relationship matrix (GRM), which had a high computing cost and required around 1 Tb of memory for this dataset. The algorithm for proven and young animals (APY) was used to approximate the inverse of the GRM. The number of core animals was set to 15,000, which was calculated as the number of eigenvalues of GRM explaining 99% of the variation. This algorithm reduced the memory usage to 40 Gb and required 10% of the computing time while slightly improving the accuracy. Another issue was the increase in computing time for calving ease evaluation, which uses a threshold model, from 12 h to 4.5 d. Resetting the preconditioned conjugate gradient iteration to solve the mixed model equations every 40 to 200 rounds helped decrease the time to 19 h. The inclusion of external EBV for Red Angus was required for evaluation of growth traits. We developed software to support genomic and external information, and the implementation of a genomic multibreed model increased the computing time only by 2.5 h. Current algorithm for approximation of accuracy of genomic EBV (GEBV) was too expensive for > 100,000 animals. A new algorithm was developed that does not require inverse of large GRM and accounts for multiple sources of information while avoiding double-counting. Correlations between accuracy from the new algorithm and true accuracy from PEV were higher than 0.85 for growth traits. Single-step GBLUP can be considered a mature methodology for commercial genomic selection in beef cattle.

Key Words: beef cattle, genomic selection

0304 Single-step GBLUP using APY inverse for protein yield in U.S. Holstein with a large number of genotyped animals. Y. Masuda*[1], I. Misztal[1], and P. M. VanRaden[2], [1]*University of Georgia, Athens,* [2]*Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD.*

The objective of this study was to provide initial results in an application of single-step genomic BLUP with a genomic relationship matrix (G^{-1}_{APY}) calculated using the Algorithm of Proven and Young (APY) to 305-d protein yield for U.S. Holsteins. Two G^{-1}_{APY} were tested; one was from 139,057 genotyped bulls with 12,895 core animals (APY140K) and the other one was from 764,029 genotyped animals with 12,913 core animals (APY760K). The predictor data set consisted of phenotypes recorded after 1989 and pedigrees limited to 3 generations back from recorded or genotyped animals. Genomic predictions (GPTA2011) were calculated for predicted bulls that had no recorded-daughters in 2011 but had at least 50 such daughters in 2015. We used the official daughter yield deviations published in 2015 (DYD2015) for the predicted bulls (N = 3797). We also used the official GPTA published in 2011 with a multistep method as a comparison, although official methods have improved since then. Coefficient of determination (R^2) and slope (b_1) were calculated from a linear regression of DYD2015 on GPTA2011. Using APY140K, the R^2 was 0.50 compared with 0.51 from the official GPTA. The b_1 was much better (0.98) compared with 0.81 from the official GPTA. With APY760K, the R^2 was 0.46 and b_1 was 1.08. Incorporating effect of a SNP related to DGAT1 increased R^2 to 0.51 for APY140K and 0.48 for APY760K. The decrease in R^2 with APY760K compared with APY140K could be due to inclusion of lower quality genotypes, or biases caused with the use of all genotypes with incomplete phenotypes. All the computations finished within 11 h including 4.2 h to set up APY-inverse with APY760K. Based on the linearity of the computation cost, using 1 million genotyped animals with the same model would require 14 h of computations. Single-step GBLUP can provide genomic predictions for all genotyped bulls and cows while accounting for pre-selection. Further research will determine the impact of various factors affecting the reliability such as validation methodology, weighting SNP markers, and quality of genotyped data.

Key Words: genomic evaluation, Holstein, ssGBLUP

0305 Heteroskedastic extensions for genome-wide association studies. Z. Ou*[1], R. J. Tempelman[2], J. P. Steibel[3,4], C. W. Ernst[3], R. O. Bates[3], C. Chen[3], and N. M. Bello[1], [1]*Department of Statistics, Kansas State University, Manhattan,* [2]*Michigan State University, East Lansing,* [3]*Department of Animal Science, Michigan State University, East Lansing,* [4]*Department of Fisheries and Wildlife, Michigan State University, East Lansing.*

Bayesian multiple regression models based on genomic marker information are commonly used for genomic prediction and selection and are being increasingly utilized in genome-wide association (GWA) analyses to search for genomic regions associated with economical important traits in agriculture. These models jointly fit all markers, thereby circumventing the limitations of "one-marker-at-a-time" of traditional GWA inference. We have recently validated and tested extensions of genomic prediction models to account for residual heteroskedasticity, which is prevalent in livestock field data. Our objective was to evaluate the impact of not accounting for potential residual heteroskedasticity in GWA inference. Using simulated data scenarios that reflected a gradient of increasing residual heteroskedasticity, we fitted homoscedastic and heteroskedastic error versions of hierarchical Bayesian genomic prediction models assuming either normal (RR-BLUP) or heavy-tailed (BayesA) prior specifications on the effects of genomic markers. For each marker, we then constructed a posterior z-score using prediction error variance of the estimated marker effect to detect associations between genomic regions and phenotypes of interest. Under conditions of extreme heterogeneity of residual variances, heteroskedastic models showed an increase in power of up to 10% points for GWA discovery with little impact on false positive rate (i.e., change of 0 to 3% points), compared with the homoscedastic model counterparts.