

Genomic-polygenic EBV for reproduction, ultrasound-carcass, and tenderness traits in the Florida multibreed Brahman-Angus population

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Summary

The objectives of this research were to estimate genomic-polygenic parameters and EBV for sets of reproduction, ultrasound-carcass, and tenderness traits as well as to assess EBV trends as Brahman percentage increased from 0% to 100% percent in the state-wide Florida multibreed Brahman-Angus population. Reproduction set heritabilities were high for yearling weight adjusted to 365 d (0.53 ± 0.05), moderate for reproductive tract score (0.26 ± 0.04), and low for age at first calving (0.17 ± 0.04) and first calving interval (0.09 ± 0.02). Ultrasound-carcass set heritabilities were high for ultrasound weight (0.57 ± 0.05), slaughter age (0.57 ± 0.04), hot carcass weight (0.57 ± 0.04), ribeye area (0.55 ± 0.03), and marbling (0.50 ± 0.05), moderate for ultrasound ribeye area (0.35 ± 0.03), ultrasound intramuscular fat (0.33 ± 0.03), and backfat thickness (0.32 ± 0.03), and low for ultrasound backfat (0.07 ± 0.01). Tenderness set heritabilities were low for Warner-Bratzler shear force (0.17 ± 0.03) and moderate for tenderness score (0.47 ± 0.06). Heritability estimates indicated that genomic-polygenic selection for the target traits of the Florida Enhancement Fund project currently underway (reproductive tract score, marbling, and tenderness) should be feasible. The wide range of EBV among animals of all breed compositions indicated that the best animals regardless of their breed composition should be chosen as replacements if genetic progress is to be optimized in this multibreed population.

Key words: beef, cattle, genomic, evaluation, multibreed

Introduction

Brahman is a key component of the Brahman-*Bos taurus* beef production system in Florida because of its great adaptability to hot and humid conditions. Brahman cattle are frequently criticized for the tenderness and marbling of their meat and for their lower fertility relative to other breeds and crossbred cattle (Johnson *et al.*, 1990; Elzo *et al.*, 2012). However, research at the University of Florida (UF) has shown that Brahman animals exhibit a range of EPD for fertility, growth, ultrasound, and carcass traits comparable to that of Angus, Brangus, and Brahman \times Angus crossbreds (Elzo *et al.*, 2015, 2016). These studies led to a Florida state-wide project initiated in 2017 with the aim of developing a selection and mating program for Brahman and Brahman crossbred cattle focused on genomic selection and assortative mating to improve tenderness, marbling, and reproductive tract score. The objectives of this research were: 1) to estimate genomic-polygenic parameters for sets of reproduction, ultrasound-carcass, and tenderness traits; 2) to obtain genomic-polygenic EBV for all these traits; and 3) to assess genomic-polygenic EBV trends as Brahman percentage increased from 0% to 100% percent in the state-wide Florida multibreed Brahman-Angus population.

Materials and Methods

Animals, feeding, and management

The research protocol was approved by the University of Florida Institutional Animal Care and Use Committee (IACUC protocol number 201003744). Animals were from four private Florida Brahman herds plus animals from the multibreed Angus-Brahman (MAB) and Brahman herds of the University of Florida (UF), Gainesville. The dataset contained 2,739 calves born from 2005 to 2016 with phenotypic data for various traits (637 bulls, 1,083 heifers, and 1,019 steers). Calves were the progeny of 218 sires and 1,170 dams. Matings in private herds were Brahman-Brahman only. Mating in the MAB herd followed a diallel design where sires from six breed groups were mated to dams of these same six breed groups. These six breed groups were: BG1 = (1.0 to 0.80) A (0.0 to 0.20) B, BG2 = (0.79 to 0.60) A (0.21 to 0.40) B, BG3 = (0.625) A (0.375) B, BG4 = (0.59 to 0.40) A (0.41 to 0.60) B, BG5 = (0.39 to 0.20) A (0.61 to 0.80) B, and BG6 = (0.19 to 0.0) A (0.81 to 1.00) B, where A = Angus and B = Brahman. There were 790 calves in BG1, 363 in BG2, 304 in BG3, 482 in BG4, 245 in BG5, and 550 in BG6. Calves were raised with their dams on bahiagrass pastures (*Paspalum notatum*) from birth to weaning and remained in these pastures until yearling. Postweaning, UF calves were supplemented with bahiagrass hay, concentrate (1.6 kg to 3.6 kg of soy hull pellets per day; 14.0 % CP), and a mineral supplement. Yearling steers remained at a contract feeder until they reached a subcutaneous fat thickness over the ribeye of 1.27 cm approximately.

Traits

The traits in the reproduction set included yearling weight adjusted to 365 d of age (YW), reproductive tract score (RTS, units; n = 516; Andersen *et al.*, 1991), age at first calving (AFC, d; n = 909), and first calving intervals (FCI, d; n = 447). The ultrasound and carcass set of traits comprised ultrasound weight (UW, kg; n = 2,734); ultrasound ribeye area (UREA, cm²; n = 2,694), ultrasound backfat (UBF, cm; n = 2,698), ultrasound percent intramuscular fat (UPIMF, %; n = 2,680), slaughter age (SLA, d; n = 815), hot carcass weight (HCW, kg; n = 803), ribeye area (REA, cm²; n = 803), backfat thickness (FAT, cm; n = 803), and marbling score (MAR, units; n = 802; 100 to 199 = practically devoid, 200 to 299 = traces, 300 to 399 = slight, 400 to 499 = small, 500 to 599 = modest, 600 to 699 = moderate, 700 to 799 = slightly abundant, 800 to 899 = moderately abundant, and 900 to 999 = abundant). The tenderness set of traits contained Warner-Bratzler shear force (WBSF, kg; n = 754), and tenderness score (TEND, units; n = 576; 1 = extremely tough, 2 = very tough, 3 = moderately tough; 4 = slightly tough; 5 = slightly tender; 6 = moderately tender; 7 = very tender; 8 = extremely tender).

Tissue sampling and genotyping

Tissue samples (blood, semen) from 782 animals (70 sires, 696 steers, and 16 heifers) were collected and stored at -80 °C between 2006 and 2015. The distribution of samples per breed group were: BG1 = 126, BG2 = 120, BG3 = 123, BG4 = 159, BG5 = 83, and BG6 = 171. DNA from blood and semen samples was extracted with a commercial kit (QIAamp DNA mini kit, Qiagen, Valencia, CA). Genotyping was done

at Neogen with GeneSeek Genomic Profiler F250 (number of SNP in autosomes and X chromosome = 221,049; Neogen, 2016). Each animal in the genotype file had 127,016 SNP autosomal and X chromosome markers after discarding SNP with minor allele frequencies below 0.05 (n = 94,033).

Genomic-Polygenic Variance Components, Parameters, and Predictions

Three separate single-step genomic-polygenic multiple-trait mixed model analyses (Aguilar *et al.*, 2010) were conducted to estimate variance components and genetic parameters. The 4-trait model for the reproduction set (YW, RTS, AFC, and FCI) contained yearling contemporary group (herd-year-season-management group), age of dam (YW only), sex of calf (YW only), direct heterosis, and maternal heterosis (YW only) as fixed effects. Fixed effects for the 9-trait model for the ultrasound-carcass set (UW, UREA, UFAT, UPIMF, SLA, HCW, REA, FAT, and MAR) were yearling contemporary group, sex of calf, ultrasound age (ultrasound traits only), and heterosis. Fixed effects for the 2-trait model for the tenderness set (WBSF, TEND) were yearling contemporary group, sex of calf, heterosis, and slaughter age. Random effects were animal direct genetic and residual for all models. The mean for random additive direct genetic effects was equal to zero, and the variance was equal to H , where H was the combined pedigree-genotype relationship matrix among animals with and without genotypes, and A was the direct additive genetic variance-covariance matrix of each of the three sets of traits. Residual effects had mean zero and variance equal to I , where I was an identity matrix, and E was the environmental variance-covariance matrix for each trait set. REML estimates of variance components and genetic parameters were obtained using an average information algorithm with the BLUPF90 family of programs (Misztal *et al.*, 2002). Standard errors of variance components were obtained as square roots of the diagonals of the inverse of the information matrix, whereas SD of heritabilities and correlations were computed using a repeated sampling procedure. Genomic-polygenic predictions were computed for each set of traits using estimates of variance components at convergence.

Results and Discussion

Heritabilities and genetic correlations

Estimates of heritability for the reproduction trait set were high for YW (0.53 ± 0.05), moderate for RTS (0.26 ± 0.04), and low for AFC (0.17 ± 0.04) and FCI (0.09 ± 0.02). Additive genetic correlations among these traits were low and with high SE. Heritability estimates for the ultrasound-carcass trait set were high for UW (0.57 ± 0.05), SLA (0.57 ± 0.04), HCW (0.57 ± 0.04), REA (0.55 ± 0.03), and MAR (0.50 ± 0.05), moderate for UREA (0.35 ± 0.03), UPIMF (0.33 ± 0.03), and FAT (0.32 ± 0.03), and low for UFAT (0.07 ± 0.01). Additive genetic correlations between ultrasound-carcass traits ranged between -0.47 to 0.81. The highest positive additive genetic correlations were between UW and HCW (0.81 ± 0.08), HCW and REA (0.80 ± 0.07), UW and UREA (0.64 ± 0.06), UREA and REA (0.63 ± 0.07), and UREA and HCW (0.3 ± 0.09). The largest negative additive genetic correlations were between UFAT and SLA (-0.47 ± 0.08), UFAT and HCW (-0.34 ± 0.09), and UREA and UPIMF (-0.25 ± 0.07). Heritability estimates for the tenderness trait set were low for WBSF (0.17 ± 0.03) and moderate for TEND (0.47 ± 0.06). The additive genetic correlation between

WBSF and TEND was negative and high (-0.97 ± 0.01). The heritabilities obtained for RTS, MAR, UPIMF, WBSF, and TEND indicated that genomic selection for the target traits (reproductive tract score, marbling, and tenderness) would be feasible in the statewide Florida Brahman-Angus multibreed population.

Genomic-polygenic EBV and trends from Angus to Brahman

High degree of variation among genomic-polygenic EBV existed for the sets of reproduction, ultrasound-carcass, and tenderness sets of traits across the spectrum of Brahman breed percentages in the statewide Florida Brahman-Angus multibreed population. Graphs of genomic-polygenic EBV for the three sets of traits showed a wide range of values for animals of all Brahman percentages. No Brahman 32nds group was overwhelmingly better than any other one, including Angus. The most visible trend from Angus to Brahman occurred for RTS, where genomic-polygenic EBV tended to decrease as Brahman fraction increased. This indicated that heifers with higher Brahman fractions tended to be less mature as yearlings than heifers with higher Angus fractions.

Conclusion

Estimates of genetic parameters in the statewide Brahman-Angus multibreed population were large enough for genomic-polygenic selection for these traits to be feasible. In particular, selection for the three target traits (reproductive tract score, marbling, and tenderness) in the Florida Enhancement Fund project is expected to be successful. The wide range of EBV among animals of all breed compositions indicated that the best animals regardless of their breed composition should be chosen as replacements if genetic progress is to be optimized in this multibreed population.

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