Breeding and Genetics I

M94 Genetic analysis of daily milk yield variability. V. S. Moncur*, L. C. Hardie, and C. D. Dechow, Penn State University, University Park, PA.

With the increased availability of daily milk yield measurements, data exists for analyses of additional traits that could be related to health and fertility. Selection for milk yield variability would be feasible if cows with more consistent milk yield exhibit greater levels of fertility or health. The objective of this study was to determine if day-to-day variation in milk yield is heritable and how it is correlated with daily milk yield (dMY). We retrieved 789,266 dMY records from 5 to 250 d in milk for 2366 lactations of 1184 Holsteins; of these, 470 had 42K genotypes. We merged dMY with the previous day’s milk yield (pMY) to derive the absolute value of dMY – pMY (ΔABS), and relative change in milk yield (ΔREL), which was ΔABS/pMY. Only lactations with at least 200 observations were retained, and the average ΔREL, ΔABS, and pMY for the first 250 d of lactation were calculated and included in a 3-trait single-step genomic evaluation in ASReml. The fixed effects included lactation group (lactations 1, 2, ≥3), age at calving, and year-season of calving, and the random effects encompassed the genomic relationship effect, permanent environment, and residual error. Pedigree and genotypic data were blended to create the genomic relationship matrix with PREGSF90. All traits were heritable with estimates of 0.23 ± 0.04, 0.15 ± 0.04, and 0.26 ± 0.05 for ΔABS, ΔREL, and pMY, respectively. The genetic correlation estimate between ΔABS and pMY was 0.76 ± 0.07, whereas the genetic correlation estimate between ΔREL and pMY was −0.15 ± 0.16. The phenotypic correlation estimates of ΔABS with ΔREL were 0.60 ± 0.02 and −0.32 ± 0.02, respectively. The 2 measures of variability were moderately correlated with a genetic correlation estimate of 0.52 ± 0.12 and phenotypic correlation estimate of 0.52 ± 0.02. Last, repeatabilities ranged from 0.32 ± 0.03 (ΔREL) to 0.41 ± 0.03 (pMY). In conclusion, daily milk yield variability was heritable and ΔREL was more independent of milk yield than ΔABS.

Key Words: milk yield variation, heritability, daily milk yield

M95 A resolution to breed identification of Pakistani Sahiwal cattle. M. Moaeen-ud Din*, G. Bilal, R. D. Muner, and N. Wahid, Laboratories of Animal Breeding and Genetics, Faculty of Veterinary and Animal Sciences, PMAS Arid Agriculture University, Rawalpindi, Punjab, Pakistan.

Molecular identification of animals is becoming increasingly important to preserve and maintain pure breeds worldwide. The issue is aggravated with rise in import of foreign animals and germplasm in Pakistan. It is becoming difficult to find pure males of Sahiwal breed for breeding purpose in public as well as private semen production units. The present study was designed to develop standard molecular markers for Sahiwal to ascertain their purity for breeding purpose. In this study, 50 and 48 unrelated males were sampled for each Sahiwal and Crossbred cattle respectively. Candidate molecular markers present in Sahiwal but absent in Crossbred and vice versa were detected using amplified fragment length polymorphism (AFLP) method. Eleven markers were developed that were converted to SNP markers for genotyping. The allele frequencies in both breeds were determined for discrimination ability using AFLP. Data were analyzed using Arlequin 3.5. The probability of identifying Sahiwal breed was 0.86 and probability of misjudgment was 0.021 using single selected markers. However, probabilities for judgment and misjudgment with 2 markers and combined with 3 markers were 0.745, 0.367 and 0.964, 0.376 respectively. Sahiwal breed and crossbred could be tested using the given markers and can be verified for purity before entering into breeding program.

Key Words: molecular marker, breed identification, Sahiwal

M96 Causes of inflation in genomic evaluations for young genotyped dairy bulls. S. Tsuruta*, D. A. L. Lourenco1, I. Miszlai1, and T. J. Lawlor2, 1University of Georgia, Athens, GA, 2Holstein USA Inc., Brattleboro, VT.

The objective of this study was to investigate causes of inflation in genomic predictions for dairy cattle. The simulated data included phenotypes, pedigrees, and genotypes, mimicking a dairy cattle population, which was selected by breeding values or not selected. With the simulated data, genomic (G)EBV were calculated with a single-step genomic BLUP and compared with true breeding values (TBV). Phenotypes and genotypes were simulated for 10 generations and the last 4 generations, respectively. Phenotypes in the last 2 generations were removed to predict breeding values using only genomic and pedigree information. For comparison, (G)EBV were also calculated using all phenotypes and genotypes in 10 generations. Pedigrees with and without inbreeding and pedigrees with unknown dams were used to construct the pedigree-based relationship matrix (A). Regression coefficients (b1) of TBV on (G)EBV were calculated to investigate inflation in GEBV. In addition to the simulation study, inflation in GEBV for 18 linear type traits of US Holsteins were examined as well. Regression coefficients of daughter yield deviations on GEBV for young genotyped bulls were calculated. The results from the simulation indicated that GEBV for bulls were inflated regardless of selection whereas EBV were not inflated with no selection. The inflation was greater with no inbreeding or with no dams in A. On the other hand, inflation in GEBV for cows were minimal with no selection or with genotypes in all generations. For linear type traits, GEBV (and parent averages) were always inflated (b1 < 1.0). To minimize the inflation, A and the genomic relationship matrix (G) should be consistent; including exact inbreeding in A is one way and using a weight (ω) < 1.0 on the inverse of A for genotyped animals (Aω−1), which increases the pedigree contribution (A−1 − ωAω−1) for genotyped animals, is another way. Smaller or current additive genetic variances could be useful. In dairy cattle, known (accurate) pedigree information and consistency between G and A (and Aω) could be essential to reduce the inflation in genomic predictions for young genotyped bulls.

Key Words: genomic prediction, linear type trait, US Holstein

M97 Genetic analysis of subclinical mastitis resistance in early lactation. S. G. Narayana*, F. Miglior2, S. A. Naqvi1, F. Malchiodi2, P. Martin2, and H. W. Barkema1, 1Department of Production Animal Health, Faculty of Veterinary Medicine, University of Calgary, Calgary, AB, Canada, 2CGLI, Department of Animal Bioe- sciences, University of Guelph, Guelph, ON, Canada, 3Canadian Dairy Network, Guelph, ON, Canada.

Subclinical mastitis (SCM) causes economic losses for producers by affecting milk production and leading to higher incidence of clinical mastitis and premature culling. The incidence of SCM in first lactating cows is usually higher during early lactation. The somatic cell count (SCC) can be used for the diagnosis of subclinical mastitis. The objective of this study was to estimate genetic parameters for SCM in early lacta-
tion in first parity Holstein. Test-day records for SCC were collected monthly between 2005 and 2009 in 90 Canadian herds participating in the national cohort of dairy farms of the Canadian Bovine Mastitis Research Network. Only the first test-day record available between 5 to 30 DIM was considered for the analysis. The final data set contained 8,518 records from first lactating Holstein heifers. Six alternative traits were defined as indicators of subclinical mastitis using different cut-off values of SCC (between 150,000 to 400,000 cells/mL). Linear and threshold animal models were used for the analysis. The prevalence of subclinical mastitis ranged from 15 to 24%. Estimated heritabilities from linear and threshold model ranged from 0.037 to 0.057 and 0.040 to 0.050, respectively. Strong genetic correlations were found among alternative SCC traits (from 0.90 to 0.99), indicating that these 6 traits were genetically similar. Despite a low heritability, estimated breeding values (EBV) predicted from both models showed a large genetic variation among sires. Higher EBV of SCM resistance corresponded to sires with higher percentage of healthy daughters. The percentage of diseased daughters varied between 5 to 13% and 19 to 33% among sires with best and worst EBV. The Spearman’s rank correlations between EBVs of sires predicted from linear (0.76 to 0.95) and threshold (0.74 to 0.95) models were moderate to high.

Key Words: mastitis, heritability, somatic cell count

M98 Genetics of functional traits related to resistance of diseases and milk yield in Friesian × Bunaji crosses. I. Adedibu1, A. Mshelia1, A. Liyola-Tunjii2, P. Barje3, C. Lakpini1, and T. O. Ososanya4, 1Ahmadu Bello University, Zaria, Kaduna State, Nigeria, 2National Agricultural Extension and Rural Liaison Services, Zaria, Kaduna State, Nigeria, 3National Animal Production Research Institute, Shika, Kaduna State, Nigeria, 4University of Ibadan, Ibadan, Oyo State, Nigeria.

This study estimated the relationship between milk yield and health trait indicators in F1 (50:50) and F2 (75:25) Friesian × Bunaji crosses (F×B) of cows. The data were collected from 500 F1 and 2 F2 F×B cows on which routine standard measures: vaccinations, control of ecto- and endo-parasites were carried out. The data were collected between 2000 and 2017. The F1 showed significantly (P < 0.01) positive genetic correlation (rP) between milk yield (MY) and lameness (LM) and between MY, foot and mouth disease (FM). The LM was significant (P < 0.01) and moderately positive rg with skin ulcer (SU); helminths (HM); FM and skin rashes (SR). Mastitis had significantly (P < 0.05) low positive rg with HM and SR. There was only significant (P < 0.05) phenotypic relationship (rP) between MY and FM but negative. The rg between SU and mastitis, SU and LM, SU and HM were highly significant (P < 0.01) and highly positive. The F2 showed significant (P < 0.01) moderate positive rP between MY and LM as well as between MY with FM. LM had significant (P < 0.01) moderate positive rP with HM, SU, SR and FM. There were moderate significant (P < 0.05) rP between MY and LM, MY and FM. The SR and HM had highly significant (P < 0.01) positive rg. Selection of F1 F×B cows for improved MY can also benefit from genetic selection against FM and LM due to antagonistic pleiotropic effect. Selection against incidence mastitis may lead to selection of cows with low resistance to ecto- and endo-parasitic incidences. The F1 F×B cows that were high milk producers in this study were likely to have lower incidences of FM. Selection of the F2 F×B cows for improved MY can be undertaken and would aid selection for population with lower incidences of LM and FM. Pleiotropic gene effect could have influenced LM, HM, SU, SR and FM in the F2 indicating that selection can be effectively utilized to improve these health traits. In the F2, the quantity of MY may not be affected by the traits LM and FM. In the F1 and F2 F×B cows, genetic relationships exist between MY and common dairy disease traits like LM and FM thus can be selected against at the onset of any breeding program.

Key Words: functional trait, milk yield, selection

M99 Development and application of the GENEX Jersey Ideal Commercial Cow Index (ICCS). H. Adams4*,1, G. Abdel-Azim1, L. James2, J. Hanson2, N. Hemauer2, S. Carson2, and R. Fourdraine1, 1CRI International Center for Biotechnology, Mount Horeb, WI, 2GENEX Cooperative Inc., Shawano, WI.

Selection indexes are a valuable way for producers to simultaneously select several significant traits in a well-adjusted formula, allowing emphasis in multiple areas such as production, health and fertility. The GENEX (Shawano, WI) Holstein Ideal Commercial Cow Index (ICCS) has already proven itself to be a well-designed and useful economic-based selection index, allowing breeders to make selection decisions based on a single ICCS value, or focus on a more specific area of improvement using sub-indexes that make up ICCS. As the GENEX ICCS was originally designed for Holstein dairy producers, surveys were conducted on some of the largest and most progressive US Jersey herds with the aim to understand the projected future direction for the Jersey breed, and identify the traits and selection areas of most importance to Jersey producers. The gathered information was used to formulate an ICCS specific to the Jersey breed. Data used in the model formulation was pulled from the CRI internal dairy research database (54 million health records on 12 million cows) utilizing 128K lactation records on 60K Jersey cows. Three sub-index categories were established: Cheese Maximizer (ChMAX$; component traits), Sustainability (SUST$; health traits), and Fertility (FERT$; cow and heifer fertility). Based on the producer survey responses, several indexes were tested using various trait combinations and corresponding economic weights that directly tie to on-farm profitability, to identify an ideal model. The final index was broken down into 43% ChMAX$, 35% SUST$ and 23% FERTS. Validation was done using active GENEX Jersey bulls measuring individual trait responses and compared with selection on JPI and NMS based on the ranking of bulls within each index. The Jersey ICCS is unique from currently available Jersey indexes in allowing individual producers to focus their selection on an area specific to their own farm’s needs using the available sub-index values. The index also places more weight on fertility and health and emphasizes milk components while staying neutral to milk yield, which sets the index apart from currently available indexes.

Key Words: Jersey, ICCS, selection index

M100 Allele frequency of β-casein gene in local dairy animals of Pakistan. G. Bila* and M. Mooneen-ud-Din, Laboratories of Animal Breeding and Genetics, Faculty of Veterinary and Animal Sciences, PMAS Arid Agriculture University, Rawalpindi, Rawalpindi, Punjab, Pakistan.

The objective of the present study was to identify the genotypes of our leading dairy cattle and buffalo breeds concerning A1 and A2 β-casein bovine milk protein. Blood samples were collected from local dairy cattle [Sahiwal (n = 13), Cholistan (n = 12), Holstein (n = 42), Crossbred (n = 18)] and buffalo (Nili Ravi; n = 15) bulls. DNA was extracted through Genetek Genomic DNA Purification Mini kit (Thermoscientific, EU, Lithuania). Allele-specific primers for A1 and A2 alleles of β casein gene were designed using Primer Premiere (Ver.6.0). Primers sequences used for A1 allele were (forward) CCCCCCTCTGGGCCCCATCCC and
Streptococcus agalactiae is a common and major cause of bovine mastitis, but the immune response related to S. agalactiae-induced mastitis is a very complex biological process. To understanding the pathophysiological process and the host immune response to S. agalactiae-induced mastitis, we used nipple tube perfusion of S. agalactiae to establish a Chinese Holstein cattle clinical mastitis model. Visual inspection, somatic cells count analysis, histopathology and transmission electron microscopy examination have confirmed the successful establishment of the S. agalactiae-induced mastitis model. Then, we used Bovine Gene Expression microarray and isobaric tags for relative and absolute quantitation (iTRAQ) to screen potential genes and proteins associated with mastitis. Compared with healthy mammary glands tissue, 129 differentially expressed genes (fold change ≥2, P ≤ 0.05) and 144 differentially expressed proteins (≥1.2-fold) were identified. Most significantly, differentially expressed genes were involved in immune and inflammatory reactions, such as complement and coagulation cascades, inflammatory mediator regulation of TRP channels, and bacterial invasion of epithelial cells. iTRAQ analysis also showed that the immune and inflammatory related proteins were significantly upregulated in the mastitis group, such as fibronectin 1, complement factor H, and von Willebrand. In conclusion, this joint analysis of transcriptomic and proteomic profiles provides an enhanced understanding of immune response to S. agalactiae-induced mastitis in bovine mammary glands.

Key Words: Streptococcus agalactiae-induced mastitis, transcriptomic analyses, proteomic analyses

M103 Genome-wide association study (GWAS) for bovine respiratory disease in pre-weaned Holstein calves. A. E. Quick*, T. L. Ollivett, B. W. Kirkpatrick, and K. A. Weigel, University of Wisconsin, Madison, WI.

Bovine respiratory disease (BRD) is one of the leading causes of morbidity and mortality in dairy calves. NAHMS (2011) reported that BRD affected 18.1% of pre-weaned heifer calves, with a mortality loss of 2.3%. The objective of this study is to establish a protocol for objective and efficient assessment of bovine respiratory disease (BRD) phenotypes in dairy calves and identify markers associated with BRD in a genome-wide association study (GWAS). 1,107 calves from 6 dairy farms in southern Wisconsin were measured at 3 and 6 weeks of age. Each calf was given a clinical score based on visual appraisal of eyes, nose, ears, attitude, cough, and temperature, as well as a subclinical score based on thoracic ultrasonography. The interaction of clinical and subclinical phenotype was represented on a 1 to 6 scale as overall BRD score. 1016 calves were genotyped with a commercially available single nucleotide polymorphism (SNP) array, and upon completion of quality control and imputation, 28,696 SNP and 1,014 individuals remained. A preliminary GWAS analysis was performed using a linear mixed model with SNP genotype as a fixed effect and with background polygenic effect as a random effect. Three- and 6-wk phenotypes were analyzed separately, and BRD scores were considered as binary (healthy or affected) or ordinal (6 levels reflecting increasing severity). At 3 wk of age, 8 and 6 significant SNP (P-value <5 × 10\(^{-5}\)) were detected in the binary and ordinal analyses, respectively, with common SNP on chromosomes 1, 7, 17, and 18. At 6 wk of age, 3 significant SNP were found in each of the binary and ordinal analyses, with common SNP on chromosomes 8 and 9. Combining the clinical and subclinical scoring systems allows objective and efficient assessment of BRD for detection of important SNP using GWAS or whole-genomic selection against BRD. Further analysis is needed to identify putative genes affecting BRD and to assess the reliability of whole-genome predictions.

Key Words: genome-wide association study (GWAS), bovine respiratory disease