# Animal Health - Livestock and Poultry: Bovine I

**388   Prediction of degree of mastitis from repeated measurements of lactate dehydrogenase (LDH) in milk.** N. C. Friggens*[1], M. G. G. Chagunda[1], M. Bjerring[1], C. Ridder[2], S. Højsgaard[1], and T. Larsen[1], [1]*University of Aarhus, Faculty of Agricultural Sciences, Denmark*, [2]*Lattec I/S, Hillerød, Denmark.*

This study aimed to test a model for mastitis detection using a logic that allows examination of time-related changes and a progressive scale of mastitis state (i.e. not using specificity/sensitivity). The model (Chagunda et al., 2006, J. Dairy Sci. 89:2980) produces a Mastitis Risk for each cow, on a scale 0 (completely healthy) to 1 (full blown mastitis). The main input is LDH (µmol/min/l) x milk yield. A test set containing 602 lactations and 849 mastitis cases was used. Proportional samples were collected from each cow at each milking and analysed for LDH and Somatic Cell Counts (SCC). The basis for the health definitions was vet treatment records. A refinement of the health definitions was made using systematic positive deviations in log(SCC) to indicate untreated infections. 2 subsets of cows were identified: mastitic cows and cows completely free of mastitis (healthy controls). The time-series profiles of these 2 groups in a 60-day window around day of vet treatment were examined. Model reliability throughout all stages of lactation and degrees of infection was examined using SCC as a continuous measure of degree of infection. The time-profile for the health controls was flat with a median Mastitis Risk of 0.02. In contrast, the profile of the mastitic cows increased above the control cows baseline from about -6 days, rising to a Mastitis Risk value of 0.20 at day 0, and declining back to the control cow level after treatment. Differences between mastitic and healthy cows were significant from –4 to +2 days from vet treatment. When cases were time-aligned to peak of infection rather than vet treatment there was a much sharper peak to the time-profile of mastitic cows. The median Mastitis Risk at peak was 0.62, the mean was 0.80, and the value of 0.62 had a less than 1% probability of actually coming from a healthy control. Testing against SCC on the whole dataset showed that only 2.1% of all Mastitis Risk values had an error greater than 0.7. This model is as accurate as the best published detection systems and was able to detect significant differences between mastitic and healthy cows 4 days before treatment.

**Key Words:** Mastitis Detection, Dairy Cow, Time Series

**389   Effects of energy balance and *Streptococcus uberis* intrammamary infection challenge on gene expression profiles in bovine mammary tissue.** K. M. Moyes*, J. K. Drackley, D. E. Morin, S. L. Rodriguez-Zas, R. E. Everts, H. A. Lewin, and J. J. Loor, *University of Illinois, Urbana.*

Cows experiencing severe postpartal negative energy balance (NEB) are at greater risk of developing mastitis than cows in positive energy balance (PEB). Objectives were to compare mammary tissue gene expression profiles during a *Streptococcus uberis* (*S. uberis*) mastitis challenge between lactating cows subjected to feed restriction to induce NEB (n = 6) and cows fed *ad libitum* to maintain PEB (n = 5). All cows had composite SCC <200,000 cells/mL prior to the study, and milk from all quarters was bacteriologically negative. Cows were paired based on parity, DIM, and milk yield. NEB cows were feed-restricted to 60% of calculated $NE_L$ requirements for 7 d, and

cows fed PEB were fed the same diet *ad libitum*. At 5 d after feed restriction, one rear mammary quarter of each cow was inoculated (IN) with 5,000 cfu of *S. uberis* (O140J). At 20 h post-IN, before the expected peak in clinical signs, both rear mammary quarters (IN and control) were biopsied for RNA extraction. A 13,257 oligonucleotide (70-mers) array and qPCR were used for transcript profiling. Annotation was based on similarity searches using BLASTN against human, mouse and bovine RefSeq, human, mouse, and bovine UniGene, and bovine TIGR. Cy3- and Cy5-labeled cDNA from mammary tissue and a reference standard were used for hybridizations. Energy balance (NEB vs. PEB) resulted in 347 differentially expressed genes (ANOVA $P < 0.05$) compared with 113 due to infection status (IN vs. control), and 23 genes for the interaction (energy balance × infection status). Among genes downregulated with NEB, Ingenuity Pathway Analysis identified small molecule biochemistry (20 genes), cancer (19), lipid metabolism (15), molecular transport (11), and cell morphology (10) as some of the most enriched molecular functions. Genes upregulated by NEB were associated with cell growth/proliferation (33), cell death (24), gene expression regulation (21), and cell signaling (19). Results indicate that energy balance and intramammary infection alter mammary gene expression.

**Key Words:** Genomics, Nutrition, Immune Response

**390   The effect of negative energy balance on immune response to *Streptococcus uberis* mastitis challenge in dairy cattle during mid-lactation.** K. M. Moyes*, J. L. Salak-Johnson, D. E. Morin, J. K. Drackley, and J. J. Loor, *University of Illinois, Urbana.*

Fourteen multiparous Holstein cows were used to determine effects of negative energy balance (NEB) on immune response to *Streptococcus uberis* (*S. uberis*) mastitis challenge during mid-lactation. Before the study, milk from all quarters of each cow were bacteriologically negative, with composite SCC < 200,000 cells/mL. Cows were paired based on parity, DIM and milk yield. At ~90 DIM, half of the cows were feed-restricted to 60% of calculated $NE_L$ requirements based on body weight and milk production to induce NEB. Feed restriction lasted 7 d. Control cows were fed the same diet ad libitum (i.e. positive energy balance; PEB). Five d after feed restriction, one rear quarter in all cows was inoculated with 5,000 cfu of *S. uberis* (O140J). Health exams were performed, and jugular blood and aseptic quarter milk samples collected daily until inoculation and every 6 h post-inoculation for 36 h. Blood was analyzed for NEFA, BHBA, triglyceride (TG), glucose, cholesterol, and albumin. Blood neutrophils were isolated for determination of chemotaxis and phagocytosis capabilities *in vitro*. Quarter milk samples were analyzed for SCC and *S. uberis* concentration. Data were analyzed with the MIXED procedure of SAS with repeated measures. All cows developed local and/or systemic signs of mastitis after *S. uberis* inoculation. The NEB cows had higher ($P < 0.01$) blood concentrations of blood NEFA, BHBA, TG and cholesterol and lower ($P < 0.01$) glucose than PEB cows. Heart rate and rectal temperature were lower ($P < 0.05$) in NEB cows than PEB cows. Neutrophil phagocytic capability was greater ($P < 0.05$) in NEB cows than PEB cows. No differences were observed with regards to neutrophil chemotaxis, SCC, or *S. uberis* concentration in milk between groups. Our results suggest that cows subjected to nutrition-induced NEB had an enhanced immune response during mid-lactation.

Therefore, energy balance status might affect immune response to invading pathogens in periparturient cows.

**Key Words:** Energy Balance, Mastitis, Dairy Cattle

**391    Multiplex PCR system for the detection of mastitis-causing pathogens.**  J. M. St-Pierre*, C. Thibault, and N. Bissonnette, *Agriculture and Agri-Food Canada, Sherbrooke, Quebec, Canada*.

Mastitis causes severe economic losses in the dairy industry each year. The need to understand the genetic factors implicated is therefore critical to help prevent the disease. Our project has many features to help determine which factors participate in the host's response to mastitis. The first phase of this experiment is to identify cows that are susceptible or resistant to the illness. As mastitis can be caused by multiple bacteria, the most prevalent ones are Escherichia coli, Staphylococcus aureus, Streptococcus agalactiae, Streptococcus dysgalactiae, Streptococcus uberis and Klebsiella pneumoniae. It has also been reported that Mycoplasma bovis is an important mastitic pathogen, but it is seldom identified because conventional culture methods can take up to 2 weeks and it is believed that it would most likely be a co-infection agent with Streptococci. We have designed a PCR multiplex system that amplifies specific genes for each of the bacterial species mentioned previously. Capillary electrophoresis is used to detect the PCR fragments as each pair of gene-specific primers is coupled to a fluorochrome that is detected by the laser of a genetic analyser. Because of the capacity of the genetic analyser to perceive many colors concurrently we are able to identify all 7 pathogens simultaneously even if they are not supposed to be present in mastitic milk at once. Therefore insuring that if an infection is caused by many microorganisms they will all be detected. The sensitivity of this method can be compared to that of microbiological methods and is more sensitive than a PCR on agarose gel though our test is more rapid than other PCRs because of the multiplexing component. Our system was tested with purified bacterial DNA. Further optimisation for the extraction of DNA directly from milk is required. As the technique is optimised we will be able to identify which animals come in contact with any of these bacterial species and develop or not the disease. This is a crucial step for our understanding of the genetic contribution to the mammary gland's immune system.

**Key Words:** Mastitis, Multiplex PCR, Pathogen

**392    Efficacy of treatment protocols for Gram negative and no growth clinical mastitis in dairy cattle.**  J. R. Wenz*, *Washington State University, Pullman*.

The purpose of this study was to compare the efficacy of intramammary (IMM) ceftiofur hydrochloride (SP) with a protocol of no IMM antibiotics (NT) for the treatment of clinical mastitis with a Gram negative (GN) or (NG) culture result on a 1500 cow commercial dairy. Milk was aseptically collected from the affected quarter(s) of cows with systemically mild clinical mastitis for bacteriologic culture. Even numbered cows received SP (125 mg once a day for 5d). Odd numbered cows received NT. Outcomes evaluated were average days in sick pen (SPD), clinical recurrence in the same quarter 15-60d later (RECUR), loss of quarter (DRIED) and death/culling within 30d

(D/C). SPD of cows with a GN culture result in the NT group were fewer than those in the SP group (P<0.0001). No difference was seen in cows with a NG culture result. The % of GN cows with >8 SPD was higher in the SP group than in the NT group (P=0.03), however, there was no difference for NG cows. There was no difference in RECUR or D&C between treatment groups, regardless of culture result. For cows with an NG culture result there were more cows in the NT group with a DRIED outcome compared with those in the SP group (P=0.02), however, there was no difference in GN cows. Results suggest SP treatment did not improve outcomes of cows with mild GN clinical mastitis compared to those receiving NT but may reduce loss of quarter in cows with mild NG clinical mastitis.

**Table 1. Outcomes of mild clinical mastitis episodes by treatment and culture result**

| Outcome | GN NT | SP | NG NT | SP |
|---|---|---|---|---|
| SPD | 6.0+/-2.1 | 8.6+/-3.0 | 7.4+/-5.1 | 7.5+/-1.8 |
| %SPD>8d | 3/27(11%) | 11/29(38%) | 20/81(25%) | 24/85(28%) |
| RECUR | 3/33(9.1%) | 4/42(9.5%) | 10/88(11%) | 9/93(9.7%) |
| D/C | 3/41(7.3%) | 5/52(9.6%) | 2/104(1.9%) | 2/114(1.8%) |
| DRIED | 1/41(2.4%) | 2/52(3.8%) | 15/104(14%) | 6/114(5.3%) |

**Key Words:** Mastitis, Gram Negative, Ceftiofur

**393    The effect of uterine infusion of ceftiofur in the immediate postpartum on uterine health in dairy cows.**  R. G. Bruno*, M. F. Sa Filho, D. F. Resende, F. S. Lima, and J. E. P. Santos, *Veterinary Medicine Teaching and Research Center, University of California Davis, Tulare*.

Objective was to evaluate the effect of intrauterine antibiotic treatment on uterine health in dairy cows. Holstein cows, 379, were randomly assigned to no treatment (Control, n=188), or a single uterine infusion (Infusion, n=191) of 500 mg of ceftiofur hydrochloride (Spectramast DC, Pfizer Animal Health) at 2 d in milk (DIM). Cows were categorized as high risk for uterine disease if they had one or more of the following: major assistance at calving, deliver of twins, retained placenta, or milk fever. Uterine discharge was evaluated using the Metricheck (Simcrotech, Hamilton, New Zealand) at 2, 15 and 29 DIM, and classified based on the aspect, color and odor as normal, clinical endometritis and metritis. An aseptic uterine flush was performed at 36 DIM, and recovered fluid was subjected to microbiologic culture and cytological examination. A threshold of 18% of polymorphonuclear leukocytes as proportion of total cells (leukocytes + endometrial cells) in the cytology categorized cows with subclinical endometritis. Ovaries were examined twice by ultrasonography to determine cyclic status at 42 DIM. Data were analyzed using the LOGISTIC procedure of SAS (2001). Infusion reduced (P=0.06) the proportion of high-risk cows that required further antibiotic treatment (27.4 vs 45.8%), but did not influence (P>0.10) median mucus score at 15 (3 vs 4) and 29 DIM (2 vs 2). Incidence of metritis was similar (P=0.88) between treatments and affected 22.5 and 22.9% of Infusion and Control cows, respectively. Treatment did not affect (P>0.10) prevalence of positive uterine culture, Arcanobacterium pyogenes, or of subclinical endometritis, which affected 37% of the cows. High risk cows had greater (P<0.05) incidence of metritis (31.9 vs 16.2%), and cows with metritis were

more likely (P=0.03) to have positive uterine culture (61.0 vs 46.3%). Treatment did not (P=0.15) affect cyclic status at 42 DIM, but cyclic cows were less (P=0.02) likely to have A. pyogenes (7.8 vs 15.6%) and to be positive for subclinical endometritis (29.8 vs 44.5%). Single infusion with 500 mg of ceftiofur did not improve uterine health of dairy cows.

**Key Words:** Ceftiofur, Dairy Cow, Uterine Health

**394    Metabolic profiles of dairy cows that develop metritis.** J. M. Huzzey*[1], T. F. Duffield[2], S. J. LeBlanc[2], D. M. Veira[3], D. M. Weary[1], and M. A. G. von Keyserlingk[1], [1]*University of British Columbia, Vancouver, Canada*, [2]*University of Guelph, Ontario, Canada*, [3]*Pacific Agri-Food Research Centre, Agassiz, BC, Canada*.

The aim of this study was to describe the metabolic profiles of Holstein cows with severe metritis (SM; n=12), mild metritis (MM; n=27), and without metritis (n=23). Holstein dairy cows were monitored from 2 wks before to 3 wks after calving. Individual DMI was monitored continuously and serum NEFA, BHBA, calcium and haptoglobin were measured on d -20±5, -6±2, -2±1 and d 0 relative to calving, and then every 3 d until d+21. Vaginal discharge, rated on a 5-point scale, was assessed every 3 d until d+2; these scores and daily rectal temperatures were used to assess metritis severity. Clinical diagnosis of SM and MM was made on d 5.3±1.9 and d 9.1±3.9 after calving, respectively. NEFA levels were higher in the SM and MM cows relative to healthy cows on d-6 (P=0.02). On this day, cows with a NEFA concentration ≥0.3mmol/L were 4.3 times more likely to be diagnosed with severe or mild metritis (P=0.03). The sensitivity and specificity for this predictive threshold were 40% and 87%, respectively. There were no differences in BHBA among health groups. Calcium levels were lower in the SM cows, particularly between d+3 to d+12 after calving (P≤0.02), likely because DMI was lower in this group compared to healthy cows (P<0.01). Haptoglobin was 0.51g/L higher in the MM and 0.63g/L higher in the SM cows relative to the healthy animals between d0 and d+12 (P<0.05), with peaks on d +3 for the healthy and MM cows and on d+6 for the SM cows. On d+3 cows with a haptoglobin concentration of ≥1g/L were 6.3 times more likely to develop severe or mild metritis (P=0.004). The sensitivity and specificity for this predictive threshold were 49% and 87%, respectively. Because differences in measures of energy metabolism and inflammation occurred before metritis developed, NEFA concentrations at d-6 and haptoglobin concentrations at d+3 relative to calving may be useful for monitoring the risk of metritis in dairy cows.

**Key Words:** Metabolites, Metritis, Periparturient

**395    JDIP – Direction for Johne's research.** K. E. Olson*[1], S. J. Wells[2], and V. Kapur[2], [1]*KEO Consulting, Schaumburg, IL*, [2]*University of Minnesota, St. Paul*.

The Johne's Disease Integrated Program (JDIP) is a consortium whose mission is to promote animal biosecurity through development and support of projects that enhance knowledge, promote education, develop real-world solutions and mitigate losses from Johne's disease (JD). Approximately 140 individuals from 30+ academic, government and industry organizations are part of JDIP. A primary benefit is the networking that facilitates translation of results from cutting edge research programs to practical solutions with field application. Primary funding is from a USDA–CSREES–NRI CAP program competitive grant. Through JDIP, Johne's research and education needs are prioritized, with modest competitive grants awarded to address priorities. The initial round of funding ends in 2007. Five project areas have been identified for future JDIP activity: Project 1 – Epidemiology and Transmission - Determine within farm transmission dynamics of *Mycobacterium avium subsp paratuberculosis (MAP)* along with its molecular epidemiology and evaluate effectiveness of recommended management practices on reducing the incidence of infection; Project 2 – Diagnostics and Strain Differentiation – Use information gained from initial JDIP projects to develop and validate more accurate, rapid diagnostic tests, and tools to better quantify positive samples; Project 3 – Basic Biology and Pathogenesis – Build on prior work to develop a better understanding of mechanisms that impact virulence and survivability of *MAP*, helping to improve diagnostics and identify vaccine candidates; Project 4 – Host Genetics, Immunology, and Vaccine Development – Identify genetic markers for susceptibility to JD in cattle, compare efficacy of mutant vaccines in animal models, test candidate vaccines on the immune response and in vivo survival of *Map*; Project 5 – Education and Extension – Complete national survey of barriers to participation in JD program, identify stakeholder educational needs and design programs to meet them. Increase awareness of JDIP by outreach to producer media and meetings. The JDIP program is developing a strong translational pipeline for development of real world solutions to mitigate losses associated with JD.

**Key Words:** Johne's Disease, MAP, JDIP

**396    Serum non-esterified fatty acid (NEFA) and beta-hydroxybutyrate (BHB) through the transition period of Holstein cows in different regions of North America.** M. E. Carson*[1], T. F. Duffield[1], S. J. LeBlanc[1], K. E. Leslie[1], S. M. Godden[2], M. B. Capel[3], M. W. Overton[4], and D. Vallejo[5], [1]*University of Guelph, Ontario, Canada*, [2]*University of Minnesota, St Paul*, [3]*Perry Veterinary Clinic, Perry, NY*, [4]*University of Georgia, Athens*, [5]*University of California, Davis, Tulare*.

The objective of this field study was to evaluate the concentrations of serum non-esterified fatty acid (NEFA) and beta-hydroxybutyrate (BHB) through the transition period of Holstein cows in four different regions. Data were collected from 1812 cows in 45 herds across Midwest, Northeast (including Ontario, Canada), Southeast and Western United States. Each herd in the Midwest and Northeast regions had approximately 35 cows per herd enrolled in the study, whereas in the Southeast and Western herds included approximately 60 and 80 cows per herd, respectively. Cows were sampled 1 week prior to the expected calving date, and again in weeks 1, 2, and 3 postpartum. All serum collected was shipped to the Animal Health Laboratory at the University of Guelph for NEFA and BHB analysis. Results for NEFA and BHB by region and time relative to calving are shown in Table 1. Cows in the West showed a smaller prevalence of NEFA levels ≥0.4 mmol/L in the week prior to parturition, whereas herds in the Northeast had the greatest prepartum NEFA with 44% of cows ≥0.4mmol/L. Similarly, the Northeast had the greatest mean BHB at week 1 postpartum. The prevalence of subclinical ketosis in week 1 postpartum was greatest in Northeast and Midwest herds and smallest in West and Southeast herds. It appears that regional differences may exist for

serum NEFA and BHB levels and prevalence of subclinical ketosis during the transition period. The reasons for these apparent differences merit further investigation.

**Table 1. Distribution of prepartum non-esterified fatty acid (NEFA) and postpartum beta-hydroxybutyrate (BHB) concentrations in dairy cows in North America.**

| Region | No. of Cows | No. of Herds | Mean (±SD) NEFA | Proportion of cows with high NEFA (≥0.4 mmol/L) | Mean (± SD) BHB | Proportion of cows with subclinical ketosis (BHB ≥1400 µmol/L) |
|---|---|---|---|---|---|---|
| Midwest | 570 | 17 | 0.38 (±0.3) | 39% | 940 (±715) | 15% |
| Northeast | 652 | 20 | 0.41 (±0.3) | 44% | 1044 (±772) | 20% |
| Southeast | 177 | 3 | 0.37 (±0.3) | 40% | 867 (±1015) | 8% |
| West | 413 | 5 | 0.26 (±0.2) | 20% | 798 (±569) | 9% |

**Key Words:** Dairy Cows, Transition, Metabolic Parameters

**397    An evaluation of meloxicam (Metacam®) as an adjunctive therapy for calves with neonatal calf diarrhea complex.**  C. G. Todd*[1], D. R. McKnight[2], S. T. Millman[1], T. F. Duffield[1], and K. E. Leslie[1], [1]*University of Guelph, Guelph, ON, Canada*, [2]*University of Guelph, Kemptville, ON, Canada*.

Diarrhea is a significant health problem among neonatal dairy calves. In some countries, calves with diarrhea may be treated with supportive therapies, such as non-steroidal anti-inflammatory drugs. The aim of this research was to examine the efficacy of meloxicam as an adjunctive therapy for calves with diarrhea, as determined by measures of calf performance, behavior and health. For this double-blind controlled trial, 62 Holstein bull calves were purchased at birth and transported to a calf research facility. At the naturally occurring onset of diarrhea, the calves were enrolled in the study, and randomly assigned to receive a single subcutaneous injection of meloxicam (0.5 mg/kg BW) or an equal volume of placebo solution. Individual milk, water and calf starter ration intakes were determined daily for all calves until 56 days of age. Daily fecal consistency scores and weekly body weight measurements were also collected for each study calf. Following the onset of diarrhea, calf feeding behavior and general activity, as well as lying and standing postures were observed for five consecutive days. During this trial, 56 calves developed diarrhea and were treated with meloxicam (n=28) or placebo (n=28). Meloxicam-treated calves began consuming starter ration significantly earlier than placebo calves (p<0.05), had improved starter intakes (p<0.05) and experienced greater body weight gain over the study period (p<0.05). There was no difference in weaning weight among the study calves (p>0.05); however, meloxicam-treated calves tended to wean at an earlier age (47 days versus 41 days, respectively, p=0.16). Compared to calves receiving placebo, meloxicam-treated calves were more sedentary for the first two days after developing diarrhea, and then became considerably more active during the remainder of the observation period (p<0.05). The occurrence of abnormal lying postures did not differ among the study calves (p>0.05). These results provide evidence of improved calf well-being and indicate that meloxicam may be an appropriate supportive therapy for calves with diarrhea.

**Key Words:** Calf, Diarrhea, Non-steroidal Anti-inflammatory Drug Therapy

**398    A diagnostic algorithm, in a dashboard environment for common dairy cow health concerns.**  D. T. Galligan*[1], D. Remsburg[1], J. Ferguson[1], R. Munson[1], and G. Licitra[2,3], [1]*University of Pennsylvania, Kennett Square*, [2]*CoRFiLaC, Regione Siciliana, Ragusa, Italy*, [3]*DACP University of Catania, Catania, Italy*.

Dairy producers are often confronted with cows displaying various clinical signs indicative of various **health conditions** (ketosis, DA (+/- torsion), mastitis, RP, metritis, pneumonia, hardware, lameness, milk fever etc). The interpretation of these clinical signs (heart rate, temperature, respiration, rumen sounds, posture, neurological signs, ketosis test results, serum protein level) as well as historical information (lactation number, production profile etc) will often determine a **presumptive diagnosis** as well as a standard treatment response. The presumptive diagnosis in this program is based on an algorithm that looks at the hierarchy of clinical signs associated with a disease condition. A graph of the relative % matching signs for each of the disease condition is presented to the user as well as a treatment window for the conditions diagnosed. Often the decision to treat a cow is based on her expected value relative to a replacement (or alternative opportunity) as well as the immediate therapeutic cost and expected prognosis to the current condition. The expected prognosis is based on the increased risk of culling associated with the difference diagnosed conditions. A dashboard (Flash) file was developed with the algorithm based on interviewing several veterinarians with considerable practice experience and reports in the literature estimating the increased odds of culling due to a given condition. The dashboard environment allows the use of sliders for data entry and a response gauge estimating survival to the next lactation. The program can be run on a stand alone computer or off the web.

**Key Words:** Health, Algorithm

**399    Effects of reduced freestall access during the dry period upon cellular immune function and transition health of dairy cows.**  T. F. Gressley*, K. K. Fried, J. M. Velasco, E. D. Reid, T. C. Hausman, K. M. Moyes, J. L. Salak-Johnson, and G. E. Dahl, *University of Illinois, Urbana*.

The objectives of this study were to determine if limiting freestall access of dry cows impacted immune function or transition health. Our model examined one aspect of overcrowding, reduced freestall availability, without changing feed access, water availability, or area per cow. Twenty Holstein cows were randomly assigned to either a 70% stall availability treatment (70SA; n=10) or a 100% stall availability treatment (100SA; n=10) 1 wk following dry off on d 51 ± 6 prior to expected calving. Cows on the 70SA treatment only had access to 7 freestalls in a 10-freestall bay, whereas cows on the 100SA treatment had access to all 10 freestalls. Short-term treatment effects on neutrophil phagocytosis and chemotaxis and lymphocyte proliferation were measured 4 and 24 h after treatment assignment. Lymphocyte proliferation was measured again at 2 and 5 wk post-treatment. Locomotor scores and postpartum disease prevalence were also recorded for these 20 cows and a second cohort of 20 cows subjected to the same treatments. In the short-term, immune cell activity was enhanced among cows on the 70SA treatment compared to cows on 100SA. Lymphocyte proliferation was increased in response to ConA (P = 0.02) and tended to increase in response to PHA (P = 0.14), suggesting an increased responsiveness of T-cells. The percentage of neutrophils engulfing 1 or more fluorescent beads was greater

among 70SA cows than the 100SA cows (P < 0.05). Long-term there was a tendency for cows in the 70SA treatment to have increased LPS-induced B-cell proliferation compared to 100SA cows (P = 0.09). Postpartum disease prevalence was similar for cows on both treatments. There were interactions between treatment and cohort and week and cohort on locomotor score (P < 0.05). Locomotor score did not change over time for cohort 1 cows or for the 100SA cows in cohort 2, but it worsened over time for the 70SA cows in cohort 2. A moderate reduction in freestall access in dry cow facilities should not adversely affect immune function, but it may negatively impact hoof health.

**Key Words:** Transition Cows, Freestall Availability, Immune Function

# Beef Species I

**400    Post-weaning growth performance of heifers grazing Tasmanian native pastures and the estimation of inbreeding levels using random amplified polymorphic DNA markers.** A. E. O. Malau-Aduli*[1] and M. Dunbabin[2], [1]*University of Tasmania, Hobart, Tasmania, Australia*, [2]*'Bangor', Dunalley, Tasmania, Australia.*

The aims of this study were to evaluate the growth performance of Hereford, Angus, Hereford × Angus and Hereford × Saler heifers within the same herd grazing native pastures and to estimate homozygosity and inbreeding coefficients using random amplified polymorphic DNA (RAPD) markers. Post-weaning liveweight (BW), average daily gain (ADG) and body condition score (BCS) on a scale from 0 to 5 were monitored monthly from 2005 to 2006. Genomic DNA was extracted from blood samples, amplified using RAPD primers, fragments resolved by gel electrophoresis and banding patterns elucidated under UV light. Estimation of homozygosity through band sharing patterns was utilised in determining within-breed inbreeding levels. Regardless of breed, LWT, BCS and ADG of heifers followed a typical sigmoid curve pattern characterised by a decline in average BW from 200 kg in May to 188 kg in June, a continuous monthly increase through to March 2006 when it reached a peak (380 kg) before a final decline to 375 kg in May. The BCS ranged from 1.6 to 3.6 while ADG ranged from -0.4 to 1.5 kg/d. Significant genetic variation was observed between the different breeds in that BCS and BW of purebred Angus heifers were lower than those of purebred Hereford and their crosses with Angus and Saler. Average BW of the Angus breed ranged from 164-349 kg, with BCS ranging from 1.4 to 3.3 compared to the Hereford (186-383 kg, 1.6-3.6), Hereford × Angus (192-383 kg, 1.7-3.6) and Hereford × Saler (192-385 kg, 1.6-3.7), respectively. The ADG of the Angus was not different from those of Hereford and their crosses indicating that the Angus was perhaps better in terms of feed efficiency since they probably ate less and gained the same weight as the heavier breeds that must have eaten more commensurate with their maintenance requirements. The strongest residual correlation (r=0.98) was between BW and BCS. Average band sharing frequencies ranged from 0.60 in the crossbreds to 0.96 in the purebreds with estimated inbreeding coefficients ranging from 0.5% to 3%, respectively, which is very low.

**Key Words:** RAPD Markers, Post-weaning Growth, Beef Cattle

**401    Influence of breed on postpartum interval and estrous cycle length in beef cattle.** R. A. Cushman*, M. F. Allan, R. M. Thallman, and L. V. Cundiff, *USDA, ARS, Roman L. Hruska U.S. Meat Animal Research Center, Clay Center, NE.*

Before genetic markers can be generated for fertility in beef cows, greater characterization of reproductive phenotypes is needed. The present study tested the hypotheses that 1) breeds vary in postpartum interval (PPI) and estrous cycle length, 2) a longer estrous cycle immediately prior to breeding increased pregnancy rates, and 3) a greater number of cycles prior to breeding increased pregnancy rates. Postpartum interval, estrous cycle length, and number of cycles prior to breeding were examined in F1 cows (n = 519) obtained from mating Hereford, Angus and USMARC III cows to Hereford, Angus, Simmental, Limousin, Charolais, Gelbvieh, and Red Angus sires. Cows were classified as having 0, 1, 2, or 3 observed estrous cycles prior to breeding, and breed effects on PPI, number of cycles, and estrous cycle length were examined using the MIXED procedure of SAS. Sire breed of the cow influenced the length of the PPI and number of cycles prior to the start of breeding (P < 0.001). Simmental-sired cows had the shortest PPI and greatest number of cycles prior to breeding; Limousin-sired cows had the longest PPI and least number of cycles prior to breeding. Cows with a greater number of cycles prior to breeding did not have greater pregnancy rates than cows that had not exhibited estrus prior to breeding (P = 0.87). In cows that cycled prior to breeding, the length of the estrous cycle immediately prior to breeding was influenced by dam breed and body condition score (BCS, P < 0.01). Cows out of Hereford dams had shorter estrous cycles than cows out of USMARC III or Angus dams, and estrous cycle length increased as body condition score increased. Pregnancy rate decreased as length of the estrous cycle prior to breeding increased (P = 0.05, -2.2% per day of cycle length), suggesting that there may be an influence of length of the estrous cycle immediately prior to breeding on conception rates due to prolonged follicles with lower quality oocytes. Breed differences in PPI and estrous cycle length suggest that there are genetic components to these traits.

**Key Words:** Beef Breeds, Pospartum Interval, Reproductive Efficiency

**402    Effect of an artificial sweetener and yeast product combination on immune function measurements, growth performance, and carcass characteristics of beef heifers.** R. R. Reuter*[1,2], J. A. Carroll[2], M. S. Brown[3], N. E. Forsberg[4], Y.-Q. Wang[4], R. Mock[5], J. D. Chapman[6], and M. L. Galyean[1], [1]*Texas Tech University, Lubbock,* [2]*USDA-ARS Livestock Issues Research Unit, Lubbock, TX,* [3]*West Texas A&M University, Canyon,* [4]*Oregon State University, Corvallis,* [5]*Texas Veterinary Medical Diagnostic Laboratories, Amarillo, TX,* [6]*Prince Agri-Products, Quincy, IL.*

One hundred ninety-nine crossbred beef heifer calves (205 ± 7.9 kg initial BW) were used in a 44-d receiving trial with 2 dietary