance comes at little cost to the bacterium under these experimental conditions. Preliminary experiments indicate, however, that phage may overcome resistance in as few as 5 h. Future studies are aimed at more clearly characterizing this phage capacity.

Key Words: phage resistance, *E. coli* O157:H7, phage therapy

761 The effect of phage on the growth of *E. coli* O157:H7 and release of shiga toxins. J. Zhang*, K. Walton, Y. Pan, Y. Hong, S. Hayes, and P. Ebner, *Purdue University, West Lafayette, IN.*

E. coli O157:H7 is often associated with cattle and ground beef products and can produce and release powerful shiga toxins. As such, infections with *E. coli* O157:H7 can lead to renal failure and death, especially in the young, elderly or immunocompromised. It was recently shown that antibiotic treatment can lead to increased release of shiga toxins. Here we aimed to determine whether phage-based technologies could limit *E. coli* O157:H7 without the concomitant increase in shiga toxin production and release. We isolated *E. coli* O157:H7 phages from wastewater treatment samples. Based in in vitro growth kinetics and killing efficiencies, we chose 3 phages from this library to develop a treatment cocktail. The eclipse periods for these phages ranged from 14.6 to 23.7 min. The latent periods ranged from 23.9 to 31.5 min. The burst sizes ranged from 4.0 to 89.9 PFU. We then compared the phage cocktail to common antibiotics fosfomycin and ciprofloxacin in terms of bactericidal properties and associated shiga toxin production. Phages were added to log phase growth *E. coli* O157:H7 at an MOI = 0.1, 1 or 10. At 8 h, the concentration of bacteria in phage treated samples was reduced 98.5% (MOI = 0.1), 99.9% (MOI = 1.0) and 99.95% (MOI = 10). Similar treatment with fosfomycin or ciprofloxacin reduced bacterial concentrations by 99.95% and 99.7%, respectively. Phage concentration increased by approximately 3 $\log_{10}$ over the 8 h period regardless of MOI. At 8 h, treatment with fosfomycin and phage (MOI = 1 or 10, but not MOI = 0.1) resulted in higher concentrations of shiga toxin 1 compared with untreated controls. There were no differences among treatments in shiga toxin 2 productions. Thus, phage therapy was similar to fosfomycin and ciprofloxacin in terms of antibacterial activity. Future studies will focus on optimizing phage conditions to maximize bactericidal activity while minimizing the effect on shiga toxin production and release.

Key Words: *E. coli* O157:H7, phage, shiga toxin

762 Arginine and glutamine alleviate the impairment induced by DON stress and enhance immunity in growing pigs. W. Wang*[1,2], L. Wu[2], T. Zhou[3], L. Yang[1], H. Zhang[4], J. Yin[2], T. Li[2], K. Yao[2], Q. Wang[3], R. Huang[2], and Y. Yin[2], *[1]College of Animal Science, South China Agricultural University, Guangzhou, China, [2]Research*

Center of Healthy Breeding of Livestock and Poultry, Hunan Engineering and Research Center of Animal and Poultry Science, and Key Laboratory of Agro-ecological Processes in Subtropical Region, Institute of Subtropical Agriculture, Chinese Academy, Changsha, Hunan, China, [3]Guelph Food Research Centre, Agriculture and Agri-Food Canada, Guelph, ON, Canada, [4]China National Key Laboratory of Animal Nutrition, Beijing Animal and Veterinary Science Institute, Chinese Agricultural Academy, Beijing, China.

Deoxynivalenol (DON) is a mycotoxin, which reduces feed intake and animal performance, especially in swine. Arginine and glutamine play an important role in swine nutrition. The objective of present study was to investigate the effects of dietary arginine and glutamine supplementation on alleviating the impairment induced by DON stress to enhance immunity in growing pigs. A total of 30, 60-d-old healthy growing pigs (Landrace × Yorkshire) with a mean body weight (16.28 ± 1.54Kg) were divided into 5 groups randomly. Before experiment, 3 amino acid groups fed 1.0% arginine (Arg), 1.0% glutamine (Gln) and 0.5% Arg + 0.5% Gln respectively for 21 d for immune-fortification. Control group and toxic group fed diet with 1.64% Ala for isonitrogenous control. After immune-fortification, the toxic group and amino acid groups fed DON-contaminated diet with the final DON concentration 6mg/kg in diet for 30 d. Amino acid groups continually fed with amino acids supplementation as before. The control group fed with DON-free commercial diet at same time. No big difference between DON group and amino acid groups was observed for the average daily gain (ADG) of pig, the average daily feed intake (ADFI) of amino acid groups were significantly higher than that in toxic group ($P < 0.01$). As to the relative weight of liver, spleen and kidney, there were no significant difference among these groups. For serum biochemistry characters, values of BUN, ALP, ALT and AST in amino acid groups were lower than that in toxic group. GLU and ALB were not different between control and amino acid groups. IGF1, GH and SOD in amino acid groups were significantly higher than that in toxic group ($P < 0.01$). IL-2 and TNFαvalues in amino acid groups were similar with that in control group, which were significantly lower than that in toxic group ($P < 0.01$). These results showed that dietary arginine and glutamine could alleviate the impairment induced by DON stress and enhance the immune system in growing pigs.

Key Words: deoxynivalenol, arginine, growing pig

765 Evaluation of nonprotein nitrogen-based protein supplements to enhance low-quality forage utilization by cattle. C. C. Stefan*, J. E. Sawyer, and T. A. Wickersham, *Texas A&M University, College Station.*

Efficacy of 4 NPN-based protein supplements for stimulating intake and digestion in cattle consuming low-quality forage (6.8% CP) was evaluated. Five ruminally cannulated steers (238 kg ± 9.1 kg) were used in a 5 × 5 Latin square consisting of 4 supplements and a negative control (CON). Supplements were infused directly into the rumen, before feeding and included a 40% CP mineral mix (40MM; 100% of CP from biuret), 60% CP mineral mix (60MM; 100% of CP from biuret), 25% CP liquid (25L; 61% of CP from slow-release N source; RumaPro, Anipro/Xtraformance Feeds), or 35% CP liquid (35L; 74% of CP from RumaPro). Mineral mixes were provided at 114 g/d and liquids at 310 g/d. Periods were 14 d; 8 d adaptation to treatment and 6 d sample collection. Forage OM intake tended to be greater for 25L (5.56 kg/d; $P = 0.06$) and 35L (5.53 kg/d; $P = 0.08$) than CON (5.20 kg/d), but was similar to CON for 40MM (5.34 kg/d; $P = 0.44$) and 60MM (5.13 kg/d; $P = 0.71$). Total OM intake was greater ($P < 0.01$) for both liquid supplements (5.81 and 5.79 kg/d; 25L and 35L, respectively) than CON (5.20 kg/d) but 40MM (5.38 kg/d; $P = 0.33$) and 60MM (5.18 kg/d; $P = 0.92$) were comparable to CON. There were no differences ($P \geq 0.11$) between supplements and CON for total tract OM digestion, which ranged from 56.0 – 58.6%. Total digestible OM intake was greater ($P < 0.01$) for 25L (3.4 kg/d) and 35L (3.36 kg/d) compared with CON (2.94 kg/d), but not for 40MM (3.03 kg/d; $P = 0.43$) or 60MM (3.06 kg/d; $P = 0.27$). Average ruminal NH_3 concentrations were greater ($P < 0.01$) with supplementation, 0.33 m*M* (CON) versus 1.06, 1.96, 1.71, and 2.09 m*M*, for 40MM, 60MM, 25L, and 35L; respectively. Ruminal VFA concentrations were greater (84.7 vs 98.7 m*M*) with supplementation ($P < 0.06$). These data suggest a potential benefit to providing readily fermentable OM when delivering supplemental NPN to cattle consuming forage near a 7% CP threshold, below which protein supplementation typically stimulates forage utilization.

Key Words: cattle, nonprotein nitrogen, supplementation

766 The effect of Mediterranean saltbush (*Atriplex halimus*) treated with exogenous enzymes on feed intake, nutrient digestibility and ruminal fermentation in sheep. H. N. Alsersy[1], A. Z. M. Salem*[1,2], H. Gado[3], B. E. Borhami[1,3], M. M. El Adawy[1], and M. H. Yacuot[4], *[1]Faculty of Agriculture, Alexandria University, Egypt, [2]Facultad de Medicina Veterinaria y Zootecnia, Universidad Autonoma de Estado de Mexico, Mexico, [3]Animal Production Department, Faculty of Agriculture, Ain Shams University, Qalubia, Egypt, [4]Animal Production Institute, Ministry of Agriculture, Dokki, Cairo, Egypt.*

This research was conducted to assess the effects of Mediterranean saltbush (*Atriplex halimus*) treated with exogenous enzymes on feed intake, nutrient digestibility and ruminal fermentation in sheep. Three Barki rams were used in consecutive digestibility trials while 3 ewes fitted with permanent rumen fistula were used as the source of inoculum for in vitro rumen fermentation trials. The treatments comprised: (1) D1, *A. halimus* (leaves and stems) plus barley grain (300 g/head/day), (2) D2, *A. halimus* treated with 2 L of ZAD per ton and 5% molasses ensiled for 30 d plus barley grain (300 g/head/day), (3) D3, *A. halimus* plus barley grain (300 g/head/day) containing ZADO (4 g/head/day) and (4) D4, *A. halimus* treated with 2 L of ZAD per ton with 5% molasses ensiled for 30 d plus barley grain (300 g/head/day) containing ZADO (4 g/head/day). Enzyme product of ZADO (powder) or ZAD (liquid) is commercially available multi-enzyme feed additive in a powder form produced from *Ruminococcus flavefaciens* and manufactured by the Academy of Scientific Research and Technology in Cairo, Egypt. The *A. halimus* was offered ad libitum to animals twice daily at 0900 and 1600 h, while barley grain was given once daily at 1000 h. Results showed that total DM intake of D2 and D4 were lower ($P < 0.05$) than D1 and D3; while ZADO was minor increase ($P < 0.05$) the feed DM intake. D4 recorded highest ($P < 0.05$) value of DM, OM, CP and EE digestibilities than D2, D3 and D1, except nitrogen free extract. Addition of ZAD or ZADO increased ($P < 0.05$) N balance, ruminal fermentation such as total VFA and NH_3-N, microbial protein production, as well as rumen DM digestibility and rumen volume, while decreased ($P < 0.05$) N intake and rumen outflow rate. It could be concluded that addition of ZAD or ZADO to sheep diets can improve the efficiency of roughage digestibility and alter ruminal fermentation.

Key Words: *Atriplex halimus*, digestibility, exogenous enzymes

767 Volatile profile of Hyblean cultivated and native pasture detected by gas chromatography/mass spectrometry/olfactometry. T. Rapisarda*[1], C. Pasta[1], G. Licitra[1,2], and S. Carpino[1], *[1]CoRFiLaC, Ragusa, Italy, [2]DISPA, Catania University, Catania, Italy.*

The Hyblean area is the major dairy producer of southeastern Sicily. Cattle farms producing cheese are based on semi-extensive systems, implying animals to graze pasture. Previous studies (Licitra et al., 1997; Carpino et al., 2003; Carpino et al., 2004a) reported that Hyblean pastures show a great variety of plants that influence milk and cheese quality. This work was a further investigation on the aroma active compounds to detect differences in flavor profile of 2 Hyblean pasture types: cultivated vs. spontaneous. Forage samples were gathered twice, at the beginning (I Period) and at the end of April (II Period). Detection and identification of odor-active compounds (OACs) were performed by gas chromatography/mass spectrometry/olfactometry (GC/MS/O) analysis. The extraction of OACs was carried out using the steam distillation technique. Then, OACs were detected and chemically identified in 7 classes: alcohol, aldehyde, ester, ketone, pyrazine, sulfur and terpene. Not identified compounds were also included in a "Not Identified" (NI) class. Data from GC/MS/O were subsequently subjected to statistical analysis performed with JMP 8.2 (SAS Institute Inc., Cary, NC) software by applying Chi-squared test at a significant level of $\alpha = 0.05$. Overall, spontaneous pasture showed a significant higher number of OACs compared to cultivated pasture ($P < 0.01$). Reflecting the natural forages growing trend, OACs were higher in Period I compared with Period II in each pasture type but only significantly higher in the spontaneous one ($P < 0.05$). In both pasture types, chemical classes were significantly different ($P < 0.0001$): alcohol, aldehyde, ketone and terpene classes presented a higher number of OACs compared to pyrazine, sulfur, and NI classes, but similar to esters. In conclusion, spontaneous pasture showed richer odor profile than cultivated pasture, confirming that this type of forage is an important marker tied to the production area that might influence the aroma properties of milk and dairy products. Further studies are needed to investigate the pasture season effect on milk flavor.

Key Words: odor active compounds, pasture, forbs

768 Effects of cutting height, time of day, and nitrogen fertilization on nutrient content of Bermudagrass (*Cynodon dactylon*). B. McIntosh*, D. McIntosh, J. Beeler, and G. Bates, *University of Tennessee, Knoxville.*

Bermudagrass (*Cynodon dactylon*) is a warm-season grass commonly used for pasture and hay for horses in the southeastern United States. The objective of this study was to determine the effects of cutting height, time of day at harvest, and nitrogen fertilization on the nutrient content of Bermudagrass (Vaughn's No.1, Hybrid). A randomized complete block design with 4 replications on 48 test plots (9.3 m^2) was performed at 2 locations over 2 growing seasons. Nitrogen was applied at 0 (NONE), 33.4 (MED) and 67.2 (HIGH) kg/ha. Harvest was conducted at 0700 (a.m.) and 1900 (p.m.) with cutting heights of 38.1 (SHORT) and 50.8 (TALL) cm. All plots were harvested using a flail small-plot harvester to capture total forage plant material in June, July, and August. Forage samples (n = 312) were oven-dried at 60°C in a forced air oven for 72 h to determine dry matter (DM) and analyzed for CP, ADF, NDF, Ca, P, K, Mg, WSC and sugar using a Foss 6500 near-infrared spectrometer. Data were analyzed using the mixed model method for randomized complete block design with repeated measures (SAS V. 9.3, SAS Institute 2012). Data are reported as LS Means ± SEM as a percent of DM. Cutting height, time of day, and nitrogen rate affected CP, ADF, NDF, Ca, P, K, Mg, WSC and sugar content ($P < 0.05$). However, the magnitude of the differences between treatments was slight and insignificant to the nutritional management of horses. Notable differences include the effect of the SHORT vs. TALL cutting height on CP (9.8 ± 0.3 vs. 8.5 ± 0.2), ADF (33.9 ± 0.2 vs. 35.0 ± 0.2), NDF (65.6 ± 0.1 vs. 67.6 ± 0.1), Ca (0.22 ± vs. 0.16 ± 0.0), and sugars (6.3 ± 0.2 vs. 5.7 ± 0.2). Lower concentrations of sugars and WSC were observed in samples collected during a.m. (5.5 ± 0.2; 7.6 ± 0.2, respectively) when compared with p.m. (6.5 ± 0.2; 8.9 ± 0.2). The HIGH nitrogen application also resulted in increased sugar and WSC (6.3 ± 0.3 and 8.7 ± 0.3, respectively) compared with NONE (5.5 ± 0.3 and 7.7 ± 0.3, respectively). Production strategies can alter the nutrient content of Bermudagrass and should be considered when managing forages for horses.

Key Words: horse, forage, nutrition

769 Effect of bale feeder, forage, and monensin on hay waste, disappearance, and cow performance. W. A. Moore* and W. J. Sexten, *University of Missouri, Columbia.*

Forty-eight spring-calving crossbred cows, 124 ± 8 d in gestation were used in a 3X2 factorial arrangement within a Latin square design to evaluate the effect of 3 bale feeders and 2 forages on hay waste. Cows were stratified by age (4 ± 2.5 years), weight (517 ± 68.8 kg) and 12th rib ultrasound measured fat thickness (0.4 ± 0.16 cm) into 6 replicate pens with 8 cows per pen. Supplemental treatments were 1 $kg \cdot hd^{-1} \cdot d^{-1}$ supplement with 182 g/ 909 kg monensin (Mon) or without monensin (Con). Bale feeders evaluated were open bottom with 17 slanted feeding stations (Open) (2.4 m diam., 1.2 m height), sheeted bottom with 15 slanted feeding stations and tapering sides (Taper) (2.1 m diam. top, 2.4 m diam. bottom, 1.2 m height, 0.5 m sheeting), and sheeted bottom and top with 16 straight feeding stations and chain cone (Cone) (2.3 m diam., 1.7 m height, 0.6 m bottom sheeting, 0.5 m top sheeting). Forages were alfalfa haylage (HQ) (41% DM, 17% CP, 49% NDF) or fescue hay (LQ) (92% DM, 7.5% CP, 66% NDF). We hypothesized that cone and sheeting would reduce waste with LQ, but not affect HQ waste, in addition monensin would improve efficiency. HQ waste was collected at 24, 48, and 72 h while LQ was collected at 24, 48, 72 and 96 h. Total DMI was reduced ($P < 0.05$) for Mon (2.2% BW) compared with Con (2.3% BW) while ADG, final BW, G:F and final 12th rib fat depth did not differ ($P > 0.10$). An interaction ($P < 0.05$) for percent bale wasted was observed between forage and feeder where LQ Open was greatest ($P < 0.05$) (19.2%), LQ Taper was intermediate ($P < 0.05$) (13.6%) but greater than ($P < 0.05$) LQ Cone (8.9%). However, LQ Cone was not different ($P > 0.10$) from HQ Open (7.0%), or HQ Cone (6.4%) but was greater than HQ Taper (4.9%). 24, 48, 72 h and total HQ waste was not different ($P > 0.10$) due to feeder. 24 and 48 h LQ waste was greater ($P < 0.05$) for Open and Taper compared to Cone. However, 72 and 96 h LQ waste was greater ($P = 0.06$) for Open and Cone compared to Taper. Cone feeder and bottom sheeting are both effective at reducing waste of LQ while monensin reduced forage intake with no effect on cow performance.

Key Words: bale feeder, hay waste, monensin

770 Liveweight, rectal temperature and plasma prolactin responses in lambs grazing tall fescue with novel endophytes. M. Friend*, I. Allen, J. Broster, and S. Robertson, *Graham Centre for Agricultural Innovation (NSW Department of Primary Industries and Charles Sturt University), Wagga Wagga, NSW, Australia.*

An experiment was conducted between January and May 2012 at Wagga Wagga, Australia, to evaluate lamb responses to grazing novel endophytes of tall fescue. Three treatments utilized Martin 2 tall fescue with either no endophyte (E-), novel endophyte 647 (M647) or novel endophyte E3 (ME3). A fourth treatment utilized Tower tall fescue with endophyte 647 (T647), while Kentucky 31 (KY31) containing wild endophtye was also included. Crossbred lambs (n = 300, 10 per plot) grazed 0.4 ha plots (3 replicates/treatment) over 2 separate 6 week periods. Liveweight was assessed fortnightly, while rectal temperatures and blood samples (for prolactin) were taken at the start of each grazing period and then again on hot days during each grazing period. Herbage mass and quality, including ergovaline content, was estimated twice in each grazing period. Live herbage mass was always lowest in KY31, but except for late in grazing run 2 the herbage mass was unlikely to have restricted intake. Herbage quality did not differ between treatments, but declined over time ($P < 0.05$) in each grazing run. Ergovaline was detected at low levels (<0.2 ppm) in herbage from KY31 plots only. Liveweight did not differ between treatments at any time, with lambs gaining an average of 5.7 ± 0.22 kg and 7.8 ± 0.20 kg in each grazing period. On hot days, KY31 lambs had the highest rectal temperatures, although this was not always significantly greater than that of lambs in the other treatments. Compared to E-, lambs grazing M647 had a similar rectal temperature at all measurements except one. Plasma prolactin levels were lower ($P < 0.05$) in lambs grazing KY31 and ME3 treatments than for lambs grazing other treatments, in both grazing runs. Plasma prolactin levels were similar ($P > 0.05$) at all sampling times in lambs grazing E-, M647 and T647 treatments. The results show no evidence that endophyte 647 produced ergovaline in sufficient quantities to initiate toxicoses in sheep. Based on plasma prolactin levels, the E3 endophyte may pose a risk for fescue toxicoses.

Key Words: fescue, endophyte, lamb

771 Intake, digestibility, and passage rate of three warm-season grass hays consumed by beef steers. K. E. Turner*[1], S. W. Coleman[1], and C. C. Chase Jr.[2], *[1]USDA ARS, El Reno, OK [2]USDA ARS, Clay Center, NE.*

Florida-44 bermudagrass [*Cynodon dactylon* (L.) Pers.] is a fine-stemmed forage selected from a Tifton-44 field near Brooksville, FL, that had drifted from the original and is highly desired for horses. The

objective here was to assess quality of warm-season grass hays at different maturities in stall-fed beef steers. Florida-44 bermudagrass (FL44); Tifton-85 bermudagrass (TF85); and Tifton-9 bahiagrass (*Paspalum notatum* Flueggé; TF9) were staged and harvested as hay at 5-wk and 7-wk intervals beginning 25 June from the ARS Station in Brooksville. Thirty-six steers were allotted to 1 of 6 hays fed in individual pens. After a 13-d adaptation, individual steers received a continuous release bolus containing C32 and C36 alkane wax as external markers to estimate fecal output, and a pulse-dose of Yb-labeled forage to estimate passage rate. Fecal samples were collected daily while forage and refusal samples were collected weekly. Fecal and forage samples were lyophilized and analyzed for n-alkane concentrations by GC and Yb by ICP. Forage digestibility (D) was estimated as the mean of D by the ratio of C31, C33, and C35 n-alkanes in forage and feces. Rate of passage was calculated by non-linear regression of Yb appearance on time from dosing. There was a hay × maturity stage interaction for DMI (g/kg BW; $P < 0.05$), D ($P < 0.03$) and passage rate ($P = 0.09$). Intake of hays at 5-wk regrowth was not different, but at 7-wk, rank was FL44 > TF85 > TF9. The DMI of 5- and 7-wk regrowth were similar for FL44 (mean 21 g/kg) and TF85 (mean 19 mg/kg), while DMI of 5-wk TF9 (18 g/kg BW) hay was greater ($P < 0.05$) than 7-wk TF9 hay (15 g/kg BW). The D of TF85 and TF9 (mean 59.4%) at 5-wk regrowth was greater ($P < 0.01$) than FL44 (52.8%) at 5-wk regrowth, whereas D of TF85 (57.3%) was greater ($P < 0.02$) than TF9 (52%) at 7-wk regrowth. Passage rate of the 3 hays at 5-wk regrowth were all similar (mean 4%/h), while at 7-wk regrowth TF85 and FL44 were similar (mean 5%/h); both were greater ($P < 0.01$) than TF9 (3%/h). Quality of TF9 bahiagrass declined more rapidly than bermudagrass.

Key Words: warm-season grass, intake, alkanes

772 Does addition of cofactors to exogenous fibrolytic enzymes increase digestion of bermudagrass by the enzymes? J. J. Romero*[1], Z. X. Ma[1], F. H. Kamada[1], U. Carneiro[1], C. F. Gonzalez[2], C. R. Staples[1], and A. T. Adesogan[1], *[1]Department of Animal Sciences, IFAS, University of Florida, Gainesville, [2]Department of Microbiology and Cell Science, IFAS, University of Florida, Gainesville.*

The objective was to determine if adding different doses of cofactors to exogenous fibrolytic enzymes (EFE) increases their hydrolytic effect on Tifton 85 bermudagrass haylage (BH). Nanopure water or each of 3 cellulase-xylanase enzymes (2A, 11C, 13D) from *Trichoderma longibrachiatum* were applied (4.5, 10, and 7.5 g EFE/kg, respectively) with 0, 0.1, 1 and 10 mM of Mn^{2+} or Fe^{2+} cofactors to BH. Mn^{2+} was added to 11C and Fe^{2+} was added to 2A or 13D based on sugar release potential from BH in earlier studies. Treatments were applied to BH (0.5 g, 1 mm) in quadruplicate, incubated for 24 h at 25°C before addition of buffered rumen fluid and further incubation for 24 h at 39°C in 2 runs. Data for each enzyme were analyzed separately as a randomized complete block design with a 2 × 4 factorial arrangement and a model including enzyme (E), cofactor dose (C), run, and interaction effects. Increasing the Mn^{2+} rate with or without 11C linearly increased ($P < 0.01$) digestibility of DM, NDF, cellulose and ADF but DMD and NDFD responses were greatest when 11C and 10 m*M* of Mn^{2+} were applied (E × C, $P < 0.05$). Adding 10 m*M* of Mn^{2+} with 11C increased NDFD by 8.2% beyond the 15.3% increase due to 11C alone, whereas 10 m*M* of Mn^{2+} alone only increased NDFD by 6.2%. Adding 10 m*M* of Mn^{2+} with 11C also increased total VFA and decreased acetate to propionate (A:P) beyond values observed with 11C alone (E × C, $P < 0.05$). Increasing the rate of Fe^{2+} application linearly decreased ($P < 0.01$) digestibility of DM, NDF, hemicellulose, ADF and cellulose. Similar but less pronounced decreases occurred when 13D was added to the Fe^{2+} doses (E × C, $P < 0.05$), but no effects were detected when 2A was added to the Fe^{2+} doses. Hence, adding Fe^{2+} to 13D and 2A attenuated or prevented decreases in BH digestibility caused by Fe^{2+} alone, whereas adding Mn^{2+} to 11C synergistically increased the digestibility of BH.

Key Words: forage, enzyme, cofactor dose

773 Nutrient digestibility of annual summer forages using different indigestible markers and fecal collection schedules in growing beef heifers. C. A. Njombwa, F. M. Ciriaco*, D. D. Henry, V. R. G. Mercadante, M. J. Ruiz-Moreno, G. C. Lamb, and N. DiLorenzo, *North Florida Research and Education Center, University of Florida, Marianna.*

Twelve Angus crossbred heifers were used to determine the effects of indigestible markers and fecal sample collection schedules on apparent total tract digestibility of nutrients in 3 annual summer forages. Forages were Mulato II (hybrid Brachiaria), pearl millet, and sorghum Sudan. On d 0 heifers were randomly assigned to treatments (2 heifers/pen) and were offered daily fresh cuts of each forage treatment for the duration of the study. Intake was monitored using a GrowSafe system. From d 7 to 19, heifers received 10 g/d of Cr_2O_3 and 10 g/d of TiO_2 at 1200 h. Fecal samples were collected from d 15 to 19 by rectal grab at 0800, 1200 and 1600 h, and composited within heifer using 2 samples/d (2s; 0800 and 1600 h only) or 3 samples/d (3s; all sampling times). Indigestible NDF (iNDF) was used as an internal digestibility marker. Data were analyzed as a split-split plot design with the whole plot testing forage treatment effect, the split plot testing the fecal collection schedule (2s vs. 3s) and the split-split plot testing the marker. No effect ($P > 0.10$) of forage or forage × marker interaction was found for nutrient digestibility. Across forage treatments, mean apparent nutrient digestibility in the total tract were 60.1%, 69.1%, 71.2%, 54.3% and 38.7% for DM, OM, CP, NDF, and ADF, respectively. A sampling schedule × marker interaction ($P < 0.05$) was found for nutrient digestibility of DM, OM, CP, and NDF. Under a 2s schedule, digestibility of nutrients was underestimated ($P < 0.05$) when using Cr_2O_3 or TiO_2 vs. iNDF. Under a 3s schedule, digestibility of all nutrients was underestimated with Cr_2O_3 vs. iNDF and tended ($P < 0.10$) to be underestimated for DM, OM, CP, and NDF digestibility when using TiO_2 vs. iNDF. Digestibility of ADF was underestimated ($P < 0.05$) with TiO_2 and Cr_2O_3 vs. iNDF, regardless of sampling schedule. No difference ($P > 0.10$) was observed in nutrient digestibility between 2s and 3s when using iNDF as a marker. The use of iNDF as an internal digestibility marker with a 2s fecal sampling schedule appears most suitable to evaluate nutrient digestibility in summer annual forages.

Key Words: forage, digestibility, marker

774 The effects of rumen digestion and in vitro exposure of small intestinal fluid on viability and germination of common Indiana weed seeds. L. Unruh Snyder*[1], E. Kiley[1], K. Burger[2], N. Baird[2], R. Lemenager[2], S. Lake[3], and J. Santini[2], *[1]North Carolina State University, Raleigh, [2]Purdue University, West Lafayette, IN, [3]University of Wyoming, Laramie.*

An experiment was conducted to examine the germination of velvetleaf (*Abutilon theophroasti*), Venice mallow (*Hibiscus trionum*), and redroot pigweed (*Amaranthus retroflexus*) after exposure to various digestion treatments. The objective of this study was to see if seed germination was affected by digestion either in vitro or in situ and if time within the rumen influenced germination rates of the weed seeds either going through the intestinal digestion phase or not. These weed species were

selected because they are the most common pasture weeds in Indiana. To recover seeds a sample tube made of PVC which contained the seeds that where were placed into 2 different bag types: the Ankom fiber filter bags (F57) with a 25-µm porosity with a size of 5 cm by 4 cm and a polyester monofilament bag with a 53-µm (±10) porosity cut to the same size of 5 cm by 4 cm, all nitrogen free and sealed closed. We tested if the type of bag influenced our results whether in the in vitro or in situ digestion setting. The seeds had 2 fates either they were exposed only to rumen digestion phase or continued on to an in vitro intestinal incubation phases to see if the additional exposure time would influence seed germination. We tested the hypothesis that ruminal incubation (for 12 or 24 h) and a more complete digestion process affects germination regardless of incubation bag type used. After 7 d, germination rates were determined and seeds were evaluated for hard or non-living seed. Redroot pigweed germination was enhanced by 20 to 25% going through the entire digestion process, mostly like because it was one of the smallest (1.2 mm) seeds investigated and needed more time to imbibe water. Velvetleaf germination decreased going through the small intestinal procedures and having the longest retention time in the rumen. Velvetleaf has been reported to have a seed coat that is highly lignified, which would enable the seed to survive for longer periods of harsh conditions. Venice mallow with a seed size of (2 mm) germinated and was most successful when going through the longest period of digestion.

Key Words: digestion, pasture, weed

775 Supplemental fumaric acid restored growth performance of weanling pigs fed 10% full-fat diatom microalgae. B. Y. Jung, K. K. Lum*, K. R. Roneker, and X. G. Lei, *Cornell University, Ithaca, NY.*

Previous research in our laboratory demonstrated a growth depression of weanling pigs by adding 7.5 to 15% of defatted microalgae diatom biomass in the diet to replace soybean meal and(or) corn. Subsequent chemical and fecal analyses suggested high ash contents of the diatom products as a potential negative effector on acid-base balance and utilization of trace elements Cu, Se, and Zn in diets of weanling pigs. The present study was conducted to determine if supplementing organic acid and the selected trace elements overcome or alleviated such effects of a full-fat diatom (Cellana, Kailua-Kona, HI). A total of 40 individually housed weanling pigs (BW = 9.6 ± 0.8 kg) were allotted to 4 groups (n = 10/treatment) and fed a corn-soybean meal basal diet (BD), BD + 10% diatom, BD + 10% diatom + 2% fumaric acid (Univar, Morrisville, PA), and BD + 10% diatom + 50% more Cu, Se, and Zn in the vitamin/mineral premix for 6 wk. Growth performance and blood biochemical responses were measured biweekly. Overall average daily gain and feed efficiency were 7% and 2% lower in pigs fed 10% diatom than those control pigs fed the BD. While supplementing 2% fumaric acid in the diatom-containing diet restored the growth performance of pigs, the additional Cu, Zn, or Se produced an opposite effect ($P < 0.05$). The diatom-fed pigs had marginal increases ($P = 0.06$) in packed cell volume and blood hemoglobin concentration compared with the BD-fed pigs. However, there were no differences in daily feed intake or plasma inorganic phosphorus concentration, alkaline phosphatase activity, and tartrate-resistant acid phosphatase activity among treatment groups at any time point. In conclusion, feeding weanling pigs with 10% full-fat diatom depressed their growth and feed use efficiency, but those losses could be obviated by supplementing 2% fumaric acid. (Supported in part by a USDA/DOE Biomass R&D Initiative grant).

Key Words: algae, trace mineral, organic acid

776 Weanling pigs fed 10% defatted green microalgae maintained normal growth performance and plasma biochemistry. R. D. Ekmay*, K. R. Roneker, K. K. Lum, and X. G. Lei, *Cornell University, Ithaca, NY.*

A green marine microalgal strain (*Desmodesmus* sp.) was tested for biofuel production and the defatted biomass contained 31% crude protein. The objective of the present study was to determine if this defatted microalgal biomass could replace a portion of soybean meal in diets for weanling pigs and if adding exogenous protease improved its protein digestibility. A total of 32 weanling pigs (5-wk old) were divided into 4 groups (n = 8) and fed a corn-soybean meal diet containing 0 or 10% of the defatted green microalgae (Cellana, Kailua-Kona, HI) and (or) an exogenous protease (Ronozyme ProAct, 0.06% of the diet, DSM Nutritional Products Inc., Parsippany, NJ) for 4 wk. Body weights and feed intakes were recorded biweekly and blood samples of individual pigs were collected at the same periods to measure plasma biochemistry. Data were analyzed as 2 × 2 factorial arrangements with time-repeated measurements. Neither the defatted microalgae nor the exogenous protease affected growth performance of pigs at any time point. Likewise, there was no dietary treatment effect on plasma alanine aminotransferase, alkaline phosphatase, and tartrate-resistant acid phosphatase activities or plasma concentrations of uric acid and total amino acids. However, supplemental protease decreased plasma urea nitrogen concentration by 45% ($P < 0.01$) when pigs were fed the defatted microalgae at wk 2. The same trend also remained at wk 4, but the protease effect was not statistically significant. In conclusion, including the defatted green microalgae in the corn-soybean meal diet of weanling pigs at 10% did not exert any adverse effect on their growth performance or plasma biochemical status. (Supported in part by a USDA/DOE Biomass R&D Initiative grant).

Key Words: green microalgae, protease, swine nutrition

777 Defatted microalgae diatom biomass may replace a portion of soybean meal and corn in broiler diets. R. E. Austic, A. Mustafa, B. Y. Jung, and X. G. Lei*, *Cornell University, Ithaca, NY.*

Previous research in our laboratory has shown effectiveness of defatted microalgae diatom biomass from biofuel production in replacing a portion of soybean meal in diets for layer hens and weanling pigs. Two experiments were performed to evaluate responses of broiler chickens to the same defatted diatom (DD) biomass (Cellana, Kailua-Kona, HI). In Exp.1, duplicate cages per sex of 5 broiler chicks were fed starter (0–3 wk) and grower (4–6 wk) diets containing synthetic amino acids and DD at 0% (control), 7.5% to replace soybean meal or 7.5% or 10% to replace soybean meal and corn. Chicks fed 7.5% DD replace only soybean meal had 11–18% lower ($P < 0.05$) body weight gain than the controls. Chicks fed 7.5% DD and 10% DD to replace soybean meal and corn had 5–13% and 16–21% lower ($P < 0.05$) body weight gain, respectively, than controls. The differences were statistically significant only in the starter period. Male chicks fed 10% DD also had lower ($P < 0.05$) plasma uric acid and liver triglyceride concentrations than the controls at wk 6. A follow-up experiment was conducted to determine if adding exogenous protease (Ronozyme ProAct, 0.06% of the diet, DSM Nutritional Products Inc., Parsippany, NJ) or more amino acids to the 7.5% DD (to replace only soybean meal) diet restored the growth performance of chicks. Five diets were fed to 6 replicates of 7 male chicks each for 6 wk. Compared with the control, the 7.5% DD diet resulted in a 5% decrease ($P < 0.05$) in overall gain/feed efficiency. The loss was prevented by the addition of more amino acids, but not by the protease. Responses of plasma and liver biomarkers and gross examination of digestive tract indicated no evidence of toxicity of DD in both experiments. In conclusion, the defatted diatom biomass could substitute for 7.5% of soybean alone, or in combination with corn, in diets for broiler chicks when appropriate amino acids are supplemented. (Supported in part by a USDA/DOE Biomass R&D Initiative grant).

Key Words: soybean meal, amino acid, protease

778 Effect of dietary fat sources on tissue α-tocopherol concentration in pig. D. P. Preveraud*[1], E. Devillard[1], and P. Borel[2], *[1]Adisseo France SAS-CERN (Center of Expertise and Research in Nutrition), Commentry, France, [2]UMR NORT (Nutrition Obésité et Risque Thrombotique) 1062 INSERM/1260 INRA/Aix-Marseille Université, Marseille Cedex 5, France.*

Vitamin E (VE) is essential for growth, health and reproduction in pig but its bioavailability is affected by many dietary factors. Our study evaluates the effect of dietary fat sources on tissue α-tocopherol (TOL) content in pig. After weaning at 28 d, 96 piglets were fed for 2 wk a semi-purified diet not supplemented with VE. Piglets were then randomly assigned to 5 isoenergetic diets with 100 ppm VE as dl-tocopheryl-acetate: a control diet (CTRL; with no added fat) and 4 other diets containing either

3% linseed oil (LIN), 3% hydrogenated coconut oil (COC), 3% olive oil (OLI) or 3% safflower oil (SAF). After 42 d, pigs were sacrificed; blood, muscle (Longissimus Dorsi), backfat, and whole liver (without gallbladder) were collected and analyzed for their TOL concentrations by HPLC. For all tissues, LIN and SAF diets led to lower TOL concentrations as compared with the CTRL group: −63% ($P < 0.02$) and −67% ($P < 0.03$), respectively. TOL concentrations in plasma, liver and backfat were higher in the COC group as compared with the CTRL group ($P < 0.001$). OLI diet led to higher TOL concentration in plasma (+21%; $P < 0.01$) and liver (+92%; $P < 0.01$) as compared with CTRL diet, but has no significant effect in muscle and backfat. Plasma and liver TOL showed the same differences among treatments, suggesting that TOL status in these 2 tissues is closely related. In conclusion, our study shows that polyunsaturated fatty acids (FA) found in LIN (48% n-3) and SAF (52% n-6) diets tend to decrease TOL concentration, whereas saturated FA (99% in COC) increase it. We hypothesized that polyunsaturated FA confer changes in mixed micelles size or charge, resulting in decreasing VE bioaccessibility, a necessary step before absorption.

Table 1. Mean TOL concentrations in plasma and tissues

	Fat source[1]				
	CTRL	LIN	COC	OLI	SAF
Plasma (μg/mL)	1.59[b]	0.51[c]	2.15[a]	1.93[a]	0.33[d]
Muscle (μg/g)	4.99[a]	1.75[b]	5.39[a]	4.88[a]	1.43[b]
Liver (μg/g)	6.97[c]	3.21[d]	9.17[b]	13.42[a]	2.71[d]
Backfat (i μg/g)	7.12[b]	2.41[c]	11.00[a]	4.50[bc]	2.91[c]

[a–d]Within a row, means without a common letter significantly differ ($P < 0.05$).
[2]CTRL = control diet with no added fat; LIN = 3% linseed oil; COC = 3% coconut oil; OLI = 3% olive oil; SAF = 3% safflower oil.

Key Words: vitamin E bioavailability, dietary fatty acid, swine

779 Ingredients of plant and animal origin in diets for nursery pigs. K. M. Jones*, J. D. Hancock, and K. M. Sotak, *Kansas State University, Manhattan.*

A total of 224 weanling pigs (avg. initial BW of 6.4 kg and avg age of 21 d) were used in a 34-d growth assay to determine the effects of diet ingredients on growth performance. The pigs were weaned, sorted by sex and ancestry, blocked by BW, and assigned to pens (7 pigs/pen and 8 pens/treatment) in a randomized complete block design. For d 0 to 10, treatments were arranged as a 2 × 2 factorial with main effects of primary protein sources (plant vs. animal) and inclusion of soybean meal (none vs. 30%). The plant protein sources were wheat gluten and corn gluten and the animal protein sources were spray-dried plasma protein and fishmeal. Soybean meal was used to replace corn on a kg/kg basis with no attempt made to reduce protein excess. All diets were formulated to be at least 120, 120, and 110% of requirements for essential amino acids, vitamins, and minerals, respectively, as suggested in the 1998 National Research Council guidelines for swine feeding. For the remainder of the experiment (d 10 to 34) pigs were fed a common diet to allow determination of any carryover effects from the diets fed immediately after weaning. As for results, there were no interactions for d 0 to 10, 10 to 34, or 0 to 34 ($P > 0.13$) among the protein sources and inclusion of soybean meal for ADG, ADFI, or G/F. However, use of animal products increased ($P < 0.02$) ADG by 61% and G/F by 16% for d 0 to 10 and ADG by 7% for d 0 to 34. Also, soybean meal increased ADG by 31% for d 0 to 10 ($P < 0.001$) and by 5% for d 0 to 34 ($P < 0.07$). In conclusion, the use of animal products (plasma protein and fishmeal) and soybean meal (30% of the diet) enhanced rate of gain in weanling pigs.

Table 1.

	Plant		Animal		
Item	0%	30%	0%	30%	SE
d 0 to 10					
ADG, g	111	173	212	249	13
ADFI, g	149	164	219	222	10
G/F, g/kg	745	1055	968	1122	51
d 0 to 34					
ADG, g	474	489	498	530	15
ADFI, g	590	622	628	640	15
G/F, g/kg	803	786	793	828	19

Key Words: animal protein, soybean meal, pig

780 Growth performance of weanling pigs fed diets containing copra meal, palm kernel expellers, or palm kernel meal. N. W. Jaworski*, J. C. Gonzalez-Vega, and H. H. Stein, *University of Illinois at Urbana-Champaign, Urbana.*

Three experiments were conducted to separately evaluate copra meal (CM), palm kernel expellers (PKE), and palm kernel meal (PKM) in phase 2 diets for weanling pigs. In Exp. 1, 128 pigs (initial BW = 9.2 ± 1.2 kg) were randomly allotted to 4 diets that were fed for 20 d. There were 4 pigs per pen and 8 replicate pens per treatment. The control diet was based on corn, soybean meal, and 4% fish meal. Three additional diets were formulated by including 5, 10, or 15% CM at the expense of corn and soybean meal. Diets were formulated to contain equal quantities of digestible AA and P, and ME. Individual pig BW was recorded at the start of the experiment, on d 10, and at the conclusion of the experiment. Daily feed allotments were recorded and feed left in the feeders were recorded on the same day as pigs were weighed. In Exp. 2, 128 pigs (initial BW = 9.8 ± 1.0 kg) were randomly allotted to 4 diets. This experiment was similar to Exp. 1 with the exception that 0, 5, 10, or 15% PKE rather than CM was included in the diets. Exp. 3 was also similar to Exp. 1 with the exception that 0, 5, 10, or 15% PKM were used and a total of 160 pigs (initial BW = 8.4 ± 1.3 kg) were allotted to the 4 treatment diets with 5 pigs per pen and 8 replicate pens per diet. Linear and quadratic effects of including increasing levels of CM, PKE, and PKM were determined using orthogonal CONTRAST statements in SAS. Results indicated that weanling pigs fed increasing levels of CM had a linear reduction ($P < 0.05$) in final BW (19.5, 19.1, 18.9, and 18.5 kg), overall ADG, and overall ADFI, but overall G:F was not influenced by CM in the diet. Pigs fed increasing levels of PKE also had a linear reduction ($P < 0.05$) in final BW (20.3, 19.6, 19.9, and 19.2 kg) and overall ADG, but overall ADFI and G:F were not influenced by PKE in the diet. However, if PKM was used, no differences in final BW and overall ADG, ADFI, or G:F were observed. In conclusion, if diets are formulated based on digestible nutrients and ME, phase 2 diets for weanling pigs may include up to 15% PKM without affecting overall performance, but this is not the case for CM and PKE.

Key Words: copra meal, palm kernel products, pig

781 Nutritive value of low phytate peas and barley based diets fed to growing pigs. R. K. Kahindi*[1], P. A. Thacker[2], and C. M. Nyachoti[1], *[1]University of Manitoba, Winnipeg, MB, Canada, [2]University of Saskatchewen, Saskatoon, SK, Canada.*

Five ileal cannulated barrows (BW of 42.8 ± 1.3 kg) were used in a 5 × 5 Latin square design to determine apparent (AID), standardized (SID) ileal digestibility of N and AA in low phytate barley (LPB), peas (LPP), and

normal peas (NP) and total tract (ATTD) digestibility of Ca and P of diets containing these ingredients, and the effect of phytase supplementation. Five experimental diets were formulated to contain 86.93% LPB, 86.81% LPP or 86.95% NP; phytase was supplemented at 500 FTU/kg to the LPP and NP diets to produce 2 additional diets. The ingredients contained Ca (0.13, 0.23, 0.21%), P (0.41, 0.47 and 0.43%), and phytate P (0.04, 0.07 and 0.20%) for LPB, LPP, and NP, respectively. Inorganic Ca was added in all diets to meet recommended values, while inorganic P was added only in peas containing diets to obtain 65% available P recommended by NRC (1998) for 20 to 50 kg pigs. The ingredients were the sole source of protein and SID of N and AA were calculated using published values for ileal basal endogenous AA losses from our laboratory. Titanium dioxide (0.3%) was used as indigestible marker. Daily feed allowance was set at 4% of BW at the beginning of each period and offered in 2 equal portions at 0800 and 1600 h. Each experimental period lasted for 8 d; d 1 to 4 for adaptation, 5 to 6 for ileal digesta collection, and 7 to 8 for urine and fecal collection. The ATTD of Ca and P were significantly higher ($P < 0.0001$) in LPB than in LPP and NP diets. Supplementing LPP and NP diets with phytase increased ($P < 0.05$) ATTD of Ca and P. The AID of N and AA except Met were higher ($P < 0.05$) in LPP and NP than LPB, and similar ($P > 0.05$) for LPP and NP. Phytase supplementation increased ($P < 0.05$) AID of Arg, Ile, Leu, Phe, Pro, Ser, Tyr, and Val. The average SID values for Lys (73.4, 89.5, 89.5%), Met (73.2, 75.7, 74.4%) and Thr (68.8, 81.6, 81.5%) in LPB, LPP and NP, respectively. The results show that the pea varieties had higher AID of AA than LPB. Additionally, LPP diet had higher ATTD of Ca and P compared with NP diet and enzyme supplementation improved nutrient digestibility.

Key Words: low phytate peas, nutritive value, pig

782 Effects of acidified protein feed on growth performance, digestive characteristics, and gut bacterial communities in growing and finishing pigs. J. Chen*, Y. Xiao, X. Li, Q. Hong, and A. Chen, *College of Animal Sciences, Zhejiang University, Hangzhou, Zhejiang, China.*

A new protein feed resource was developed in this study. Corn protein powder and citric acid mycelium which was the residue of production of citric acid were combined in proportion of 3 to one to make the acidified protein feed (APF). The contents (g/kg, 90.60% DM) of CP, Lys, Met, and Thr of ADF were 294.52, 8.71, 6.35, and 7.69, respectively. Potential effects of APF as a substitute for a portion of soybean meal and corn of diet on growth performance, intestinal digestive characteristics and bacterial communities in growing and finishing pigs were investigated. A total of 240 pigs of 30 ± 1.2 kg were randomly assigned into 2 groups: (1) APF group (20% APF added to basal diet instead of 10% corn and 10% soybean meal), (2) control group. There were 6 replications per group and 20 pigs per replication. Fat powder and Lys were added to meet requirements on a true ileal digestible basis. The pH value of APF-treated diet was 6.01, and the control was 6.28. Growth performance were evaluated based on each replication by *t*-test, while 6 pigs per group were euthanized to assay intestinal pH value, digestive enzyme activity, apparent ileal digestibility (AID), and ileal and cecal bacterial communities by PCR-DGGE on d 50 and d 105. Results showed that ADG increased by 6.8% ($P > 0.05$) on d 50, whereas F:G decreased by 10.2% ($P < 0.05$). Addition with APF decreased ($P < 0.05$) the pH value in duodenum of pigs. The trypsin activity increased ($P < 0.05$) in duodenum and jejunum of the APF-treated pigs. The AID of Thr, Lys, Leu, Val, Ala and Ser increased ($P < 0.05$) by 8.02%, 6.01%, 10.86%, 7.57%, 7.50%, and 7.13% in APF group on d 50, respectively, as Lys increased by 5.89% on d 105. It was observed that the total number of DGGE bands and Shannon index of diversity for ileal and cecal content samples were greater in APF group. In conclusion, the APF as a substitute for the proportion of basal diet in the form of corn and soybean meal can modify the intestinal digestive characteristics and bacterial communities to improve the growth performance in growing and finishing pigs.

Key Words: acidified protein feed, digestive characteristics, pig

Production, Management and the Environment Symposium: Confinement Animal Agriculture Sustainability

783 Navigating sustainability. J. L. Capper*[1] and R. R. White[2], *[1]Livestock Sustainability Consulting, Bozeman, MT, [2]Washington State University, Pullman.*

Sustainable livestock production may be defined as: "a system that meets the needs of the present without compromising the ability of future generations to meet their own needs." As the global population increases, livestock production sustainability necessitates providing sufficient safe, affordable food to supply societal needs, while balancing 3 key metrics: economic viability, environmental responsibility, and social acceptability. Systems that fail to achieve a balance between these 3 metrics will ultimately cease to exist. In contrast to historical systems in which economic viability was the most important metric, growing consumer awareness of food production systems has led to an increased focus upon the environmental and social consequences of dietary choices. This has been highlighted by the increasing popularity of "Meatless Mondays" campaigns in recent years. System-wide changes in US beef, dairy and swine industries over time have demonstrated the positive environmental effects of improved productivity through intensification, which has also facilitated decreases in economic costs of production and thus retail prices. However, although environmental impacts (resource use and carbon emissions) are increased in extensive compared with intensive production systems, philosophical concerns relating to conventional livestock production impacts upon biodiversity, animal welfare and human health are difficult to address scientifically and may lead to a lack of consumer confidence. Sustainability is theoretically irrespective of size or system, however it may only be achieved providing that a consumer willingness to pay (WTP) exists for the product. Although the stated WTP is often greater than the actual WTP for livestock products, data indicates that consumers show a greater WTP for perceived health benefits than for environmental indicators, although quality indicators are more important than either health or environmental metrics. Sustainability will continue to be a key focus for all food production stakeholders—the challenge facing the livestock sector is to find appropriate messages to address consumer concerns that tend toward philosophical ideology rather than scientific fact.

Key Words: sustainability, livestock, consumer

784 The US Swine Industries Carbon Footprint. R. Ulrich*, G. Thoma, J. Popp, and G. Rodriguez, *University of Arkansas, Fayetteville.*

The greenhouse gas footprint of confinement-based pig production facilities was compiled and, based on this LCA, an emission model was constructed to be used as a tool in identifying infrastructure and operational parameters to reduce emissions in a cost-effective manner. The LCA indicated that the main contributors to GHG emissions is methane from on-farm manure handling systems and carbon dioxide from feed production resulting from fertilizer manufacture and crop handling. The emissions model is built upon a detailed pig production model that predicts the required usage of electricity, gas, propane, water, and feed along with the expected manure amount and composition. These overheads are used to calculate the emissions of carbon dioxide, methane and nitrous oxide from the various parts of the pig farm. Since the user does not have to enter in the amount of consumables, the model can be used to predict the effect of infrastructure and operational changes on GHG emissions. An economic module calculates the dollars per kg of equivalent carbon dioxide avoided. The model indicates that one of the easiest ways to reduce GHG emissions is to build manure handling facilities to avoid seasonal high temperatures in the system.

Key Words: greenhouse gas emissions, pig farm, modeling

785 Nutrient management and environmental and societal issues affecting sustainability of feedlot finishing systems. N. A. Cole*[1], R. W. Todd[1], H. Waldrip[1], K. Hales[2], and J. C. MacDonald[3], *[1]USDA-ARS-CPRL, Bushland, TX, [2]USDA-ARS-MARC, Clay Center, NE, [3]Univ. of Nebraska, Lincoln, NE.*

Cattle evolved on a diet consisting primarily of forages. Thus, it is often assumed that the "ideal" system for producing cattle is pasture-based. In contrast to much of the world, beef cattle in North American typically spend a portion of their life in feedlots where they are fed diets high in grains and/or by-products. Feeding cattle nutritionally balanced, high-energy diets in confinement has many advantages over pastoral systems. However, feeding cattle in confinement leads to a concentration of nutrients into a small geographic area. Significant environmental and economic concerns include accumulation of nutrients, extraneous losses of nutrients to ground and surface water, removal of accumulated manure, excretion of pathogens and physiologically active compounds (PAC), and emissions of ammonia, greenhouse gases (GHG), odors, and dust. The public often views with concern, animal welfare and the use of growth promoters and antibiotics. Nutrition and management practices influence the quantity of nutrients excreted by the animal, transformations and movements of those nutrients, as well as losses of ammonia, volatile organic compounds, particulate matter, GHG, and PAC. Fortunately, ruminants can readily utilize a variety of high-fiber by-products to produce high-quality protein. The growth of the grain-based bio-fuel and corn sweetener industries has provided cattle feeders with a large supply of by-products (distillers grains, corn gluten feed, etc.) that can be substituted for feed grains. Because these byproducts are usually high in fiber, N, P, and S, when fed at high dietary concentrations, manure production, N, P, and S excretion, enteric methane emissions, and ammonia, nitrous oxide, and hydrogen sulfide emissions from manure are all increased. However, feeding lower concentrations (<30% of DM) of these by-products and use of grain processing techniques such as steam flaking may actually decrease the environmental footprint of feedlots by decreasing the quantity of feed grains required.

Key Words: beef cattle, feedlot, sustainability

786 Nutrient management, environmental issues and societal issues affecting confinement dairy sustainability. J. H. Harrison*, *Washington State University, Puyallup.*

Management on dairy operations has become more complex as society demands more attention be placed on environmental stewardship. During the past 2 decades most emphasis has been placed on nutrient management in the context of nitrogen and phosphorus. With this effort there has been a need for dairy operations to focus on nutrients at a whole-farm level. The emphasis of contemporary integrated nutrient management should be placed on 3 areas: reducing imports, enhancing within farm efficiencies (both cropping and cow efficiencies), and seeking export opportunities for excess nutrients not utilized for crop production on the

farm. Emerging areas of concern are the fate and transport of pharmaceuticals in the environment. Management of nutrients and pharmaceuticals at the whole-farm level needs to be accompanied by an effort to inform the public and environmentally concerned groups about the proactive efforts that producers have adopted to protect the environment. To be sustainable, integrated nutrient management will require an expanded effort to reconnect the nutrient cycle and link the movement of nutrients between sites of feed production and feed utilization. Resources need to be focused on clearly defining the fate and transport of pharmaceuticals so that effective management practices can be developed to minimize movement of pharmaceuticals into air and water.

Key Words: sustainability, nutrient, pharmaceutical

Production, Management and the Environment: Surveys and Models II

787 Mortality rate of dairy calves in a calf rearing farm (CRF). D. Aponte[1], J. Rossi[3], J. Raciti[4], and P. Celi*[1,2], *[1]Faculty of Veterinary Science, The University of Sydney, Narellan, NSW, Australia, [2]Melbourne School of Land and Environment, The University of Melbourne, Parkville, VIC, Australia, [3]Departamento de Producción Animal, Facultad de Agronomía, Universidad de Buenos Aires, Ciudad Autónoma de Buenos Aires, Argentina, [4]Manfrey Cooperativa de Tamberos de Comercio e Industria, Freyre, Córdoba, Argentina.*

Calf rearing farms (CRFs) in Argentina are properties where calves are custom raised until they are approximately 90–120 d old. Both heifers and male calves are reared on CRFs with the number of male calves increasing over the past few years due to the opportunity cost in meat price for heavier and leaner animals. Little information has been published about CRFs and the performance of calves reared on these farms is unknown. Therefore the aim of this study was to evaluate CRFs due to the opportunities they offer to overcome the limitations faced by the dairy industry, including lack of labor, land and increased costs of production. Data was collected from the CRF's database and included 39,340 calves (21,028 heifers and 18,312 bulls) from 26 farms reared between 1994 and 2012. From the day of their arrival on the CRF up to 90 d of age, calves were individually tied up to a stake which held a stand used to place the buckets for feeding milk (4 L/head/day) and concentrate (Calf Starter; 0.1–3 kg/head/day). From 90 to 120 d of age, calves were housed in-group pens (30 calves per pen) with shade, and shared feeding and watering facilities. Effects of farm of origin, sex, live weight (LW) at entry, condition of entry, distance traveled from farm to CRF, month and year of birth on mortality rate and survival time were analyzed by multiple logistic regression models using Genstat version 14. Farm of origin, sex, condition of entry, distance traveled from farm to CRF, month and year of birth had no significant effect on mortality rate and survival time. The overall mortality rate observed was 4.2% which is well below to that reported in private farms in Argentina (7.5–15.4%) and reflects the high standard of management offered in this CRF. It was observed that survival time was associated with LW at entry ($P < 0.001$), with calves surviving 0.83 d longer for each extra kg of LW at the time of entry. Simple interventions during the peripartum period (separation calf-dam and colostrum management) might have the potential to significantly reduce the effect of calf LW on calf mortality and survival on CRFs.

Key Words: dairy calf, calf rearing farm, mortality

788 A mechanistic model for estimating water excretion in dairy cows. J. A. D. R. N. Appuhamy*[1], E. Kebreab[1], and J. France[2], *[1]University of California, Davis, [2]University of Guelph, Guelph, ON, Canada.*

Reliable estimates of fresh manure water contents would improve predictions of nutrient transformations during manure storage. The objective of present study was to propose a mechanistic mathematical model to determine water excretions in urine (WU) and feces (WF) of dairy cows. The model included 3 body water pools; rumen water (Q_R), post-rumen water (Q_{PR}), and absorbed-water (Q_{AB}). Inflows to Q_R pool were saliva, drinking water and water in feed, and outflows from the pool were absorbed water and water passing to the Q_{PR}. Water from Q_R and drinking water bypassing rumen were inputs to Q_{PR}, and absorbed water and water to feces were outflows. The Q_{AB} pool had inputs from absorbed water flows from Q_R and Q_{PR}, and outflows were water in urine, milk, saliva, water for growth and maintenance and evaporated water. Saliva flows were determined with a function of dry matter intake (DMI). Drinking water flows were estimated with a linear function of DMI, dry matter (DMP), organic matter (OMP) and crude protein (CP) contents of feed. Fractional rates of absorption flows from Q_R and Q_{PR} were respectively adjusted for DMI and dietary acid detergent fiber (ADF) contents. Water flow to urine was determined as a linear function of Q_{AB}, CP, and milk yield. Water flow to milk was calculated with milk yield and a coefficient of water content in milk. Model was internally evaluated using 600 observations of daily WF and WU from dairy cows with respect to DMI, DMP, OMP, CP, ADF, and milk yields. Mean square prediction error (MSPE) was calculated and decomposed to systematic (SB) and random (RB) bias. Root MSPE was expressed as a percentage of mean observed values (RMSPE). Predictions of WF and WU were associated with 19 and 28% RMSPE respectively and about 97% of the MSPE was due to RB. The model was externally evaluated with an independent data set of 594 observations. Predictions of WF and WU had 29 and 34% RMSPE respectively with10 to 25% coming from SB. The proposed model appeared to reasonably predict WF and WU of dairy cows. Model reparameterizations addressing the SB could further improve model prediction accuracies.

Key Words: dairy cow, mathematical model, water excretion

789 Predictors of the heat stress response in lactating Holstein cows. S. K. Stoakes*[1], M. Abuajamieh[1], M. V. Sanz-Fernandez[1], J. S. Johnson[1], D. B. Snider[1], R. P. Rhoads[2], and L. H. Baumgard[1], *[1]Iowa State University, Ames, [2]Virginia Polytechnic Institute and State University, Blacksburg.*

Heat stress (HS) threatens the economic stability of the dairy industry and global food security. Study objectives were to identify predictors of the HS response in lactating dairy cattle. Data from 6 studies (Rhoads et al., 2009, 2010; Shwartz et al., 2009; Skrzypek et al., 2010; Wheelock et al., 2010; Baumgard et al., 2011) were combined into one data set. All cows (n = 123) were in a thermoneutral period (TN; P1; 19 ± 1.1°C) followed by either a HS (cycling 30.0 to 38.7°C; n = 82) or a pair-fed thermoneutral (PFTN; n = 41) period (P2) for 7 d. Correlations between indices of rectal temperature (Tr), respiration rate (RR), milk yield (MY), and dry matter intake (DMI) during TN, HS and PFTN were examined using a Pearson correlation in SAS. During P1, only MY ($P < 0.01$, r = −0.46), Tr ($P < 0.04$, r = −0.23), and RR ($P = 0.03$, r = 0.24) were associated with MY decrease during HS, and only P1 MY ($P < 0.01$, r = −0.43) and DMI ($P = 0.03$, r = −0.34) were associated with the MY decrease during PFTN. P2 DMI was negatively associated ($P < 0.01$) with the percent MY decline for both HS (r = −0.46) and PFTN (r = −0.56). Tr response on d 1 of HS was associated with percent P2 MY decline (r = 0.63), total MY loss (r = 0.56), MY slope (r = −0.49), and average MY decline per d (r = 0.56). Average P2 daily RR was correlated with Tr ($P < 0.01$, r = 0.31); however, morning RR was a better indicator of average daily Tr during HS ($P < 0.01$, r = 0.40) compared with evening RR ($P = 0.03$, r = 0.25). In summary, only TN MY and Tr response slightly predicted MY decrease during HS and this supports the dogma that high-producing dairy cows are more susceptible to heat stress.

Key Words: heat stress, dairy cow, production parameters

790 Visualization of lifetime profitability curves in Quebec dairy cattle. H. Delgado*[1], R. Cue[1], A. Sewalem[4], R. Lacroix2,1, D. Lefevre[2], E. Bouchard[3], J. Dubuc[3], and K. Wade[1], *[1]Dairy Information Systems Group, McGill University, Montreal, QC, Canada, [2]Valacta, St. Anne de Bellevue, QC, Canada, [3]Université de Montreal, St. Hyacinthe, QC, Canada, [4]Agriculture and Agri-Food Canada, Guelph, ON, Canada.*

Data from veterinary-health and dairy-herd improvement (DHI) sources were combined (56,121 animals from 663 herds) to perform a diagnosis and analysis of the different factors affecting lifetime profitability in Québec dairy cattle. Lifetime profit was calculated by deducting costs for heifer rearing, feed, breeding and health from current milk prices. DHI-recorded events were used to calculate age at first calving and the cumulative lifetime events (health episodes and breeding services). Costs for these various events were estimated based on current Québec figures. Information was normalized and compiled, and lifetime records were created using SAS 9.2. Animals in the data set started their first lactation between 2000 and 2011. For the lifetime analysis, all animals were required to have a code for "left herd reason" and a corresponding date. Individual curves were developed for animals with reported health episodes, and compared to animals with no reported health problems. This visualization of the curves allowed for the monitoring of an individual animal's lifetime profit and especially demonstrated how it may be affected by age at first calving, extended calving intervals and health issues. To maximize the validity of the analysis, animals were selected from herds that routinely recorded health events. From this resulting subset of the data, first-lactation animals with mastitis, displaced abomasum or ketosis were found to incur an additional 73.69%, 28.08% and 32.54% in costs respectively over those first-lactation animals reported as not having health problems. The equivalent costs for second-lactation animals were 17.99%, 11.79% and 13.00% respectively, while those for third-lactation animals were 21.71%, 12.51% and 15.02% respectively. For that same data set, average productive life estimates for animals culled for involuntary culling reasons, for mastitis, and for displaced abomasums were 35.59, 37.24 and 31.77 months respectively. Such lifetime profit measures will allow producers to more accurately evaluate the impact of health events on individual cow profitability and hence improve overall selection for profitability.

Key Words: lifetime, profitability, visualization

791 Stochastic economic evaluation of dairy farms' reproductive performance. A. S. Kalantari* and V. E. Cabrera, *University of Wisconsin-Madison, Madison.*

The objective of this study was to evaluate reproductive performance in dairy cattle under farms uncertain and variable conditions. Consequently, this study introduced stochasticity into a Markov chain model. A Markov chain model with 21 d stage length and 3 state variables—parity, days in milk, and days in pregnancy—was developed. Uncertainty was added to all main transition probabilities -involuntary culling, pregnancy rate, abortion risk, and milk production level- step by step to explore the effect of adding a single random variable at a time. Randomness was introduced in 1 of 2 ways: (1) using a polynomial regression model to build a white noise around the observed historical data for involuntary culling and abortion; and (2) using distributions -such as normal distribution for milk production levels and triangular distribution for pregnancy rates. The model was run for 10,000 replications after introducing each random variable. After verifying model's behavior, the model was run for 2,000 replications to study the effect of incrementing the 21-d pregnancy rates from 10 to 25% with one-unit-percentage intervals. An overall increase in the net return ($/cow per yr) from 10% 21-d pregnancy rate to 25% was observed. This marginal increment was greater at the lower pregnancy rates ($9 ± 6.8/cow per yr) and decreased to $5 ± 5.1/cow per yr in higher pregnancy rates. The reason for this difference among net returns of different reproductive performances was mainly due to the increment in the calf revenue and decrement in the culling and reproductive costs. There was a slight reduction in the overall milk revenue after increasing 21-d pregnancy rate, which was mainly due to the defined shapes of the milk lactation curves used in this study.

Key Words: Markov chain, stochastic, reproductive performance

792 A 50-year comparison of the environmental impact and resource use of the US swine herd: 1959 vs. 2009. R. A. Cady*[1], G. Boyd[2,3], L. Wittig[3], G. Bryan[4], P. J. Holden[5], A. L. Sutton[6], and D. Anderson[7], *[1]Elanco, Greenfield, IN, [2]Prasino Group, Topsail Beach, NC, [3]Camco, Broomfield, CO, [4]Camco, London, UK, [5]Iowa State University, Ames, [6]Purdue University, West Lafayette, IN, [7]Anderson Associates, Loveland, CO.*

Cradle-to-gate lifecycle assessments compared environmental impact and resource use of US swine production in 1959 to 2009. The functional unit is one kg of hot dressed carcass weight (HDCW). Boundaries were from crop sowing to market-ready hogs at the farmgate. A process-based deterministic model tracked yearlong pig flow through swine production. Age-sex subclass census were adjusted to account for mortality and live hog import/export. USDA-NASS, USDA-ERS and the 1959 Agricultural Census provided hog demographics, crop statistics, irrigation, and crop inputs. The 2006 NAHMS swine reports, NRC 10th Edition of Nutrient Requirements of Swine, and the 2011 National Life Cycle Carbon Footprint Study for US Swine provided hog management data. Emission factors came from ASAE and Ecovent. Annual feed requirements were estimated using era-typical diets. Water intake and manure excretion were estimated. Cropland requirements were estimated using yield and input data for pesticides, energy use, and irrigation. Land use was discounted for by-product feeds. Emission factors were obtained for hog production, cadaver disposal, cropping, feed processing and transport, manure handling, and energy use. Prediction of live hogs to market was within ±0.1% of actual. The 2009 carbon emissions (CO_2e) were within 10% of the livestock portion US National Swine Lifecycle report and fell within the 95% CI. Marketed hogs increased from 87,600,000 to 112,600,000 from a 39% smaller breeding herd. HDCW yield increased from 5.49 million metric tonnes (MMT) to 10.34 MMT; an increase of 1,012 kg of HDCW harvested per sow-year. Total feed increased 25% resulting in whole population feed conversion improving from 6.6 kg feed/kg HDCW to 4.4 kg/kg. Added gains in crop yields and by-product feed use led to a 59% decrease of land required resulting in a 78% decrease in land per kg HDCW. Annual animal water consumption increased from 123.6 billion L to 137.1 billion L. However, water consumption decreased from 22.5 L/kg HDCW to 13.3 L/kg. CO_2e emissions increased from 45.7 MMT to 56.1 MMT while kg CO_2e/kg HDCW declined 35% from 8.3 kg/CO_2e to 5.4 kg/CO_2e.

Key Words: carbon footprint, sustainability

793 Effects of of 2-hydroxy 4-(methylthio) butanoic acid iso-propyl ester (HMBi) and DL-Met on in vitro fermentation characters of high-yielding dairy cow diets. B. B. Nobari*[1], A. Taghizadeh[1], M. Khorvash[2], S. Alijani[1], J. Shodja[1], and F. Parnian, and K. Dizaj[1], *[1]Department of Animal Sciences, Faculty of Agriculture, University of Tabriz, Tabriz, Eastern Azarbaijan, Iran, [2]Department of Animal Science, College of Agriculture, Isfahan, Isfahan, Iran.*

An in vitro gas production and degradability study has been conducted to investigate the effects of 4 treatments including: no supplement (cnt), 0.065% HMBi/ DM diet (HMBi-1), 0.13% HMBi/ DM diet (HMBi-2) and 0.088% DL-Met/ DM diet (DL-Met) on typical dairy cow diets. Two diets with 17.7% (HCP, high crude protein) and 15.7% (LCP, low crude protein) CP have been formulated by different ingredients for early lactating Holstein dairy cows (DIM 55 ± 7, BW 650 and Milk yield 55 ± 6.4). Results revealed that digestibility of DM were significantly increased by HMBi and DL-Met addition while digestibilities of ADF, NDF and HEMI was decreased for the DL-Met treated diets compared with the diet containing the equivalent amount of Met supplied as HMBi-2. Asymptote gas production (A) has been affected by HBMi and DL-met supplementation ($P < 0.01$) but fractional gas production rate (c) parameter of gas production has not affected by treatments. Regarding fermentation parameters, pH has not been affected by supplements or CP levels. Also, there are linear and quadratic effects of HMBi incremental levels on ammonia-N, whereas its concentration decreased with addition of HMBi. Supplementation of HMBi and low crude protein diets can reduce excess ammonia-N load in rumen and increase N utilization in dairy industry which will modify animal health as well as environment friendly farming.

Table 1. Nutrient digestibility, gas production and fermentation parameters of two diets in batch culture including two concentrations of HMBi or DL-Met

	HMBi (%)					Contrasts					*P*-value	
Item	0	0.065	0.13	dl-met	SEM	L	Q	HMBi2 vs. dl-met	Cnt vs All	M	CP	M × CP
GP parameters												
A (ml)												
HCP	214.6	224.6	212.9	223.0	0.96	<0.01	<0.01	<0.01	<0.01	<0.01	<0.01	<0.001
LCP	217.1	221.6	199.6	187.6								
c (%/h)												
HCP	0.061	0.063	0.060	0.063	0.003	0.989	0.594	0.251	0.510	0.616	<0.001	0.721
LCP	0.068	0.075	0.075	0.075								
Lag (h)												
HCP	0.30	0.25	0.56	0.63	0.16	0.117	0.457	0.201	0.407	0.368	0.916	0.266
LCP	0.51	0.46	0.20	0.61								
Fermentation parameter												
pH												
HCP	5.39	5.38	5.40	5.37	0.02	0.164	0.426	0.164	0.564	0.404	0.323	0.400
LCP	5.36	5.37	5.42	5.38								
Ammonia-N (mg/dL)												
HCP	5.57	5.31	4.91	5.30	0.40	0.016	0.312	0.002	0.031	0.012	0.607	0.850
LCP	5.37	5.25	4.93	5.37								

Key Words: degradability, fermentation, HMBi

794 Study of the effect of flavonoid substances on methanogenesis on in vitro fermentation of rumen liquor coming from different experimental diets in beef cattle. A. R. Seradj*[1], J. Balcells[1], H. J. Morazan[1], D. V. Mata[1], J. Crespo[2], and M. Fondevila[3], *[1]Dept. Animal Production, University of Lleida, Lleida, Spain, [2]Interquim, S.A. (Ferrer HealthTech), Barcelona, Spain, [3]Dept. Animal production and nutrition, University of Zaragoza, Zaragoza, Spain.*

Two in vitro incubation trials in a randomized complete block design were conducted to evaluate the effect of Neohesperidine (NH) and Bioflavex (BF) at 5 mg/L compared with an unsupplemented control (CTR) on total gas and methane production. Two groups of steers given a total mixed ration (TMR) and concentrate plus straw were used as donors of rumen liquid, which was filtered and immediately used as inoculum. Bottles of 120 mL were filled in anaerobic conditions with 80 mL of incubation solution including 20% strained rumen fluid, and kept at 39 °C for 72 h in triplicate. The pressure measurements were carried out at different incubation times and converted to volume. From 12h, a gas sample (0.1 mL) was taken manually using a gas tight syringe and immediately analyzed for methane concentration using gas chromatography (GC). One bottle from each treatment was opened under anaerobic conditions and sampled for pH and volatile fatty acids (VFA) using GC at 0, 12 and 72 h. A nonlinear model for rate determination with lag time [$y = a (1 - e^{-b (t-c)})$] was applied to determine the potential cumulative gas production, fractional rate and discrete lag time. No effect of BF and NH was recorded ($P > 0.05$) on gas production despite the diet given to donor animals; however, NH produced more gas ($P < 0.05$) than BF and CTR Both BF and NH reduced ($P < 0.01$) the production and proportion of methane respect to CTR in rumen liquid from both origins. Compared with NH, BF showed lower methane production (170.2 vs. 188.6 mL; SEM 3.37; $P < 0.01$) and methane percentage (13.52 vs. 13.88% SEM 0.22; $P > 0.05$). Total VFA concentration decreased with BF ($P < 0.01$) and NH ($P > 0.05$), and both BF and NH decreased ($P < 0.01$) the acetate to propionate ratio as compared with control. The 2 sources of flavonoids did not affect gas production pattern. However, VFA concentration increased and acetate to propionate molar proportion decreased, and consequently methane production was reduced.

Key Words: Bioflavex, methanogenesis, Neohesperidine

795 Gastrointestinal bacterial and methanogenic archaea diversity in response to feeding condensed tannins-containing pine bark diet to goats using 16S rDNA amplicon pyrosequencing. B. R. Min*[1], S. Solaiman[1], R. Shange[1], and J. S. Eun[2], *[1]Tuskegee University, Tuskegee, AL, [2]Utah State University, Logan.*

Eighteen Kiko-cross goats (33.4 ± 0.98 kg; n = 6) were used to measure gastrointestinal (GI) bacteria and methanogenic archaea (MA) diversity when fed condensed tannins (CT)-containing pine bark (PB). The GI fecal collection was performed during 7 d in 2 different periods. Three dietary treatments were tested: control diet (0% PB and 30% wheat straw (WS; 0.17% CT DM); 15% PB and 15% WS (1.6% CT DM), and 30% PB and 0% WS (3.2% CT DM). Populations of the GI bacteria and MA were measured using a 16S rDNA bacterial tag-encoded FLX amplicon pyrosequencing technique to characterize and elucidate changes in GI bacteria and MA diversity among the diets. All the statistical analyses were conducted using the MIXED procedures of SAS, and orthogonal polynomial contrasts were performed to determine linear and quadratic effects of feeding PB in the diets. Total 416 bacteria (60 unknown spe-

cies) and 26 MA genera were detected in goat samples. *Proteobacteria* was the most dominant phyla with mean relative abundance values ranging from 39.7% (30% PB) to 46.5% (control) and 47.1% (15% PB). The remaining phyla accounted for fewer than 25% of the relative abundance observed. Of these groups, *Gammatoproteobacteria* ($P < 0.05$), *Flavobacteria* ($P < 0.01$), *Proteobacteria* ($P < 0.05$), and Bacteroides ($P < 0.05$) were linearly decreased ($P < 0.05$) with increasing dietary PB concentration. However, Clostridia ($P < 0.01$) and *Firmicutes* ($P < 0.05$) were linearly increased with increasing PB concentration. Predominant GI genera among methanogens were *Methanobrevibacter* (75, 72, and 49%), *Akkermansia* (17, 23, and 41%), *Methanosphaera* (3.3, 2.3, and 3.4%), and *Methanobacteriaceae* (1.2, 0.6, and 0.7%) population in control, 15, and 30% PB, respectively, and they were linearly decreased or increased with increasing PB concentration ($P < 0.05$). Other 22 GI fecal MA genera population (<1%) varied among treatments. These results indicated that feeding PB selectively reduced bacteria and main MA populations in the GI tract of meat goats.

Key Words: bacteria, methanogenic archaea, pine bark

797 Effect of polymer-coated urea and sodium bentonite on digestibility, nitrogen retention and rumen fermentation in sheep fed high levels of corn stalk. A. R. Chegeni[1,2], Y. L. Li*[1], C. G. Jiang[1], Q. Y. Diao[1], *[1]Feed Research Institute, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Lorestan Agricultural and Natural Resources Research Center, Khorramabad, Lorestan, Iran.*

The experiment of this study was conducted to evaluate the effect of polymer-coated urea (Optigen II, Alltech Inc., Nicholasville, KY) and sodium bentonite (SB) on nutrient digestibility, nitrogen retention and rumen fermentation in sheep fed high level of corn stalk. Four ruminally cannulated thin-tailed Han × Dorper crossbreed wethers were used in a 4 × 4 Latin square design experiment with 4 isonitrogenous and isocaloric diets composed with 60% corn stalk (DM basis) and 40% concentrate (DM basis). The 4 treatments were control (CON), PCU (replacing soybean meal with 1.8% Optigen on control diet), SB (supplementing 2% SB on CON diet), and PCUSB (supplementing 2% SB on PCU diet). The objective of this study was to evaluate if Optigen could be used as a substitution for soybean meal and if SB could improve N utilization. There were no differences in DMI for different treatments. The digestibilities of OM ($P = 0.02$) and nitrogen ($P < 0.01$) for PCU were greater than those in other treatments. The fecal N were numerically lower ($P = 0.09$) for treatments with Optigen (PCU and PCUSB), and nitrogen retentions were numerically ($P = 0.09$) greater. The pH and total VFA were not influenced by different treatments, whereas the proportions of propionate were greater ($P < 0.01$) for treatments with Optigen than those without Optigen. The concentrations of NH_3-N in sheep fed Optigen were greater ($P < 0.05$) at the beginning after feeding, but decreased to the same level with other treatments at the time of 7h. The results showed that using Optigen as N source to replace soybean meal in sheep fed high levels of corn stalk improved parts nutrient digestibilities, likewise increased nitrogen retention and the proportion of propionate. However, adding SB to Optigen had no further beneficial effects on N utilization. It is concluded that Optigen could be used as a substitution for soybean meal in sheep fed high level of corn stalk and had no negative effect on nutrient digestibility, nitrogen retention and rumen fermentation.

Key Words: polymer-coated urea, sheep, sodium bentonite

798 Essential oils modify rumen bacterial compositions in vitro as revealed by microarray analysis. A. K. Patra[1,2] and Z. Yu*[1], *[1]The Ohio State University, Columbus, [2]West Bengal University of Animal and Fishery Sciences, Kolkata, West Bengal, India.*

This experiment was conducted to examine the effect on rumen bacterial composition of 3 different types of essential oils (EOs): origanum oil (ORO), garlic oil (GAO) and peppermint oil (PEO), using a rumen microarray that was developed recently in our laboratory. Each of the EOs was used at 0.50 g/L of the fermentation medium. The number of bacterial operational taxonomic units (OUTs) in the phylum *Firmicutes* was lowered, especially in the class Clostridia by ORO and GAO, but increased by PEO compared with control. The number of OTUs in the genus *Butyrivibrio* was lowered by all the EOs. However, OTUs in the phylum *Bacteroidetes* were increased by ORO and PEO, but not affected by GAO. Increases of OTUs in *Bacteroidetes* mainly resulted from increases of Prevotella OTUs. Overall, 113 individual OTUs showed significant differences ($P \leq 0.10$) among the EOs. Among the predominant OTUs, some OTUs assigned to *Syntrophococcus sucromutans*, *Lachnospiraceae incertae sedis*, and unclassified *Ruminococcaceae* were decreased, while others classified to *Succiniclasticum ruminis*, *Prevotella*, and unclassified *Bacteroidales*, *Lachnospiraceae*, and *Prevotellaceae* were increased markedly by ORO. Garlic oil increased some OTUs related to *S. ruminis*, *Prevotella*, *Clostridium*, *Mogibacterium*, and unclassified *Ruminococcaceae*, while decreasing some OTUs of *Lachnobacterium bovis* and *Bacillus* substantially. For PEO, some OTUs belong to *S. sucromutans*, *S. ruminis*, and unclassified *Ruminococcaceae* and *Lachnospiraceae* were decreased, but other OTUs mainly related to *Roseburia*, *Prevotella*, *Pseudobutyrivibrio*, and unclassified *Ruminococcaceae*, *Lachnospiraceae*, *Clostridiales* and *Bacteroidales* were increased notably. However, principal component analysis indicated that PEO resulted in a distinct ruminal bacterial community, but not GAO or ORO. In conclusion, this study demonstrated that EOs can affect the population dynamics of several bacteria, especially those in the families *Prevotellaceae*, *Lachnospiraceae* and *Ruminococcaceae* depending upon the EO types, resulting in modification on rumen fermentation.

Key Words: essential oil, rumen bacterial composition, microarray

799 Chemical composition and digestion kinetic of urea-molasses treated wheat straw ensiled with exogenous enzyme in ruminally cannulated buffalo bulls. M. Nisa, M. Sarwar, O.A. Khan*, A. Rehman, and M. A. Shazad, *Institute of Animal Nutrition and Feed Technology, University of Agriculture Faisalabad, Faisalabad, Punjab, Pakistan.*

Two experiments were conducted to evaluate the chemical composition and digestion kinetics of urea molasses treated wheat straw (UMWS) ensiled with varying level of exogenous fibrolytic enzyme. Thirty-six laboratory silos, 9 each in completely randomized design of UMWS were treated with 4% urea and 6% molasses with 0 (E0), 1 (E1), 2 (E2) and 3 g (E3) enzyme /kg UMWS on DM for 21 d. Dry matter, OM, NDF, ADF, crude protein, true protein and pH were analyzed. For digestion kinetics, 4 ruminally cannulated Nili Ravi buffalo bulls were used in 4 × 4 Latin square design. The 4 test diets were placed in the rumen of bulls alternatively during 4 periods of 5 d each. Fractional digestion rate was calculated by regressing natural log of potentially digestible fraction remaining at different time intervals over time. The data were analyzed using GLM procedures of SAS. Dry matter, NDF, ADF, crude protein and true protein of UMWS ensiled without or with enzyme remained unaltered. The pH of UMWS without or with enzyme ranged from 8.42 to 8.47 and remained unchanged across all treatments. The lag time, digestion rate, in situ digestibility and extent of digestion of DM, NDF and ADF did not change across all treatments. In conclusion, ensiling UMWS with enzyme did not influence its chemical composition and digestion kinetics.

Key Words: digestion kinetic, exogenous enzyme

800 Effects of nitrate, saponins, sulfate, and their combinations on rumen methanogenesis, fermentation and microbial communities in vitro. A. K. Patra*[1,2] and Z. Yu[1], [1]*The Ohio State University, Columbus,* [2]*West Bengal University of Animal and Fishery Sciences, Kolkata, West Bengal, India.*

This study investigated the anti-methanogenic effects of quillaja saponins (QS), nitrate, and sulfate, and their effects on rumen fermentation and ruminal microbial communities in vitro. Nitrate (5 m*M*), sulfate (5 m*M*), and QS (0.6 g/L) were tested individually and in all possible combinations. All the treatments (8 in total) except sulfate decreased methane production compared with control. Sulfate and its combinations with nitrate or QS did not show cumulative depression in methane production. In contrast, combinations of nitrate with QS or/and sulfate additively lowered methane production, with the lowest (45.7% reduction) methanogenesis caused by the combination of QS, nitrate and sulfate. The combination of these 3 compounds did not affect dry matter or fiber digestion. Concentrations of total volatile fatty acids and molar percentage of acetate were not affected by any of the treatments. Inclusion of QS in the medium, except when nitrate was also added, increased ($P < 0.05$) the molar percentages of propionate. Conversely, molar percentages of butyrate were lowered ($P < 0.05$) by the combination of QS with the other 2 inhibitors. The acetate to propionate ratios were lower ($P < 0.05$) than control when QS and sulfate were added together. Neither any of the compounds nor their combinations altered the abundances of total bacteria or *Ruminococcus albus*. Adding QS alone or together with nitrate or/and sulfate stimulated the growth of *Fibrobacter succinogenes* and *Ruminococcus flavefaciens*, whereas nitrate and sulfate did not. Rumen archaeal populations did not differ among the treatments except between nitrate and the combination of all 3 compounds. Addition of QS, either individually or in combinations, inhibited ($P < 0.05$) the growth of protozoa. The archaeal and bacterial diversity differed ($P < 0.05$) among the treatments. This study demonstrated that feeding QS, nitrate and sulfate together at low concentrates might effectively decrease methanogenesis in an additive manner, while not adversely affecting, even improving, rumen fermentation characteristics.

Key Words: saponin-nitrate-sulfate combination, methanogenesis, rumen fermentation

801 Effects of starch infusion on body condition, lactation performance, and fecal content in lactating cows. Y. Zou*, Y. Guo, Z. Yang, Y. Du, S. Li, and Z. Cao, *State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing, China.*

The effect of ruminal or abomasal starch infusion on body condition, lactation performance, and fecal content of lactating cows was measured. Six Holstein cows (3 multiparous and 3 primiparous) fitted with permanent ruminal cannulas were arranged into 2 complete 3 × 3 Latin squares, infused in the rumen or abomasums with starch solution (800 g/d) or not infused (control) for 15 d. The abomasal infusion was through a plastic tube (6 mm i.d.) inserted into the abomasums through the rumen and held in place with a flexible rubber disk (18 cm i.d.). Extra energy supplementation was balanced with the decreased DMI (0.77 kg/d, $P = 0.26$), thereby milk yield was decreased (0.63 kg/d for abomasal treatment). The decrease ($P = 0.32$) of starch percentage in feces (0.44 vs. 0.51% of DM; starch infusion vs. control) indicated a higher intestinal absorption efficiency, which was in consistent with the data concerning starch digestibility, starch digestibility of cows receiving starch infusion abomasally (93.04%) was greater ($P = 0.39$) compared with ruminally (88.86%). An increase of backfat thickness (BFT) by 1.83 mm (ruminally) and 2.37 mm (abomasally) when starch was infused indicated a decrease in mobilization of adipose reserves and stimulation in lipid anabolism. The results indicated that supplementation of starch at a concentration of 800 g/d in the abomasums could stimulate the body lipid metabolism and storage other than transport to the mammary gland.

Table 1. Body condition, lactation performance, and fecal content of lactating cows infused starch with 800 g/d in the rumen, or the abomasum

Item	Control	Rumen	Abomasum	SEM
DMI, kg/d	18.58	17.96	17.67	0.30
DM digestibility, %	59.01	59.48	60.39	3.34
Starch digestibility, %	88.50	88.86	93.04	1.89
BW, kg	584.5	590.5	600.7	8.35
BCS	2.71	2.75	2.79	0.06
BFT, mm	17.50	19.33	19.87	0.61
Ruminal propionate, mmol/L	17.32	18.28	17.27	0.95
Feces DM, %	16.72	16.84	17.75	0.27
Feces starch, % of DM	0.51	0.44	0.43	0.02
Milk yield, kg/d	20.38	20.35	19.75	0.30
Milk fat, %	3.43	3.42	3.35	0.03
Milk protein, %	2.89	2.91	2.88	0.02
Milk lactose, %	4.94	4.98	4.94	0.03

Key Words: backfat thickness, lactating cow, lactation performance

802 Benefits of using milk fat to true protein ratio to evaluate on farm transition dairy cow lipid metabolism and effect of transition cow success on milk production. Z. Sawall* and N. B. Litherland, *University of Minnesota, St. Paul.*

Three early lactation studies using multiparous cows (n = 176) were evaluated to determine the efficacy of utilizing fat to true protein ratio (FPR) as a determinant of success of transition cow management. To evaluate FPR cut point for risk of lipid related disorders, cows were divided into 2 groups post hoc, < or >1.4 FPR during the first month postpartum. Analysis was conducted using PROC MIXED in SAS with model including, year, diet × year and treatments of < or >1.4 FPR. Cows with a FPR >1.4 vs. < 1.4 had greater serum BHBA mmol/L and NEFA μEq/L on d 1, 7 and 14 postpartum indicating cows >1.4 FPR had subclinical ketosis. Cows with FPR > 1.4 vs. < 1.4 had greater liver triacylglycerol % (TAG) on d 7 and 14. Cows with FPR > 1.4 lost more kg body weight (BW) through the first 4 weeks of lactation. Yield of ME 305d milk yield, kg tended to be greater for cows >1.4 FPR. Utilizing FPR > 1.4 as a minimum cut point is an adequate diagnostic tool sensitive to detecting cows with a mean BHBA > 1.2 mmol/L, which is the lower value for determining subclinical ketosis. Detecting and managing the negative effects of elevated serum BHBA, NEFA and liver triglycerides as indicated by FPR >1.4 has potential to increase ME 305d milk yield. First month FPR is a low cost indicator of transition cow lipid metabolism.

Table 1. Effects of fat to true protein ratio on early lactation lipid metabolism and milk production

	FPR <1.4	FPR >1.4	SEM	*P*-value
BHBA d 1, mmol/L	0.96	1.22	0.08	0.01
BHBA d 7, mmol/L	0.86	1.34	0.12	<0.01
BHBA d 14, mmol/L	0.77	1.25	0.13	<0.01
NEFA d 1, μEq/L	442.14	603.57	45.24	<0.01
NEFA d 7, μEq/L	575.29	857.44	51.23	<0.001
NEFA d 14, μEq/L	513.31	715.50	42.96	<0.001
Liver TAG 7, %	3.80	9.53	0.99	<0.001
Liver TAG 14, %	4.11	7.70	0.73	<0.001
BW change, kg	−33.58	−59.62	5.80	<0.001
ME 305d milk, kg	10,593.00	11,544.00	418.31	0.08

Key Words: fat:protein ratio, lipid metabolism, transition cow

803 Effects of three levels of energy intake during the close-up period on blood metabolites of dairy cows. A. Pineda*, F. C. Cardoso, and J. K. Drackley, *University of Illinois, Urbana.*

Dairy cows start facing negative energy balance few wk before calving leading to blood metabolites imbalance, predisposition to metabolic disorders, and compromised cow performance. The objective of this study was to evaluate the effects of controlled energy intake prepartum on blood metabolites in the peripartum period. Twenty-seven multiparous Holstein cows dried-off 50d before expected calving date were blocked by lactation, body weight, body condition score, and randomly assigned to one of 3 dry period diets. Cows were individually fed throughout the experiment. Dietary treatments were: controlled-energy group (CE; n = 11), fed a high-fiber diet to supply 100% of NRC requirements for energy and all nutrients ad libitum; high-energy group (HE; n = 7), fed a diet formulated to supply 160–180% of energy (NEL) requirements at ad libitum intake; and restricted-energy group (RE; n = 8), fed to 80% of their calculated NEL requirements by controlled intake of the high-energy ration. After calving a single lactation diet to supply 100% NRC requirements was fed to all cows. Blood samples were obtained 3× per wk from 21d until calving, daily 5 d after calving, and then 3× per wk until 21d after calving. Plasma samples were analyzed for concentrations of BHBA, calcium (Ca), and magnesium (Mg). Cows remained in the experiment until 28d after calving. Data were analyzed using the MIXED procedure of SAS. There were no differences ($P >$ 0.30) among treatments for Ca, Mg, and BHBA concentrations. How-

ever, differences ($P < 0.01$) were observed by d in Ca, Mg, and BHA concentrations during the transition period. BHBA concentration began to increase from 0.74 ± 0.17 mg/dL 1 wk before 1.56 ± 0.30 mg/dL 1wk after calving. Calcium concentration dropped from 9.40 ± 0.20 mg/dL to 7.89 ± 0.43 mg/dL 2 d before calving and increased to 9.01 ± 0.44 mg/dL at d 5 after calving. In conclusion, blood metabolites measured in this study were greatly affected by days relative to calving but not by treatment.

Key Words: dairy cow, dry period, transition period

804 Grain processing methods for Nellore bulls fed high grain finishing diets. C. Sitta, M. A. P. Meschiatti, P. R. B. Campanili, L. T. C. Mello, W. F. Angolini, J. de Souza, F. Batistel, V. N. Gouvêa, M. Lovaglio, A. H. F. Melo, J. R. R. Dórea, D. F. A. Costa, and F. A. P. Santos*, *University of São Paulo, Piracicaba, São Paulo, Brazil.*

Feedlot cattle fed high grain diets usually have high energy intake. Grain processing methods can increase energy availability by disrupting the protein matrix encapsulating starch granules and by increasing the surface area allowing more starch to be digested. One positive outcome of grain processing methods, such as flaking or grinding may be a higher animal performance. The objective of this trial was to evaluate the use of 2 processing methods of corn grain (fine ground and flaked corn) on animal performance. Two hundred thirty-nine Nellore bulls (350 kg BW ± 1.42) fed diets containing 5% sugarcane bagasse; 50% corn; 28.9% citrus pulp; 10% cottonseed; 4% soybean meal; 1.1% urea; 1% mineral and vitamin premix, were blocked by initial body weight and randomly allocated to 40 pens in groups of 6 animals. The parameters evaluated were dry matter intake (DMI), average daily gain (ADG) and feed efficiency (FE = ADG.kg DMI^{-1}).The experiment lasted 117 d and the data was analyzed using Mixed procedure of SAS package. Animals fed flaked corn were heavier by the end of the experiment and had higher ADG and FE. It was concluded that corn flaking is an efficient way to improve performance of feedlot Nellore cattle in comparison with fine ground corn.

Table 1. Performance of Nellore bulls receiving finishing diets with two corn grain processing methods (fine ground and flaked)

	Fine ground	Flaked
Initial BW, kg	350	351
Final BW, kg	498[b]	512[a]
DMI, kg	8.51	8.47
Average daily gain, kg	1.26[b]	1.36[a]
Feed efficiency (ADG/DMI)	0.148[b]	0.160[a]

[a,b]Different superscripts across the rows indicate significant differences between treatments ($P < 0.05$).

Key Words: Nellore, feedlot, grain processing

805 Effects of wet distillers grains and condensed distillers solubles on growth performance and carcass characteristics of finishing steers. H. D. Hughes*, M. S. Brown, R. Butler, K. J. Kraich, J. Simroth-Rodriguez, and J. O. Wallace, *West Texas A&M University, Canyon.*

Few data exist describing the feeding value of condensed distillers solubles (CDS) in diets typical of the southern High Plains. Crossbred steers (n = 384) were adapted to a common finishing diet, blocked by BW, and assigned to treatments of CDS concentration (0, 7.5, or 15% of diet DM) in diets containing 15% wet distillers grains with solubles (WDGS; represented by 0/15, 7.5/15, and 15/15, respectively) or to a control treatment containing 0% CDS and 0% WDGS. Cattle were housed in 36 soil-surfaced pens (9 pens/treatment). Diets contained equal fat and crude protein content across treatments. The WDGS and CDS replaced portions of steam-flaked corn, cottonseed meal, yellow grease, and urea. Cattle were fed twice daily for 167 d (initial BW = 360 ± 11 kg). Dry matter intake tended to increase ($P = 0.12$) with increasing CDS concentration (9.05, 9.10, and 9.27 ± 0.18 kg/d for 0/15, 7.5/15, and 15/15, respectively), but DMI was not different between the control (8.97 kg/d) and the average of remaining treatments ($P = 0.58$). Steer ADG on a live basis was 7.3% greater in cattle fed WDGS and CDS diets (1.53, 1.50, and 1.52 ± 0.03 kg/d for 0/15, 7.5/15, and 15/15, respectively) compared with cattle fed the control diet (1.42 kg/d; $P = 0.007$), but ADG was not different among CDS concentrations ($P > 0.43$). Cattle fed the control were 4.2% less efficient on either a live or carcass basis than the average of those fed CDS ($P = 0.005$), and gain efficiency decreased linearly on a live basis only ($P = 0.09$; $P = 0.25$ on a carcass basis) as more CDS was fed. Hot carcass weight ($P = 0.02$) and 12th rib fat thickness ($P = 0.09$) were both greater for cattle fed WDGS and CDS compared with the control. Based on cattle performance, the NEg of WDGS and CDS were 100 and 85%, respectively, of the NEg of steam-flaked corn. Results suggest that including up to 15% of ration DM as CDS, in combination with WDGS, may negatively affect gain efficiency.

Key Words: feedlot cattle, wet distillers grains with solubles, condensed distillers solubles

806 Individual limitation of total daily concentrate consumption reduces between-day variation of concentrate consumption and carcass weight in Holstein bulls fed high-concentrate rations during the finishing period. M. Verdu*[1], A. Bach[2,1], and M. Devant[1], *[1]Department of Ruminant Production-IRTA, Torre Marimon, Caldes de Montbui, Barcelona, Spain, [2]ICREA, Barcelona, Spain.*

A total of 116 bulls (321 ± 2.9 kg BW, 234 ± 7.4 d of age) were divided into 2 treatments: (1) concentrate consumption fed ad libitum (AD) and (2) daily individual concentrate consumption limited to 7.5 kg/d (DCL) to evaluate their effects on performance, eating pattern, and carcass of Holstein bulls. Individual concentrate intake and eating pattern were recorded daily with a computerized concentrate feeder, and BW every 28 d. Animals were slaughtered after 107 d and HCW, and carcass quality were registered. Data were analyzed using a mixed-effects model with repeated measures. As concentrate consumption of AD bulls (6.5, 6.9, and 7.2 ± 0.17 kg/d, 1st, 2nd, 3rd mo, respectively) increased ($P < 0.05$) throughout the study, concentrate consumption of DCL bulls increased ($P < 0.05$) from the 1st to the 2nd mo (6.2 to 6.5 ± 0.17 kg/d, respectively), but no increase was observed in the 3rd mo (6.6 ± 0.17 kg/d). The CV of concentrate intake in DCL was less and constant throughout the study (12 ± 0.85%) compared with AD bulls which increased ($P < 0.01$) in the 3rd mo (18, 17, 19 ± 0.85%). In the 3rd mo, the number of daily meals in the 3rd mo increased ($P < 0.01$) in the DCL (9.0 ± 0.45) compared with the AD bulls (8.6 ± 0.45). Limiting daily total concentrate intake did not affect ADG, but tended ($P = 0.09$) to improve efficiency in the 3rd mo (0.20 and 0.18 ± 0.007 kg/kg for DCL and AD, respectively). However, HCW ($P < 0.05$) was less in DCL compared with AD bulls (245 and 250 ± 1.6 kg, respectively). Limiting daily individual total concentrate consumption is effective reducing the CV of concentrate consumption, concentrate consumption and efficiency, but reduces carcass weight, compared with bulls fed ad libitum.

Key Words: beef, concentrate limitation, eating pattern

807 Fattening Holstein heifers feeding high-moisture corn (whole or ground) separately from concentrate and straw ad libitum: Effects on behavior, rumen fermentation, digestibility, and nitrogen balance. M. Devant*[1], B. Quintana[1], and A. Bach[2,1], *[1]Department of Ruminant Production-IRTA, Torre Marimon, Caldes de Montbui, Barcelona, Spain, [2]ICREA, Barcelona, Spain.*

Twenty-four Holstein heifers (199 ± 5.5 kg BW and 157 ± 9 d age) housed in individual pens were assigned to 3 treatments where high-moisture corn (HMC), either whole or ground, concentrate (25% CP, 3.5 ME Mcal/kg), and straw were fed separately and ad libitum. Treatments were (1) whole HMC, concentrate (25% CP, 3.5 ME Mcal/kg), straw (WHMC), (2) ground HMC, concentrate (17% CP, 3.3 ME Mcal/kg), straw (GHMC), and (3) concentrate and straw (Control). Concentrate, HMC, and straw consumption was recorded daily, and BW weekly. At the beginning, middle, and end of the study rumen fluid was collected through rumenocentesis to determine rumen pH and VFA concentrations, and apparent nutrient digestibility and N balance were determined. Feeding behavior was monitored throughout the study. Animals were slaughtered after 134 d, HCW, rumen wall and cecum lesions, and liver abscesses were recorded. Data were analyzed using a mixed-effects model with repeated measures. Treatment did not affect total DMI, feed efficiency, ADG, final BW, carcass weight or classification. Concentrate consumption of Control heifers (6.6 ± 0.35 kg/d) was greater ($P < 0.001$) than that of GHMC (4.1 ± 0.35 kg/d) and WHMC (2.8 ± 0.35 kg/d) heifers, and GHMC heifers consumed less ($P < 0.001$) HMC than did the WHMC heifers (2.3 ± 0.31 and 4.2 ± 0.31 kg/d, respectively). Straw intake was greater ($P < 0.05$) in Control (0.84 ± 0.063 kg/d) and GHMC (0.75 ± 0.063 kg/d) compared with WHMC heifers (0.59 ± 0.063 kg/d). Treatments did not affect rumination, self-grooming, non-nutritive oral behaviors, and rumen pH. However, rumen acetate to propionate ratio decreased ($P < 0.01$) when heifers received HMC (2.82 ± 0.276) compared with Control (1.77 ± 0.276). Total-tract starch apparent digestibility was greater ($P < 0.001$) in Control (97.7 ± 0.47%) and GHMC (99.4 ± 0.47%) than in WHMC (95.2 ± 0.47%) heifers. Treatments did not affect N retention. Feeding HMC, either whole or ground, separately from concentrate and straw results in similar performance and behavioral patterns than feeding only concentrate and straw.

Key Words: beef, digestibility, feed consumption

808 Effect of increased dietary grain inclusion on growth performance of prepubertal dairy heifers. T. S. Dennis*, J. E. Tower, H. Schmitz, A. Mosiman, and T. D. Nennich, *Purdue University, West Lafayette, IN.*

The objective of this study was to evaluate the effect of increasing dietary grain:forage ratio on growth, dry matter intake (DMI), and feed efficiency of prepubertal dairy heifers. Seventy-eight Holstein heifers (133.1 ± 27.4 kg, 125 ± 22 d of age) were randomly allocated by body weight (BW) to 1 of 15 pens. Pens were randomly assigned to dietary treatments balanced for CP and ME containing grain:forage ratios of 80:20 (80%), 60:40 (60%), or 40:60 (40%) and fed for 56 d. Following the treatment period, all pens were switched to a common diet containing 40% grain and 60% forage and fed for an additional 56 d. Body weights were collected every 2 wk, and hip and withers heights, body condition score (BCS), heart girth, and hip width were measured monthly. Data were analyzed as repeated measures using PROC MIXED of SAS with pen as the experimental unit. Heifers fed 80% were 13.7 and 27.1 kg heavier than 60% and 40%, respectively, at the end of the treatment period ($P < 0.01$). Similarly, ADG, DMI, feed efficiency, and skeletal growth were improved during the treatment period for 80% compared with 60% and 40% ($P < 0.01$). There was a treatment × time interaction for DMI (% of BW), with 80% consuming 3.4 and 3.0% of BW, respectively, compared with 40% consuming 2.8 and 3.3% of BW on d 56 and 112, respectively ($P < 0.01$). Additionally, ADG was increased for heifers fed 40% and 60% compared with 80% on d 70 ($P = 0.02$) and 84 ($P = 0.01$) during the common period. Feed efficiency was improved for heifers fed 60% compared with 80% on d 84 of the common period, with 60% averaging 0.166 compared with 0.125 kg ADG/kg DMI for 80% ($P = 0.04$). Intake of total NDF was greater for 80% during the treatment period ($P < 0.01$), but total NDF intake was greater for 40% on d 84 ($P = 0.04$) and 98 ($P = 0.01$) of the common period. Skeletal growth and BCS were similar between treatments during the common period from d 56 to 112 ($P > 0.10$). Dairy heifers had greater ADG when fed high amounts of grain, but ADG and feed efficiency were reduced compared with heifers fed moderate to low amounts of grain after switching to a high-forage diet.

Key Words: dairy heifer, grain inclusion, intake

809 Effects of varying periparturient dietary starch amount and supplementation with *Propionibacterium* on multiparous dairy cow performance, metabolism, and health. Z. Sawall*[1], W. Weich[1], D. Lobao da Silva[1], T. Parrott[2], and N. B. Litherland[1], *[1]University of Minnesota, St. Paul, [2]Dupont Industrial Biosciences, Waukesha, WI.*

Multiparous dairy cows (n = 17/treatment) were used in a 2 × 2 factorial design to determine if daily supplementation with *Propionibacterium* (P169) direct fed microbial (DFM) altered response to periparturient diets varying in starch concentration. Cows were fed low or high starch diets pre- and postpartum 42 d pre- through 56 d postpartum with or without DFM 21 d pre- to 56 d postpartum. Dietary starch concentration was adjusted by replacing corn silage and soy hulls with ground corn to yield 2 pre- and 2 postpartum diets; low starch (15.5%) pre- and (20.1%) postpartum or high starch (26.7%) pre- and (29.7%) postpartum. Either DFM carrier or DFM (providing approximately 60 billion cfu/head/day *Propionibacterium*) were added to each cows TMR daily. Factors combined to produce 4 treatments; 1) low starch + Control (DFM carrier) (LSC), 2) low starch + DFM (LSM), 3) high starch + Control (HSC), 4) high starch + DFM (HSM). Data were analyzed using PROC MIXED in SAS as a 2 × 2 factorial with model effects of starch, DFM and week. We hypothesized that DFM would increase milk yield in both low and high starch diets. Prepartum DMI for LSC, LSM, HSC and HSM averaged 13.1, 11.2, 13.0 and 12.5 ± 0.5 kg/d and was decreased ($P < 0.05$) by DFM but unaffected by dietary starch concentration ($P = 0.14$). Postpartum DMI averaged 22.1, 18.8, 21.7 and 21.4 ± 1.1 kg/d for LSC, LSM, HSC and HSM and tended ($P = 0.08$) to be lower for DFM vs. Control but unaffected by starch ($P = 0.24$). Milk yield through d 56 averaged 45.5, 43.3, 43.8 and 47.2 ± 1.5 kg/d for LSC, LSM, HSC and HSM and was greatest ($P = 0.04$) for HSM but 3.5% FCM yield was similar among treatments. Feed efficiency (3.5%FCM/DMI) averaged 2.15, 2.46, 2.09 and 2.22 ± 0.12 for LSC, LSM, HSC and HSM and was greater ($P < 0.05$) for DFM vs. Control. Serum NEFA, BHBA and liver concentrations of triacylglycerol and glycogen were similar among treatments. In summary, the combination of high starch and DFM resulted in the greatest milk yield. Feed efficiency was increased by DFM for both low and high concentrations of dietary starch.

Key Words: direct fed microbial, starch, transition cow

810 Effect of duodenal leucine infusion on pancreatic exocrine function of dairy cow. K. Liu, Y. Liu, and J. Yao*, *College of Animal Science and Technology, Northwest A&F University, Yangling, Shaanxi, China.*

The experiment was conducted to evaluate the effects of duodenal leucine infusion on pancreatic exocrine function of dairy cow. Four intravenously Holstein cows (215 ± 7 kg) with duodenal catheters were used in a 4 × 4 Latin square experiment with 4 levels of leucine infusion (0, 29.1, 59.1 and 88.6 μmol·kg^{-1}·h^{-1}). Concentrations of plasma insulin and cholecystokinin increased with increasing leucine infusion ($P < 0.05$), and pancreatic α-amylase secretion (U/h) responded quadratically ($P < 0.01$), with greatest value observed at 29.1 μmol·kg^{-1}·h^{-1}. Duodenal leucine infusion could also affect concentration (U/mL; α-amylase, $P < 0.001$; U/L; chymotrypsin, $P = 0.014$), specific activity (U/mg; α-amylase, $P < 0.001$; lipase, $P < 0.001$) and secretion (U/h; chymotrypsin, $P = 0.016$) of enzymes. These data indicated that leucine could regulate pancreatic enzyme secretion, and there appeared to be a dose-effect relationship between them. Changes in hormones, such as insulin and cholecystokinin, may be involved in the changes of enzyme secretion.

Key Words: dairy cow, leucine infusion, pancreatic exocrine function

811 Effects of starch infusion on plasma metabolic and gene expression in lactating cows. Y. Zou*, Z. Yang, Y. Guo, S. Li, and Z. Cao, *State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing, China.*

The effect of ruminal or abomasal starch infusion on plasma metabolic, gene expression abundance of gluconeogenesis and lipid metabolism of lactating cows was measured. Six Holstein cows (3 multiparous and 3 primiparous) fitted with permanent ruminal cannulas were arranged into 2 complete 3 × 3 Latin squares, infused in the rumen or abomasums with starch solution (800 g/d) or not infused (control) for 15 d. The abomasal infusion was through a plastic tube (6 mm i.d.) inserted into the abomasums through the rumen and held in place with a flexible rubber disk (18 cm i.d.). Ruminal and abomasal infusion did not affect ($P > 0.05$) plasma metabolism in lactating cows, only a numerical change was detected. The increase in insulin ($P > 0.05$) with starch promote glycogen and lipid synthesis, and all these might have been in response to increased ($P > 0.05$) propionate production and absorption. The decrease ($P > 0.05$) in BHBA and NEFA concentrations indicated a decrease in mobilization of adipose reserves and stimulation in lipid anabolism, which is in agreement with the increased ($P > 0.05$) backfat thickness by 1.83 (ruminally) and 2.37 mm (abomasally) when starch was infused. Messager ribonucleic acid abundance of PPAR-gamma and GLUT-4 in subcutaneous adipose also indicated a lipid accumulation in lactating dairy cows. Starch infusion abomasally can certainly been carried down to the intestine directly to ameliorate energy supplies. The results indicated that supplementation of starch at a concentration of 800 g/d in the abomasums could decrease plasma adipose mobilization and stimulate lipid accumulation mRNA abundance.

Table 1. Plasma concentrations and relative mRNA abundance of cows infused starch with 800 g/d in the rumen, or the abomasum

Item	Control	Rumen	Abomasum	SEM
Glucose, mg/dL	58.6	63.5	71.7	3.73
Insulin, μIU/mL	17.3	18.3	19.4	0.62
BHBA, mmol/L	0.52	0.51	0.49	0.03
NEFA, mmol/L	0.40	0.37	1.35	0.03
Backfat thickness, mm	17.50	19.33	19.87	0.61
Liver				
PC	1.39	0.67	0.92	0.22
PEPCK-C	0.60	0.57	0.47	0.07
PPAR-α	1.25	0.95	1.15	0.10
GLUT-2	1.30	0.94	0.90	0.12
Adipose				
InsR	1.01	1.28	1.36	0.17
PPAR-γ	1.30	1.24	1.04	0.07
GLUT-4	0.84	1.22	0.98	0.29

Key Words: expression abundance, lactating cow, plasma and liver metabolism

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