13 Weaning management of newly received beef calves with or without continuous exposure to a persistently infected bovine viral diarrhea virus pen mate: Effects on rectal temperature, peripheral blood leukocytes and serum proinflammatory cytokine concentrations. J. T. Richeson*[1], E. B. Kegley[1], J. G. Powell[1], R. G. Schaut[2], R. E. Sacco[3], and J. F. Ridpath[3], *[1]University of Arkansas, Fayetteville, [2]Iowa State University, Ames, [3]USDA-ARS, National Animal Disease Center, Ames, IA.*

Exposure to animals persistently infected (PI) with bovine viral diarrhea virus (BVDV) results in immunomodulation in cohorts. It is hypothesized that the extent of modulation differs for preconditioned (PC) vs. auction market (AM) cattle. Our objective was to compare immune responses of PC or AM calves in presence (PI) or absence (CON) of a PI-BVDV pen mate using a 2 × 2 factorial arrangement. Crossbred PC steers (n = 27) from a single ranch-origin were selected randomly, weaned, dewormed, vaccinated, tested for PI-BVDV, and kept on the ranch for 61 d. Subsequently, PC steers were transported to a stocker receiving unit (RU), weighed (282 ± 1.6 kg), stratified by d −1 BW, and assigned randomly to treatment (PCPI or PCCON) with no additional processing. Simultaneously, crossbred AM calves (n = 27) were assembled from regional auction markets and delivered to the RU 24 h before PC arrival. The AM calves were weighed (268 ± 2.3 kg), stratified by gender and d −1 BW, processed under the same regimen used for PC steers at their origin ranch except bull calves were castrated, then assigned randomly to treatment (AMPI or AMCON). Treatment pens (50 m × 15 m) were arranged spatially so that PI did not have fence-line contact with CON. For cytokine and hemagram analyses, serum or whole blood was analyzed from d 0, 1, 3, 5 (hemagram only), 7, and 14. In AM calves, RT increased ($P < 0.001$) sharply on d 1. Exposure to PI cohort decreased ($P = 0.01$) the percentage of neutrophils, and increased ($P = 0.02$) percentage lymphocytes resulting in a tendency ($P = 0.07$) for a decreased neutrophil:lymphocyte ratio. Serum concentrations of TNF-α tended to increase ($P = 0.09$) for PI cohort. Interferon-γ concentrations on d 7 and 14, IL-6 concentrations on d 14, and platelets on d 7 were greatest for AMPI ($P \leq 0.05$). Results indicate weaning management and PI exposure alter the immune status of newly received calves. These effects may be additive because alterations were greatest for AMPI.

Key words: bovine viral diarrhea virus, cytokine

14 Effect of oral meloxicam on performance and health of stocker calves after castration. J. F. Coetzee*[1], L. N. Edwards[1], R. A. Mosher[1], A. M. O'Connor[2], B. Wang[2], B. KuKanich[1], and D. A. Blasi[1], *[1]Kansas State University, Department of Animal Science and Industry, Manhattan, [2]Iowa State University, Ames.*

Castration of weaned calves affects profitability by reducing ADG and increasing susceptibility to disease. This study investigated the effect of meloxicam on performance and health of stocker calves after surgical castration. British × Continental calves (n = 258; BW = 193 – 285 kg) were transported for 12 h in 3 truckloads (d −1), weighed and randomly treated with either lactose placebo (CONT; 1 mg/kg) or meloxicam (MEL; 1 mg/kg). Doses were suspended in water and administered per os 24 h before castration. On d 0, bulls were surgically castrated (CAST) and steers were submitted to simulated castration (SHAM). Plasma meloxicam concentrations at the time of castration (d 0) were determined by LC-MS. DMI and ADG determined using BW obtained on d 14 and d 28 were analyzed using PROC GLIMMIX in SAS. Animals were classified as sick based on a depression score of ≥2 on a 5-point scale and a rectal temperature of ≥39.78°C. Relative risk of disease was calculated using PROC NLMIXED in SAS and cumulative pull rate, crude morbidity and BRD morbidity were compared using Kaplan-Meier survival analysis and log-rank tests. On d 0, 1 and 14, calf temperament in the squeeze chute was evaluated using a 4-point scale. Plasma meloxicam concentrations at the time of castration were not significantly different ($P = 0.87$). Castration was found to reduce ADG and DMI over the first 14 d after surgery ($P < 0.001$) but meloxicam administration did not significantly improve performance parameters compared with placebo-treated control calves ($P = 0.48$). Meloxicam treatment significantly reduced the first pull rate in castrated calves ($P = 0.04$) and tended to reduce the BRD morbidity rate ($P = 0.14$). Also, more CONT-CAST calves were pulled ($P = 0.016$) and treated for BRD ($P = 0.023$) over time than MEL-CAST calves. There were a greater percentage of CAST calves with a temperament score ≥2 as compared with SHAM calves. These findings suggest that meloxicam administration before castration in post-weaning calves may reduce the number of animals identified as requiring treatment by feedlot personnel and may extend the time to first treatment for BRD.

Key words: castration, NSAID, performance

15 Characterization and antibiotic susceptibility of *Mycoplasma* isolates from mastitic buffaloes. I. Hussain*[1], S. ur Rahman[2], F. A. Atif[1], and M. Arif[1], *[1]University College of Agriculture, University of Sargodha., Sargodha, Punjab, Pakistan, [2]University of Agriculture Faisalabad, Faisalabad, Punjab, Pakistan.*

The objective of the study was isolation and identification of *Mycoplasma* isolates from mastitic buffaloes and to evaluate the antibiotic resistance of *Mycoplasma bovis* in Faisalabad, Pakistan. A total of 235 buffalo milk samples were collected from 4 private small holder dairy farms located around Faisalabad district of Pakistan. Clinical samples were identified through visual changes and sub-clinical samples with surf field mastitis test. The overall occurrence of mastitis was 40.42% (95/235). The incidence of clinical and sub clinical mastitis was 24.21% (23/95) and 75.78% (72/95) respectively. Mastitic samples were subjected to various passages for the purification of *Mycoplasma* species. *Mycoplasma* species were identified based on colony characteristics and biochemical tests. A total of 19 isolates belonged to 2 species i.e., *Mycoplasma bovis* (18) and *Mycoplasma dispar* (1) were isolated. *Mycoplasma bovis* and *M. dispar* were prevalent in 8.33 and 1.67 % respectively. Highest antibiotic resistance was observed for Tylosin (MIC50 = 8µg/ml) followed by Tetracycline (MIC50 = 7µg/ml), Spiromicin (MIC50 = 4µg/ml) and Gentamicin (MIC50 = 3µg/ml). The results of the study suggested that there should be testing for *Mycoplasma* in routine bacterial examination, while considering other causes of mastitis.

Key words: mastitis, *Mycoplasma*, antibiotic

16 Development of detecting kit for bovine myeloperoxidase using enzyme-linked immunosorbent assay. J. Shi, Q.-Z. Li*, Y. Yang, Y. Lv, and X.-J. Gao, *Key Laboratory of Dairy Science of Ministry of Education, Northeast Agricultural University, P.R. China.*

Myeloperoxidase (MPO) is a heme glucoprotein found in the primary granules of mammalian neutrophils. At the site of infection, MPO is

released extracellularly or into phagocytic vacuoles. It has shown that MPO is abundant in milk taken from mammary glands of cows with mastitis and that the amount of MPO in milk is well correlated with the somatic cell count in mastitis milk. To evaluate the potential of using MPO in the diagnosis of mastitis in cows, this study developed a specific enzyme immunoassay for MPO in milk. Bovine MPO was isolated and purified from bovine whole blood by Sephadex G-200 chromatography and ConA-Sephrose 4B affinity chromatography. Antiserum against bovine MPO were produced using the purified MPO with conA as a coated "antibody," and mouse anti-bovine antiserum against MPO as a second detection antibody, and chicken HRP-labeled polyclonal antibody as a anti-antibody, a special sandwich ELISA for MPO was established. ELISA kit was developed. Evaluating kit by methodology showed good specificity, reproducibility (variant coefficient: 1.09% ~7.2% in batch and 1.47% ~6.7% between batches), and the detection limit was 1.1ug/mL. The experiment certified that this kit could maintain over one year and the detection time of the kit was about 3.5h.

Key words: bovine myeloperoxidase, purification, ELISA kit

17 The identification of candidate genes and candidate gene structural variation for bovine spongiform encephalopathy. J. Thomson*, V. Bowles, J. Choi, P. Stothard, and S. Moore, *University of Alberta, Edmonton, AB, Canada.*

Previous work in our lab identified several regions throughout the bovine genome associated with classical BSE in European cattle. There are a total of 64 regions found to be associated with BSE incidence ($P < 0.05$). All of the genes under those regions were analyzed using gene ontology information as well as current literature findings and 100 candidate genes were identified. Data from 10 mRNA sequence libraries and 2 whole genome sequences, created using the SOLiD next generation sequencing system from Applied Biosystems, was interrogated to identify structural variation in these candidate genes. mRNA seq libraries including liver, adipose, hypothalamus, muscle, duodenum, kidney, lung, peyers patch, cortex, and blood were used for single nucleotide polymorphism identification. Whole genome re-sequencing was performed on both a Holstein and a Black Angus bull. Utilizing both the mRNA-sequence libraries and the whole genome re-sequencing, structural variation was found in 98 of the 100 candidate genes identified as positional candidates for BSE susceptibility. This structural variation included 107 non-synonymous mutations, 18 synonymous mutations, 111 intronic mutations, and 19 3′and 5′ UTR region mutations. The identified polymorphisms will be tested in a family based data set of 302 BSE affected and 179 unaffected half-sib Holsteins from 6 sire families. The results of this research will give indicators of the gene pathways underlying BSE disease progression and enhance our understanding of the disease in its host species.

Key words: BSE, single nucleotide polymorphisms, animal health

18 Genomic regions associated with incidence of disease in cattle using DNA pooling and a high-density single nucleotide polymorphism array. E. Casas*, L. A. Kuehn, T. G. McDaneld, T. P. L. Smith, and J. W. Keele, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Genomic regions associated with general disease (respiratory disease, foot rot, and pinkeye) in beef cattle were identified using treatment records on 2,849 animals. General disease cases included animals treated for bovine respiratory disease, foot rot, or pinkeye. Untreated cohorts, matched on breed composition and contemporary group, for cases were included as controls. Fifteen pools of DNA with 102 cases/pool and 13 pools with an average of 101 controls/pool were genotyped using 777,000 single nucleotide polymorphisms (SNP). Mixed model methods were used to estimate differences in allele frequency between cases and controls while accounting for technical variation (specific to SNP array platform), binomial sampling and pool construction error. Hidden population structure unaccounted by the matching procedure was considered statistically using eigenvectors of the correlation among pools across all SNP. Single nucleotide polymorphisms residing on chromosomes 3, 6, 7, 20, 23, and X were highly significant (nominal $P < 0.00001$). Three of these SNPs reside on chromosome 3 between 25 megabase (Mb) and 26 Mb. Fourteen additional SNPs were also significant ($P < 0.001$) in this chromosomal region. On chromosome 6, one highly significant SNP ($P < 0.00001$) is located between 63 and 64 Mb. In this genomic region, 10 additional SNPs were also significant ($P < 0.001$). Two SNPs were highly significant ($P < 0.00001$) on chromosome 7. One resides on Mb 56, while the other resides on the telomeric end of the chromosome. One SNP was highly significant ($P < 0.00001$) on chromosome 20 (on 55 Mb), and one on chromosome 23 (on 20 Mb). Three SNPs on chromosome X were highly significant ($P < 0.00001$). These SNPs reside at 12, 21, and 94 Mb. Results from this study, combined with future studies in a meta-analysis, should provide strong evidence for these genomic regions as harboring genes associated with defense mechanisms against pathogens.

Key words: cattle, diseases, DNA pooling

19 In vitro and in vivo anthelmintic activity of *Amomum subulatum* Roxb. seeds. Z. Iqbal*, N. Badar, M. Khan, and Z. Sindhu, *Department of Parasitology, University of Agriculture, Faisalabad, Punjab-Pakistan.*

This study was carried out to validate the anthelmintic activity of *Amomum subulatum* seeds used in traditional veterinary medicine in Pakistan. Crude aqueous methanol extract (CAME) and its different solvent fractions were tested in vitro employing adult motility assay and egg hatch tests using mature *Haemonchus contortus* and its eggs, respectively. In vivo, CAME and crude powder (CP) were tested employing fecal egg count reduction test in sheep naturally parasitized with gastrointestinal nematodes. In adult motility assays, 73.3% mature H. contortus exposed to CAME @ 50 mg/ml were found dead compared with no mortality in the worms kept in PBS by 10 h post-exposure. There was 100% mortality of worms exposed to the standard drug (levamisole) @ 0.5 mg/ml. Ethyle acetate fraction of CAME was the most effective resulting in 100% mortality of worms @ 50 mg/ml followed by chloroform (76.7%), aqueous (50%) and petroleum spirit (46.7%) fractions. In egg hatch test, CAME was found an effective ovicidal with LC_{50} 13.1872 µg/ml. Chloroform and ethyle acetate fractions had comparable LC_{50} values (18.1413 and 18.6102 µg/ml, respectively) which followed in increasing order by aqueous (20.4178 µg/ml) and petroleum spirit (253.9106 µg/ml) fractions. The LC_{50} values of plant extracts were, however, far greater than that of standard drug, albendazole (0.0345 µg/ml). The maximum reduction (74.45%) in eggs per gram of feces (EPG) was recorded in sheep treated with CAME @ 3 g/kg body weight on d 12 post-treatment (PT). CP was less effective as maximum reduction in EPG was recorded as 57.45% @ 3 g/kg body weight on d 12 PT. There was 100% reduction in EPG by d 8 PT in sheep treated with standard drug, levamisole. Therefore, use of *A. subulatum* seeds in traditional veterinary medicine as an anthel-

mintic is valid. Large-scale control studies, however, are suggested to identify the active principles in the plant material tested in this study.

Key words: *Amomum subulatum*, anthelmintic, sheep

20 Lentisk (*Pistacia lentiscus* L.) browse prevents gastro-intestinal nematode infection in goats. S. Y. Landau*[1], A. H. Azaizeh[2], H. Muklada[1], T. A. Glasser[3], E. D. Ungar[1], and A. Marcovics[4], *[1]Agricultural Research Organization, the Volcani Center, Department of Agronomy and Natural Resources, Bet Dagan, Israel, [2]Institute of Applied Research, The Galilee Society (Affiliated with University of Haifa), Shefa-Amr, Israel, [3]The Ramat Hanadiv Nature Park, Zikhron Ya'akov, Israel, [4]Department of Parasitology, Kimron Veterinary Institute, Bet Dagan, Israel.*

Gastro-enteritis caused by infection with gastro-intestinal nematodes (GIN) is widespread among goats in the Middle-East. It is characterized by extreme emaciation, diarrhea, and mortality. In a 2-year survey, we observed that the Damascus and Mamber breeds of goats that graze on brushland rich in lentisk (*Pistacia lentiscus* L.) had very low fecal egg counts (FEC). Lentisk contains 20% polyethylene glycol (PEG, MW 4,000)-binding tannins on a dry matter basis. We tested possible mechanisms of protection against GIN. In a series of in vitro experiments, we showed that ethanol 70% and, to a less extent, water and ethanol 100% extracts of lentisk prevent exsheathment of L3 larvae, thus impairing nematode maturation to the egg-producing adult stage. In addition, we showed that feeding lentisk foliage to young goats infected with mixed GIN species resulted in a drastic decrease in FEC (241 vs. 1293, $P < 0.001$; n = 14). When goats were administered daily 20 g of PEG (which binds to and thereby neutralizes the tannins), the effect of lentisk on FEC was approximately halved to 705 epg. This suggests that tannins are not the only anthelmintic moiety in lentisk. The daily intake of tannins needed to eliminate fecal egg excretion was 1 g·kg BW^{-1} d^{-1}. After lentisk feeding was stopped, FEC returned to the control level, implying that the effect of lentisk on GIN was suppressive but not lethal. Our data suggest that daily ingestion of lentisk—5 to 15% of DM ingested—prevents egg formation and possibly larval maturation all year-round, resulting in effective control of GIN populations. This seems to be a passive mechanism, and not an active mechanism of adaptive feeding behavior to a worm challenge.

Key words: tannin, browse, self-medication

21 Withdrawn

22 Occurrence of paratuberculosis in the hilly regions of Himachal Pradesh, India. J. S. Sohal*, S. V. Singh, P. K. Singh, and A. V. Singh, *Central Institute for Research on Goats, Mathura, UP, India.*

In India paratuberculosis has been studied widely in the plain regions, however, to our knowledge there have been no reports from hilly regions. Present study was attempted to study the occurrence of paratuberculosis in hilly regions of northern parts of country. A total of 4 flocks (sheep and goat) belonging to Chamba District of Himachal Pradesh, India were studied in the present investigation. These flocks usually come to plain regions of the state in search of fodder in the winter season. A total of 52 animals were sampled for feces from these flocks. In total 12 (8- sheep, 4- goats), 15 (10- sheep, 5- goats), 9 (7- sheep and 2- goats) and 16 (12- sheep, 4- goats) animals belong to flock 1, 2, 3 and 4, respectively. Animals were tested for direct fecal examination, fecal DNA PCR and culture for the presence of MAP. The positive PCR samples were subjected to IS1311 PCR-REA to know the genotype of infecting strain.

Key words: paratuberculosis, hilly regions, genotyping

23 Status of *Mycobacterium avium* subspecies *paratuberculosis* Infection in the Cow Shelters (Goshalas/Pinjarapoles) in India. S. V. Singh*[1], A. V. Singh[1], P. K. Singh[1], B. Singh[1], A. Kumar[1], B. S. Chandel[3], A. Srivastav[2], S. Gupta[1], H. Singh[1], A. Mittal[1], and S. Yadav[2], *[1]Central Institute for Research on Goats, Mathura, Uttar Pradesh, India, [2]College of Veterinary Sciences, Mathura, Uttar Pradesh, India, [3]College of Veterinary Science, Dantiwada, Gujarat, India.*

India possesses huge population (>480 million) of domestic livestock, however, per animal productivity remains poor. Due to poor per animal productivity, large number of low or unproductive goats, sheep and buffaloes go for early slaughter. Slaughtering of cows (even those suffering from incurable diseases) is banned in India. Such cows are either let off or sent to Cow Shelters by farmers. Cow shelters (or Goshalas in North India and Pinjarapoles in Western India) provide shelters for un-productive and homeless cows. Number of these cow shelters is very large in country and depend on charity money. Cows in these shelters survive on low plane of nutrition and are in poor health and suffer from varieties of health problems and are rarely screened for diseases including Johne's disease. Mycobacterium avium subspecies paratuberculosis (MAP), the cause of JD, is responsible for huge losses in production and is endemic in farm and farmer's herds. Study estimated status of MAP in 4 Goshalas in Mathura, UP (region A) and 3 in Dantiwada, Gujarat (region B) using microscopy, indigenous ELISA kit and Blood PCR. 211, 143 and 183 cows were screened by microscopic examination (feces), ELISA (serum) and PCR (blood), respectively. Whereas, of the 3 Goshalas in region B, 37 and 135 cows were screened by microscopy (fecal) and ELISA (serum), respectively. In region A, 57.4 and 55.9 and 36.1% cows were positive in microscopy, ELISA and PCR, respectively. In region B, 48.6 and 62.2% cows were positive by microscopy and ELISA, respectively. Load of MAP infection was high in cow shelters and serve as reservoir and need special attention for the control of MAP at National level.

Key words: Johne's disease, ruminants, prevalence

24 Finishing performance and carcass traits of heifers previously managed with three respiratory disease protocols. J. L. Wahrmund*[1], D. B. Burken[1], B. K. Wilson[1], S. J. Terrill[1], C. R. Krehbiel[1], D. L. Step[2], S. M. Trost[3], C. L. Goad[4], and C. J. Richards[1], *[1]Oklahoma State University, Department of Animal Sciences, Stillwater, [2]Oklahoma State University, Department of Veterinary Clinical Sciences, Stillwater, [3]Strategic Solutions International, Stillwater, OK, [4]Oklahoma State University, Department of Statistics, Stillwater.*

This experiment evaluated the finishing performance and carcass traits of 331 heifers (BW = 351 ± 51 kg) previously managed for 56 d with 3 bovine respiratory disease (BRD) health management protocols. The protocols were: visual monitoring (CON), visual and ruminal temperature monitoring (TEMP), or visual monitoring following a d 0 metaphylactic treatment (MET). Heifers were blocked by BW and randomly allotted to 24 pens for the receiving phase. At finishing, 169 heifers from 12 pens were blocked by BW and reallocated to 30 pens based on receiving treatment, and all heifers were adapted to a 94% concentrate diet. Percentage of heifers receiving 0, 1 or 2 treatments for BRD were 57, 37 and 8% for CON; 26, 49 and 25% for TEMP;

and 81, 10 and 9% for MET; respectively. Heifers treated twice for BRD began the finishing phase weighing 16.9 kg less ($P < 0.01$) than all other heifers. Interactions were observed between health protocol and number of times treated for final BW and overall ADG ($P \leq 0.02$). Final BW of CON heifers treated twice was 32.2 kg less ($P \leq 0.04$) than other CON heifers, while number of times treated did not affect ($P \geq 0.13$) final BW of TEMP and MET heifers. CON heifers treated twice gained 0.16 kg/d less ($P = 0.01$) than other CON heifers. TEMP heifers treated twice gained 0.11 kg/d more ($P = 0.03$) than those never treated and MET heifers' ADG was unaffected ($P \geq 0.12$) by times treated. Heifers treated twice for BRD had 11.4 kg lighter ($P \leq 0.04$) HCW than those receiving 0 or 1 treatment. Heifers not treated for BRD had 1.1% greater dressing percent ($P < 0.01$), 7.6% greater marbling score ($P \leq 0.04$) and 0.25 cm greater fat thickness ($P \leq 0.02$) compared with those treated once or twice. Carcass value showed a health protocol × number of times treated interaction ($P = 0.04$). Carcasses from CON heifers treated twice were valued at $91.48 less ($P \leq 0.02$) than those from other CON heifers, while carcass value of TEMP and MET heifers was not affected ($P \geq 0.27$) by number of times treated. Results indicate that metaphylaxis and remote temperature monitoring may spare some of the detrimental effects of BRD on performance and carcass value.

Key words: respiratory disease, performance, carcass