American Horse Council requesting that horses be counted in the same manner as feedlot cattle, however EPA chose to continue counting each horse as two animal units. Thus, any operation that has 150 or more horses in confinement (including stalls or dry lots) for a total of 45 days or more in any 12-month period or is otherwise designated as a CAFO has a duty to seek coverage under an NPDES permit. Many stables, breeding farms, and exhibition facilities that have not previously been affected may now have to meet the requirements of the new regulations, including a provision to be able to contain all of the runoff from a 25-year, 24-hour storm event. The economic cost could be devastating to the industry.

Key Words: Equine industry, CAFO regulation, Environmental regulations

Southern Branch ADSA Symposium: How can we best work together to serve tomorrow's dairy industry?

332 How best can we work together to serve tomorrow's dairy industry: university extension faculty perspective. L. O. Ely*, *University of Georgia*.

The Cooperative Extension Service was created with the Smith-Lever Act of May 8, 1914. Extension work was to "consist of giving instruction and practical demonstrations in agriculture and home economics to persons not attending or resident in said colleges in the several communities, and imparting to such persons information on said subjects through field demonstrations, publications and otherwise". At this time the population of the US was rural and education for most was finished at the eighth grade level. Basic information in animal and human nutrition was being discovered. Today extension work has the same objective but the audience is much different. Only a small percent of the US population is rural and engaged in agriculture. The education level is post high school. The need is not for basic information but for fine tuning management decision-making. Producers are looking for ways to handle the overload of information and records that are available to them. Extension can provide resources that will aid in utilization of record keeping systems and decision-making programs that analyze these records. These programs may be web based for independent use by producers instead of one on one or group meetings between producers and extension specialists. Society has demanded impact and accountability statements that have left agriculture with low scores because of small clientele numbers. Evaluation of quality is not part of these scores, as it is not easily quantified. Other countries have privatized their extension services. In the US there has been an increase in private companies developing their sales force into an extension service that competes with the land grant system. The new objective may be that extension service and industry must cooperate to provide programs and resources to the dairy industry. How does the leadership in college administration evaluate this paradigm shift?

Key Words: Dairy industry, Extension service, Function

Animal Health: Diseases and mammary health

333 Changes in the mechanical properties and the lesion score of the sole horn in first lactation dairy heifers. B. Winkler and J. K. Margerison*, *University of Plymouth, Seale Hayne*.

This experiment compares mechanical tests of the sole horn toughness with the pattern of lesion formation, in the pre- and postpartum heifers. Mechanical tests were completed on samples of sole hoof horn taken from 20 heifers at 2 months before parturition (p1) and 100 days postpartum (p2). Simultaneously, all claws were assessed for the lesions score levels (LS) of sole horn. Heifers were kept at pasture prepartum and housed loose in a straw-bedded yard postpartum. Hoof samples were collected from all claws and analysed for elastic modulus (ELM) and puncture resistance (PR). Each measurement was replicated five times on the same area of each claw. PR force required fracture sole horn was significantly greater in front claws (FC) when compared to hind claws (HC) ($P<0.05$) (FC 9.7, HC 8.8N), but there was no significant difference between the inner and outer claws. PR force, ELM and LS significantly increased postpartum compared with prepartum ($P<0.01$) (p1- 7.8N, 86.9N/mm2 and 73.1; p2- 10.7N, 118.0N/mm2 and 186.5). LS was significantly greater in the HC compared with the FC during the postpartum period ($p<0.001$) (HC 223.7, FC149.3). In the HC the outer claws presented a significantly ($p<0.05$) greater LS when compared to the inner claws in both periods. In the FC the LS was significantly higher in the inner claws ($P<0.01$) postpartum. Prepartum ELM and PR force were not correlated with lesion score either pre or postpartum. However, postpartum ELM and PR force were significantly negatively correlated ($p<0.01$) to the increase in lesion score between periods ($R=0.65$). Differences of EML and PR between FC and HC may be related to the different pressure distribution in these claws. Mechanical tests reflected increases in sole lesions and LS following

Key Words: Lameness, Sole tissue, Mechanical testing

334 Muscle protein tyrosine nitration patterns during chronic subclinical intramuscular parasitism: Co-localization to fiber type and ubiquitin. T. H. Elsasser*[1], S. Kahl[1], J.L. Sartin[2], R. Fayer[1], A. Martinez[3], F. Cuttitta[3], and J. Hinson[4], [1]*USDA-ARS, Beltsville, MD,* [2]*Auburn University, Auburn, AL,* [3]*NIH-NCI, Bethesda, MD,* [4]*University of Arkansas, Little Rock, AR*.

The present study was conducted to determine whether the inflammatory oxidative response to chronic intramuscular parasitism, as modeled with the protozoan parasite *Sarcocystis cruzi*, results in protein nitration damage and whether a pattern to it localization can be characterized. Holstein steer calves (n=10; av.wt.= 124 kg) were assigned equally to control (C) and infected (I, 25,000 Sarco sporocysts) groups. Calves were slaughtered on d56 postinfection and samples of rectus femoris (RF) and psoas major (PM) harvested. Xanthine oxidase (XO) was measured in muscle homogenates by fluorescence (resorufin, 587 nm). Frozen sections (9 μ) were immunostained (IHC; horseradish peroxidase/DAB) for nitrotyrosine (NT) or ubiquitin (UBI) or co-localization of NT with fibertype (staining v nonstaining with mouse anti-myosin fast twitch), or NT with UBI via confocal immunofluorescence. Extracted muscle proteins were extracted, separated on 4-20% SDS PAGE gels, transferred to nitrocellulose, and probed for nitrated proteins using a anti-NT or antibovine-UBI. XO activity, a source of superoxide, was 2.3 times greater in I than C ($P<0.01$). Western blot demonstrated that >80% of the increase in NT was associated with an increased number of protein bands ($P<0.04$, I v C)with Mr >75 kD. IHC demonstrated very low levels of both NT and UBI staining in RF and PM of C but increased NT (42% more NT+ fibers, $P<0.05$) in both RF and PM of I. NT immunostaining could be categorized into three distinct forms: a) peripheral fiber (I and C), b) dispersed intrafiber (I), and c) cyst-specific (I). Both fast and slow fibers displayed the peripheral localization of NT and UBI. Only slow twitch oxidative fibers displayed extensive co-localized intrafiber NT staining regardless of muscle source. The sarcocyst itself was highly nitrated and muscle proteins in the immediate vicinity of the cyst displayed increased NT co-localized with UBI. The data suggest that the oxidative inflammatory response to chronic low-level muscle-resident parasitism generates nitrated muscle proteins. The nitration appears to be more pronounced in slow oxidative fibers and supports prior observations of more severe impact of this parasitism on muscles with higher percentages of slow twitch fibers.

Key Words: Stress, Health, Muscle

335 A relative comparison of diagnostic tests for Johne's disease. T. Duffield[1], D. Kelton[1], K. Leslie[1], K. Lissemore[1], and M. Archambault[2], [1]*Department of Population Medicine, University of Guelph,* [2]*Animal Health Laboratory, University of Guelph*.

Prevention and control of Johne's disease (JD) could be improved if diagnostic tests were reliable, rapid and economical. The objective of this study is to evaluate a commercial milk ELISA test relative to other diagnostic tests. 32 dairy herds in Ontario with a suspected high prevalence of JD had fecal and serum samples collected from all milking and dry

cows. Serum was tested for antibodies with an IDEXX ELISA (AHL). Preserved milk samples were collected at the following Dairy Herd Improvement (DHI) test day. These milk samples were sent to Antel Bio Corp. (Lansing, MI) for an in-house milk ELISA test. Cows positive on either the serum or milk ELISA test had their corresponding fecal sample tested with all three of the following: traditional fecal culture (FC) (Antel Bio), an IDEXX fecal PCR probe (AHL), and radiometric FC (BACTEC culturing system) (AHL). 286 of the 2148 serum samples were positive (13.4%). 124 of the 1699 cows milking on DHI test day were positive on milk ELISA (7.3%). The kappa between the milk and serum ELISA for the 1699 cows tested was 0.45 (0.38, 0.52). 326 cows were positive on one or both of the ELISA tests. 144 of the ELISA positive cows (either milk or serum) were positive on traditional FC (44.2%), while only 62 were identified positive on fecal PCR (24.1%). The BACTEC culture results are still pending. 686 fecal samples from ELISA negative cows are still being cultured. In total, complete FCs from nine herds (874 cows) will be analysed. Preliminary statistics were calculated for 257 cows having milk, serum, fecal PCR and FC results. Relative to FC, the positive predictive value for the milk and serum ELISA was 61.3% and 45.2%, respectively. The kappa between fecal PCR and FC was 0.57 (0.47, 0.68). The milk ELISA test reasonably predicts fecal shedding status and because of its convenience and cost, it has utility as a herd screening test.

Key Words: Johne's disease, Fecal culture, Milk ELISA

336 Detection of *Aspergillus fumigatus* in hemorrhagic bowel syndrome in dairy cattle. S. Puntenney*, Y.-Q. Wang, and N. Forsberg, *Oregon State University, Corvallis OR.*

The goal of the research was to investigate the association between *Aspergillus fumigatus*, *Clostridium perfringens* and hemorrhagic bowel syndrome (HBS) in lactating dairy cattle. Samples of gastrointestinal (GI) contents, GI wall, mesenteric lymph nodes and blood were obtained from HBS cows and from control cows in 4 states (IA, ID, OR and WA). Concentrations of *A. fumigatus* DNA in the samples were evaluated with a real-time quantitative Sybr Green PCR method using an ABI7700 thermocycler. A standard curve was constructed with purified *A. fumigatus* genomic DNA. Melt curve analysis was completed to ensure that only *A. fumigatus* DNA was detected in each assay. We also tested for the presence of *Clostridium perfringens* in the samples using a multiplex PCR which detected five of the major *C. perfringens* toxins. Seven HBS cows were obtained and each of them contained high concentrations of *A. fumigatus* in hemorrhaging GI contents, GI wall, mesenteric lymph nodes and blood. Two idiopathic cases of abomasal hemorrhage (one dairy cow and one gazelle)were also evaluated. Both cases were positive for *A. fumigatus*. *C. perfringens* alpha and epsilon toxin genes were detected in some HBS samples; however, their presence was not associated with HBS. Some HBS cows did not harbor *C. perfringens* toxin genes. In humans, *A. fumigatus* is pathogenic in immunocompromised patients. It is harmless in immunocompetent individuals. Dairy cattle may be immunosuppressed, particularly in early stages of lactation. Several studies have shown potential for *A. fumigatus* to infect the ruminant GI tract and to cause hemorrhage. Hence, we propose that *A. fumigatus* has similar potential in lactating dairy cattle. These observations do not preclude other pathogenic organisms from participating in HBS. Instead, we propose that *A. fumigatus* contributes to the etiology of a multi-factorial disease. Management of feed storage to minimize mold may reduce or eliminate incidence of HBS.

Key Words: Jejunal hemorrhage syndrome, Mold, Dairy herd health

337 The potential of infrared thermography as an early detection method for mastitis: Seasonal effects on predictability. R. J. Berry[1], A. D. Kennedy*[1], S. L. Scott[2], D. Fulawka[1], F. I. L. Hernandez[2], and A. L. Schaefer[3], [1]*University of Manitoba, Winnipeg, Manitoba, Canada,* [2]*Ag Canada Research Station, Brandon, Manitoba, Canada,* [3]*Ag Canada Research Station, Lacombe, Alberta, Canada.*

In order to determine the potential of using Infrared thermography (IRT) for early detection of mastitis, seasonal variation in udder temperature was determined and a prediction model based on the results was developed. Two groups of 10 dairy cows (lactation range 1-6) were monitored every other day starting 5 days before calving until 120 days into lactation. A "summer" group was studied over the time period 5/1/01-10/15/01 and a "winter" group was studied between 12/24/01-5/3/02. IRT images of the posterior surface of the udder were collected approximately 2 h before milking, and stored onto digital video cassettes. Rectal temperatures were taken concurrently. Barn temperatures were monitored remotely every 10 min. A lagged regression model was applied at the individual level. Model description is as follows: UStemp = Lag1UStemp + Lag2UStemp + EtempH2 + Max EtempH2 + EtempH24 + Max EtempH24 + EtempH48 + Max EtempH48. Where: UStemp=mean udder surface temp; Lag1 & Lag2Ustemp= lagged mean udder surface temp for the previous 1 or 2 measures, respectively; EtempH2, EtempH24, & Etemph48= mean environmental temperature for the previous 2, 24 and 48 h, respectively; MaxEtempH2, MaxEtempH24, & Max EtempH48= max environmental temperature for the previous 2, 24 and 48h, respectively. The model was significant for all animals in both groups ($p<0.05$), giving r^2 ranges of 0.41-0.88 and 0.27-0.63 for the Summer and Winter groups, respectively. Residuals for the model showed that the model more accurately predicted UStemp for the Summer group (mean residual =0.71, range 0.34-1.04; Winter group mean residual= 0.91, range 0.61-1.25). Residuals were below an endotoxin infusion-induced rise in UStemp of 2.3 C reported an earlier study by Scott et al (2000). Therefore, IRT shows potential as an early detection method for mastitis.

Key Words: Thermography, Dairy cattle, Mastitis

338 Protective efficiency of a mix DNA-protein vaccination strategy against *Staphylococcus aureus* mastitis in dairy cows. L. Shkreta*[1], B. G. Talbot[1], M. S. Diarra[2], and P. Lacasse[2], [1]*University of Sherbrooke, QC, Canada,* [2]*Dairy and Swine R&D Centre, Lennoxville, QC, Canada.*

The objective of this study was to test the protective efficiency of a vaccination strategy against *Staphylococcus aureus* mastitis. Four pregnant heifers were not vaccinated and used as control while four others were injected intramuscularly twice with a DNA vaccine (7 and 4 wks prior to calving) and once subcutaneously with a protein vaccine 17 days later. The DNA vaccine contained 2 mg of the bicistronic plasmid pCI-D1D3-ClfA that encodes epitopes of the *S. aureus* adhesins Clumping factor A (ClfA) and Fibronectin binding protein A (D1D3) and 2 mg of the plasmid pCI-GM-CSF that encodes the bovine Granulocyte macrophage-colony stimulation factor. The protein vaccine consisted of 200 μg of recombinant D1D3 and 300 μg of recombinant ClfA in incomplete Freund's adjuvant. Three weeks after calving, 3 quarters per cows were challenged through the teat canal with 900 CFU/quarter of *S. aureus* Newbould 305 while the fourth quarter was infused with saline. The DNA immunizations did not increase significantly the serum levels of anti-ClfA or anti-D1D3. However, the protein boost significantly increased the serum levels of anti-ClfA - IgG, IgG-2, IgG-1, IgM and IgA (respectively P<0,03; <0,01; < 0,01; < 0,05; and P<0,07), but only slightly those of anti-D1D3. Both antibodies were detected (P<0.05) in milk although levels of anti-D1D3 antibodies were low. The lymphoproliferative response induced by DNA vaccination was highly significant for both antigens (P< 0,001). All inoculated quarters developed mastitis. Over the following 3 weeks, the number of bacteria remained relatively constant in control cows but decreased gradually (time x treatment, P<0.05) in vaccinated cows. At the end of this period, the number of bacteria averaged 3.3 logCFU/ml in control and 1.4 (P<0.05) in vaccinated cows. Bacteria were still present in 11of 12 quarters for the controls and 5 of 12 quarters in vaccinated cows. In the period 24-72 hrs post challenge, vaccinated cows tended to have lower serum haptoglobin (P<0.09), cardiac rhythm (P<0.04) and body temperature (P<0.09) than control cows. In conclusion, this mixed DNA and protein vaccination strategy against *S. aureus* adhesins induced not only humoral and cellular immune responses but also partial protection in dairy cows.

339 Effectiveness of an internal teat sealant in the prevention of new intramammary infections during the dry and early lactation periods in dairy cows when used with an intramammary antibiotic. S. Godden*[1], P. Rapnicki[1], S. Stewart[1], A. Johnson[2], R. Bey[1], and R. Farnsworth[1], [1]*University of Minnesota, St. Paul, MN,* [2]*Total Herd Management Services, Clintonville, WI.*

The primary objective of this study was to describe whether quarters treated with an internal teat sealant in addition to an antibiotic at dry off (treated) would develop fewer new intramammary infections (IMI) during the dry period and early lactation, as compared to quarters

treated with antibiotic alone (control). Secondary objectives were to describe the effect of treatment on the prevalence of IMI and linear score (LS) after calving, and on the incidence of clinical mastitis between dry off and 60 DIM. The study enrolled 437 cows from two dairy farms in western WI. On the day of dry off all four quarters were sampled for bacteriological culture and SCC measures. After the final milking all four quarters were routinely infused with a commercially available long-acting antibiotic. Two contra-lateral quarters (LF/RH or RF/LH) were then randomly assigned the treatment of infusion with an inert internal teat sealant (Orbeseal, Pfizer Animal Health, Groton, CT). The teat sealant was stripped out at first milking after calving and the quarters re-sampled at both 1- 3 DIM and 6-8 DIM for bacteriological culture and SCC analysis. The incidence of new IMI occurring between dry off and 1-3 DIM was 25.9% and 20.6 % for control vs. treated quarters, respectively (odds ratio$_{treated}$ = 0.72, P < 0.05). The prevalence of IMI at 1-3 DIM was 29.5% and 23.3%, for control vs. treated quarters, respectively (odds ratio$_{treated}$ = 0.71, P < 0.05). Mean LS was significantly lower for control vs. treated quarters at 1-3 DIM (control = 5.5; treat = 5.2, P < 0.05) and at 6-8 DIM (control = 3.2; treat = 2.9, P < 0.05). Finally, there were significantly fewer clinical mastitis events between dry off and 60 DIM occurring in quarters treated with teat sealant and an antibiotic (5.9%) than in quarters treated with antibiotic alone (8.0%) (odds ratio$_{treated}$ = 0.72, P < 0.05).

Key Words: Internal teat sealant, Mastitis, Dry period

Breeding & Genetics: Beef cattle breeding

340 Factors to adjust birth and weaning weights of Red Angus calves for age of dam. J. M. Rumph*[1], L. S. Gould[2], R. L. Hough[2], and L. D. Van Vleck[3], [1]*University of Nebraska, Lincoln,* [2]*Red Angus Association of America, Denton, Texas,* [3]*USDA, ARS, USMARC, Lincoln, Nebraska.*

Age-of-dam adjustment factors now used by the Red Angus Association of America (RAAA) were evaluated to determine if they were still applicable for the current Red Angus population. After edits, 61,322 records were available for birth weight on bull calves, 64,056 for birth weight on heifer calves, 29,663 for weaning weight on bull calves, and 31,073 for weaning weight on heifer calves. Records of bulls and heifers were analyzed separately to estimate age-of-dam adjustment factors for bulls and heifers for each weight. Statistical models were similar to those used for national genetic evaluations by the Red Angus Association of America. Additive factors to adjust to a mature (5 – 10 yr old) dam basis for birth weight of bull calves were determined to be 3.13, 1.41, 0.41, and 1.13 kg for 2-, 3-, 4-, and 11-yr-old and older dams, respectively. For birth weight of heifer calves, adjustment factors were determined to be 3.08, 1.32, 0.45, and 1.04 kg for the same dam classifications. For weaning weight, adjustment factors for bull calves were 32.97, 17.19, 7.30, and 11.97 kg and for heifer calves were 25.80, 13.70, 4.90, and 10.48 kg. The adjustment factors currently used by the Red Angus Association of America under adjust birth weights at all ages for both sexes compared to these new estimates. For weaning weight, the adjustment factors currently used under adjust weaning weights for calves with 2-yr-old dams and with dams that are 11 yr of age or older. Weaning weights for calves out of 3- and 4-yr-old dams are slightly overadjusted with the adjustment factors now used for both sexes, but the magnitude of differences for bull calves is greater than for heifer calves. New adjustment factors for age-of-dam are recommended for use in RAAA genetic evaluations.

Key Words: Adjustment factors, Beef cattle, Genetic evaluations

341 Effects of genetic groups to account for selection on estimates of genetic parameters for a line of Hereford cattle. L. D. Van Vleck*[1], K. J. Hanford[1], and M. D. MacNeil[2], [1]*USDA, ARS, USMARC, Lincoln, NE,* [2]*USDA, ARS, LARRL, Miles City, MT.*

Robin Thompson originated the idea of an accumulated groups model to account for prior selection. Robin Westell's rules made the coefficient matrix for group models as easy to compute as the A-inverse rules of Henderson and Quaas made use of the numerator relationship matrix for calculation of predicted breeding values given components of the phenotypic variance. The effects of groups in the model on estimates of variance components, however, seem to be unpredictable. Groups were assigned arbitrarily instead of sire identification for some or all of 3,884 weaning weight records of Line 1 Herefords. With usual sire identification, estimates of parameters were 0.20, -0.38, 0.16, 0.19, 0.52 for direct heritability, direct-maternal genetic correlation, maternal heritability, and proportions of variance due to maternal permanent environmental and residual environmental effects. With 22 groups (to replace about one sire for each intake of sires), estimates were 0.13, -0.23, 0.11, 0.20, and 0.58. With 49 groups (all sires of an intake group assigned to that group), estimates were 0.05, 0.41, 0.11, 0.20, and 0.61. With each sire (160) assigned as a group, estimates were 0.06, 1.00, 0.01, 0.24, and 0.67. As another extreme, all sires were coded as missing and were not grouped. Estimates were 0.30, -0.72, 0.08, 0.28, and 0.45. For birth weight, usual estimates were 0.36, -0.06, 0.14, 0.03,and 0.49. With arbitrary groups, estimates were affected but less extremely than for weaning weight. With a dam effect replacing maternal genetic and permanent environmental effects in the model, substitution of group effects for sires had little effect on estimates of heritability for birth weight but did affect estimates of heritability for weaning weight (although less extremely than for the direct-maternal genetic models). More extensive analytical or simulation studies of effects of genetic groups on estimates of genetic parameters seem warranted.

Key Words: Beef cattle, Genetic correlation, Heritability

342 Maternal performance of Hereford, Angus, Red Angus, Simmental, Gelbvieh, Limousin, and Charolais sired two-year-old crossbred females. L. V. Cundiff*, *USDA, ARS, Roman L. Hruska U.S. Meat Animal Research Center.*

The objective of this experiment was to characterize reproduction and maternal traits of F1 cross females calving at 2 years of age in cycle VII of the Germplasm Evaluation Program at the U.S. Meat Animal Research Center. The females were produced in the spring of 1999 and 2000 as a result of artificial insemination matings of Hereford (H, 21 sires), Angus (A, 22), Red Angus (Ra, 21), Simmental (S, 20), Gelbvieh (G, 23), Limousin (L, 20), and Charolais (C, 22) bulls to Hereford, Angus, and composite MARC III (1/4 each Angus, Hereford, Red Poll, and Pinzgauer) cows. Data were obtained on 681 females exposed, 565 calves born, and 489 calves weaned in the fall of 2001 and 2002 as a result of natural service multi-sire matings to MARC III bulls. Data on calf crop born (CB, %) and weaned (CW, %), calving difficulty score (CDS, score), unassisted births (UB, %), birth weight (BW, kg), survival to weaning (SW), and 200-d weaning weight of progeny (WW, kg) were analyzed by least squares procedures using a model that included random effects for maternal grandsire in maternal grandsire breed, and fixed effects for maternal grandsire breed, maternal grandam breed, sex of calf (for BW, SW, WW only), birth year, and maternal grandsire breed x maternal grandam breed. Effects of maternal grandsire breed were significant (P<.05) for WW but not for any other trait. The means for WW of progeny with H, A, Ra, S, G, L, and C maternal grandsires were 187.4, 192,2, 188.1, 200.3, 195.2, 194.7 and 195.2 kg for WW, respectively. The mean least significant difference among maternal grandsire breed means for WW was 9.5 kg (P<.05). Breed of maternal grand sire means for S and G differed significantly from H and Ra, but not from any other breeds. Breed of maternal grandsire effects did not differ among H, A, Ra, L, and C breeds. Results for WW indicate that contrasts between British (H and A) and Continental European breeds (S, G, L, and C) are less than half as great for direct (3.5 vs 9.5 kg) and maternal (4.8 vs. 11.5 kg) breed effects in the current evaluation (Cycle VII of the GPE Program) as they were 25 to 30 years ago (Cycle I and II of the GPE Program).

Key Words: Beef cattle, Breeds, Germplasm

343 Genetic trends resulting from selection based on an index of birth weight and yearling weight. M. D. MacNeil*, *USDA-ARS, Fort Keogh LARRL, Miles City, MT.*

The CGC population is a stabilized composite of 1/2 Red Angus, 1/4 Charolais, and 1/4 Tarentaise germplasm. The objectives of this research were to estimate genetic parameters for weight traits of CGC and to evaluate genetic responses resulting from selection based on the