

SYMPOSIA AND ORAL PRESENTATIONS

Animal Health: Respiratory Health, Viruses

767 Newly received feedlot heifers managed with three respiratory disease protocols. J. L. Wahrmond*¹, D. B. Burken¹, B. K. Wilson¹, S. J. Terrill¹, D. L. Step², C. R. Krehbiel¹, C. L. Goad³, and C. J. Richards¹, ¹Oklahoma State University, Department of Animal Science, Stillwater; ²Oklahoma State University, Department of Veterinary Clinical Sciences, Stillwater; ³Oklahoma State University, Department of Statistics, Stillwater.

Commingled heifers were purchased and administered ruminal temperature monitoring devices in LA (n = 180, BW = 248.7 ± 35.7 kg) and KY (n = 162, BW = 243.9 ± 21.4 kg). Within purchase group, heifers were allotted to 12 pens for 56 d. Pens were assigned to 3 bovine respiratory disease (BRD) management treatments with pulls based on: visual signs (CON, n = 110), visual signs and(or) elevated ruminal temperature (TEMP, n = 116), or visual signs after metaphylactic tulathromycin treatment (MET, n = 116). Antimicrobial treatments for BRD included tulathromycin, fluoroquinolone, and ceftiofur-HCl. Effects of management and number of BRD treatments required were analyzed using the MIXED procedure of SAS. Heifers on CON, TEMP, and MET treatments were treated 0.55, 1.47, and 1.27 times for BRD, respectively. Final BW of TEMP heifers was 5.3 kg greater ($P < 0.05$) than CON, and MET heifers gained 0.12 kg/d more than CON heifers ($P < 0.05$). Interactions of management × number of BRD treatments required were observed ($P < 0.05$) for final BW and overall ADG. Final BW of CON heifers requiring one or 2 BRD treatments were 12.9 kg and 38.6 kg less ($P < 0.05$), respectively, than those never treated. Final BW of MET heifers requiring no additional BRD treatment were 18.9 kg greater ($P < 0.05$) than those requiring 3 treatments. Final BW of TEMP heifers receiving 2 or less treatments were not different ($P > 0.05$); however, BW of those treated 3 times was 15.1 kg less ($P < 0.05$) than those treated once. CON heifers requiring zero or one treatment gained 0.58 kg/d more ($P < 0.05$) than heifers requiring 2. MET heifers receiving no additional treatments gained 0.23 kg/d more ($P < 0.05$) than those receiving 3. TEMP heifers treated once or twice gained 0.46 kg/d more ($P < 0.05$) than heifers treated 3 times. Of heifers treated once for BRD, MET heifers gained 0.16 kg/d more ($P < 0.05$) than CON heifers. Of heifers treated twice, MET and TEMP heifers gained 0.64 kg/d more ($P < 0.05$) than CON. Management did not affect ($P > 0.05$) ADG of heifers treated 3 times. Ruminal temperature monitoring and metaphylactic antimicrobial treatment have positive effects on feedlot health and performance.

Key Words: disease, performance, temperature

768 Muscle gene expression in an acute model of bovine respiratory disease. 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) has been shown to negatively impact carcass characteristics by leading to lighter carcasses, decreased *longissimus dorsi* (LD) area, and poorer carcass quality. To understand the effects of BRD on muscle gene expression, 8 beef steers (284 ± 37.4 kg) were exposed to 2 calves persistently infected with bovine viral diarrhea

virus type 1b (BVDV) for 72h followed by intratracheal inoculation with *Mannheimia hemolytica* (MH). Muscle biopsies were taken from the LD before exposure to pathogens (PRE) and 24 h (24H) following inoculation. Total RNA was extracted, reverse transcribed, and expression levels analyzed using quantitative PCR. Glutamine synthetase (GS) was induced (+8.12, $P < 0.001$) and regulatory factor X-associated ankyrin-containing protein (RFXANK) and a homolog of tropomyosin 4 (TPM4) tended to be upregulated (+2.61 and +1.48, respectively; $P < 0.10$) in the 24H group. Glutamine synthetase induction is a hallmark of muscle deterioration. RFXANK is a regulatory protein known to bind major histocompatibility complex class II (MHCII) promoters inducing MHCII expression involved in antigen presentation. Tropomyosin 4 is an actin-binding protein shown to affect muscle contraction in striated and smooth muscle tissue in humans. Results indicate that muscle proteolysis is occurring based on GS expression. MHCII may be upregulated in muscle histiocytes as demonstrated by increased levels of RFXANK transcripts. Glutamine status has been shown to affect immune status; therefore, the induction of these 2 proteins may be indicative of cooperation between macrophages and myofibers. These results suggest that cattle challenged with BRD pathogens may experience acute cachexia within 24h post-infection with BVDV and MH. Such myopathy may partially explain lighter carcass weights associated with cattle treated for BRD.

Key Words: beef cattle, bovine respiratory disease, skeletal muscle

769 Bovine respiratory disease related metabolic fingerprints in beef steers. S. J. Terrill*, R. D. Madden, J. W. Dillwith, L. O. Burciaga-Robles, D. L. Step, R. W. Fulton, A. W. Confer, M. Montelongo, and C. R. Krehbiel, Oklahoma State University, Stillwater.

Bovine respiratory disease (BRD) is the most costly disease in North American feedlots; however, diagnosis is subjective. Metabolomics, or the study of the total metabolic profile of a biological tissue or fluid, may provide a way for objective diagnosis. The objective was to identify biomarkers of BRD using metabolomic techniques (i.e., GC/MS). Twenty-four Angus crossbred steers were divided into 4 treatment groups in a completely randomized design (n = 6). Treatments were: 1) exposure to 2 BVDV persistently infected (PI) steers for 72 h (BVDV); 2) exposure to the 2 PI-BVDV steers for 72 h and intratracheal challenge with *Mannheimia hemolytica* on d 0 (BVDV+MH); 3) intratracheal challenge with *M. hemolytica* on d 0 (MH); and 4) no challenge (CTRL). Blood samples were collected at -72, 12, 24, and 48 h of *M. hemolytica* challenge. Using a GC/MS platform, total metabolic fingerprints of plasma were obtained. Normalized abundance values were analyzed and means separated using Tukey's procedure (GeneSpring MS 1.2; Agilent Technologies, Santa Clara, CA), and metabolites were identified using the NIST '05 MS Database (NIST, Gaithersburg, MD). At 12 h after infection, glutamic acid was lower ($P = 0.003$) across all treatments compared with CTRL, whereas threonic acid was greater ($P = 0.04$). Citric acid was greater ($P < 0.001$) in BVDV+MH and BVDV steers compared with CTRL. BVDV+MH steers had greater ($P = 0.003$) levels of isoleucine than CTRL, but the MH treatment had lower ($P = 0.003$)

isoleucine. At 48 h after infection, valine and leucine were lower ($P < 0.01$) in BVDV+MH cattle compared with CTRL, but greater ($P < 0.01$) in BVDV steers. Phenylalanine was lower ($P = 0.006$) in both BVDV+MH and MH steers compared with CTRL, but was greater ($P = 0.006$) in BVDV steers. Glycine was lower ($P = 0.02$) in both BVDV+MH and BVDV treatments. There were no significant changes detected at 24 h after infection. Results suggest significant changes in AA profiles at 12 and 48 h after BVDV exposure and *M. hemolytica* infection. GC/MS metabolic fingerprinting is a promising technique that may provide for better diagnosis and identification of BRD.

Key Words: amino acids, bovine respiratory disease, metabolomics

770 Evaluating timing of weaning stress on response to BVD2 vaccinations in Angus calves. E. D. Downey^{*1}, E. C. Conrad¹, J. F. Ridpath², R. G. Tait Jr.¹, and J. M. Reecy¹, ¹Iowa State University, Ames, ²National Animal Disease Center/ARS/USDA, Ames, IA.

This study was designed to evaluate the impact of environmental factors and genetic controls on response to vaccination against bovine viral diarrhea virus type 2 (BVDV2) in Purebred American Angus beef cattle. This study utilized 362 Angus calves born in the spring ($n = 211$) and fall ($n = 151$) of 2007. Two doses of modified live Bovishield Gold-5 (initial and booster) were administered 3 weeks apart. The herd was managed with 2 calving seasons, fall and spring. Calves, from each season, were allotted to one of 2 weaning/vaccination management protocols based on dam management group. In protocol 1, calves were weaned at initial vaccination. In protocol 2, calves were weaned at the time of booster vaccination. Viral neutralizations were conducted using cytopathic BVDV2 to determine antibody titer at initial vaccination, at booster vaccination, and 3 weeks post booster vaccination. Titer levels at initial vaccination were significantly influenced by calf age ($P < 0.001$), calving season ($P < 0.001$), and gender ($P < 0.05$). There was no significant difference ($P = 0.219$) in the initial titer level between the 2 protocol groups. Response to initial vaccination was calculated by finding the difference between the booster titer score and the initial titer score; response to booster vaccination was the difference between the titer score 3 weeks post booster injection and at booster injection. The overall response was calculated as the titer score 3 weeks post booster injection minus initial titer score. Response to initial vaccination, response to booster vaccination and overall response were significantly ($P < 0.001$) affected by the titer level at the beginning of the specified response period. All 3 response variables were significantly ($P < 0.05$) different across the 2 weaning protocol. The interaction between weaning protocol and the respective titer level was significant ($P < 0.05$) or suggestive ($P < 0.10$) of an effect on all 3 response variables. Based on this preliminary data, management of weaning/vaccination stress in conjunction with titer level at initial vaccination can affect the antibody response developed in Angus calves.

Key Words: beef cattle, vaccination, weaning

771 Alterations in the somatotrophic axis during an infectious bovine rhinotracheitis viral (IBRV) challenge in beef steers. S. M. Falkenberg^{*1}, T. B. Schmidt¹, D. H. Keisler², J. L. Sartin⁴, J. O. Buntyn¹, and J. A. Carroll³, ¹Mississippi State University, Mississippi State, ²University of Missouri, Columbia, ³Livestock Issues Research Unit, USDA-ARS, Lubbock, TX, ⁴Auburn University College of Veterinary Medicine, Auburn, AL.

The objective of this trial was to identify the cytokine response following IBRV exposure and the impact on the somatotrophic axis. 12 steers (228.82 ± 22.15 kg) were randomly assigned to a Control (CON) or an

IBRV challenged group. Prior to the challenge steers were fitted with an indwelling rectal probe and a blood sample was obtained. On d 0, IBRV steers received an intra-nasal dose of IBRV (2 mL/nostril ; Cooper strain, 1×10^7 PFU/mL) and CON steers received an intra-nasal dose of saline (2 mL/nostril). IBRV steers were placed in a paddock isolated from the CON cattle as well as all other cattle on the research farm. The first 48 h post-challenge, blood was collected via single jugular venipuncture. At 72 h post-challenge steers were fitted with indwelling jugular catheters, and then moved to individual stanchions. Blood samples were intensively collected on d 4–8 post-challenge. IBRV steers had elevated rectal temperatures as compared with CON steers ($P < 0.05$) starting on d 2, peaking on d 4 (40.8 ± 0.54 vs. $39.5 \pm 0.54^\circ\text{C}$), and returning to baseline on d 6. The response patterns for cortisol (CORT), interferon- γ (IFN- γ), and growth hormone (GH) all followed a similar pattern for IBRV steers starting on approximately d 2, peaking on d 4, and tapering off on d 6. The peak concentration on d 4 for CORT (pg/mL; 136.96 ± 67.70 vs. 74.5 ± 45.76), IFN- γ (ng/mL; 133.41 ± 126.45 vs. 27.98 ± 10.38), and GH (ng/mL; 48.43 ± 7.66 vs. 32.74 ± 12.67) for the IBRV steers as compared with CON. While there was a difference ($P < 0.05$) in GH concentrations between the IBRV and CON steers, IGF-1 concentrations did not differ ($P > 0.05$) between the 2 groups. Collectively the data revealed alterations in the somatotrophic axis that were not associated with a large increase in circulating concentrations of pro-inflammatory cytokines. We conclude that the low dose of the virus used in the present study, while sufficient to elicit a febrile response, it did not result in the calves becoming septicemic which would explain the lack of a detectable cytokine response.

Key Words: cattle, cortisol, cytokines

772 Identification of genetic regions associated with bovine viral diarrhea-persistently infected cattle. R. Zanella^{*1}, J. Wenz¹, E. Casas², J. S. Neibergs¹, D. Moore¹, and H. L. Neibergs¹, ¹Washington State University, Pullman, ²United States Meat Animal Research Center, Clay Center, NE.

Bovine viral diarrhea virus (BVDV) is one of the etiologies involved in bovine respiratory disease (BRD). BVDV infection can also cause reproductive disorders and acute fatal hemorrhagic disease resulting in poor performance and economic losses to the cattle industry. Infection with BVDV can be transient or persistent. Transient infections are temporary and last until the animal builds immunity to the virus. Persistent infections (BVD-PI) occur when a cow and her fetus are infected with BVDV at approximately 40 to 140 d of gestation. BVD-PI animals shed virus throughout their lives. Previous studies have found bovine chromosomes (BTA) 2 and 26 to be linked to BRD. The objective of this research was to determine if these regions were associated with BVDV-PI infection. Ear notches of 8624 commercial beef calves were tested by qRT-PCR for the presence of BVDV. Calves positive for BVDV were confirmed to be BVD-PI by ELISA at the Washington Animal Disease Laboratory. Sixty-five BVD-PI calves, their dams, and 60 contemporary calves (controls) from the same herd were genotyped for 6 microsatellites on BTA 2 and 7 microsatellites on BTA 26. Allele frequencies were compared between BVD-PI calves and controls, dams of BVD-PI calves and controls with a Fishers exact test. BTA 26 was associated with persistent infection when BVD-PI calves ($P = 0.01$) and dams of BVD-PI calves ($P = 2.8 \times 10^{-6}$) were compared with controls. Strong evidence for an association with BTA 2 and persistent infection was demonstrated for BVD-PI calves ($P = 1 \times 10^{-10}$) and the dams of BVD-PI calves ($P = 1 \times 10^{-13}$). These results are congruent with the BRD linkage results and suggest that BTA 2 and BTA 26 harbor loci that influence both BRD and BVD-PI.

Key Words: BVD-PI, loci, association

773 Economic analysis of persistently infected bovine viral diarrhoea disease prevalence in Washington beef herds. J. S. Neiberger*, H. L. Neiberger, J. Wenz, and D. Moore, *Washington State University, Pullman.*

Studies have identified that bovine viral diarrhoea virus (BVDV) causes economic losses throughout the beef production chain primarily through persistently infected (PI) calves. The purposes of this study were to identify BVDV-PI prevalence in Washington cow-calf herds, identify herd health management risk factors associated with positive PI prevalence, determine economic losses, and to evaluate the economic efficacy of disease management. A state-wide voluntary BVDV-PI testing program tested 8,624 calves from 60 herds, identifying 80 (0.92%) BVDV-PI calves in 8 herds (13.3%). Two herds had catastrophically high prevalence with 13% and 52% PI positive calves. Washington PI prevalence was substantially higher than comparable studies. Managers with positive herds were interviewed to collect production and economic performance data using NCBA SPA economic methods. Herd economic losses ranged from \$1.34 to \$236.75 per cow. Total ranch losses ranged from \$482 to \$20,124 reflecting differences in losses due to the proportion of BVDV-PI calves in the herd. Losses are the market value losses of removing PI calves from the commercial production chain and detected losses in reproduction efficiency through the SPA analysis. The presence of PI calves was due to poor bio-security practices in the 2 herds with catastrophic prevalence. Purchased replacements were not quarantined or BVDV-PI tested. Two PI cows produced PI calves among the other herds. Specific risk factors were not identified in the remaining herds. BVDV health management recommendations are: to test calves to determine herd prevalence, test replacements and quarantine new animals, and implement a BVDV vaccination program. Annual testing of all calves is not economically effective, because once a herd is determined to be BVD-PI free to eliminate production losses, the regional market does not provide a price premium for tested negative calves. New cost effective disease control methods such as genetic selection for disease resistance are needed to reduce BVDV-PI prevalence and its associated economic losses.

Key Words: BVD-PI, economics, prevalence

774 Pre-arrival management of newly received beef calves with or without exposure to a persistently infected bovine viral diarrhoea virus type I calf affects health, performance, bovine viral diarrhoea virus type I titers, and circulating leukocytes. J. T. Richeson* and E. B. Kegley, *University of Arkansas, Fayetteville.*

Calves persistently infected (PI) with bovine viral diarrhoea virus (BVDV) are a major source of the virus; however, consequences of exposure to a PI-BVDV calf in preconditioned (PC) vs. auction market (AM) cattle may differ. Our objective was to compare treatments of PC or AM origin, with (PI) or without (CON) exposure to a PI-BVDV calf in a 2×2 factorial arrangement to evaluate effects on health and performance in a randomized block design using the MIXED procedure of SAS. Four sets (block) of PC steers ($n = 236$) from 3 ranches were selected randomly, weaned, dewormed, vaccinated, tested for PI-BVDV status, and kept on the ranch for ≥ 42 d. Subsequently, PC calves were transported to a stocker unit (SU), weighed (251 ± 2 kg), bled, and assigned randomly to treatment (PCPI or PCCON) with no additional processing. Simultaneously, 4 sets of AM calves ($n = 292$) were assembled for delivery to the SU within 24 h of PC arrival. The AM calves were weighed (245 ± 1.3 kg) and administered the same processing procedures as PC; however, bull calves were castrated, stratified by sex, and AM calves were assigned randomly to treatment (AMPI or AMCON). Calves were fed identically and followed the same antibiotic treatment protocol. Daily gain for the entire 42 d was greater ($P < 0.001$) for PC (1.2 kg) than AM (0.85 kg). There was an exposure effect ($P = 0.002$) on ADG from d 28 to 42; CON gained 1.12 kg vs. 0.90 kg for PI. Morbidity rate was greater ($P < 0.001$) in AM (70%) than PC (7%). Treatment with a third antibiotic occurred more often ($P = 0.04$) for PI, likewise the greatest number of chronic cattle were AMPI ($P = 0.06$). BVDV type I titer levels were greater on d 0 for PC (treatment \times day, $P < 0.001$), and seroconversion to BVDV on d 0 was 100% for PC vs. 23% in AM. Neutrophil:lymphocyte was greater ($P < 0.001$) for AM on d 14 and 28. Results suggest that PC gain faster and require fewer antibiotic treatments; whereas, PI-BVDV exposure reduced gain and increased antibiotic treatment cost, particularly in AM.

Key Words: beef calves, preconditioned, BVDV