University of Florida Report (2016-2017)
S-1064: Genetic improvement of adaptation and reproduction to enhance sustainability of cow-calf production in the Southern United States

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Research Areas

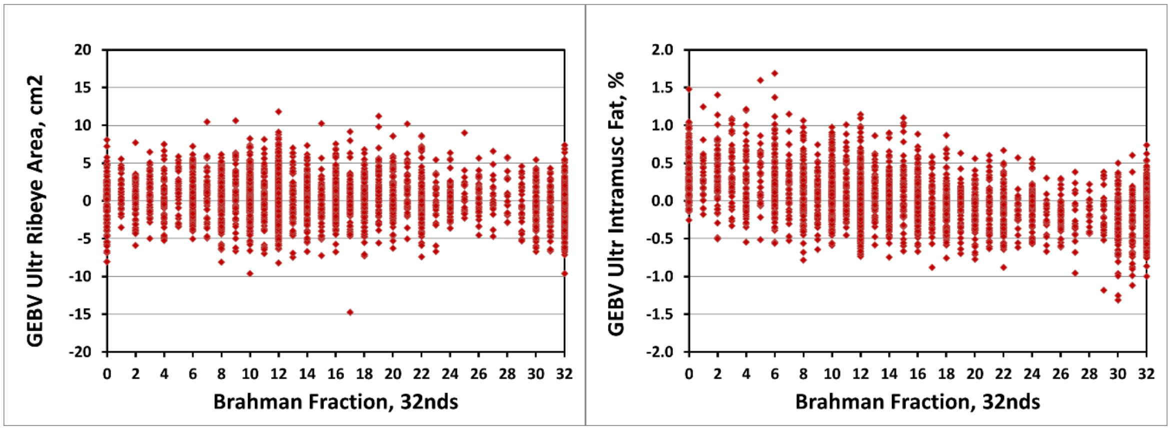
1) **Objective 2:** Meta-analyses of economically important traits of cow productivity and fertility to assess breed and production system combinations
2) **Objective 4:** Investigation of early cow-life performance (first four parities) affecting lifetime production in Brahman and Brahman-Angus cows

Activities

1) Collection of health, survival, fertility, growth, ultrasound, carcass, and meat palatability data from animals from the multibreed Angus-Brahman (MAB) and Brahman herds from the University of Florida (UF). Utilization of embryo transfer to increase the size of the Brahman herd.
2) Updating and maintenance of the MAB and Brahman herd databases containing health, survival, fertility, preweaning growth, postweaning growth, carcass and meat palatability data (n = 7,523).
3) Collection of blood samples from calves (n = 314), and semen or blood from new sires (n = 14) used in the MAB and Brahman herds (stored at UF).
4) Genomic-polygenic and polygenic predictions for nine ultrasound and carcass traits in Angus-Brahman multibreed cattle using three sets of genotypes.
5) FORTRAN software updates for editing of phenotypes, genotypes, and pedigree data and construction of input data files for imputation from lower to higher-density genotyping chips followed by genomic-polygenic evaluation using single-step methodology.
6) SAS programs updates for editing, statistical description, and mixed model analysis of feed intake, growth, ultrasound, carcass, and meat palatability traits in the MAB and Brahman populations.
7) Development of a statewide Brahman and Brahman-Angus database that includes pedigree and phenotypic information for fertility, growth, ultrasound, carcass, and meat palatability traits from private Brahman and UF herds.
8) Development of a statewide Brahman and Brahman-Angus tissue sample repository with blood, ear-notches, and semen samples from private Brahman and UF herds.
9) Association of SNPs and haplotypes in µ-calpain and calpastatin genes with Warner-Bratzler Shear Force in a multibreed Brahman-Angus population (R. Mateescu).
10) Influence of Brahman genetics on muscle fiber properties, protein degradation, and tenderness in the Angus-Brahman multibreed herd (T. Scheffler).
11) Colonization dynamics of Cefotaxime resistant bacteria in beef cattle raised without Cephalosporin antibiotics (K. C. Jeong).
12) Influence and regulation of vitamin D on the immune system, health, and growth of beef calves (C. D. Nelson).

Research Outcomes

1) Genomic-polygenic and polygenic predictions for nine ultrasound and carcass traits in Angus-Brahman multibreed cattle using three sets of genotypes. The objectives of this study were to estimate variance components, genetic parameters, EBV, accuracies, and rankings for nine ultrasound and carcass traits in a multibreed Angus-Brahman population using three genomic-polygenic models and one polygenic model (PM). The genomic-polygenic models used the complete GeneSeek GPF250k SNP set (GPM), top 5% SNP (GPMR1), and 5% SNP evenly spread across the genome (GPMR2). Yearling ultrasound traits were weight (UW), ribeye area (UREA), backfat (UFAT), and percent intramuscular fat (UPIMF). Carcass traits were slaughter age (SLA), hot carcass weight (HCW), ribeye area (REA), backfat thickness (FAT), and marbling score (MAR). The 9-trait GPM, GPMR1, GPMR2, and PM contained fixed contemporary group, age of calf (ultrasound traits only), sex of calf, and direct heterosis effects, and random animal and residual effects. Variance components and genetic parameters were computed using AIREMLF90. Comparable heritabilities were obtained with GPM and PM for UW (GPM: 0.54 ± 0.05; PM: 0.51 ± 0.05), UREA (GPM: 0.36 ± 0.03; PM: 0.34 ± 0.03), UFAT (GPM: 0.12 ± 0.02; PM: 0.11 ± 0.02), UMPIMF (GPM: 0.34 ± 0.03; PM: 0.30 ± 0.03), SLA (GPM: 0.59 ± 0.07, PM: 0.61 ± 0.06), HCW (GPM: 0.58 ± 0.06, PM: 0.52 ± 0.07), REA (GPM: 0.48 ± 0.04, PM: 0.45 ± 0.05), FAT (GPM: 0.41 ± 0.05, PM: 0.30 ± 0.05), and MAR (GPM: 0.56 ± 0.07, PM: 0.51 ± 0.08). Additive genetic correlations between pairs of ultrasound and carcass traits were all between -0.31 and 0.81. The highest positive additive genetic correlations were between UW and UREA, UW and HCW, UW and REA, UREA and HCW, UREA and REA, UFAT and FAT, and between HCW and REA. The largest negative additive genetic correlations were between UREA and UPIMF, UFAT and SLA, UFAT and HCW, UPIMF and REA, and between REA and MAR. High similarity among genomic-polygenic EBV and accuracies from GPM, GPMR1, and GPMR2 as well as high-rank correlations for sires, dams, and progenies indicated that the two reduced genotype sets were appropriate alternatives to the complete GPF250k SNP set for animal evaluation and selection in this multibreed Angus-Brahman population. High EBV variability among animals of all Angus and Brahman percentages indicated that optimization of genetic progress through selection in multibreed Angus-Brahman populations should be based solely on genetic merit regardless of breed composition. As an example, **Figure 1** below shows genomic-polygenic EBV (GEBV) for two ultrasound traits (ribeye area and intramuscular fat) and their corresponding carcass traits (ribeye area and marbling).



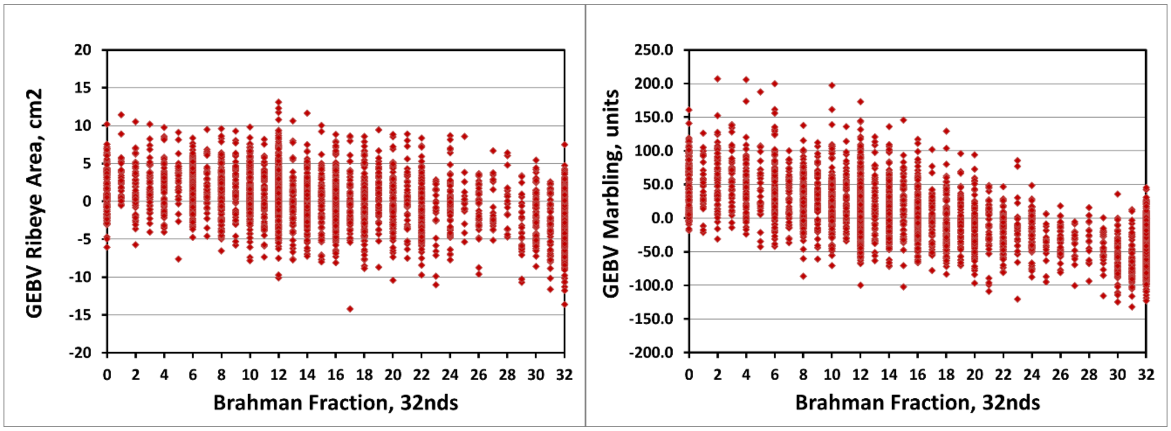


Figure 1. Genomic-polygenic EBV (GEBV) for two ultrasound traits (ribeye area and intramuscular fat) and their corresponding carcass traits (ribeye area and marbling)

2) The Florida Brahman genomics project. This two-year project was initiated in January 2017. Its aim is to develop a statewide selection and mating program for Florida Brahman cattle focused on genomic selection and assortative mating to improve three target traits of high economic importance: meat tenderness, marbling, and reproductive tract score, a trait closely associated with fertility and age at first calving. Currently there are seven Brahman breeders contributing to the project with pedigree and phenotypic data as well as tissue samples (blood, ear notches, semen) for genotyping with GeneSeek GGP250k or GGP50k. The American Brahman Breeders Association supplied pedigree (n = 15,844) and growth data (n = 7,358) files containing accumulated information from 1976 to 2016. The UF multibreed Angus-Brahman and the Brahman herds will contribute with pedigree (n = 8,302), phenotypes for reproduction, growth, ultrasound, carcass, and meat palatability traits (n = 6,755), and existing genotypes (Illumina 3k, GeneSeek GGP 150k, GeneSeek GGP 250k). Current work includes acquisition of 2016 and 2017 pedigree and phenotypic data from Florida Brahman breeders, semen and ear notch samples for genotyping, and integration of the ABBA, UF, and Florida Brahman breeder pedigree and phenotypic datasets. This will be followed by the testing of multiple-trait genomic-polygenic analyses for several sets of traits (e.g., reproductive tract score, age at first calving, and first calving interval; weaning weight, ultrasound weight, ultrasound ribeye area, ultrasound marbling; ultrasound weight, ultrasound ribeye area, ultrasound marbling, slaughter age, hot carcass weight, ribeye area, marbling, tenderness). Subsequently, the use of these genomic-polygenic predictions will be explained to Florida Brahman and discussed in the context of their individual herds as well as the complete Florida Brahman population. **Table 1** below shows the number of pedigree and phenotype records, tissue samples, and GeneSeek GGP250 genotypes as of April 2017.

Table 1. Records, Tissue Samples, and Genotypes (April 2017)

Dataset	Pedigree file	Phenotype file	Tissue Samples	GeneSeek GGP250k
Florida Brahman breeders	198	115	1,400	0
ABBA (All years; Unedited files)	15,844	7,358	0	0
UF Brahman herd	673	446	475	47
UF Brahman-Angus Multibreed herd	8,302	6,755	2,801	738

3) Brahman genetics influence on muscle fiber properties, protein degradation, and tenderness in the Angus-Brahman multibreed herd. The objective of this study was to determine influence of Brahman genetics on muscle contractile and metabolic phenotype and postmortem proteolysis. Cattle used in this study represent a continuous spectrum of Angus-Brahman genetic variation and were divided into six breed groups for analysis. Steers (n = 6 per breed group) were harvested and samples from Longissimus were collected at 1.5 h, 24 h, and 14 d postmortem. Western blotting and SDS-vertical agarose gel electrophoresis were used to assess proteolysis during the 14 d aging period, and immunohistochemistry and enzyme activity were used to evaluate muscle fiber characteristics. Tenderness at 14 d was determined by Warner-Bratzler shear force (WBSF) and a trained sensory panel. As Brahman influence increased, WBSF increased ($P = 0.0009$) and sensory tenderness decreased ($P < 0.0001$). Calpain-1 autolysis decreased as Brahman percentage increased ($P=0.0025$), and corresponded with reduced degradation of troponin-T, desmin, and titin. Increasing Brahman percentage was associated with greater citrate synthase activity and greater cross-sectional area of type IIx fibers. Brahman and Brahman-Angus crossbred cattle produced tougher steaks and exhibited decreased protein degradation. Brahman genetics influenced not only the calpain-calpastatin system, but also muscle fiber size and metabolic properties.

4) Association of SNPs and haplotypes in µ-calpain and calpastatin genes with Warner-Bratzler Shear Force (WBSF) in a multibreed Brahman-Angus population. Tenderness has been established as the most important quality trait in meat, especially in beef, and it essentially depends on the amount of connective tissue, myofibrillar protein degradation and intramuscular fat content. Myofibrillar protein degradation is a result of various autogenous proteolytic enzymes. The calpain family and their inhibitor calpastatin are the main effectors in this process of myofibrillar protein degradation.
The objectives of this study were to construct a linkage disequilibrium (LD) block analysis in µ-calpain and calpastatin genes and perform association tests per SNP and LD-Block with WBSF. Sixteen SNP in µ-calpain and 26 SNP in calpastatin were genotyped and the informative SNP were used in a LD-Block prediction test and association assay. The measurements cook loss (Pcookloss) and WBSF were recorded in steaks from 673 steers. WBSF measures the amount of force required to shear a core of cooked meat of 1.27 cm in diameter. High values of WBSF are indicative of tougher samples. The µ-calpain gene had one LD-Block (**Figure 2**), and UA-IFASA-1370 and 29-44097612 were their tagged SNP. Both SNPs are located in an intron region of µ-calpain. This LD-Block has an extension of 11 kb and includes seven exons. The last two exons are part of the 3'UTR. Calpastatin had three LD-Blocks. LD-Block 1 is located between ARS-BFGL-NGS-43901 (intron) and 7-98535683 (exon); this block has an extension of 37 kb distributed in the third intron of calpastatin and the next six exons. LD-Block 2 has 7-98542988 (intron), BovineHD0700028773 (exon) and 7-98560787 (exon) as tagged SNP; this LD-Block extends on 17 kb and covers various exons in the last third section of calpastatin. The tagged SNP of LD-Block 3 are ARS-USMARC-116 (intron) and 7-98581038 (3'UTR); this block is located in the final section of calpastatin with an extension of 14 kb and includes the 3'UTR (Figure 1). 3) The SNP marker ARSUSMARC116 was associated with WBSF. Animals with genotype CC had the highest WBSF value (4.73 ± 0.10 kg). Genotype CC yielded higher WBSF than genotypes TT (4.14 ± 0.17 kg) and CT (4.28 ± 0.11 kg). LD-Block 3 of calpastatin (ARSUSMARC116 is one of its tagged SNPs) was also associated with WBSF. LD-Block 3 diplotype CG-CG (4.75 ± 0.18 kg) had higher WBSF values than diplotype TA-CG (4.32 ± 0.12 kg), and both of them yielded hither WBSF values than diplotypes TA-TA (4.13 ± 0.11 kg) and TG-CG (3.77 ± 0.24 kg; **Figure 3**).

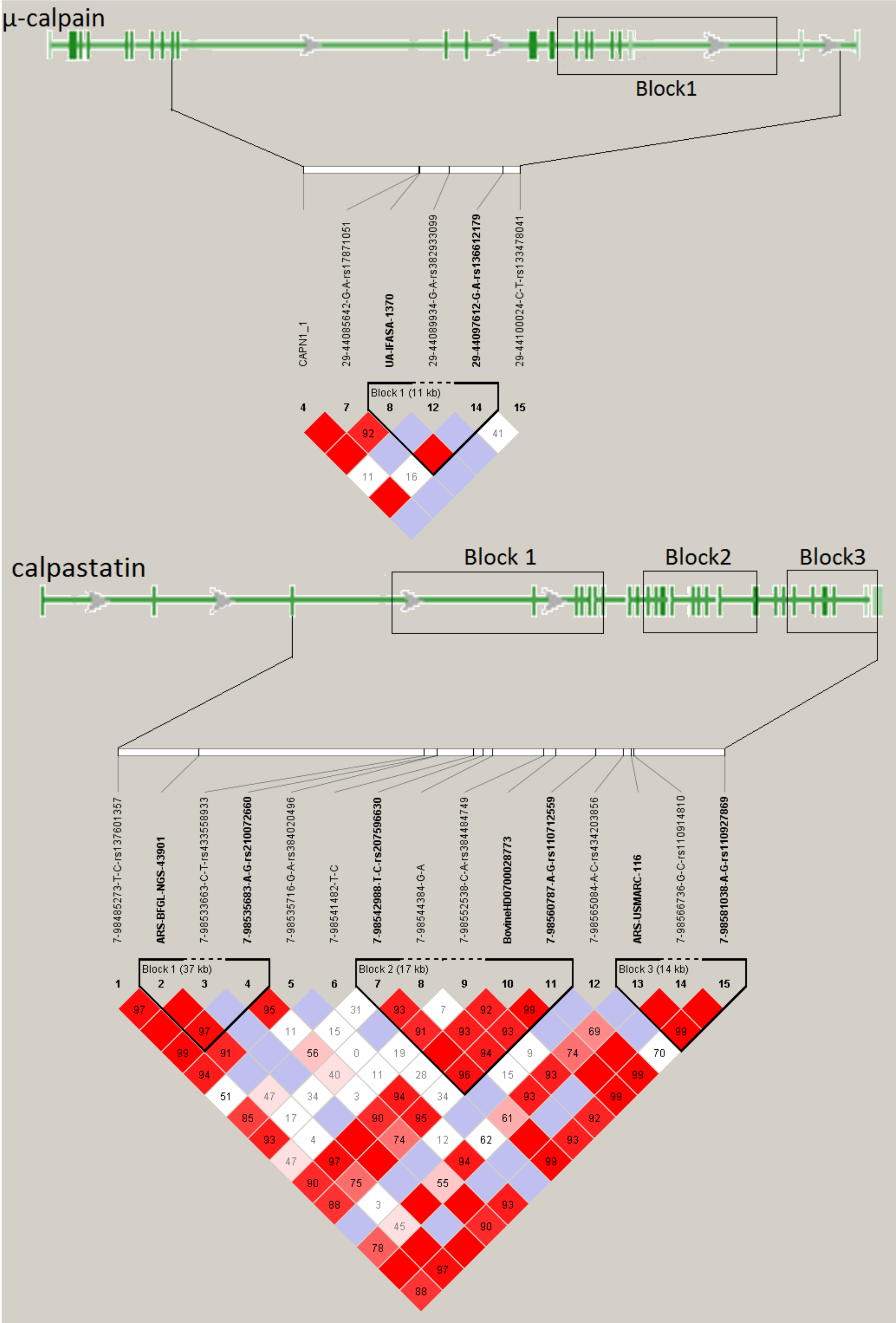


Figure 2. Linkage Disequilibrium blocks in 196 families. A. µ-calpain B. calpastatin.

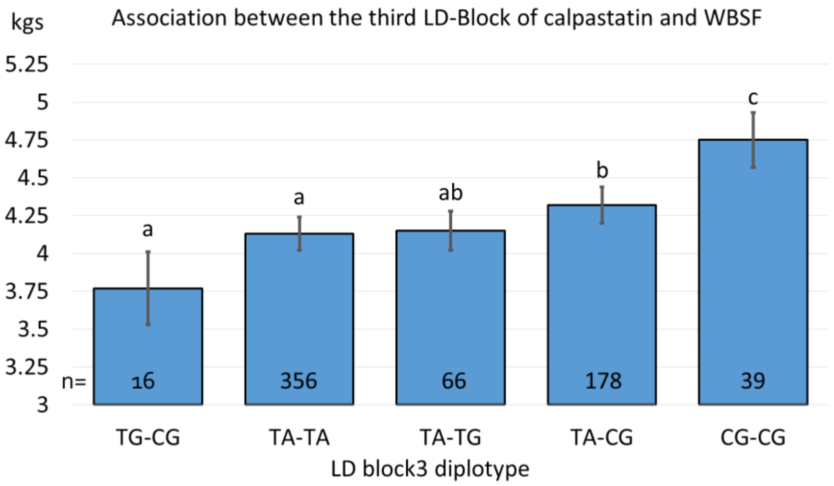


Figure 3. Association between the LD-Block 3 of calpastatin and the measurement WBSF. ARSUSMARC116 and 7-98581038 are the tagged SNPs in this LD-Block.

5) Colonization dynamics of Cefotaxime resistant bacteria in beef cattle raised without Cephalosporin antibiotics. The emergence of infections caused by antimicrobial resistant microorganisms (ARMs) is currently one of the most important challenges to public health and medicine. Though speculated to originate from the overuse of antibiotics during food animal production, we hypothesized that cattle are exposed to naturally occurring ARMs in the environment. In this cohort study, a herd of beef calves with no previous exposure to antibiotics was followed during the first year of life in order to investigate the rate of colonization by bacteria resistance to the third-generation cephalosporin cefotaxime. Fecal samples were collected from the recto-anal junction of cattle at approximately 3, 6, 9 and 12 months of age and tested for cefotaxime resistant bacteria (CRB) and the presence of extended spectrum β-lactamases (ESBLs). The colonization dynamics of CRB in calves (n = 188) was evaluated with samples collected from four periods using longitudinal statistical analyses. Colonization by CRB was a dynamic process with over 92% of the calves testing positive for CRB at least once during the first year of life. All isolates subjected to antimicrobial susceptibility test were resistant to at least five different antibiotics and carried multiple variants of the blaCTX-M genes. Metagenomic analysis revealed significant differences in microflora of the calves with and without CRB colonization at different ages. This study provided evidence that colonization of beef calves by ARMs is a natural, dynamic process that can occur in the absence of veterinary or agricultural use of antibiotics.

Publications

Elzo, M. A., R. G. Mateescu, D. D. Johnson, T. L. Scheffler, J. M. Scheffler, C. Carr, D. O. Rae, J. G. Wasdin, M. D. Driver and J. D. Driver. 2017. Genomic-polygenic and polygenic predictions for nine ultrasound and carcass traits in Angus-Brahman multibreed cattle using three sets of genotypes. Livest. Sci. 202:58-66.

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Elzo, M. A., R. Mateescu, D. D. Johnson, T. L. Scheffler, J. M. Scheffler, C. Carr, D. O. Rae, J. G. Wasdin, M. D. Driver, and J. D. Driver. 2017. Multibreed Angus-Brahman genetic parameters and predictions for nine ultrasound and carcass traits using three genomic-polygenic models and one polygenic model. Abstract 20268, ASAS Annual Meeting, Baltimore, MD, July 8-12-2017.

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Research Impacts

1) High similarity among genomic-polygenic EBV and accuracies from GPM, GPMR1, and GPMR2 as well as high-rank correlations for sires, dams, and progenies indicated that the two reduced genotype sets were appropriate alternatives to the complete GPF250k SNP set for animal evaluation and selection in this multibreed Angus-Brahman population. High EBV variability among animals of all Angus and Brahman percentages indicated that optimization of genetic progress through selection in multibreed Angus-Brahman populations should be based solely on genetic merit regardless of breed composition.
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3) The SNP marker ARSUSMARC116 was associated with WBSF. Animals with genotype CC had the highest WBSF value (4.73 ± 0.10 kg). Genotype CC yielded higher WBSF than genotypes TT (4.14 ± 0.17

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[*] Graduate Student

kg) and CT (4.28 ± 0.11 kg). LD-Block 3 of calpastatin (ARSUSMARC116 is one of its tagged SNPs) was also associated with WBSF. LD-Block 3 diplotype CG-CG (4.75 ± 0.18 kg) had higher WBSF values than diplotype TA-CG (4.32 ± 0.12 kg), and both of them yielded hither WBSF values than diplotypes TA-TA (4.13 ± 0.11 kg) and TG-CG (3.77 ± 0.24 kg).

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