

UF-Gainesville Beef Cattle News Corner

The Florida Brahman Genomic Selection Project: April 2018 Genomic EBV

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Introduction

The Florida Brahman Genomic Selection project was initiated in January 2017 with funding from the Florida Cattle Enhancement Board. ***The primary aim of this project was to develop 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.*** A crucial aspect of this statewide project was the participation of Florida Brahman breeders in addition to the involvement of the University of Florida (UF) Brahman and Multibreed Angus-Brahman herds. Currently, there are eight Florida Brahman breeders participating in this project contributing with phenotypes, pedigree, and tissue samples for genotyping. In addition, the American Brahman Breeders Association (ABBA) contributed with historical phenotypic and pedigree data files until January 2017. Phenotypic and pedigree information obtained directly from Florida Brahman breeders, ABBA, and UF Brahman and Multibreed Angus-Brahman herds were used to construct the statewide phenotype-pedigree database. Tissue samples from Florida Brahman breeder, UF Brahman, and UF Multibreed Angus-Brahman herds constituted the statewide repository housed at the UF Department of Animal Sciences. Genotypes obtained from tissue samples provided by these Florida Brahman and UF herds formed the statewide genotypic database. Phenotypic, pedigree, and genotypes from the statewide databases were utilized to conduct two genomic evaluations in 2017, and several others in March and April 2018. Here, we report the results of last genomic evaluation conducted with genotypes from GeneSeek 250k in April 2018.

Florida Brahman Genomic Evaluation of April 2018

The April 2018 genomic evaluation included 20 traits grouped into four sets: growth ($n = 5$), reproduction ($n = 4$), ultrasound-carcass ($n = 9$), and tenderness ($n = 2$). We estimated variance components, heritabilities, correlations (genetic, environmental, phenotypic), and genomic EBV for each of the four sets of traits. The traits included in each set were: a) ***Growth set:*** birth weight direct (BWD), weaning weight direct (WWD), postweaning weight direct (GWD), birth weight maternal (BWM), and weaning weight maternal (WWM); b) ***Reproduction set:*** 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:*** 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:*** Warner-Bratzler shear force (WBSF) and tenderness score (TEND).

The number of animals contributing with one or more phenotypic records to this genomic evaluation was 15,642 (9,327 Brahman and 6,315 Angus and Brahman-Angus crossbreds), and the

number of animals in the pedigree file was 23,958 (16,993 Brahman and 6,988 Angus and Brahman-Angus crossbreds). Genotypic data came from 2,364 Brahman, Brahman-Angus, and Angus animals from cooperating Florida Brahman breeder, UF Brahman, and Multibreed Angus-Brahman herds genotyped with the GeneSeek GGP250k chip. Estimates of heritabilities ranged from moderate to high for all traits. ***Heritability estimates indicated that sufficient genetic variation existed for all evaluated traits, thus selection for tenderness, marbling, and reproductive tract score and any other of the 20 evaluated traits would be effective in the Florida Brahman population.*** To illustrate the genetic variation present in Florida Brahman, graphs of genomic EBV for six of the twenty evaluated traits are shown below (animals are ordered by sequential pedigree number). Depending on the herd and the group of traits used to select animals, desirable animals would generally be those with genomic EBV values above zero.

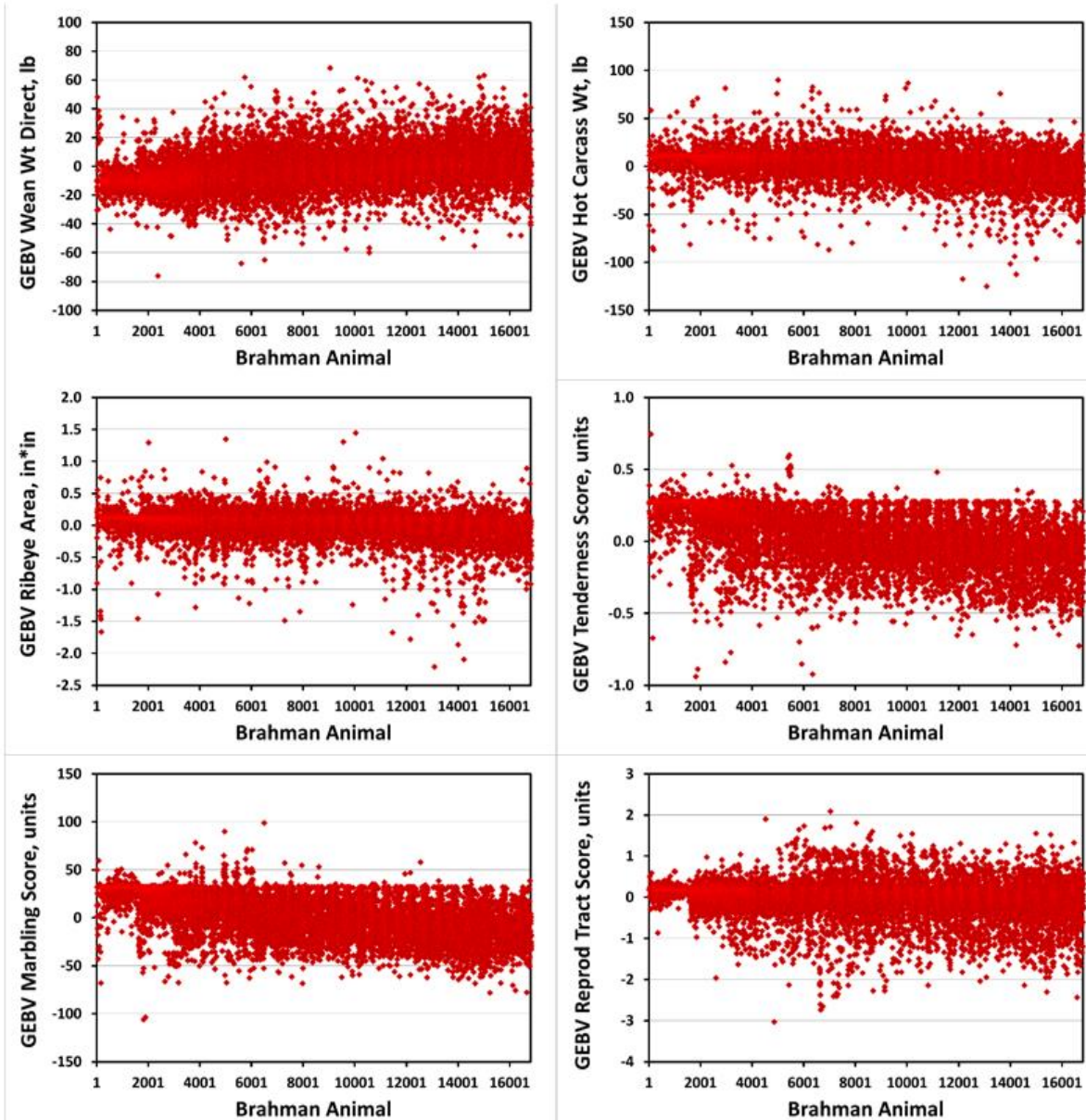


Table 1 shows the number of animals as well as minimum and maximum values of genomic EBV for the four sets of traits evaluated in April 2018. Genomic EBV were deviated from the average of the genomic EBV of purebred Brahman cattle.

Table 1. Numbers of evaluated animals, minimum, and maximum values of genomic EBV			
Growth Set	N	Min	Max
BWD, lb	23958	-30.04	24.63
WWD, lb	23958	-90.68	77.39
GWD, lb	23958	-90.29	91.34
BWM, lb	23958	-11.39	22.63
WWM, lb	23958	-64.92	67.65
Reproduction Set	N	Min	Max
YW, lb	23958	-229.48	177.79
RTS, units	23958	-3.02	2.10
AFC, d	23958	-147.53	105.29
FCI, d	23958	-92.86	124.38
Ultrasound-Carcass Set	N	Min	Max
UW, lb	23958	-141.39	184.00
UREA, in ²	23958	-1.62	1.90
UBF, in	23958	-0.15	0.27
UPIMF, %	23958	-1.05	1.77
SLA, d	23958	-72.36	69.63
HCW, lb	23958	-124.79	155.68
REA, in ²	23958	-2.21	3.07
FAT, in	23958	-0.39	0.80
MAR, units	23958	-105.52	286.78
Tenderness Set	N	Min	Max
WBSF, lb	23958	-1.97	2.02
TEND, units	23958	-1.34	1.41

We presented and discussed the April 2018 genomic EBV and accuracies with Florida Brahman breeders in a meeting held on April 27, 2018 in the conference room of the UF Department of Animal Sciences. In that meeting, we stressed the importance of collecting as much phenotypic information from Florida herds as possible to obtain genomic EBV that are both accurate and applicable to Florida subtropical conditions. We also discussed the need to collect phenotypes, pedigree, and genotypes from Brahman crossbred animals to enhance the accuracy of EBV of Brahman cattle particularly for traits infrequently measured in purebred Brahman animals such as carcass. Phenotypic information from Brahman crossbred animals will also help identify Brahman sires that produce desirable crossbred progeny under Florida subtropical conditions.

The meeting in April 2018 was followed by emails to each cooperating Florida Brahman breeder containing Excel files with phenotypic and pedigree information for all their animals in our database as well as the genomic EBV for each of the 20 evaluated traits. Subsequently, we sent a second

email with an Excel file containing genomic EBV for all evaluated animals in April 2018 (n = 23,958). We will continue to increase the size the statewide phenotypic, pedigree, and genotypic databases as well as the statewide tissue sample and DNA repository in future phases of this project in the hope that it will help further improve Brahman selection and mating programs in Florida.