Breeding and Genetics: Genomic Selection

T196 Genome-wide association study of cholesterol and polyunsaturated fatty acids of beef from crossbred cattle. L. N. Schiermiester*, C. M. Ahlberg, J. T. Howard, C. Calkins, and M. L. Spangler, University of Nebraska, Lincoln.

Crossbred cattle of varying percentages of Angus, Simmental, and Piedmontese were used to investigate the proportion of phenotypic variation explained by the BovineSNP50 assay for the traits of cholesterol (CH), polyunsaturated fatty acids (PUFA), and monounsaturated fatty acids (MUFA). Steers and heifers (n = 239) were split into 4 groups and placed in a feedlot over a 2-year period between 2010 and 2012. After harvest, half-inch thick steaks were sampled from the eye of round (eye) and the longissimus dorsi (strip) and trimmed to a 1/8 inch of subcutaneous fat for nutrient analysis. All animals were genotyped with the BovineSNP50 assay and had a call rate above 97.5%. Illumina data analysis software was used to assign quality scores (GenCall) for each genotype. If genotypes were missing or a GenCall score was below 0.20, genotypes were replaced with the mean allele frequency across each genotype. A Bayes C algorithm was employed fitting group as a fixed effect using the GenSel software including a chain length of 150,000 samples with the top 0.5% windows (n = 13) were compared across cuts within a trait. Windows in common between the 2 cuts for protein included 6 regions on BTA2. There was only one window in common between the 2 cuts for potassium and iron, both on BTA2. There were no windows in common between the 2 cuts for sodium. The influence of regions on BTA2 suggest that the Myostatin mutation (C313Y) segregating in some of these animals influences protein and the content of some minerals in beef.

Key Words: beef cattle, genome-wide association study, nutrient profile

T197 Genome-wide association study of protein and mineral content of beef from crossbred cattle. C. M. Ahlberg*, L. N. Schiermiester, J. T. Howard, C. Calkins, and M. L. Spangler, University of Nebraska, Lincoln.

Crossbred cattle of varying percentages of Angus, Simmental, and Piedmontese were used to investigate the proportion of phenotypic variation explained by the BovineSNP50 assay for the traits of protein, iron, potassium and sodium. Steers and heifers (n = 239) were split into 4 groups and placed in a feedlot over a 2-year period between 2010 and 2012. After harvest, half-inch thick steaks were sampled from the eye of round (eye) and the longissimus dorsi (strip) and trimmed to a 1/8 inch of subcutaneous fat for nutrient analysis. All animals were genotyped with the BovineSNP50 assay and had a call rate above 97.5%. Illumina data analysis software was used to assign quality scores (GenCall) for each genotype. If genotypes were missing or a GenCall score was below 0.20, genotypes were replaced with the mean allele frequency across all animals. No SNP were culled based on minor allele frequency. A Bayes C algorithm was employed fitting group as a fixed effect using the GenSel software including a chain length of 150,000 samples with the top 0.5% windows (n = 13) were compared across cuts within a trait. Windows in common between the 2 cuts for protein included 6 regions on BTA2. There was only one window in common between the 2 cuts for potassium and iron, both on BTA2. There were no windows in common between the 2 cuts for sodium. The influence of regions on BTA2 suggest that the Myostatin mutation (C313Y) segregating in some of these animals influences protein and the content of some minerals in beef.

Key Words: beef cattle, genome-wide association study, fatty acids
High variation of follicle numbers in cows during the estrus cycle can influence their reproductive performance. Animals with high follicle count (HFC) have a better reproductive performance when compared with low follicle count (LFC) animals (Mossa et al. 2012). Moreover animals with HFC can be more responsive to reproductive biotechniques such as superovulation, ovum pick-up and in vitro fertilization. Identifying these animals with superior genetic potential for fertility would be desirable to increase farm profitability. The SNP profile of 72 Nelore (32 HFC and 40 LFC) and 48 Angus heifers (21 HFC and 27 LFC) was determined using high-density SNP chip (BovineHD Illumina). Initial data cleanup was performed to remove poorly performing and nonautosomal probes from the analysis, considering as criteria for SNP or samples exclusion minor allele frequencies >0.02, call rates >0.98, significant deviations from Hardy-Weinberg equilibrium with P < 10^{-5} and samples with call rate <0.90. Fast score test (qtscore) method, equivalent to the Armitage test, was used for case–control comparisons (GenABEL package). A total of 181 SNPs from the Nelore heifers and 201 from the Angus heifers met genome wide significance (P < 10^{-5}). These SNP were genotyped on 47 purebred Angus, Braford, and Brahman bulls on a forage based performance bull test. The mixed model traits included average daily gain, birth weight, weaning weight, hip height, and back fat. These SNP were genotyped on 47 purebred Angus, Braford, and Brahman bulls on a forage based performance bull test. The measured traits included average daily gain, birth weight, weaning weight, hip height, intramuscular fat (IMF), ribeye area (REA), and scrotal circumference (SC). The mixed model procedure of SAS was utilized to evaluate associations of the 49 SNPs and measured traits. Associations were reported as significant if P < 0.05 and as a trend if P < 0.1. Seven SNP exhibited a trend for ADG (rs109022910, rs109199979, rs110266103, rs132665612, rs132951819, rs109327701 and rs110959643). No SNP for BW were significantly associated; however, 3 SNP (rs109327701, rs136939207, and rs137140434) displayed a trend. For finwt, 2 SNP (rs109275907 and rs132951819) were of significant and 7 SNP (rs109022910, rs109199979, rs109327701, rs110266103, rs110959643, rs132665612, and rs133980322) displayed a trend. Hip height and SC were both significantly associated with 1 SNP (rs133980322). Intra muscular fat exhibited a trend with 3 SNP (rs132951819, rs139380322, and rs137651874). No significant associations for REA were identified while 6 SNP (rs109022910, rs109199979, rs110266103, rs110959643, rs132665612, and rs137651874) displayed a trend. In total, one SNP within the GH1 gene was significantly associated with finwt, and 2 SNP within the IGF-1 gene were significantly associated with finwt, HH, and SC. Eleven different SNPs displayed trends associated with ADG, BW, finwt, HH, IMF, REA, and SC. The objectives were to estimate the fractions of additive genetic variances for 4 postweaning feed efficiency and growth traits explained by 40,276 actual and imputed SNP genotypes, to compare EBV rankings from genomic-polygenic (GP), genomic (G), and polygenic (P) models, and to

**Key Words:** cattle, growth trait, carcass

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The objective of the current study was to evaluate the association of single nucleotide polymorphisms (SNP) on 3 candidate genes for growth and performance traits in bulls participating in forage based performance bull test. Single nucleotide polymorphisms on 3 candidate genes including calpastatin (CAST), growth hormone (GH1), and insulin-like growth factor 1 (IGF-1) were utilized for association analysis. Single nucleotide polymorphisms were selected that were evenly distributed and represented the total length of the candidate gene. Of the 49 SNP genotyped, 20 were chosen for CAST, 9 for GH1, and 20 for IGF-1. These SNP were genotyped on 47 purebred Angus, Braford, and Brahman bulls on a forage based performance bull test. The measured traits included average daily gain, birth weight, weaning weight, hip height, intramuscular fat (IMF), ribeye area (REA), and scrotal circumference (SC). The mixed model procedure of SAS was utilized to evaluate associations of the 49 SNPs and measured traits. Associations were reported as significant if P < 0.05 and as a trend if P < 0.1. Seven SNP exhibited a trend for ADG (rs109022910, rs109199979, rs110266103, rs132665612, rs132951819, rs109327701 and rs110959643). No SNP for BW were significantly associated; however, 3 SNP (rs109327701, rs136939207, and rs137140434) displayed a trend. For finwt, 2 SNP (rs109275907 and rs132951819) were of significant and 7 SNP (rs109022910, rs109199979, rs109327701, rs110266103, rs110959643, rs132665612, and rs133980322) displayed a trend. Hip height and SC were both significantly associated with 1 SNP (rs133980322). Intra muscular fat exhibited a trend with 3 SNP (rs132951819, rs139380322, and rs137651874). No significant associations for REA were identified while 6 SNP (rs109022910, rs109199979, rs110266103, rs110959643, rs132665612, and rs137651874) displayed a trend. In total, one SNP within the GH1 gene was significantly associated with finwt, and 2 SNP within the IGF-1 gene were significantly associated with finwt, HH, and SC. Eleven different SNPs displayed trends associated with ADG, BW, finwt, HH, IMF, REA, and SC.

**Key Words:** forage performance bull test, SNP

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**T202** Genomic-polygenic evaluation of multibreed Angus-Brahman cattle for feed efficiency and postweaning growth using actual and imputed Illumina 50k SNP genotypes. M. A. Elzo*,1, M. G. Thomas², C. A. Martinez³, G. C. Lamb⁴, D. D. Johnson¹, I. Misztal¹, D. O. Rae¹, J. G. Wasdin¹, and J. D. Driver¹, 1University of Florida, Gainesville, 2Colorado State University, Fort Collins, 3University of Georgia, Athens.

The objectives were to estimate the fractions of additive genetic variances for 4 postweaning feed efficiency and growth traits explained by 40,276 actual and imputed SNP genotypes, to compare EBV rankings from genomic-polygenic (GP), genomic (G), and polygenic (P) models, and to
T204 Genetic variants and genetic parameters of feed efficiency from univariate and multivariate analyses.


Average daily gain (ADG) and dry matter intake (DMI) are two main components of feed efficiency in beef cattle. Univariate analysis of these components hinders the ability to evaluate the genetic correlation between them, the identification of genomic variants with pleiotropic effects on both components, and could result in lower statistical power. The goals of this study were to assess the genetic variation and co-variation of ADG and DMI and to identify single nucleotide polymorphisms (SNPs) associated with these traits using multivariate analyses, and to compare the results to univariate analyses. Records from 1,321 feedlot steers across 5 farms and 4 years were analyzed. The steers pertained to one of 5 crosses between Angus and Simmental and received one of 5 diets. Univariate and bivariate animal models including the fixed effects of crossbreeding, diet, contemporary group, age and the random effect of animal were used to estimate the genetic parameters using Wombat. Similar univariate and multivariate models including a fixed SNP effect were evaluated using Qxpak and a univariate linear model including all fixed effects was evaluated in PLINK. The heritability estimates (and standard errors) for ADG and DMI were 0.14 (0.06) and 0.24 (0.08), respectively and the genetic correlation was 0.30 (0.11). Seven SNPs were associated with ADG (P-value <0.0001) in the linear fixed effects model. Genes containing or in the proximity of the SNPs detected have functions associated with growth including calmodulin regulated spectrin-associated protein 1-like 1 (CAMSP1L1), Kruppel-like factor 6 (KLF6), Fanci anemia, complementation group F (FANCF) and pseudo gene fucosidase α-L-1 tissue-like (Fuca1, LOC100140646). The bivariate mixed-effects analysis identified the highest number of variants (11 SNPs) and the DMI and ADG mixed effects analyses identified 9 and 8 associations, respectively. The total number of SNP detected was 28, mapping to 19 unique SNPs and 9 unique genes. These results can help in the identification of variants with favorable effect on both components of feed efficiency in beef cattle.

Key Words: SNP, heritability, multi-trait analysis

T205 Accuracy of genomic predictions in Nelore cattle with different marker densities.


The objective of this study was to investigate the improvement in accuracies of genomic predictions associated with increasing the number of markers from 50,000 (50K) to 770,000 (770K) in the Brazilian Nelore breed. Expected progeny differences (EPD) for growth, reproductive, carcass, and conformation traits were available in the study. All animals genotyped with the BovineSNP50 BeadChip were imputed to 770K using FImpute software based on a reference data set with 763 records associated with these traits using multivariate analyses, and to compare the results to univariate analyses. Records from 1,321 feedlot steers across 5 farms and 4 years were analyzed. The steers pertained to one of 5 crosses between Angus and Simmental and received one of 5 diets. Univariate and bivariate animal models including the fixed effects of crossbreeding, diet, contemporary group, age and the random effect of animal were used to estimate the genetic parameters using Wombat. Similar univariate and multivariate models including a fixed SNP effect were evaluated using Qxpak and a univariate linear model including all fixed effects was evaluated in PLINK. The heritability estimates (and standard errors) for ADG and DMI were 0.14 (0.06) and 0.24 (0.08), respectively and the genetic correlation was 0.30 (0.11). Seven SNPs were associated with ADG (P-value <0.0001) in the linear fixed effects model. Genes containing or in the proximity of the SNPs detected have functions associated with growth including calmodulin regulated spectrin-associated protein 1-like 1 (CAMSP1L1), Kruppel-like factor 6 (KLF6), Fanci anemia, complementation group F (FANCF) and pseudo gene fucosidase α-L-1 tissue-like (Fuca1, LOC100140646). The bivariate mixed-effects analysis identified the highest number of variants (11 SNPs) and the DMI and ADG mixed effects analyses identified 9 and 8 associations, respectively. The total number of SNP detected was 28, mapping to 19 unique SNPs and 9 unique genes. These results can help in the identification of variants with favorable effect on both components of feed efficiency in beef cattle.

Key Words: SNP, heritability, multi-trait analysis

T203 Genetic parameters and single nucleotide polymorphism of feed utilization in beef cattle.


Three widely used indicators of feed utilization, residual feed intake (RFI), residual average daily gain (RADG), and residual intake gain (RIG) place different weights on the 2 main components of the system, input and output. Variation in intake and growth are at the center of RFI and RADG, respectively meanwhile RIG is an index of both indicators. The previous differences are expected to affect the total genetic variation and specific single nucleotide polymorphisms (SNPs) corresponding to each indicator. The aim was to estimate the genetic variation and co-variation of the 3 feed efficiency indicators and to uncover SNPs associated with these indicators that could explain the genetic variation. Phenotypic and genotypic measurements were available on approximately 1,300 Angus, Simmental and crossbred steers, assigned to 5 feeding treatments. The pedigree matrix included 3331 individuals across 3 generations. A model including a random animal effect and the fixed effects of breed composition, treatment, contemporary group, and age was implemented in Wombat to estimate the genetic parameters. The fixed effect of genotype was added to the model and fitted on a per-SNP basis using Qxpak. The heritability estimates (standard errors) for RFI, RADG and RIG were 0.40 (0.10), 0.17 (0.07), and 0.40 (0.10), respectively and the genetic correlation were −0.43 (0.09), −0.99 (0.002) and 0.55 (0.08) for RFI with RADG, RFI and RIG, and RADG and RIG, respectively. Seven, 9, and 8 SNP were associated (P < 0.0001) to RFI, RADG and RIG, respectively. The RFI SNPs were anotated to genes containing Ciliary neurotrophic factor receptor (CNTFR) and Transmembrane protein 40 (TMEM40). The RADG SNPs were associated to genes including KDEL Lys-Asp-Glu-Leu containing 1-like (KDELCL2), ELMO/CED-12 domain containing 1 (ELMOD1), and PAK1 interacting protein 1 (PAK1IP1). The RIG SNPs were also annotated to KDELCL2. In total, 24 SNP on 5 genes were associated with the 3 indicators. The genetic parameter and SNP estimates can support genome-enabled selection programs to improve feed utilization in the beef cattle industry.

Key Words: feed efficiency, genetic parameter, SNP

Sixty percent of the animals with the highest accuracy EPDs for each individual trait comprised training data sets, and the remaining animals were used for validation. Marker effects were estimated using BayesC as implemented in Gense software. The training data set was clustered into 5 groups based on genotype similarity using an identical-by-descent strategy. Estimated marker effects were used to calculate direct genomic values (DGVs). A 5-fold cross validation was performed on the training data set. The average correlations across all traits, between DGVs and EPDs obtained with 50K, 770K and 770K, trait were 0.50, 0.50 and 0.59, respectively for the cross-validation, and 0.63, 0.63 and 0.62, respectively, for the external validation. Cross-validation correlations were higher when markers were pre-selected. However, the correlations observed for individual traits in the external validation were similar for 50K, 770K and 770K, trait data sets. The results demonstrate that increasing marker density from 50K to 770K did not improve genomic prediction accuracies as measured by correlations between DGVs and EPDs, supporting published results in dairy populations.

**Key Words:** Nelore, HD genotype, prediction accuracy

**T206** Genomic evaluation and identification of a haplotype affecting fertility for Ayrshire dairy cattle. T. A. Cooper*, G. R. Wiggans, D. J. Null, and J. L. Hutchison, Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD.

Genomic evaluation of dairy cattle in the United States has been available for Holstein, Jersey and Brown Swiss since 2009. As of February 2013, there were 1,100 genotyped Ayrshires in the North American database including 646 bulls with traditional evaluations allowing for the evaluation of this breed. Gains in reliability due to genomics were determined by comparing parent averages and genomic evaluations from August 2008 to January 2013 daughter performance for bulls born on or after January 1, 2000 who received a traditional evaluation by January 2013. The number of bulls tested ranged between 147 and 180 bulls by trait. The average gain in reliability over parent average for all traits was 8.2. The highest gains were found in milk yield (16.6), protein yield (16.9) and stature (16.2). These evaluations were calculated based on the North American population and may not be suitable to all red dairy cattle because linkage disequilibrium probably differs by population. There are 12 SNP in Ayrshire that can be used for breed determination because they are nearly monomorphic (>90%) in Ayrshire and have fewer than 30% of animals homozygous for that allele in Holstein, Jersey and Brown Swiss. There are fewer breed determining SNP in Ayrshire than in Holstein, Jersey and Brown Swiss, mostly due to the similarity of Ayrshire and Holstein. A haplotype affecting fertility was located on chromosome 17. This haplotype first originated in the genotyped population with Selwood Betty’s Commander (b. 1953). The carrier frequency for genotyped haplotype first originated in the genotyped population with Selwood A haplotype affecting fertility was located on chromosome 17. This haplotype and Brown Swiss, mostly due to the similarity of Ayrshire and Holstein. Jersey and Brown Swiss. There are fewer breed determining SNP in Ayrshire than in Holstein, Jersey and Brown Swiss, mostly due to the similarity of Ayrshire and Holstein. 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**Key Words:** dairy cattle, genomic evaluation, fertility haplotype

**T207** Regression metamodels of an optimal genomic testing strategy in dairy cattle when selection intensity is low. A. De Vries*1, J. B. Cole2, and D. T. Galligan3. 1University of Florida, Gainesville, 2Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD, 3University of Pennsylvania, Kennett Square.

Genomic testing of dairy cattle increases reliability and can be used to select animals with superior genetic merit. Genomic testing is not free and not all candidates for selection should necessarily be tested. One algorithm used to compare alternative genomic testing decisions is time-consuming and not easily applicable in practice. Therefore, the objective of this study was to develop regression metamodels that predict increases in estimated breeding value (EBV) of net merit (SNM) in selected animals based on the reliability of pre-ranking of animals, reliability of the genomic test, proportion of animals that are genetically tested, and selection intensity. First, the increase in EBV SNM in selected animals (>50% of the population) was calculated using Monte Carlo methods when all animals were pre-ranked for EBV SNM with reliabilities varying from 0 to 100% in increments of 10 percentage points (PP). After pre-ranking all animals, the genomic test was applied to all ranges of pre-ranked animals in 10 PP increments (n = 36,300 scenarios). Selection was applied after the second ranking and the gain in EBV SNM was recorded. For example, gain in EBV SNM with 20% pre-ranking reliability, testing the 60 to 90 percentiles of the pre-ranked animals, 60% genomic test reliability, and 90% selection intensity was $80. Second, the SAS procedure glmselect was used to develop regression metamodels that predict gain in EBV SNM given 30 variables constructed from reliabilities, ranges of genetically tested animals, selection intensity and their logs, squares and reciprocals. Models constrained to 5, 10, 20, or 40 variables including 2-way interactions had RMSE of $14.90, $10.98, $6.47 and $5.11, respectively. The R-squared ranged from 94.4% to 99.4%. The same 4 models including 4-way interactions had RMSE of $12.20, $6.61, $3.62, and $2.45. The R-squared ranged from 96.3% to 99.9%. In conclusion, the larger metamodels accurately predicted gain in EBV SNM and can easily be implemented in decision support aids. The cost of genomic testing may be added to find the optimal range of pre-ranked animals that should be genomically tested.

**Key Words:** genomics, reliability, regression

**T208** Prioritizing sequence polymorphisms for potential association with phenotype. W. M. Snelling1, G. L. Bennett1, R. M. Thallman1, A. K. Lindholm-Perry1, L. A. Kuehn1, T. G. McDaniel1, S. D. Kachman1, M. L. Spangler2, H. Koshinsky1, and T. S. Kalbfleisch1,5. 1USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, 2University of Nebraska, Lincoln, 3Eureka Genomics Inc., Hercules, CA, 4Intrepid Bioinformatics, Louisville, KY, 5University of Louisville, Louisville, KY.

The millions of SNP, insertions and deletions revealed by next generation sequencing (NGS), are certain to include polymorphisms responsible for phenotypic variation. Distinguishing causal from benign variants may allow genomic predictions that are robust across populations. While variants underlying phenotypic variation may never be known with certainty, classifying NGS variants according to expected effects on gene function may reveal likely candidates. Associations between phenotypes and available genotypes of markers flanking each variant may further indicate those likely to affect phenotype through altered gene function. Low-coverage NGS of 96 sires used in a 7-breed population of crossbred beef cattle revealed 10,028,578 variants. 1,309 were classified as having a high impact on protein coding genes, and 1,503 occurred in non-coding RNA, which may regulate protein coding genes. Potential impact of these variants on birth weight was assessed using 2,940 birth weight records from the 7-breed population, 3,812 records from a somewhat related 16-breed population, and imputed high-density SNP genotypes for both populations. Genomic heritability estimates (SE) in the 7-breed population were 0.38 (0.03) with 3,810 SNP flanking the high-impact and non-coding RNA variants, 0.25 (0.02) with 291 SNP surrounding 217 variants with the largest flanking SNP effects, 0.64 (0.03) with the full set of high-density SNP, and 0.38 (0.05) for the 300 high-density
SNP with the largest effects. Genetic correlations between 16-breed birth weights and genomic EBV predicted from 7-breed SNP effects were 0.42 (0.05) for the 3,810 SNP and 0.58 (0.05) for the 291 SNP around selected variants. Estimated birth weight-genomic EBV genetic correlations were 0.51 (0.04) for all high-density SNP and 0.48 (0.05) for the top 300. Genomic predictions with SNP flanking variants affecting gene function may be more robust than predictions based only on associations with phenotype. Further assessment of direct genotypes for the functional variants is needed. USDA is an equal opportunity provider and employer.

Key Words: cattle, DNA sequence variant, genomic prediction

T209 Accuracy of mixed model methods for genomic prediction and variance component estimation of additive and dominance effects using SNP markers. S. Wang, G. Hu*, C. Wang, and Y. Da, Department of Animal Science, University of Minnesota, St. Paul.

The accuracy of GREML and GBLUP methods for additive and dominance effects were evaluated using simulation data for various heritability levels of additive and dominance effects. SNP marker sets included 1K causal variants, 1K, 3K and 7K inter-QTL SNP markers, and 41K SNP marker with minor allele frequency > 0.05 including the 1K causal variants. Genomic additive and dominance relationship matrices using SNP markers were consistent with theoretical expectations. GREML and GBLUP using genome-wide SNP markers were able to capture small additive and dominance effects each accounted for 5 \(10^{-5}\)–3 \(10^{-5}\) of the phenotypic variance. Accuracy of GREML and GBLUP increased as the heritability increased for both additive and dominance effects. GBLUP of total genetic values as summation of breeding values and dominance deviations had higher accuracy breeding values or dominance deviations. GREML was more sensitive than GBLUP to the true additive and dominance heritability levels and to the density of SNP markers. Low density of non-causal SNP markers (3K or less) had a tendency to underestimate additive and dominance variance components by GREML. The 41K that included the 1K causal variants overestimated the variance components for the phenotype with 1006 underlying QTL and performed better for the phenotype with 100 underlying QTL than lower density inter-QTL SNPs. Causal variants had the highest accuracy of GREML and GBLUP and adding whole genome SNP markers to the causal variants did not improve accuracy.

Key Words: genomic prediction, variance component, dominance

T211 Accounting for heterogeneous pleiotropy in whole genome selection models. N. M. Bello*, J. P. Steibel1, and R. J. Tempelman2, 1Kansas State University, Manhattan, 2Michigan State University, East Lansing.

The additive genetic correlation between economically relevant traits is generally considered a critical factor determining the relative advantage of multi-trait models over single-trait models for whole genome prediction of genetic merit. Yet, the additive genetic correlation between traits may be considered an aggregate summary of between-trait correlations at the individual QTL level, thereby defining pleiotropic mechanisms by which individual genes have simultaneous effects on multiple phenotypic traits. Pleiotropic effects, in turn, may be gene specific and heterogeneous across the genome. In this study, we present a hierarchical Bayesian extension to bivariate genomic prediction models that accounts for heterogeneous pleiotropic effects across SNP markers. More specifically, we elicit a function of the SNP marker-specific correlation between traits as heterogeneous across markers following a square-root Cholesky reparameterization of the marker-specific covariance matrix that ensures necessary positive semidefinite constraints. We use simulation studies to demonstrate the properties of the proposed methods. We assess the relative performance of the proposed method by comparing prediction accuracy for genomic breeding values and for SNP marker effects for each of 2 traits across putative scenarios of homogeneous and heterogeneous pleiotropic genetic mechanisms. We also consider extensive model comparisons for cases of null and non-null additive genetic correlations under conditions of high and low heritability of the traits of interest. Overall, the relative advantage of genomic prediction bivariate models that account for heterogeneous pleiotropy relative to their univariate counterparts depended upon trait heritability and genetic architecture of the pleiotropic mechanisms and was of small magnitude (~1% net gain in predictive accuracy) when at all present. The trade-off between methodological and computational modeling complexity and net gain in prediction accuracy is also discussed.

Key Words: genomic evaluation, unknown parent group

T210 Bias in genomic evaluations attributable to unknown parent group estimates. S. Tsuruta*, D. A. L. Lourenco, and I. Misztal, University of Georgia, Athens.

The objective of this study was to investigate bias in genomic evaluations due to unknown parent group estimates. Genomic (G)BLUP was predicted for final score in US Holsteins, 305-d milk yields in 3 parities in Israeli Holsteins, and multiple traits in pigs, using genomic and phenotypic combined data. The US Holstein data consisted of 10,167,604 records for 884,250 pigs and 906,660 animals in pedigree including 4853 genotyped animals with 63,219 SNP. Original unknown parent groups (UPG) were defined based on year of birth by sex, year of birth by sex by breed, and year of birth for US Holstein, Israeli Holstein, and pig data, respectively. Genomic (G)EBV and UPG estimates were compared using original and refined UPG and separating additive genetic effects into those with UPG from pedigree and those without UPG from genotypes. The BLUP90IOD program using a single-step approach was used to estimate UPG effects and GEBV. The last UPG effect for US Holstein was significantly overestimated. The last UPG effects for Israeli Holstein bulls were overestimated. The UPG estimates in pigs were similar in original and refined UPG. For US Holstein, Israeli Holstein, and pig data sets, correlations between GEBV from original and refined UPG models were 0.99, 0.95–9.97, and 0.97–0.99, respectively. Those correlations between GEBV from original and 2 additive models were 0.91, 0.91–0.93, and 0.96–0.98, respectively. Refinement of UPG improved convergence in GBLUP by 4%, 55%, and 35% for US Holstein, Israeli Holstein, and pig data sets, respectively. Refinement of UPG is recommended to reduce bias in GEBV and improve computing speed in GBLUP.

Key Words: genomic evaluation, unknown parent group