**SUMMARY**

The objectives were to estimate the fractions of additive genetic variances for four postweaning growth and feed efficiency traits from Angus to Brahman in a multibreed population, and to determine EBV trends from Angus to Brahman in a multibreed population under subtropical conditions. Tissue sampling and genotyping were completed at the University of Florida, Gainesville, FL; Colorado State University, Fort Collins, CO; and University of Georgia, Athens, GA.

**RESULTS AND DISCUSSION**

Table 1 shows means and SD by calf breed group and all calves. Table 2 presents posterior means and credible intervals (95% CI) for additive genomic polygenic EBV (PhenVar) from genomic-polygenic models and for polygenic EBV. The data were analyzed using linear regressions with additive genomic, polygenic, and genomic-polygenic EBV on Brahman fraction. Thus, EBV from Angus to Brahman were evaluated using linear regressions of genomic-polygenic, polygenic, and genomic EBV on Brahman fraction.

**References**