each trait. The APY algorithm may allow routine genomic evaluation for any number of genotyped animals with any model at a cost not much above BLUP.

Key Words: genome selection, genomic recursion, genomic relationship matrix

537 Effect of increasing the number of single nucleotide polymorphisms from 60,000 to 85,000 in genomic evaluation of Holsteins. George R. Wiggans*, Tabatha A. Cooper, Paul M. VanRaden, Curt P. Van Tassell, Derek M. Bickhart, and Tad S. Sonstegard, *Animal Genomics and Improvement Laboratory, Agricultural Research Service, USDA, Beltsville, MD.*

The periodic need to restock reagent pools for genotyping chips provides an opportunity to increase the number of single nucleotide polymorphisms (SNP) on a chip. As an improved replacement for the GeneSeek Genomic Profiler HD for dairy cattle, a set of >140,000 SNP was selected that included all SNP on the current chip, all SNP used in genomic evaluations, SNP that are possible functional mutations, and other informative SNP. Most added SNP were selected from the Illumina Bovine HD Genotyping BeadChip based on the magnitude of effects on evaluated traits. Some SNP with lower minor allele frequency were considered because of their potential for better tracking of causative variants. Genotypes already available from other chips were used to impute and evaluate the SNP set. Effects for 134,511 usable SNP were estimated for all breed-trait combinations; SNP with the largest absolute values for effects were selected (5,000 for Holsteins, 1,000 for Jerseys, and 500 each for Brown Swiss and Ayrshires for each trait), which resulted in 78,032 SNP after removing duplicates. An additional 9,130 SNP with many parent-progeny conflicts after imputation were removed, which resulted in 72,843 SNP. Of those, 38,515 were among the 60,671 SNP currently used in genomic evaluation. To minimize possible accuracy loss,12,094 of the SNP currently used but not already selected and with the largest effects were added for a total of 84,937 SNP. Three cutoff studies were conducted with 60,671, 84,937, and 134,511 SNP to determine gain in reliability over parent average when evaluations based on data from August 2011 were used to predict genetic merit from December 2014. Across all traits, mean gains were 32.5, 33.4, and 32.0 percentage points, respectively. Previous experience indicates that gains from the highest number of SNP will increase as the number of genotypes from the new SNP set increases. The gain of 0.9 percentage points from adding nearly 25,000 SNP justifies the extra computation time needed. However, the gain may be overestimated because data used to select the most informative SNP were also the data used to determine gain.

Key Words: dairy cattle, genomic evaluation, single nucleotide polymorphisms

538 Genome-wide association study of fertility traits in dairy cattle using high-density single nucleotide polymorphism marker panels. Kristen L. Parker Gaddis[1] and John B. Cole*[2], *[1]Department of Animal Sciences, University of Florida, Gainesville, FL, [2]Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD.*

Unfavorable genetic correlations between production and fertility traits are well documented. Genetic selection for fertility traits is slow, however, due to low heritabilities. Identification of single nucleotide polymorphisms (SNP) involved in reproduction could improve reliability of genomic estimates for these low heritability traits. Additionally, high-density marker panels can increase the power of resultant GWAS by providing increased coverage and stronger linkage disequilibrium between markers and causal variants. The objective of this study was to identify SNP associated with 3 fertility traits in dairy cattle, daughter pregnancy rate (DPR), heifer conception rate (HCR), and cow conception rate (CCR), using high-density marker panels. Deregressed predicted transmitting abilities were available for 10,000 bulls sampled from the National Dairy Database that had high-density genotypes. Of those, 725 had been genotyped with the Illumina BovineHD Genotyping BeadChip. The remaining bulls had genotypes from various chip densities that were imputed up to the same level. After editing, 312,614 markers were included in the analyses. Univariate analyses were performed for DPR, HCR, and CCR using REMLF90 (version 1.79) with genomic options. postGSf90 (version 1.170) was used to calculate SNP effects and 10-SNP window variances. The largest proportion of variance explained for DPR (0.126%) was located on chromosome 6. Peaks were also identified on chromosomes 5, 18, and 28 associated with DPR. For HCR, the region explaining the largest proportion of variance (0.155%) was located on chromosome 1. Large peaks were also identified for HCR on chromosomes 6, 8, 14, and 17. The largest proportion of variance explained for CCR (0.181%) was located on chromosome 18. Large peaks associated with CCR were also identified on chromosomes 6, 15, and 19. Numerous markers and regions aligned with those previously identified. Significant SNPs could be used in genomic selection programs as well as in identification of genes and networks involved with fertility.

Key Words: fertility, genomic evaluation, high-density genotype

539 Segment-based methods to calculate weights for weighted single-step GBLUP. Xinyue Zhang*, Daniela A. L. Lourenco, and Ignacy Misztal, *University of Georgia, Athens, GA.*

The purpose of this study was to explore additional options for calculating weights in weighted single-step GBLUP (WssGBLUP). In GWAS by ssGBLUP, GEBV are converted to marker (SNP) effects. Unequal variances for markers are then derived from SNP solutions and subsequently incorporated into a weighted genomic relationship matrix. Improvements on the SNP weights were obtained iteratively by recomputing both the SNP effects and the GEBV. Six options were used to calculate the weights: (1) proportional to u_i^2 where u_i is the effect of the i-th SNP; (2) proportional to u_i^2 + constant; (3) weights as $\nu^{|s-2|}$, where ν is a scale standing for the departure from normality, and *s* is number of standard deviation from mean for each u_i^2 where p_i is frequency of the second allele; (4) as the largest effect (u_i^2) among every 20 SNP; (5) as the mean effect of every 20 SNP; (6) as the summation of effects of every 20 SNP. A simulated data set was used that included 15,600 animals in 5 generations, of which 1,540 were genotyped for 50k SNP. The simulation involved phenotypes for a trait with heritability of 0.5 and affected by 5, 100, and 500 QTL. Accuracy between TBV and GEBV for genotyped animals in the last generation was used for evaluation. Comparisons also involved BayesB and BayesC with deregressed proofs or EBV from BLUP, and $\pi = 0.99$, 0.9 or 0.5. In single-step, SNP effects were tracked along 10 iterations and weights were equal to 1.0 in the first iteration. Option 5 was the best in identifying simulated QTL without background noise and with precision in most of the regions. Option 2 kept accuracy of GEBV at the plateau after 2 iterations and was 0.81 as opposed to 0.70 for BayesC and 0.48 for BayesB under 500 QTL scenario. All methods reached better accuracies than BayesB and BayesC when number of QTL approached or exceeded 100 (0.2% of all SNP) due to automatically including PA in GEBV. Weights based on a sum of SNPs may be superior to those based on individual SNPs.

Key Words: weighted SNP, single-step genomic BLUP (ssGBLUP), BayesB