

125 Prevention and control of the Bovine Viral Diarrhea virus. J. Sackmann*, *Washington State University, Pullman.*

The Bovine Viral Diarrhea (BVD) virus is an RNA virus of the *Pestivirus* genus of the *Flaviviridae* family of viruses. This virus, as a disease agent causes respiratory and reproductive problems in cattle that can be economically devastating. The BVD virus affects animals at various stages of life. Pregnant cowsTM fetuses can become infected during the latter stages of gestation, resulting in an aborted calf, or a calf that is persistently infected, a carrier. Carrier calves fail to thrive and can die before maturity. Carrier animals shed the virus in their feces, blood, nasal mucus, saliva and urine. Testing is possible in blood and tissue samples. Once an animal has become infected, it must be removed from the herd, as there is no cure for the infection. However, there are methods of preventing BVD. Over 140 vaccines are available in the United States to help build an animal's resistance. These BVD vaccines are available as killed or modified live. Though there are various vaccination programs available for prevention of BVD, a vaccination program alone is not a herd health program. Strict screening processes, testing all calves, coupled with culling of positive calves and implementing a closed herd policy, are methods of limiting the exposure of unaffected cattle. Implementing a vaccination program for incoming cattle, as well as segregating them from the herd until determined to be BVD negative, is also a method of preventing spread. Although there are various methods of prevention and control for this disease, an alarmingly low percentage of dairies utilize prevention and control methodsTM as many as 75.5% of herds do not require testing of animals before incorporation into a herd. Only 10% of beef and dairy operations tested for BVD in purchased cattle in 2001. In summary, BVD is a viral disease decreasing the profitability of cattle; however, simple strategies for prevention and control of this disease are available. Therefore, it would be economically advantageous for producers to implement BVD prevention and control measures.

Key Words: BVD, Prevention, Control

126 The effects of heat stress on reproductive efficiency in dairy cattle. L. Buttles*, *University of Wisconsin, River Falls.*

Heat stress causes many negative effects within dairy cattle. These negative effects include, but are not limited to, decreased milk production, decreased reproductive efficiency, increased semen cost, and uneven calving intervals. Activity levels decline during estrus within periods of heat stress. Furthermore, the fertility of ova produced is also compromised. Synchronization protocols and embryo transfer offer options to combat reproductive problems related to heat stress but are associated with higher cost to the producer. Misters and fans are additional tools used to combat heat stress.

Key Words: Reproduction, Heat Stress

127 Management considerations with shortened dry periods. D. Maulfair*, *Penn State University, University Park.*

Recent studies have indicated that dry periods shorter than 60 d may be profitable. Research trials in Florida, Arizona, and Wisconsin have shown that although cows produce up to 4% less in the next lactation following a 30 d dry period, this is more than offset by the income from extra days added to the current lactation. Break-even milk yield based on production and expected calving date should be a primary determinant in shortening dry periods. Parity is another consideration because studies suggest that 30 d dry periods between the first and second lactation are not as economical; these cows show a larger drop in milk yield than older cows in the next lactation. Other management factors to consider include accuracy of breeding records, antibiotic use, feeding programs, and housing utilization. The importance of accurate breeding records is multiplied because there is much smaller margin for error with a shorter dry period. Because some dry cow treatments have withholding times longer than 30 d, their use must be carefully monitored. The dry cow ration also requires attention because these cows may be able to be fed a high energy ration for their entire dry period. Lastly, capacity of the parlor and cow facilities must be taken into account because shortening dry periods effectively increases milking herd size, possibly resulting in excessive overcrowding.

Key Words: Dry Period, Milk Production

128 National Animal Identification: What is its future? M. Aguiar* and E. Jaster, *California Polytechnic State University, San Luis Obispo.*

The subject of animal identification is not new to the dairy industry. However, with such recent events such as the outbreak of Foot and Mouth Disease in the United Kingdom and the detection of Bovine Spongiform Encephalopathy (BSE) in the U.S., the dairy and animal industry has been alerted to the potentially devastating effects of an outbreak in the United States. Dairy producers within the U.S. have voluntarily participated in the Dairy Herd Improvement Association (DHIA) Programs for over 30 years. Being enrolled in DHIA requires the dairy producers to have individual animal identification with attached readable tags. Although DHIA provides an identification and tracking program at present it is a voluntarily operation and does not include the entire dairy and beef industry. Therefore, a reliable program that would trace any possibly infected animals is necessary to reduce economic losses and minimize loss of consumer confidence in dairy and beef products. With the implementation of an effective National Animal Identification System (NAIS) any animal suspected of being infected could be traced to its point of origin. This information could be used to determine all animals that have been exposed to this suspected animal. This would allow for immediate quarantine of suspected populations and or recall adulterated products. This early detection and remediation would drastically reduce the negative effects on producers.

Key Words: National Identification, Dairy Cattle

Breeding and Genetics: Sheep, Swine, and Dog Breeding

129 Assessing connectedness in across-flock genetic evaluations. R. M. Lewis^{*1,3}, R. E. Crump², L. A. Kuehn¹, G. Simm³, and R. Thompson⁴, ¹*Virginia Polytechnic Institute and State University, Blacksburg*, ²*AGBU, University of New England, Armidale, Australia*, ³*Scottish Agricultural College, Edinburgh, UK*, ⁴*IACR-Rothamstead, Harpenden, UK.*

Reliability of across-flock genetic evaluations depends on the extent of genetic connections among animals in separate flocks. Our objective was to assess the relationship between connectedness and errors of prediction of differences in EBV ($a_i^* - a_j^*$) between pairs of animals (i, j) in different flocks. Fifteen flocks of 40 to 120 ewes were simulated for a trait with heritability of 0.25 within-flock. Flock genetic means were drawn from a normal distribution with mean 0 and scaled variance 0.25. Flocks had opportunity to link by sharing rams from

a team of 6 reference sires (RS). Selection ensued for 15 yr. Six scenarios producing from no (no RS used) to strong (3 RS each mated to 10 ewes) across-flock connectedness were used. Connectedness was measured as the average prediction error correlation (r_{ij}) between flocks. In simulation, true breeding values (a) are known and the statistic $L_{ij} = (a_i^* - a_j^*) - (a_i - a_j)$ was obtained with expectation zero. The average square of L_{ij} for all i, j quantifies the mean square error of prediction [$M(L_{ij})$]. For each of 25 replicates of each scenario, r_{ij} and $M(L_{ij})$ were obtained for lambs born in yr 25 and summarized by flock. As RS use increased, r_{ij} increased and $M(L_{ij})$ decreased ($P < 0.01$). Their relationship was modeled as $Y = b + ce^{kX}$ where Y was the value of $M(L_{ij})$, b was the asymptote, $b + c$ the intercept, k the rate parameter, and X the value of r_{ij} . The b reflects variance, and c the squared bias without connectedness, of prediction. The function fitted well ($R^2 = 0.97$) with values of b , c and k of 0.372 ± 0.0161 ,

0.142±0.0214 and 379±149, respectively, although *b* and *k* were highly correlated (0.81). The asymptotic value of *b* was approached with only 1 RS mated to 5 ewes. In conclusion, the bias of comparisons of EBV quickly fall as connectedness increases, with adequate links established by limited sharing of rams among flocks.

Acknowledgements: We are grateful to the Meat and Livestock Commission for funding.

Key Words: Connectedness, Prediction Error, Sheep

130 Evaluating connectedness over time in a group breeding scheme using a sheep paradigm. L. A. Kuehn^{*1}, R. M. Lewis¹, and G. J. Nieuwhof², ¹Virginia Polytechnic Institute and State University, Blacksburg, ²Meat and Livestock Commission, Milton Keynes, UK.

Poor connectedness between animals in separate flocks lowers reliability when comparing EBV across flocks. The objective of this study was to assess the increase in connectedness between flocks of sheep participating in a sire referencing scheme (SRS). Pedigree and performance data for a single trait with a within-flock heritability of 0.25 were simulated (25 reps) for 15 flocks with 40 to 120 ewes per flock. Founder genetic means for each flock were sampled from a normal distribution with mean zero and SD equal to the trait's genetic SD. After 10 yrs of random mating, flocks had opportunity to join a SRS and selection began for the simulated trait. Six yearling rams were chosen as reference sires randomly from the top one-sixth of the population ranked on BLUP EBV. Every year, in each flock, three reference sires were each mated to 10 ewes. Remaining ewes were mated to homebred or purchased rams of unknown pedigrees. Connectedness was measured as the average prediction error correlation of flock genetic means (flock connectedness) or of EBV for the current crop of ram lambs EBV (lamb connectedness). Four sire referencing scenarios were considered in which all flocks participated in a SRS for: i) 15 yr (ALL); ii) 5 yr and discontinued the scheme for 10 yr (OFF5); iii) 10 yr and discontinued for 5 yr (OFF10); and, iv) 0 yr since scheme not formed (OFF). Genetic gain was on average 1.19 times higher ($P<0.01$) at yr 15 of selection in the ALL as compared to the OFF scenario. Genetic gain was intermediate in the OFF5 and OFF10 scenarios. Flock connectedness increased linearly in all scenarios while SRS was underway and leveled off when flocks discontinued SRS. Lamb connectedness increased rapidly as soon as the SRS was implemented and decreased substantially the year the flocks left the scheme ($P<0.01$). Through group breeding schemes, connectedness is rapidly increased thereby allowing producers to make equitable genetic comparisons between their breeding animals.

Acknowledgements: We are grateful to the Meat and Livestock Commission for funding.

Key Words: Connectedness, Simulation, Sheep

131 Evaluating parameters affecting on economical attributes of kordian sheep in order to estimating of genetic trend in shirvan station. S. A. Shiri^{*}, Agricultural & Natural Resources Research Center of Khorasan, Mashhad, Iran.

Data from 6215 Kordian sheep collected over 13 yr (1991-2004) at the animal breeding station of Shirvan were analysed by using the DFREML 1997 package. Traits analysed were: birth weight (BW), weaning weight (WW), pre-weaning gain (G1), post-weaning gain (G2), lamb fleece weight (LF), and adult fleece weight (AF). Effects of sex, age of dam, birth type and birth year for all growth traits were significant ($P<0.05$). Estimates of direct heritability were obtained with univariate and bivariate animal models. Heritability estimates from the univariate animal model were 0.18, 0.29 ± 0.06, 0.05 ± 0.02, 0.47, 0.37 ± 0.11, 0.09, 0.21; and from the bivariate animal model were 0.25 ± 0.05, 0.30 ± 0.01, 0.04 ± 0.004, 0.32 ± 0.03, 0.11 ± 0.003, 0.19 ± 0.02; for BW, WW, G1, G2, LF, and AF, respectively. Estimated repeatability of WW, G1, LF and AF were 0.46 ± 0.11, 0.23 ± 0.39, 0.11 ± 0.18, 0.26 ± 0.07, respectively. Genetic and (phenotypic correlations) between BW & WW, WW & 6-mo weight, G1 & G2, BW &

LF, LF & AF were: 0.11 ± 0.16 (0.25), 0.89 ± 0.05 (0.62), -0.39 ± 0.26 (-0.43), 0.54 ± 0.29 (0.05), 0.30 ± 0.40 (0.06), respectively. Genetic trends in WW, G1, LF and AF were significant ($P<0.05$) with trend in growth traits being positive and wool traits having negative genetic trend after 1995.

Key Words: Kordian Sheep, Genetic Trend, Animal Model

132 Genetic (co)variance components for ewe productivity traits in Katahdin sheep. H. B. Vanimisetti^{*}, D. R. Notter, and L. A. Kuehn, Virginia Polytechnic Institute and State University, Blacksburg.

Total litter weight weaned by a ewe is an economically important trait in sheep production but records of zero when no lambs are weaned, missing weaning weight records, or invalid weight records taken outside acceptable age windows complicate direct genetic analysis of this trait. The objective of this study was to estimate genetic (co)variance components for total litter weaning weight per ewe lambing (TW) and its components, number of lambs born (NB), number of lambs weaned (NW), and average lamb weaning weight (AW) for Katahdin sheep. The TW was the sum of 60-d age-adjusted weights of all lambs weaned in the litter; these weights were also adjusted for ewe age and lamb sex. The AW was the average 60-d age-adjusted weight of all lambs weaned in the litter; these weights were adjusted for ewe age, lamb sex, and type of birth and rearing. A total of 2,995 NB and NW records, but only 2,714 AW and 2,622 TW records, were available from 1,549 ewes over 4 yr. Ewes were progeny of 382 sires. Initially, heritabilities were estimated for each trait from univariate REML analyses. Initial estimates of genetic correlations were obtained from bi- and trivariate analyses and then used in a final four-trait analysis. The model for NB, NW, and TW included fixed contemporary group (CG) and ewe age effects and random ewe additive and permanent environmental effects. A random service sire effect was also fitted for TW. The model for AW included fixed CG and random ewe additive and permanent environmental and service sire effects. Heritabilities of TW, NB, NW, and AW from univariate analyses were 0.14, 0.13, 0.10, and 0.14 (all $P < 0.01$), respectively. Genetic correlations of TW with NB, NW, and AW were 0.42, 0.94, and 0.77, respectively, those of NB with NW and AW were 0.50 and 0.16, respectively, and that between NW and AW was 0.52. Using these genetic correlations, TW EPD can be predicted from its components by a selection index approach, thereby utilizing all available data for genetic evaluation of ewe productivity.

Key Words: Heritability, Productivity, Sheep

133 Genetic factors influencing body weights and condition scores in adult Targhee ewes. R. C. Borg^{*1}, D. R. Notter¹, R. W. Kott², and L. A. Kuehn¹, ¹Virginia Polytechnic Institute and State University, Blacksburg, ²Montana State University, Bozeman.

Genetic and phenotypic relationships among adult BW, condition score (CS), and EBV for currently evaluated production traits were analyzed in Targhee sheep. A total of 1,094 records were collected from 513 ewes over 5 yr. Ewe BW and CS (1-5 scale) were recorded three times each year: late gestation (G), early lactation (L) and post-weaning (P). Data included 863 G and P records and 1,078 L records for BW and CS. A multivariate model including fixed effects of year, ewe age, and litter size was simultaneously fit to each BW and CS. Regressions of BW and CS on EBV were also estimated in individual models including these fixed effects. The EBV were for 120-d weaning weight, maternal milk, yearling weight, yearling gain, fleece weight, fiber diameter, staple length, and prolificacy (lambs born/100 ewes lambing). Heritabilities and permanent environment effects were estimated in univariate analyses with the same fixed effects. Means for BW were 71.3, 61.3 and 67.3 kg for G, L and P, respectively, and for CS were 3.1, 2.6 and 2.8 for G, L and P, respectively. Residual correlations (*r*) among adjacent BW and CS measures averaged 0.74 ($P<0.05$) and 0.26 ($P<0.05$), respectively; for BW and CS measures taken at the same time averaged $r = 0.33$ ($P<0.05$). On average, BW increased 4.7 kg for each scoring unit increase in CS ($P<0.05$). No antagonistic relationships existed between CS and any EBV; most regressions did not differ from zero ($P<0.10$).

However, BW was associated ($P < 0.05$) with differences in all EBV except those for fiber diameter and staple length. Ewes with single litters had higher CS during L than ewes with larger litters ($P < 0.05$). Heritability estimates for CS were 0.10, 0.15 and 0.16 for G, L and P, respectively. Permanent environment effects were not significant ($P < 0.10$). The genetic relationships that exist between performance potential, BW, and CS may be useful in estimating adult ewe performance.

Key Words: Sheep, Heritability, Body Weight

134 Genomic organization and six exonic polymorphisms of the pig SLC11A1 gene. W. Zhen-Fang*, L. Wen-Hua, Z. Xi-Chuan, and Y. Guan-FU, *South China Agricultural University, Guangzhou, Guangdong, China.*

SLC11A1 gene plays a crucial role in animal disease resistance to several intracellular pathogens such as Mycobacterium, Leishmania and Salmonella. In this study, PCR amplification and sequencing were performed to obtain the genomic organization of pig SLC11A1 gene by comparative genomic analysis. Results showed that pig SLC11A1 gene consists of 15 exons and 14 introns, which is consistent with the mouse, human SLC11A1 gene. All of the introns sequence acquired have been submitted to GenBank and assigned the accession numbers AY368468, AY368469, AY368470, AY368471, AY368472, AY368473, AY368474, AY368475, AY556536, AY368476, AY368477, AY368478, AY368479, AY368480, respectively. The full gene spans 12,267 bp. Mutational analysis was performed on the exonic regions. Six single nucleotide polymorphisms (SNPs) are identified, two are nonsynonymous, three are synonymous, and one is in 3' UTR region. The SNP G80C in exon2 results in the change Asp6 to His6; and G587A in exon6 results in the change of Val175 to Ile175. The availability of the fine genomic organization of the pig SLC11A1 gene and the identification of polymorphisms will facilitate the evaluation of its functional role in several diseases resistance or susceptibility.

Acknowledgements: We thank Dr Shu-Hong Zhao from college of animal science, Huazhong Agricultural University, China, and Dr Jin-Zeng Yang from Dept of Human Nutrition, Food and Animal Sciences, University of Hawaii, USA for valuable suggestions to this paper. This study was supported in part by an agricultural key Grant-in-aid project (2002C20202) from the office of science and technology, Guangdong province, China

Key Words: Pig SLC11A1 Gene, Genomic Organization, Single Nucleotide Polymorphism

135 Detection of imprinted quantitative trait loci for growth, carcass, and meat quality traits in swine. N. Vukasinovic*, A. Clutter*, F. Du*, M. Lohuis*, L. Messer*, J. Bennewitz*, N. Borchers*, N. Reinsch*, G. Otto*, K. Sanders*, and E. Kalm*, *Animal AG, Monsanto, St. Louis, MO, ²University of Kiel, Kiel, Germany.*

Detection of imprinted quantitative trait loci (QTL) affecting growth, carcass, and meat quality was conducted in an F2 population created by crossing Pietrain boars with Large White x Landrace hybrid sows. 1014 F2 animals, their parents and grandparents were genotyped for 27 microsatellite markers on chromosomes 2, 6, and 7. Phenotypes on 31 growth, carcass, and meat quality traits

were available. Imprinting analysis was performed using the following methods: (1) the imprinting effect was fitted along with additive and dominance effect; imprinting was inferred if the model with imprinting was significantly better than the null model without QTL and the Mendelian model without imprinting (Knott et al., *Genetics* 149, 1998); (2) maternal and paternal allele effects were fitted separately; imprinting was declared if the full model (with paternal, maternal, and dominance effect) was significantly better than the model with only one parental component and no dominance (De Koning et al., *JAS* 79, 2001); and (3) Mendelian, full, paternal, and maternal models were evaluated using a decision tree to determine presence and mode of inheritance of QTL (Thomsen et al., *WCGALP Proceedings*, 2002). All three methods detected several QTL for growth, fatness, and meat color and conductivity on SSC2, most of which were (paternally) imprinted. With method (3), QTL for abdominal fat, loin eye area, and meat color were partially imprinted. Methods (1) and (2) did not infer imprinting for QTL affecting backfat, meat color, and meat reflectance. No QTL was detected on SSC6, except for a paternally imprinted QTL for birth weight detected by method (3). On SSC7, all three methods detected Mendelian QTL affecting carcass length and backfat; in addition, method (3) detected partially imprinted QTL for ham weight and percentage, and loin eye area. These results confirmed previous findings of paternally imprinted QTL for growth and fatness on SSC2 and provided evidence of additional imprinted QTL.

Key Words: Imprinting, QTL Mapping, Swine

136 Discrete time survival analysis of longevity in a colony of dog guides. J. Cole*, B. Southey*, D. Franke*, and E. Leighton*, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD, ²University of Illinois, Urbana, ³Louisiana State University, Baton Rouge, ⁴Seeing Eye, Inc., Morristown, NJ.*

Working life for 1,177 German Shepherd (GS) and 1,724 Labrador Retriever (LR) dogs that worked as guides for the blind was studied using discrete time survival analysis. Total years worked after graduation, total months worked after graduation, months worked between graduation and 18 mo (EWL), and months worked beyond 18 mo (LWL) were analyzed using complementary log-log animal and maternal effects models. Animals working 10 or more years were combined in a single group. Censoring rates were 91.76% (44.87%) and 94.90% (48.90%) for EWL (LWL) in GS and LR, respectively. Explanatory variables were duration of time interval (months or years), contemporary group, sex, and inbreeding coefficient. Estimates of explanatory variables obtained within the same period across models and different time intervals were similar. No sex differences were observed and the hazard of culling increased with increasing inbreeding coefficient. Maternal effects were small and non-significant in both breeds for all traits. Heritability estimates ranged from 0.05 to 0.12 in GS and 0.04 to 0.15 in LR and were lowest for later working life, intermediate for total working life in months or years, and highest for early working life. These estimates were higher than the previously reported estimates of 0.03 (0.02) and 0.05 (0.03) for EWL (LWL) in GS and LR, respectively, that were obtained with a Weibull sire model. Pearson's product-moment correlations among sire estimated breeding values for EWL and LWL were 0.92 and 0.83 for GS and LR, respectively, suggesting that EWL and LWL are biologically different traits. These results suggest that there is sufficient genetic variability that can be exploited to genetically improve working life.

Key Words: Dog, Heritability, Longevity

Breeding and Genetics: Statistical Methods II

137 Bayesian inferences on major genes affecting polygenic binary traits: comparison of models and application to osteochondral diseases in pigs. H. N. Kadarmideen*¹ and L. L. G. Janss*, *¹Swiss Federal Institute of Technology, Zurich, Switzerland, ²Wageningen University and Research Centre, Lelystad, The Netherlands.*

The main objective of this study was to develop and apply Bayesian segregation analysis (BSA) method to detect major genes for binary polygenic traits

and to investigate different BSA models. In order to apply developed methods, osteochondral (OC) diseases in pigs (as scores or binary data) were modeled by a mixture inheritance linear model (MILM) and threshold model (MITM) and analyzed by Bayesian-Gibbs sampling algorithms. Data, on 1163 pigs with OC (pedigree with 2891 animals), were from company, SUIAG. Both MILM and MITM included systematic environmental effects, animals polygenic effects and a major gene effect with *Mendelian* transmission probabilities. Results showed familial transmission and evidence for segregating major gene with