

UF-Gainesville Beef Cattle News Corner

The Florida Brahman Genomic Selection Project: January 2019 Genomic EBV

Mauricio A. Elzo, Raluca G. Mateescu, Chad Carr, Owen Rae, Tracy Scheffler, Jason Scheffler, K. C. Jeong, Danny Driver, and Michelle Driver
Department of Animal Sciences, University of Florida

Introduction

The Florida Brahman Genomic Selection Project entered its third year in January 2019. We conducted two mid-year genomic evaluations of the twenty reproduction, growth, ultrasound-carcass, and tenderness traits utilizing additional phenotypic and pedigree information collected during the 2018-2019 phase of this project. The Florida Brahman Genomic Selection Project is funded by the Florida Cattle Enhancement Board. ***Its primary aim is the development of a statewide selection and mating program for Florida Brahman cattle focused on genomic selection and assortative mating to improve three target traits: tenderness, marbling, and reproductive tract score.*** This project currently counts with the participation of eight Florida Brahman breeder herds plus two herds from the University of Florida (UF): a purebred Brahman herd and a Multibreed Angus-Brahman herd. All herds contribute to the project with phenotypic data on the various traits, pedigree information, and tissue samples for genotyping. In addition, the American Brahman Breeders Association (ABBA) provided existing phenotypic and pedigree information until January 2017. All the phenotypic and pedigree data from Florida Brahman breeders, ABBA, and UF Brahman and Multibreed Angus-Brahman herds were combined to construct the Florida Brahman statewide phenotype-pedigree database. Tissue samples from Florida Brahman breeder, UF Brahman, and UF Multibreed Angus-Brahman herds were used to construct the statewide tissue and DNA repository housed at the UF Department of Animal Sciences. Genotypes obtained from DNA extracted from tissue samples provided by Florida Brahman and UF herds became the statewide genotypic database. We updated the phenotype and pedigree files with the new information collected during the 2018-2019 phase of this project prior to conducting the two mid-year genomic evaluations. Results from the second of these two genomic evaluations, conducted in January 2019, are reported here.

January 2019 Florida Brahman Genomic Evaluation

This genomic evaluation included the same four sets of traits analyzed in April 2018. The traits in these four sets were: a) **Growth set (n = 5):** birth weight direct (BWD), weaning weight direct (WWD), postweaning weight direct (GWD), birth weight maternal (BWM), and weaning weight maternal (WWM); b) **Reproduction set (n = 4):** yearling weight adjusted to 305 days of age (YW), reproductive tract score (RTS), age at first calving (AFC), and first calving interval (FCI); c) **Ultrasound-Carcass set (n = 9):** ultrasound weight (UW), ultrasound ribeye area (UREA), ultrasound fat (UBF), ultrasound percent intramuscular fat (UPIMF), slaughter age (SLA), hot carcass weight (HCW), ribeye area (REA), backfat thickness (FAT), and marbling score (MAR); and d) **Tenderness set (n = 2):** Warner-Bratzler shear force (WBSF) and tenderness score (TEND). We are currently processing the DNA samples taken in the 2018-2019 phase. Consequently, we reestimated variance components, heritabilities, correlations (genetic, environmental, phenotypic), and computed Genomic EBV (GEBV) for each of the four sets of traits using the genotype file of April 2018 and the phenotype and pedigree files updated in January 2019.

The number of animals contributing with one or more phenotypic records to this genomic evaluation was 16,750 (10,040 Brahman and 6,710 Angus and Brahman-Angus crossbreds), and the number of animals in the pedigree file was n = 24,869 (17,484 Brahman and 7,385 Angus and Brahman-Angus crossbreds). Genotypic data were from the 2,364 Brahman, Brahman-Angus, and Angus animals from Florida Brahman breeder, UF Brahman, and Multibreed Angus-Brahman herds genotyped with GeneSeek GGP250k during the previous phase of this project. ***As in the April 2018 Brahman Genomic Evaluation, heritability estimates were moderate to high for all evaluated traits indicating that selection for tenderness, marbling, and reproductive tract score and any other of the 17 evaluated traits would***

bring genetic progress to the Florida Brahman population. Table 1 contains numbers of animals, minimum values of GEBV, and maximum values of GEBV for the four sets of traits evaluated in January 2019. **Genomic EBV of purebred and crossbred animals in the Florida Brahman population are deviated from the average of the Genomic EBV for purebred Brahman cattle.**

Table 1. Numbers of evaluated animals, minimum, and maximum values of Genomic EBV				
Growth Set		N	Min	Max
	BWD, lb	24,886	-30.63	25.33
	WWD, lb	24,886	-99.46	119.68
	GWD, lb	24,886	-89.44	89.05
	BWM, lb	24,886	-11.69	22.90
	WWM, lb	24,886	-65.08	69.52
Reproduction Set		N	Min	Max
	YW, lb	24,886	-155.54	181.22
	RTS, units	24,886	-0.76	1.44
	AFC, d	24,886	-296.96	187.87
	FCI, d	24,886	-25.80	28.18
Ultrasound-Carcass Set		N	Min	Max
	UW, lb	24,886	-164.85	157.33
	UREA, in ²	24,886	-1.39	1.85
	UBF, in	24,886	-0.26	0.46
	UPIMF, %	24,886	-0.92	1.64
	SLA, d	24,886	-92.35	128.54
	HCW, lb	24,886	-126.07	136.27
	REA, in ²	24,886	-2.17	3.60
	FAT, in	24,886	-0.50	0.97
	MAR, units	24,886	-116.34	327.06
Tenderness Set		N	Min	Max
	WBSF, lb	24,886	-1.71	1.74
	TEND, units	24,886	-1.24	1.24

BWD = birth weight direct, WWD = weaning weight direct, GWD = postweaning weight direct, BWM = birth weight maternal, WWM = weaning weight maternal, YW = yearling weight, RTS = reproductive tract score, AFC = age at first calving, FCI = first calving interval, UW = ultrasound weight, UREA = ultrasound ribeye area, UBF = ultrasound fat, UPIMF = ultrasound percent intramuscular fat, SLA = slaughter age, HCW = hot carcass weight, REA = ribeye area, FAT = backfat thickness, MAR = marbling score, WBSF = Warner-Bratzler shear force, TEND = tenderness score.

Percentile graphs (**Figure 1**) are useful to quickly find the approximate standing of the GEBV of an animal for a particular relative to the GEBV of all animals in the population. For example, if an animal has a GEBV of 0.50 units for Tenderness Score, we locate 0.50 units in the ordinate of percentiles for this trait (eighth graph), project a horizontal line towards the line of red diamonds until it touches the line of red diamonds, and then project a vertical line downwards towards the abscissa to find a percentile value of approximately 90%. This value means that approximately 90% of the animals have a GEBV for Tenderness Score lower than 0.50 units and that 10% of the animals have a GEBV higher than 0.50 in the Florida Brahman population.

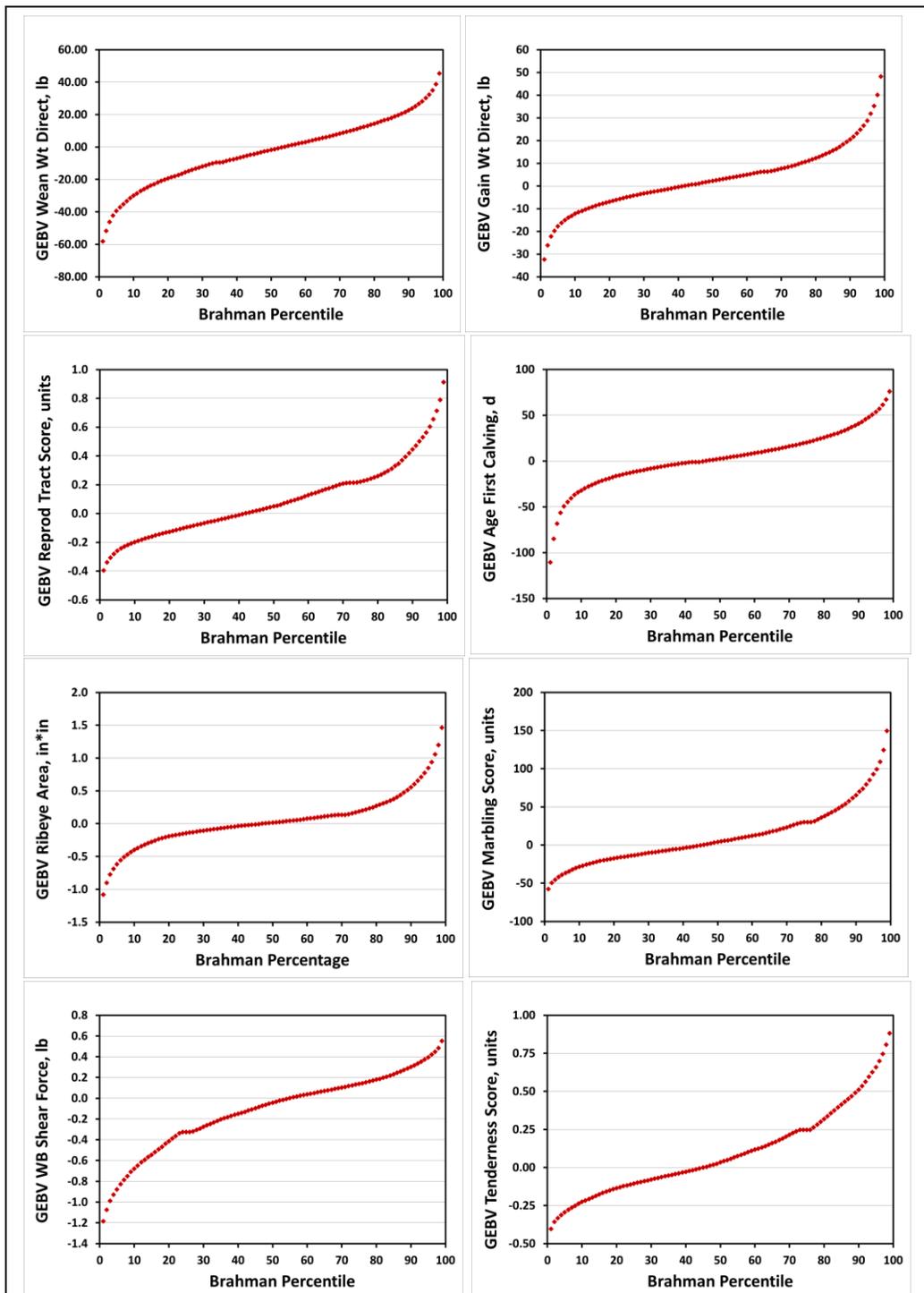


Figure 1 Graphs of Genomic EBV and their percentiles allow us to visualize the range of variation in Genomic EBV in the Florida Brahman population. Percentile graphs for Genomic EBV for eight of the twenty evaluated traits.

We will conduct another round of genomic evaluations after we receive the 2018-2019 GGP250k genotypes from GeneSeek. We will recompute Genomic EBV with the updated input files (phenotypes, pedigree, genotypes) and forward emails with Excel files containing GEBV for all animals in the Florida Brahman population to all cooperating Florida Brahman Breeders plus Excel files with GEBV only for animals in their herds. We will follow these emails with a meeting to discuss these genomic evaluations, the current status of the statewide Florida Brahman database and DNA repositories, and future steps of this project.