**SUMMARY**

The objectives of this research were to compare variance components, genetic parameters and EBV rankings using genomic-polygenic and polygenic models for birth weight (BW) direct and maternal, and postweaning gain (PmG) direct and maternal. It was hypothesized that 1) additive direct genetic effects were higher for BW direct and maternal, and PmG direct and maternal when using genomic-polygenic models and 2) to compare rankings of animals for birth weight direct and maternal, and postweaning gain direct using genomic-polygenic and polygenic models. For BW direct and maternal, and PmG direct and maternal, variance components and genetic parameters were estimated for all growth traits. Variance components were estimated using REML procedures with an average information derivative over the genotyped animals. Genetic parameter estimates were calculated with the inverse of the average information matrices. Standard deviations of 1000 samples were computed for variances of family relationships (Meyer and Houle, 2013). Estimated breeding values (EBV) were computed using the predicted breeding values (PBVs) from the genomic-polygenic model (GPM1, GPM2, GPM3) and genomic model (PM) and were distributed to all genotyped bulls, heifers, and steers. Comparisons of EBV from the four models were assessed using rank correlations. In addition, agreement for additive direct genetic effects and a dismal performance for maternal genetic effects is likely occurring in calves, as EBV differences were very low in all models indicating that genomic-polygenic models outperformed polygenic models for the top 5%, 10%, 25%, and all evaluated animals across all traits.

**Tissue Sampling and Genotyping**

Tissue samples (blood, semen) from 1,223 Brahman bulls and 1,110 Angus bulls were genotyped at the University of Florida from 2006 to 2010. There were samples from 161 parents (20 sires and 141 dams) from the smartphone genotype (PM), and 2,860 progeny (1,360 bulls, 1,500 heifers) were born from 1987 to 2013. Genomic-polygenic models (GPM1, GPM2, GPM3) were used to estimate variance components and genetic parameters. Tissue samples were processed and stored at -80 °C at New Mexico State University. Samples were genotyped using the Illumina 1M genotyping beadchip. Imputation was performed by snipSNP2 software (Li et al., 2010), and additional of vitamin-phosphate-buffered saline up to a volume of 1.0 mL. Tissue samples were recovered from 106 animals from the University of Florida (Lincoln, NE, USA) in 2010 for genotyping with the Illumina Mineland beadchip.

**Variances Component, Variance Ratios, and EBV**

Three genomic-polygenic models (GPM) and a polygenic model (PM) were used to obtain variance component estimates and breeding values for BW direct, BW maternal, PmG direct, PmG maternal, and BW and PmG direct. The three multiplicative genomic-polygenic models were: 1) GPM1, a single-step model (Aguirre et al., 2010) with genomic information and pedigrees among all animals; 2) GPM2, a single-step model with genomic information and imputation among all animals; and 3) GPM3, a single-step model with genomic information and pedigrees among all animals and imputation. The fixed effects for the three genomic-polygenic models and the three polygenic models were: 1) contemporary group (location-year for BW and PmG direct); 2) sex; 3) age; 4) days of gestation (D.O.G); 5) birth weight (BW); and 6) dam weight. Variance components were estimated using REML procedures with an average information derivative over the genotyped animals. Genetic parameter estimates were calculated with the inverse of the average information matrices. Standard deviations of 1000 samples were computed for variances of family relationships (Meyer and Houle, 2013). Estimated breeding values (EBV) were computed using the predicted breeding values (PBVs) from the genomic-polygenic model (GPM1, GPM2, GPM3) and genomic model (PM) and were distributed to all genotyped bulls, heifers, and steers. Comparisons of EBV from the four models were assessed using rank correlations.

**RESULTS AND DISCUSSION**

Estimates of additive genetic variances and covariances from the genomic polygenic model 1 were on the average, slightly larger than those from the polygenic model. The genomic information had little effect on estimates of variance components for growth traits in this dataset. For BW maternal, the EBV from the genomic-polygenic model 2 and from all estimations were not different. The largest differences were observed among EBV from the four models was assessed using rank correlations.

The opposite occurred for environmental variances and covariances across models (Table 3). Estimates of environmental variances for BW, BW maternal, and PmG maternal across all models were higher when using genomic-polygenic models than the polygenic model (mean difference = 2.32 kg²), and higher for genomic-polygenic models 2 (mean difference = 23.3 kg²) and 3 (mean difference = 46.33 kg²) than from the polygenic model (mean difference = 12.56 kg²). Estimates of phenotypic variances and covariances (Table 4) followed the same pattern as those for genetic variances and covariances. Variance components and genetic parameters for BW, BW maternal, and PmG maternal from genomic-polygenic models 2 and 3 were similar to those obtained in the polygenic model. Estimates of phenotypic variances and covariances for BW, BW maternal, and PmG maternal from genomic-polygenic models 2 and 3 were very similar, those from genomic-polygenic model 3 were similar to those obtained in the polygenic model (mean difference = -11.92 kg²) and those from genomic-polygenic model 2 (mean difference = -12.56 kg²) were larger (mean difference = 12.56 kg²).

**Variance Ratios. The pattern for estimates of variance ratios mimicked the one observed for variance components (Table 5). From genomic-polygenic model 1 and the polygenic model were very similar, while genomic-polygenic models 2 and 3 were larger. The variance ratio of heritability from the genomic-polygenic model was very similar to that of the polygenic model (mean difference = -0.04), while those from genomic-polygenic models 2 and 3 were similar to those obtained in the polygenic model (mean difference = 0.08). However, slope estimates for heritability from the polygenic model was lower than that from genomic-polygenic model 1 (mean difference = 0.02) and those from genomic-polygenic models 2 and 3 (mean difference = 0.03), though both models indicating that genomic-polygenic models outperformed polygenic model.