T196 Genome-wide association study of cholesterol and poly- and monounsaturated 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 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 incuding a chain length of 150,000 samples with the first 50,000 being discarded as burn-in. In general, there was strong agreement between the posterior heritability estimates between the 2 cuts for all traits. The resulting posterior heritability (SE) estimates were 0.46(0.11), 0.52(0.06), 0.67(0.06), 0.71(0.08), 0.61(0.07), and 0.43(0.10) for eye CH, strip CH, eye PUFA, strip PUFA, eye MUFA, and strip MUFA, respectively. SNP were blocked into 1 Mb windows and the top 0.5% windows (n = 13) were compared across cuts within a trait. Of the windows in common between the 2 cuts for MUFA, 5 were on BTA2 and one on BTA19 (7–8 Mb). For PUFA, all 8 windows in common were on BTA2 and the one window in common for CH was also on BTA2. The influence of regions on BTA2 suggest that the Myostatin mutation (C313Y) segregating in some of these animals influences CH, MUFA and PUFA content of beef.

Key Words: beef cattle, genome-wide association study, fatty acids

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 nutrent 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 incuding a chain length of 150,000 samples with the first 50,000 being discarded as burn-in. In general, there was strong agreement between the posterior heritability estimates between the 2 cuts for all traits. Posterior heritability estimates (SE) were 0.67(0.08), 0.75(0.06), 0.38(0.13), 0.33(0.09), 0.73(0.08), 0.64(0.08), 0.13(0.08), and 0.05(0.08) for strip protein, eye protein, strip iron, eye iron, strip potassium, eye potassium, strip sodium, and eye sodium, respectively. SNP were blocked into 1 Mb windows and 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

T198 Association between single nucleotide polimorphisms and sexual precocity in Nellore heifers. I. C. Regatieri[1,3], R. Espigolan[1,3], R. B. Costa[1,3], F. Baldi[1], and L. G. Albuquerque*[1,2], *[1]Universidade Estadual Paulista (UNESP) - FCAV, Jaboticabal, SP, Brazil, [2]Conselho Nacional de Desenvolvimento Cientifico e Tecnologico(CNPq), Brasilia, DF, Brazil, [3]Fundacao de Amparo a Pesquisa do Estado de Sao Paulo (FAPESP), Sao Paulo, SP, Brazil.*

Reproductive traits, such as age at first calving (AFC) and occurrence of early pregnancy (OP), are used as selection criteria in beef cattle breeding programs since these traits affect production system profitability. The measure (r^2) of linkage disequilibrium (LD) is used in genome-wide association studies to detect genetic markers and major genes (QTL) that influence economically important traits. The aim of this study was to determine the extent of LD in the genome of Nellore cattle, and examine associations between single nucleotide polymorphisms (SNP) and AFC and OP, using a panel of high-density SNPs. Data from 1,182 Nellore born in 2007 and 2008, belonging to Agropecuaria Jacarezinho were used. A total of 13 contemporary groups (CG) consisting of farm, season and year of birth, with an average of 90 animals per CG were formed. For genomic-wide association, only autosomes were used and SNPs with minor allele frequency (MAF) below 0.05, and animals with Call Rate below 0.90 were excluded, totaling 431,885 SNPs. The model of analysis for both traits, AFC and OP, included the CG and SNPs (0, 1 and 2) as fixed effects. The Bonferroni correction was applied to adjust the limit of significance (1.16×10^{-7}). The average r^2 for all autosomes was 0.18 at a distance of 4.8 kb and the average MAF was 0.25 ± 0.13. The LD decreased as the distance between markers increased: 0.35 (1 kb) to 0.12 (100 kb). Eleven SNP showed significant effects on the traits and were distributed in 7 different chromosomes (BTA1, BTA4, BTA6, BTA11, BTA17, BTA21, and BTA22). Among these, 7 SNPs were associated with AFC and 4 with OP. Three SNPs were significant for both traits (BTA1, BTA21, and BTA22). Chromosome BTA21 showed 2 SNPs associated with OP. A total of 19 chromosomes showed potential QTL regions for AFC and OP. The most evident peaks of significant SNPs, that may suggest potential QTL regions, were located on chromosomes BTA4, BTA6, BTA8, BTA17, and BTA19.

Key Words: genome-wide association, linkage disequilibrium, quantitative trait loci

T199 Genome-wide associations study for Nelore and Angus Heifers with low and high ovarian follicle count. M. G. Favoreto*[1], B. Loureiro[1], R. L. Ereno[1], A. G. Pupulim[1], A. S. Carmo[2], J. Buratini[1],

and C. M. Barros[1], *[1]UNESP - Universidade Estadual Paulista, Botucatu, SP, Brazil, [2]DEOXI biotecnologia, Araçatuba, SP, Brazil.*

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 compare 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 ($P < 10^{-4}$). The 181 SNPs from the Nelore heifers were associated on 23 different BTA chromosomes (UMD v3.1 assembly) and the 10 most significant SNPs ($P < 9.8 \times 10^{-5}$) were detected on BTA 1, 3, 7, 9, 14, 16 and 22. In the Angus population the 201 SNPs were associated on 29 different chromosomes and the highest significant SNP ($P = 1.2 \times 10^{-5}$) were located on BTA 3. This is the first time a high density SNP chip is used to identify polymorphisms in high and low follicle counts Nellore and Angus heifers. Results show biomarkers that can contribute to identification of animals with HFC. More analysis must be performed to determine which genes associated with reproduction are linked with those SNPs. This research was financed by FAPESP grant number 2011/5964-0. Scholarships for Loureiro, Ereno, Favoreto, and Pupulim were from FAPESP.

Key Words: GWAS, follicle, SNP

T200 An SNP association study evaluating modern Charolais sired calves versus multigenerational Angus sired calves for growth and carcass traits. J. Bailey*, M. S. Mizell, A. Canal, T. R. Howard, R. Hill, T. Page, and M. D. Garcia, *Louisiana State University, Baton Rouge.*

The objective of this study is to evaluate the association of single nucleotide polymorphisms with growth, performance, and carcass quality and composition characteristics in a population of cattle consisting of multigenerational Angus sired calves and modern characteristic Charolais sired calves. Previous studies have consistently indicated considerable differences in the growth and carcass quality and composition traits between the Angus and Charolais breeds. The data collected in the current study included growth and performance traits as well as raw carcass measurements. Specifically, birth weight (BW), weaning weight (WW), hip height (HH), and average daily gain (ADG) were the growth traits collected. Carcass quality and composition traits that were collected included hot carcass weight (HCW), rib eye area (REA), back fat (BF), and marbling score (MARB). Two candidate genes were selected based on their previous associations with carcass and growth traits. These genes were the calpastatin (CAST) gene located on BTA7 and the calpain 3 (CAPN3) gene located on BTA10. A total of 40 SNP were utilized for genotyping and subsequent association analyses. Calves were genotyped for 20 single nucleotide polymorphisms located equidistant across the CAST gene and for 20 single nucleotide polymorphisms located equidistant across the CAPN3 gene. Analyses to evaluate potential SNP association were conducted via the mixed model procedure of SAS and the LSMEANS function was utilized to determine significant difference in performance for specific traits between genotypes. Multiple SNP for production and carcass quality and composition traits were identified as significant ($P < 0.05$) or exhibited a trend ($P < 0.1$) for both candidate genes. Thus, identification of SNP associated with production and carcass traits in the current study require validation in association with the use of more SNP in other cattle populations.

Key Words: cattle, growth trait, carcass

T201 SNP associated with growth and performance of yearling bulls on a forage performance bull test. T. R. Howard, M. S. Mizell, K. Harborth, M. Canal, A. Canal, K. Bondioli, T. Page, and M. D. Garcia*, *Louisiana State University, Baton Rouge.*

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, final 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). Intramuscular fat exhibited a trend with 3 SNP (rs132951819, rs133980322, 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

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. Thomas[2], C. A. Martinez[1], G. C. Lamb[1], D. D. Johnson[1], I. Misztal[3], D. O. Rae[1], J. G. Wasdin[1], and J. D. Driver[1], *[1]University of Florida, Gainesville, [2]Colorado State University, Fort Collins, [3]University 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

determine EBV trends from Angus to Brahman in a multibreed population. Traits were residual feed intake (RFI), daily feed intake (DFI), feed conversion ratio (FCR), and weight gain (PWG). Phenotypes were from 807 bull, heifer, and steer calves measured at the Feed Efficiency Facility of the University of Florida from 2006 to 2010. Imputation from 2,899 SNP (Illumina 3k) to 46,909 SNP (Illumina 50k) was done with program findhap2 using a reference population of 828 Brangus heifers. Fixed effects for all models were contemporary group (year-pen), age of dam, sex of calf, age of calf, Brahman fraction of calf, and heterozygosity of calf. Random effects were additive SNP (GP and G models), additive polygenic (GP and P models), and residual. Software GS3 was used to compute variance components and heritabilities (option VCE; Markov Chain Monte Carlo), and EBV (option BLUP). Heritabilities were 0.31 for RFI, 0.38 for DFI, 0.25 for FCR, and 0.34 for PWG. The fractions of additive genetic variances explained by the 46,909 actual and imputed SNP were 0.46 for RFI, 0.36 for DFI, 0.47 for FCR, and 0.28 for PWG. These fractions were 3.0, 3.2, 1.9, and 1.8 times larger than those obtained for these 4 traits using 2,899 SNP from the Illumina3k chip. Rank correlations between EBV from GP and P and from GP and G models were high (0.89 to 0.98; $P < 0.0001$). Lower rank correlations existed between EBV from G and P models (0.69 to 0.81; $P < 0.0001$). Regressions of EBV on Brahman fraction were negative with the G model for DFI ($P < 0.0344$) and with all models for PWG ($P < 0.0171$ to $P < 0.0001$). This suggested that calves of similar EBV for RFI, DFI and FCR existed in all breed compositions, but EBV for PWG tended to decrease as Brahman fraction increased.

Key Words: cattle, imputation, multibreed

T203 Genetic parameters and single nucleotide polymorphism of feed utilization in beef cattle. D. Gonzalez-Pena*, N. V. L. Serão, J. E. Beever, D. B. Faulkner, and S. L. Rodriguez-Zas, *University of Illinois at Urbana-Champaign, Urbana.*

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 annotated to genes including 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 (KDELC2), ELMO/CED-12 domain containing 1 (ELMOD1), and PAK1 interacting protein 1 (PAK1IP1). The RIG SNPs were also annotated to KDELC2. 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

T204 Genomic variants and genetic parameters of feed efficiency from univariate and multivariate analyses. C. Zavala*, N. V. L. Serão, D. González-Peña, and S. Rodriguez-Zas, *University of Illinois at Urbana-Champaign, Urbana.*

Average daily gain (ADG) and dry matter intake (DMI) are 2 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 pleiotrophic 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), Fanconi 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. P. Boddhireddy*[1], R. B. Lobo[2], K. Prayaga[1], P. Barros[1], and S. DeNise[1], *[1]Zoetis Inc., Kalamazoo, MI, [2]Technical Centre of Genetic Evaluation (CTAG), Ribeirão Preto, Brazil.*

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 genotyped with the BovineHD BeadChip (770K). Genomic calibrations were performed using: 50K; 770K; and trait specific (770K_trait) SNPs. Trait specific SNPs were included if they were significantly associated ($P < 0.05$) in single point association analysis. The total number of informative markers from 50K and 770K platforms were 26,458 and 492,887, respectively. The number of informative markers in the 770K_trait sets ranged from 100K to 200K depending on the trait.

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 Gensel 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 Ayrshires is 23.2%. Sire conception rate was 3.0% lower for carriers of the haplotype as determined by 483 carrier by maternal grandsire carrier matings. Genomic evaluations of Ayrshire provide improved prediction over parent average, raising reliability by 8.2 over all traits.

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. Cole[2], and D. T. Galligan[3], *[1]University of Florida, Gainesville, [2]Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD, [3]University 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 ($NM) in selected animals based on the reliability of pre-ranking of animals, reliability of the genomic test, proportion of animals that are genomically tested, and selection intensity. First, the increase in EBV $NM in selected animals (>50% of the population) was calculated using Monte Carlo methods when all animals were pre-ranked for EBV $NM 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 $NM was recorded. For example, gain in EBV $NM with 20% pre-rank 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 $NM given 30 variables constructed from reliabilities, ranges of genomically 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 $NM 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. Snelling*[1], G. L. Bennett[1], R. M. Thallman[1], A. K. Lindholm-Perry[1], L. A. Kuehn[1], T. G. McDaneld[1], S. D. Kachman[2], M. L. Spangler[2], H. Koshinsky[3], and T. S. Kalbfleisch[4,5], *[1]USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, [2]University of Nebraska, Lincoln, [3]Eureka Genomics Inc., Hercules, CA, [4]Intrepid Bioinformatics, Louisville, KY, [5]University 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^{-4}) 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

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 6,586,605 cows and 9,602,031 animals in pedigree including 34,506 genotyped bulls with 42,503 SNP; the Israeli Holstein data consisted of 1,205,801 records for 713,686 cows and 829,437 animals in pedigree including 1305 genotyped bulls with 30,359 SNP; the pig data consisted of 2,923,141 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

T211 Accounting for heterogeneous pleiotropy in whole genome selection models. N. M. Bello*[1], J. P. Steibel[2], and R. J. Tempelman[2], *[1]Kansas State University, Manhattan, [2]Michigan 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 selection, bivariate model, heterogeneous correlation