

**600 Affects of climate change and environmental regulation on management of dairy farms.** W. Powers\*<sup>1</sup> and D. Meyer<sup>2</sup>, <sup>1</sup>*Michigan State University, East Lansing*, <sup>2</sup>*University of California, Davis*.

The dairy industry faces increasing environmental challenges. This is coupled with retailer pressure to discontinue use of bST, which will likely increase nutrient excretion per unit of milk produced and/or result in an increase in cow numbers to meet increasing product demand. As states adopt their own greenhouse gas reduction strategies, there is greater emphasis on adoption of a national policy. However, at the present time it is uncertain whether such a policy would include animal agriculture in a cap (e.g. a cow tax) or provide opportunities to the dairy industry to generate credits to be sold in a carbon market. Furthermore, the question remains as to whether or not greenhouse gas reduction strategies will result in increased emissions of criteria pollutants. Air quality issues remain at the forefront of challenges for the dairy industry. Recent reporting requirements under the Emergency Planning and Community

Right-to-know Act (EPCRA) for large concentrated animal feeding operations (CAFOs) signifies that regulation of air pollutants may intensify for animal agriculture. Yet, it is uncertain what pollutants will be targeted and how standards will be established. As the Environmental Protection Agency winds down its National Air Emissions Monitoring Study many are eager to see how the data will translate to policy and what pollutants will be addressed. In the meantime, states continue to set their own policies, targeting a wide array of pollutants such as odor (PA), volatile organic compounds (CA) and hydrogen sulfide (IA and MN). In the face of all these changes is the increasing activity associated with adoption of practices to promote animal well-being and the uncertainty of how those practices affect the welfare of the environment. While many are discussing and calculating the carbon footprint of the U.S. dairy industry many holes in the data exist, making it all the more difficult to manage conflicting objectives.

**Key Words:** air, environment, water

## Animal Health: Calf Health, Respiratory Disease, etc.

**601 Calf enteric mortality etiologies 2004–2008.** T. J. Baldwin, D. J. Wilson\*, R. T. Skirpstunas, J. D. Trujillo, and E. J. Kelly, *Utah State University, Logan*.

Calves (1-90 d old, < 137 kg body wt) submitted dead to the Utah Veterinary Diagnostic Laboratory from 2004-2008 and diagnosed with enteric disease were retrospectively studied. 180 dairy and 123 beef (mainly Holstein or Jersey, Angus, respectively) calves from Utah and Idaho had post-mortem enteric cause(s) of death diagnosed. Agents of mortality included: Bovine Viral Diarrhea (BVD) 38% of cases, cryptosporidia 22%, coronavirus, rotavirus, E. coli each 20%. 10 different single agents killed 52% of calves; most common were BVD 21%, E. coli 9%. There were 21 combinations of 2 agents (28% of cases) and 12 combinations of 3 agents (9%). For calves 1-7 d old, common mortality causes were: dairy-coronavirus, rotavirus, cryptosporidia; beef - BVD, E. coli. 8-14 d, dairy - rotavirus, cryptosporidia, coronavirus; beef - BVD, E. coli. 15-45 d, dairy - BVD, Salmonella; beef - BVD, coccidia. From 45-90 d old, there was little beef calf mortality, but dairy calves died mainly from E. coli and BVD. Recent literature reports the vast majority of calf diarrhea cases are antibiotic-treated. The main causes of enteric mortality are viral, protozoal or a combination thereof. There are implications for therapy and importance of BVD control.

**Key Words:** calf, mortality, BVD

**602 Assessment of the health status of newborn dairy replacement and veal calves.** K. Waalderbos\*<sup>1</sup>, K. Leslie<sup>1</sup>, T. Duffield<sup>1</sup>, T. DeVries<sup>2</sup>, and B. McBride<sup>2</sup>, <sup>1</sup>*Department of Population Medicine, University of Guelph, Guelph, Ontario, Canada*, <sup>2</sup>*Department of Animal and Poultry Science, University of Guelph, Guelph, Ontario, Canada*.

Successful raising of healthy calves can be a challenge for dairy and veal producers. To date, in Ontario calves, little research has been reported on how the transfer of passive immunity and other health indicators may relate to calf health. A cross-sectional study is being conducted with 2306 newborn calves from 16 herds in southwestern Ontario. The objectives are to determine the health status of newborn dairy replacement and veal calves, with emphasis on quantifying transfer of passive immunity; to assess the influence of other metabolic and physiological

indicators on calf health; and to evaluate differences between heifer and bull calves for these health indicators. During the study period of January to December 2008, weekly enrollment of heifer and bull calves, 1 to 7 days of age, occurred on commercial dairy farms in southwestern Ontario. At enrollment, calves were given a health score, measured for height, weight and body temperature, and two blood samples were collected. The whole blood sample was analyzed for complete blood count and selenium. Serum was harvested and analyzed for total protein, haptoglobin, magnesium and globulins. Birth records were completed for each study calf. Calves were followed until four months of age for disease events, treatment information and growth. Data analysis is in progress. In current results, the serum total protein values for 2306 calves ranged from 3.6 to 9.7g/dL, with a mean of 5.7g/dL (SD 0.68). Using a cut-off of >5.2g/dL to indicate success of passive transfer, 482 calves (20.9%) had a failure rate. Farm of origin and gender have an effect (P<0.01) on the distribution of serum total protein in calves. The distribution of whole blood selenium status for 876 newborn calves shows values ranged from 0.09 to 0.40 mg/mL, with a mean of 0.21 mg/mL (SD 0.05). Of note, the lab-provided reference interval for whole blood selenium is 0.20 to 1.2 mg/mL. Calves in this study tend toward the lower reference limit, with 369 calves (42.1%) falling below a 0.2 cut-off. These results suggest there is considerable variability in serum total protein and selenium levels of newborn calves both within and between farms.

**Key Words:** calf, total protein, selenium

**603 Targeting therapy to minimize antimicrobial use in pre-weaned dairy calves: effects on health and occurrence of antimicrobial resistance in fecal *Escherichia coli*.** A. C. B. Berge, D. A. Moore\*, T. E. Besser, and W. M. Sischo, *Washington State University, Pullman*.

Antibiotics should be used prudently in production agriculture to reduce risks for antimicrobial resistance. The objectives of this study were to assess effects of raising pre-weaned calves without antimicrobials in the milk and reducing therapeutic antimicrobial treatment for diarrhea on morbidity, mortality, weight gain and antimicrobial resistance fecal *Escherichia coli*. Newborn calves (N=358) were randomly allocated to 4 groups, housed in individual hutches and observed for 28 days. Day

2 serum IgG levels, weights on day 1, 28 and weaning were obtained. Calves in the conventional treatment (CT) group were treated by dairy staff with their protocol of bismuth-pectin, sulfisoxazole/trimethoprim, spectinomycin and penicillin for diarrhea. The targeted treatment (TT) group received bismuth-pectin and antimicrobial treatment only in cases of fever or depressed attitude. Within CT and TT groups, calves were equally stratified to receive neomycin and tetracycline in the milk for the first 2 weeks (ABMILK) or no antimicrobials (NoABMILK). Daily evaluations included fecal consistency, respiratory signs, attitude, appetite and milk and grain consumption. Fecal samples were obtained on the day 1, 14 and 28. Three fecal E. coli per sample were isolated and susceptibility-tested to 12 antimicrobials using disk diffusion. A multivariate negative binomial model evaluated the likelihood of diarrhea on any observation day. An ANOVA model assessed differences in weight gain and grain consumption. Potential covariates included serum IgG, birth weight and gender, and interaction effects. The CT calves were twice as likely to have diarrhea compared to TT calves. The ABMILK calves were 1.3 times more likely to have diarrhea compared to NoABMILK calves. The TT calves tended to have a higher average daily gain at 28 days and consumed more grain than CT calves. Antimicrobial resistance patterns in fecal E. coli showed low levels of multi-drug resistance in day-old calves but higher levels in isolates from 2 and 4 week old calves.

**Key Words:** calves, antimicrobial resistance, treatment

**604 Factors affecting performance of pre-weaned dairy calves under Kuwait's environment: Effects of immunoglobulins and age on diseases and mortality.** M. Razzaque\*, T. Al-Mutawa, S. Abbas, and M. Bedair, *Aridland Agriculture and Greenery Department, Kuwait Institute for Scientific Research, Kuwait, Safat, Kuwait.*

**Abstract:** Objectives of the study were to investigate the effects of dam vaccination, age, serum immunoglobulin (Ig) on disease syndromes and mortality in pre-weaned calves. Late pregnant Holstein Friesian dairy cows and heifers were divided into two herds from five farms: Treatment (T) vaccinated using Lactovac against Rotavirus, Coronavirus and Escherichia coli and control (C) unvaccinated. Total of 1088 newborn calves of above herds were also divided as T and C for the study from their birth to weaning at 90 d. Calves were weighed at birth, fed colostrum 12.5% of their live weight within 8 hrs from birth until 24 hrs. Serum proteins and Ig (IgG, IgM and IgA) were measured, disease syndromes, morbidity and mortality rates were evaluated until weaning of calves at 90 d. The mean birth weight ( $34.25 \pm SE 0.21$ kg) of calves did not differ between the herds ( $P=0.05$ ). Crude mortality rates (2.83 to 22.83%) in calves varied significantly ( $P < 0.01$ ) among five farms. Highly significant differences between dairy herds were observed in Ig classes: IgG (F 3.47  $P < 0.010$ ), IgM (F 3.52  $P < 0.009$ ) and IgA (F 3.66  $P < 0.008$ ). The effects of Ig levels on calf morbidity rates were significant ( $P < 0.05$ ) on three disease syndromes: pneumonia, diarrhea, and pneumo-enteritis. Vaccination of pregnant dams and oral administration of antibodies to newborn calves reduced calf morbidity and mortality rates ( $P < 0.01$ ). Predominant disease syndromes were pneumo-enteritis (34.6%), pneumonia (33.8%) and combined accounted for 68.4% of all mortality. The younger calves were greatly affected by the disease syndromes. Results showed that inadequate levels of passive immunity of young calves were commonly found in the dairy farms of Kuwait adversely affecting their performance. This first study demonstrates importance of ensuring adequate levels of serum Ig and proteins levels in calves of Kuwait's dairy herds. *Acknowledgement: Partial support of Kuwait Foundation for Advance-*

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**Key Words:** dairy calves, mortality, morbidity

**605 Associations between herd risk of high precalving NEFA and management, feed additive, and facility factors.** T. F. Duffield\*<sup>1</sup>, M. Carson<sup>1</sup>, M. Capel<sup>5</sup>, S. Godden<sup>2</sup>, M. Overton<sup>3</sup>, J. Santos<sup>4</sup>, and S. J. LeBlanc<sup>1</sup>, <sup>1</sup>University of Guelph, Guelph, ON, Canada, <sup>2</sup>University of Minnesota, Minneapolis, <sup>3</sup>University of Georgia, Athens, <sup>4</sup>University of Florida, Gainesville, <sup>5</sup>Perry Veterinary Clinic, Perry, NY.

A field study was conducted in 4 regions of Canada and the USA (ON and NY; MN and WI; CA; and GA and FL) to explore herd risk factors for high precalving serum non-esterified fatty acids (NEFA). Once weekly, blood was collected from cows in the week before calving. For this analysis data from 2048 cows in 47 Holstein dairy herds with a completed herd management survey were utilized. Median cows sampled per farm was 36 (min of 20, max of 97). The median NEFA value for all precalving cows was 0.37 mmol/L. A cutpoint of  $\geq 0.5$  mmol/L was used to define high NEFA at the cow level. Using this cutpoint, the range in the prevalence of high NEFA across herds was 6.5 to 75% and the median herd prevalence of high NEFA cows was 25%. High herd risk for elevated precalving NEFA (HNEFA, n=24 herds) was defined at a prevalence of  $\geq 25\%$  of cows with NEFA  $\geq 0.5$  mmol/L and low risk NEFA (LNEFA, n=23) herds had a prevalence  $< 25\%$ . Two by two contingency tables were constructed to screen survey variables for association with HNEFA within 3 categories: facilities, additives/therapeutics, management. Variables associated with HNEFA were then subjected to logistic regression. Bunk space, cow density, feeding frequency, and frequency of group changes through the transition period were not significantly associated with the probability of HNEFA in the close-up period. The use of anionic salts in the close-up diet was associated with a reduced risk of an HNEFA classification (odds ratio (OR) = 0.31,  $P=0.06$ ). The use of individual maternity pens versus a group calving pen was associated with HNEFA (OR=2.6,  $P=0.1$ ). The mixing of close-up heifers and cows was associated with an increased risk of HNEFA (OR=5.6,  $P=0.05$ ). These results do not refute the importance of feeding and lying space but underline that the use of single calving pens and mixing of close-up heifers with cows may be associated with social stressors that might reduce DMI and raise serum NEFA. The lowered risk of HNEFA with the use of anionic salts may represent a surrogate measure of other aspects of transition nutrition and merits more investigation.

**Key Words:** NEFA, risk factors, precalving

**606 Associations between herd risk of high precalving NEFA and dietary factors.** T. F. Duffield\*<sup>1</sup>, M. Carson<sup>1</sup>, M. Capel<sup>5</sup>, S. Godden<sup>2</sup>, M. Overton<sup>3</sup>, J. Santos<sup>4</sup>, and S. J. LeBlanc<sup>1</sup>, <sup>1</sup>University of Guelph, Guelph, ON, Canada, <sup>2</sup>University of Minnesota, Minneapolis, <sup>3</sup>University of Georgia, Athens, <sup>4</sup>University of Florida, Gainesville, <sup>5</sup>Perry Veterinary Clinic, Perry, NY.

The objective of this study was to explore possible nutritional risk factors for high serum non-esterified fatty acids (NEFA) in the close-up period. A field study was conducted in 4 regions of Canada and the USA. Once weekly, after the morning feeding, blood was collected from cows in the week before calving. For this analysis data from 1572 cows in 35 Holstein dairy herds from ON, NY, MN, and CA with a completed herd

management survey and completed feed analysis of the pre-calving TMR were utilized. The close-up TMR was sampled from each participating farm in four places in the bunk, mixed together and submitted to the same laboratory. Wet chemistry analysis was used for minerals and all other analyses were performed using near infrared spectroscopy. In addition, each TMR was evaluated for particle size using the Penn State particle separator (PS). Dietary cation anion difference was calculated using the following formula:  $DCAD = ((Na \times 435 \times 100) + (K \times 256 \times 100)) - ((Cl \text{ lorida} \times 282 \times 100) + (S \times 624 \times 100))$ . Mean herd NEFA for each farm was calculated for all cows sampled and was used as the outcome of interest. Univariable associations between each ration parameter and herd NEFA were calculated using a mixed model linear regression, controlling for the random effect of region. Variables significant at  $P < 0.2$  were submitted to a multivariable model. In preliminary screening, indicators of fiber (NDF, proportion on the top screen of the PS) and DCAD were positively associated with herd NEFA, while energy indicators (starch, ADF, fat) were negatively associated with herd NEFA. The final model revealed significant associations of NDF ( $P = 0.01$ ) and DCAD ( $P = 0.01$ ) with herd average NEFA. In this dataset, lower to moderate dietary NDF (mean = 43%, range was 32 to 52%) and limiting DCAD (mean = 64, range was -139 to 286) in the close-up diet was associated with lower herd NEFA pre-calving.

**Key Words:** NEFA, precalving diet, risk factors

**607 Rumen metabolomic profile and hierarchical clustering analysis in dairy cows fed grading amounts of grain.** Q. Zebeli, M. Lewis, S. M. Dunn, D. S. Wishart, and B. N. Ametaj\*, *University of Alberta, Edmonton, Alberta, Canada.*

Feeding dairy cows high grain diets is related to high incidence of metabolic disorders; however, the underlying mechanism(s) are not yet clear. Metabolomic profiling is a new technology that identifies and quantifies multiple small molecular weight compounds in biological fluid samples. The aim of this study was to explore changes in rumen fluid metabolomic profile in dairy cows fed graded amounts of barley grain using NMR and GC-MS technologies as well as hierarchical clustering analysis. Eight primiparous Holstein lactating cows (~100 DIM) were assigned to one of the 4 mixed diets containing 0, 15, 30, and 45% barley grain (on DM basis) in a double  $4 \times 4$  Latin square design with 21-d periods. After an 11-d adaptation period, samples of rumen fluid were collected shortly before morning feeding on d 1, 3, 5, 7, and 10 of measurements period. Across all diets, the average linkage hierarchical clustering analysis revealed a minimum similarity of 55% in the expression patterns of the 24 organic compounds identified in the rumen fluid. The highest similarity provided the cluster built by leucine, valine, and acetate (90%) followed by a cluster of butyrate, alanine, lactate, and valine (83%) as well as clusters of 3-phenylpropionate (3PP) and 3-hydroxy-phenylacetate (3HP; 71%). Increasing the level of barley grain in the diet linearly increased the concentration of methylamine (MET;  $P = 0.01$ ), phenylacetate (PHE;  $P = 0.02$ ), and 3HP ( $P = 0.08$ ) but decreased that of 3PP ( $P < 0.01$ ). The analysis also showed negative quadratic relationship between MET and dimethylamine to rumen pH ( $P < 0.01$ ). The results showed positive correlations between MET and PHE and rumen lipopolysaccharide (LPS;  $P < 0.001$ ), a highly pro-inflammatory compound, as well as negative correlation between LPS and 3HP ( $P < 0.001$ ). In conclusion, rumen metabolomic cluster analysis reliably describes changes in the rumen fluid during feeding of high-grain diets and suggest further research to better understand rumen physiology.

**Key Words:** dairy cow, rumen metabolomics, clustering analysis

**608 Intrapulmonary *Mannheimia haemolytica* (MH) challenge increases nitrooxidative stress (NOxS) in heifers phenotypically selected for tumor necrosis factor- $\alpha$  (TNF- $\alpha$ ) hyper-responsiveness.** T. Elsasser\*<sup>1</sup>, J. Goff<sup>2,3</sup>, R. Briggs<sup>2</sup>, S. Kahl<sup>1</sup>, H. Lehmkuhl<sup>2</sup>, M. Ackerman<sup>3</sup>, C. Li<sup>1</sup>, and R. Horst<sup>2</sup>, <sup>1</sup>USDA-ARS, Beltsville, MD, <sup>2</sup>USDA-ARS, Ames, IA, <sup>3</sup>Iowa State University, Ames.

We assessed the degree to which NOxS contributes to the pulmonary and extrapulmonary pathological consequences of MH infection. Two populations of 8-mo old Angus  $\times$  Hereford heifers were selected based on the patterns of plasma TNF- $\alpha$  evoked following 2 endotoxin (LPS, *E. coli* 055: B5, 0.2  $\mu\text{g}/\text{kg}$  BW) challenges 4 d apart; normal animals (N) presented low TNF- $\alpha$  responses and displayed tolerance to the second LPS challenge and hyper-responsive heifers (H) presented higher plasma concentrations of TNF- $\alpha$  and failed to display LPS tolerance. Animals were transported from Beltsville, MD to Ames IA, unloaded, and challenged with MH (NADC D153 serotype 1; intrapulmonary,  $9 \times 10^8$  CFU/animal). Blood samples, rectal temperature and clinical observations were made at time 0, 24 h and 48 h postinfection (PI). Animals were euthanized at 48 h PI. Lungs and livers were excised, weighed, and scored for appearance; samples were fixed in buffered formalin for subsequent immunohistochemical (quantitative image analysis) examination. Animals included in the statistical analysis (N,  $n = 6$ ; H,  $n = 5$ ) had no clinical signs at time 0 and met 4 of 5 criteria (fever, respiratory signs, lung score  $\geq 1$ , appropriate positive tissue gram stain, increased white blood cell count) of infection after MH. Lung weight (as a % BW) increased to a greater extent in H than in N. Mean lung TNF- $\alpha$  immunoreactivity was 47.7% greater in H than in N ( $P < 0.04$ ). Mean protein tyrosine nitration immunoreactivity, a biochemical marker for peroxynitrite (ONOO)-mediated NOxS damage in cells overproducing nitric oxide and superoxide anion, was higher in H than N in liver (87%,  $P < 0.03$ ) and lung (34%,  $P < 0.04$ ) after MH. The data suggest that MH infection generates ONOO in the lung and liver where tissue damage is more extensive in animals with a propensity to overrespond to Gram-negative proinflammatory challenge.

**Key Words:** *Mannheimia haemolytica*, respiratory disease, cattle

**609 Transcriptome analysis of muscle tissue from calves infected with bovine viral diarrhea virus and *Mannheimia haemolytica*.** R. L. Mills\*, L. Carlos-Valdez, L. O. Burciaga-Robles, D. Stein, D. L. Step, R. W. Fulton, U. DeSilva, and C. R. Krehbiel, *Oklahoma State University, Stillwater.*

Bovine respiratory disease (BRD) is the most economically important ailment of cattle in the U.S. Cattle with this disease produce lighter carcasses with decreased dressing percentages and *longissimus dorsi* area. To understand the effects of common BRD pathogens on muscle gene expression, 8 crossbred beef steers ( $283.6 \pm 37.4$  kg) were exposed to a calf persistently infected with bovine viral diarrhea virus type 1b for 72h followed by intratracheal inoculation with *Mannheimia haemolytica* serotype A. Muscle biopsies were taken prior to exposure to either pathogen and 24h following inoculation. Total RNA was extracted and bovine oligonucleotide microarray hybridization performed ( $n = 6$ ). Genes were categorized according to biological process and/or function. Significance was set at fold change greater than 1.5 and  $P < 0.01$ . We found 30 genes were induced and 32 genes were suppressed by 24h of infection. Protein metabolism, transcription regulation, and the cell cycle were the predominant biological processes affected. Among upregulated genes, protein metabolism, transcription regulation, cell cycle, and signal transduction processes were most affected. Among downregulated genes, transcription regulation, binding, and

cell cycle genes were most affected. We observed mRNA for several genes involved in tissue remodeling and regeneration to be induced by 24h of infection (tropomyosin 4, 2.84 fold; ankyrin repeat domain 2, 2.29 fold; cathepsin H, 2.09 fold). Genes involved in the cell cycle were coordinately regulated to promote cell proliferation and differentiation (eukaryotic translation initiation factor, 1.59 fold, calreticulin, -1.63 fold, and prolyl endopeptidase, -1.77 fold). Results from this experiment indicate that cattle challenged with BRD pathogens alter gene expression to promote cellular proliferation and differentiation with concomitant tissue regeneration. A corollary to this would suggest that during the first 24h of infection by BRD pathogens, skeletal muscle deterioration is occurring which may partially explain the lighter carcass weights associated with cattle treated for BRD.

**Key Words:** beef cattle, bovine respiratory disease, gene expression

**610 Effect of times treated for bovine respiratory disease during preconditioning on gene expression in muscle and adipose tissue of beef heifers.** J. Johnson\*, D. R. Stein, L. O. Burciaga-Robles, B. P. Holland, D. L. Step, J. W. Ritchey, U. DeSilva, and C. R. Krehbiel, *Oklahoma State University, Stillwater.*

Bovine respiratory disease (BRD) is the most costly disease to the cattle feeding industry. Our objective was to determine the effects of BRD on gene expression in economically important tissues. Tissue biopsy samples from the LM and s.c. fat (SCF) were collected between the 12th and 13th rib from heifers never treated against BRD (HEALTHY; n = 5), treated once (n=5), treated twice (n=5), treated three times (n=5), and heifers classified as chronically morbid (CHRONIC; n = 5) after a 63 d preconditioning period. CHRONIC was defined as animals with at least three antimicrobial treatments and loss of BW during the previous 21 d on feed. Microarray comparisons were performed against HEALTHY and CHRONIC animals to determine differentially expressed genes important in pathways that decrease growth and performance or are involved in immunological functions. Subsequently, 14 genes were evaluated using RT-PCR including tumor necrosis factor alpha (TNF $\alpha$ ), interleukin 6, toll-like receptor 4, and nuclear factor kappa B (NF $\kappa$ B). The Proc Mixed procedure of SAS was used to evaluate the significance of number of antimicrobial treatments. Components of the ubiquitin pathway were different among treatments, including greater ( $P<0.09$ ) expression of Fbox WD repeating domain 12 in SCF, and greater ( $P=0.10$ ) expression of 26S proteasome subunit ATPase 1 in LM. TNF $\alpha$  was more highly expressed ( $P<0.007$ ) in muscle of CHRONIC than HEALTHY heifers. Other genes that were differently expressed in adipose tissue of CHRONIC vs. HEALTHY animals were haptoglobin (down regulated;  $P<0.02$ ) and NF $\kappa$ B (up regulated;  $P<0.10$ ). These results suggest that muscle wasting via the ubiquitin pathway, as well as increased expression of TNF $\alpha$  may decrease growth potential in heifers treated several times for BRD.

**Key Words:** animal growth, bovine respiratory disease, gene expression

**611 Evaluation of enzymatically hydrolyzed yeast in vitro and in vivo for control of *Cryptosporidium parvum* infections in dairy calves.** S. Jalukar\*<sup>1</sup> and J. Nocek<sup>2</sup>, <sup>1</sup>Varied Industries Corporation, Mason City, IA, <sup>2</sup>Spruce Haven Farm and Research Center, Auburn, NY.

Effect of enzymatically hydrolyzed yeast and yeast culture (EHY) (Celmanax<sup>®</sup>, Varied Industries Corporation, IA, USA) was evaluated

to determine efficacy on *Cryptosporidium parvum* challenge. EHY contains complex sugars like galactosamine, mannose and mannan oligosaccharide (MOS) which have been shown to interfere with *Cryptosporidium spp* attachment to intestinal epithelium. Experiment 1 evaluated EHY (40, 20 or 2 mg/mL) treated *C. parvum* sporozoites to interfere with the binding and infection of Madin - Derby bovine kidney (MDBK) cells and live porcine intestinal cells (IPEC-J2) by an in vitro immuno-fluorescence assay. Experiment 2: Sixteen calves (10-12 days old) naturally infected with *C. parvum* were randomly assigned to two treatments: without and with 4ml/calf/twice a day EHY for 5 days. Fecal samples were taken at initiation and completion of the trial for oocysts count, consistency and calves were scored for dehydration. Experiment 1: There was a decrease ( $P < 0.001$ ) in the number of attached sporozoites to bovine MDBK cells when EHY was present at 40 and 20 mg/mL, compared to un-treated control (11.97 and 19.60 vs. 40.80 sporozoites/field, respectively). Ability of *C. parvum* sporozoites to infect porcine IPEC-J2 cells decreased with increase in EHY concentration in a cell-monolayer assay. A 90% decrease in infection was noted with 40 mg/mL EHY treatment compared to control. Experiment 2: Calves supplemented with EHY demonstrated 3 fold less oocyst shedding within 5 days after supplementation. Fecal and dehydration scores were significantly less for calves supplemented with EHY. Enzymatically hydrolyzed yeast plus yeast culture (Celmanax<sup>®</sup>) demonstrated the ability to bind and prevent *C. parvum* from infecting tissue in vitro, reduced oocyst shedding, improved fecal consistency and hydration status in infected calves.

**Key Words:** cryptosporidiosis, calf

**612 Neem-tree extract as a feed-additive against ticks in sheep.** S. Y. Landau\*<sup>1</sup>, D. R. Gardner<sup>2</sup>, J. A. Pfister<sup>2</sup>, E. L. Knoppel<sup>2</sup>, D. Kababya<sup>1</sup>, F. D. Provenza<sup>3</sup>, C. Peterson<sup>3</sup>, and J. J. Villalba<sup>3</sup>, <sup>1</sup>Agricultural Research Organization, Bet Dagan, Israel, <sup>2</sup>SDA-ARS Poisonous Plant Research Laboratory, Logan, UT, <sup>3</sup>Utah State University, Logan.

Ticks are affected by the composition of the blood of their hosts. Immersion in solutions of fruit and kernel extracts from trees of the Meliaceae family inhibits egg production and embryogenesis in *Hyalomma spp* and *Boophilus spp.* ticks in vitro. The tetranor-triterpenoid Azadirachtin A (AzA) is the main acaricidal compound in these extracts. We investigated the effects of an extract of the neem tree (*Azadirachta indica* Juss.) containing 43% AzA, given as a feed additive to lambs artificially infested with adult engorging *Dermacentor variabilis* ticks. We assessed feed acceptance and toxicity to lambs, AzA concentration in peripheral blood using a novel LC/MS assay, and tick engorgement and egg production. After tick attached, the lambs were allotted to 3 dietary treatments: AzA0 (Control, n=10), AzA0.3 (n=5), and AzA0.6 (n=5), with feed containing 0, 0.3, and 0.6% AzA on a DM basis. Four days after attachment, ticks were sprayed in half of the AzA0 lambs with an ethanol:water:soap emulsion containing 0.6% AzA (AzA0S). In spite of its very pungent odor, the neem extract was well accepted by all but one lamb. No differences were found between groups in muscle and liver enzymes in blood, and there was no indication of toxicity. Plasma AzA concentrations after 7 and 14 days of feeding AzA were (3.32; 4.81) and (1.88, 4.35  $\mu$ g/ml) for the AzA0.3 and AzA0.6 treatments, respectively, suggesting increased liver detoxication during the second week. Treatments were not lethal to ticks, but tick weight at detachment was 0.64, 0.56, 0.48, and 0.37 g for ticks from the AzA0, AzA0.3, AzA0S, and AzA0.6 treatments ( $P<0.004$ ), suggesting that blood AzA was detrimental to ticks. As Azadirachtin affects embryo development and ticks at the moulting stages, we expect that one-host ticks will be more

affected than the three-host tick *D. variabilis*. Our results thus suggest that ingestion by herbivores of plants containing compounds such as AzA may reduce external parasites.

**Key Words:** lamb, tick, azadirachtin

## Beef Species: Health, Efficiency and Beef Quality

**613 mRNA expression of genes regulating oxidative phosphorylation in the muscle of beef cattle divergently ranked on residual feed intake.** A. K. Kelly\*<sup>1</sup>, S. M. Waters<sup>2</sup>, M. McGee<sup>2</sup>, C Carberry<sup>1,2</sup>, D. H. Crews Jr<sup>3</sup>, T. M. Boland<sup>1</sup>, and D. A. Kenny<sup>1</sup>, <sup>1</sup>*School of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Belfield, Dublin 4, Ireland*, <sup>2</sup>*Animal Bioscience Centre, Teagasc, Grange Beef Research Centre, Dunsany, Co. Meath, Ireland*, <sup>3</sup>*Colorado State University, Fort Collins.*

The objective was to evaluate the effects of ranking on phenotypic residual feed intake (RFI) and diet type on the transcription of genes coding for mitochondrial biogenesis in the muscle of beef cattle. Individual dry matter intake and growth was recorded for 90 yearling Limousin × Friesian heifers offered a high energy TMR diet over 120 days. All animals were ranked retrospectively on phenotypic RFI. The 10 highest (inefficient) and 10 lowest (efficient) animals were selected for this study. Animals were then re-allocated to a grass silage diet and feed intake was recorded for a six week period. The experiment was therefore arranged in a 2 (high v low RFI) × 2 (high v low energy diet) factorial design. Biopsies of the *M. longissimus dorsi* were harvested at the end of each dietary period. Total RNA was extracted and real-time PCR was used to quantify mRNA transcripts of genes coding for five enzymes from the respiratory chain complex, two electron carriers, mitochondrial protein and five transcription factors. mRNA expression of the transcription factors PGC1- $\alpha$  and PPAR- $\gamma$  were 2.0 and 2.8-fold higher ( $P < 0.01$ ) respectively, in inefficient compared with efficient animals. There was a phenotype × diet interaction ( $P < 0.05$ ) for *ant-1* mRNA involved in exchange of ADP and ATP between the mitochondrial matrix and the cytosol. A tendency ( $P = 0.09$ ) for a phenotype × diet interaction was also observed for *atpase*, a critical regulator of the ATP-synthesizing enzyme complex. These data suggest an association between mitochondrial biogenesis and RFI in cattle and could be useful in the development of molecular markers for this trait.

**Key Words:** residual feed intake, muscle, gene expression

**614 Relationship between metabolic hormones, metabolites and energetic efficiency in growing beef heifers.** A. K. Kelly\*<sup>1</sup>, M. McGee<sup>2</sup>, D. H. Crews Jr.<sup>3</sup>, T. M. Boland<sup>1</sup>, and D. A. Kenny<sup>1</sup>, <sup>1</sup>*School of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland*, <sup>2</sup>*Teagasc, Grange Beef Research Centre, Dunsany, Co. Meath, Ireland*, <sup>3</sup>*Colorado State University, Fort Collins.*

Measurement of residual feed intake (RFI) is expensive and thus identification of cost-effective physiological indicators is necessary to facilitate wide-scale adoption. Our objective was to examine the potential of selected metabolic hormones and metabolites as indicators of energetic efficiency in growing beef heifers. Individual dry matter intake and growth was recorded for 90 yearling Limousin × Friesian heifers offered a high energy TMR diet for 120 days. Blood samples (n=4) were collected by jugular venipuncture on a monthly basis for each animal. Concentration of plasma IGF-1 was measured using

RIA, insulin was quantified using fluoro-immunoassay, while selected metabolites were measured using an automated biochemical analyzer. Residual feed intake was computed, for each animal, as the residuals from the regression of DMI on ADG and mid test BW<sup>0.75</sup> (MWT). Residual feed intake averaged 0.00 kg/d and ranged from -1.25 to 1.87 kg/d. As expected, RFI was not correlated with MWT or ADG, but was correlated ( $P < 0.001$ ) with DMI ( $r = 0.48$ ) and FCR ( $r = 0.46$ ). Plasma IGF-1 was positively correlated ( $P < 0.05$ ) with ADG ( $r = 0.25$ ) but not ( $P > 0.10$ ) with DMI, FCR or RFI. Correlations coefficients between insulin and DMI, ADG, FCR or RFI were not different from zero ( $P > 0.10$ ). Plasma glucose was negatively correlated ( $P < 0.05$ ) with FCR ( $r = -0.20$ ) but not associated with DMI, ADG or RFI. Urea concentrations were related to DMI ( $r = 0.33$ ) and FCR ( $r = 0.31$ ) but not ADG or RFI. Plasma NEFA was negatively associated ( $P < 0.05$ ) with DMI (-0.36), FCR (-0.36) and RFI (-0.23). Positive associations ( $P < 0.05$ ) were observed between BHB and DMI (0.34), FCR (0.25) and RFI (0.39) but an association with ADG was not detected. It is unlikely that the plasma analytes measured here, *per se*, will be useful in the early identification of energetically efficient cattle.

**Key Words:** residual feed intake, plasma analytes

**615 Predicting body weight in beef heifers using various body measurements.** A. G. Fahey\*, A. K. Kelly, R. P. McDonnell, and D. A. Kenny, *School of Agriculture, Food Science, and Veterinary Medicine, University College Dublin, Belfield, Dublin 4, Ireland.*

Accurate assessment of body weight (BW) is an important management tool in commercial beef enterprises. However, many farmers may not have easy access to weighing facilities. Body measurements (BM) such as wither height or depth of chest require inexpensive equipment. In order to determine the potential of various BM as predictors of BW, back length, wither height, pelvic width, chest depth, and chest girth were measured along with BW. Heifers were divided into two age groups; 6-13 months (mean = 286.8 ± 44.7 d; n = 87 heifers, 176 records), and 17-24 months (mean = 642.3 ± 45.6 d; n=60 heifers, 106 records). Body weight was regressed on BM, and linear, quadratic and cubic effects of the BM variables were considered:  $Y = b_0 + \text{age} + b_1X + b_2X^2 + b_3X^3 + \epsilon$ . Where Y = body weight,  $b_0$  = the intercept, X = independent variable (i.e. wither height, back length, chest depth, chest girth, or pelvic width). Cubic regression models with and without age were best predictor equations for BW for both age groups. The R<sup>2</sup> value was used to determine the variation accounted for by the various regression models (Table 1). Overall, the cubic regression models had a better fit for the 6-13 month group for all measurements with the exception of chest girth which was stronger for the 17-24 month heifers. The cubic regression equation for chest depth + age had the best fit for the 6-13 month group, while chest girth + age was the best BW prediction model for the 17-24 month group. These results indicate the potential for the use of BM as indicators of BW, although different BM may have to be used depending on the age of the animal.