The Florida Brahman Genomic Selection Project: April 2019 Genomic EBV

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Introduction
The Florida Brahman Genomic Selection Project will complete its third year in June 2019. During this phase of the project, we conducted two mid-year and one final genomic evaluation in April 2019 for twenty reproduction, growth, ultrasound-carcass, and tenderness traits utilizing all available phenotypic, pedigree, and genotypic information. *The primary goal of the Florida Brahman Genomic Selection Project 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*. Herds involved in this project encompassed eight herds from Florida Brahman breeders and two herds from the University of Florida (**UF**): a purebred Brahman herd and a Multibreed Angus-Brahman herd. These herds provided the project with phenotypic data on the twenty traits, pedigree information, and tissue samples for genotyping. In addition, the American Brahman Breeders Association (**ABBA**) contributed with accumulated phenotypic and pedigree information from December 1967 to January 2017. All phenotypic and pedigree data from Florida Brahman breeders, ABBA, and UF Brahman and Multibreed Angus-Brahman herds were merged into the Florida Brahman statewide phenotype-pedigree database. Tissue samples taken in Florida Brahman breeder, UF Brahman, and UF Multibreed Angus-Brahman herds were used to create the Florida statewide tissue and DNA repository stored at the UF Department of Animal Sciences. Genotypes determined from DNA extracted from tissue samples formed the Florida statewide genotypic database. The statewide phenotype, pedigree, and genotype databases were updated with all the new information obtained in 2018-2019 before conducting the two mid-year and the final genomic evaluations. Results from the final genomic evaluation for the 2018-2019 phase of the Brahman Genomic Selection Project are presented here.

**April 2019 Florida Brahman Genomic Evaluation**
The April 2019 Florida Brahman Genomic Evaluation evaluated animals for the same four sets of traits analyzed in previous genomic evaluations of this project. For completeness, the traits included in these trait 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 reestimated variance components, heritabilities, correlations (genetic, environmental, phenotypic) in January 2019. We utilized these newly estimated variance components to compute the Genomic EBV (**GEBV**) for the four sets of traits of the final genomic evaluation of the 2018-2019 phase in April 2019.

The number of animals with phenotypic records for one or more traits in the April 2019 genomic evaluation was 17,239 (10,137 Brahman and 7,092 Angus and Brahman-Angus crossbreds), and the number of animals in the pedigree file was 25,379 (17,601 Brahman and 7,778 Angus and Brahman-Angus crossbreds). Genotypic data came from 3,429 Brahman, Brahman-Angus, and Angus animals from Florida Brahman breeder, UF Brahman, and UF Multibreed Angus-Brahman herds genotyped with GeneSeek

GGP250k. *As in previous Florida Brahman Genomic Evaluations, heritability estimates in January 2019 were moderate to high for all evaluated traits indicating that selection for tenderness, marbling, and reproductive tract score and any other of the 20 evaluated traits would move the Florida Brahman population in the desired direction.* **Table 1** contains numbers of animals, minimum GEBV values, and maximum GEBV values for the four sets of traits in the April 2019 genomic evaluation. *Purebred and crossbred animal Genomic EBV were deviated from the average of the Genomic EBV for purebred Brahman cattle in the Florida population.*

Table 1. Numbers of evaluated animals, minimum, and maximum values of Genomic EBV			
Growth Set	**N**	**Min**	**Max**
BWD, lb	25379	-30.93	25.21
WWD, lb	25379	-97.34	149.46
GWD, lb	25379	-88.74	89.85
BWM, lb	25379	-11.42	23.24
WWM, lb	25379	-65.24	65.92
Reproduction Set	**N**	**Min**	**Max**
YW, lb	25379	-159.80	182.67
RTS, units	25379	-0.70	1.49
AFC, d	25379	-453.93	190.73
FCI, d	25379	-25.70	28.27
Ultrasound-Carcass Set	**N**	**Min**	**Max**
UW, lb	25379	-163.77	158.84
UREA, in^2	25379	-1.36	1.83
UBF, in	25379	-0.26	0.44
UPIMF, %	25379	-93.15	164.03
SLA, d	25379	-94.31	142.20
HCW, lb	25379	-122.78	136.15
REA, in^2	25379	-2.22	3.59
FAT, in	25379	-0.48	0.94
MAR, units	25379	-118.27	311.14
Tenderness Set	**N**	**Min**	**Max**
WBSF, lb	25379	-1.76	1.69
TEND, units	25379	-1.19	1.31

To facilitate visualization of the existing variability among Genomic EBV in the Florida Brahman population, Genomic EBV were plotted against their percentiles for each of the 20 evaluated traits. Percentile graphs for one trait from each of the four sets are shown below: 1) *Growth set:* weaning weight direct; 2) *Reproductive set:* reproductive tract score; 3) *Ultrasound-carcass set:* marbling; and 4) *Tenderness set:* shear force.
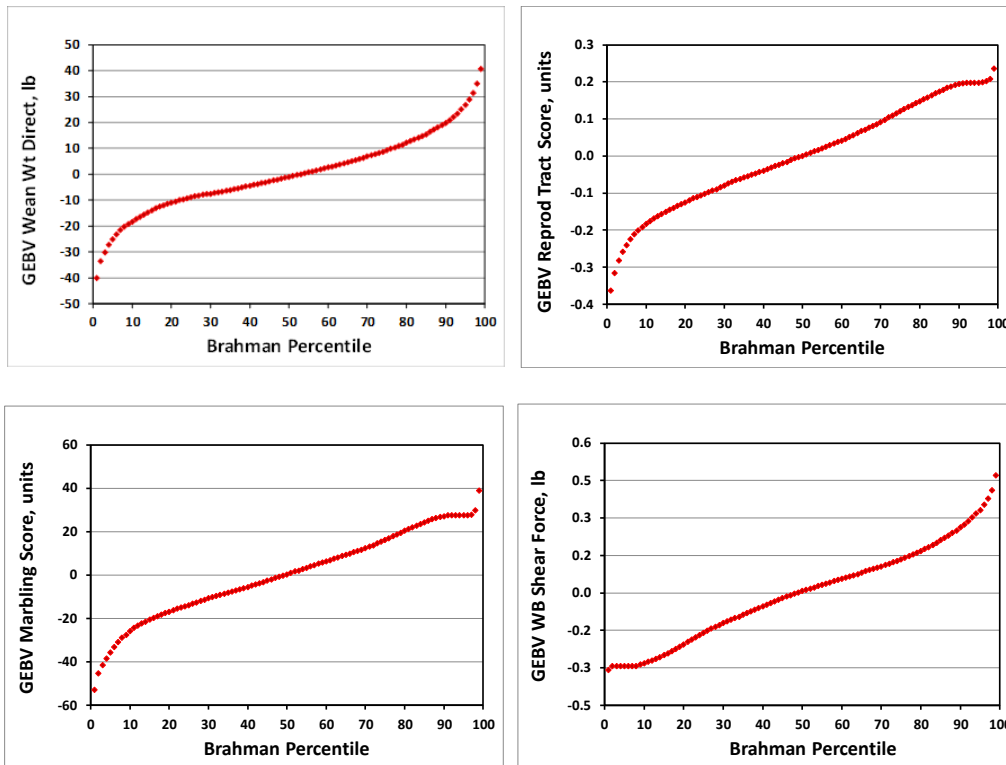
These percentile graphs permit to quickly determine the approximate standing of a Brahman animal Genomic EBV for a given trait relative to the Genomic EBV of all animals in the population. For example, if an animal has a GEBV of -0.2 lb for Warner-Bratzler Shear Force, we locate -0.2 lb in the ordinate of the graph for WB Shear Force (seventh graph), project a horizontal line towards 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 30%. This percentile means that approximately 30% of the animals have a Genomic EBV for WB Shear Force lower than -0.2 lb and that 70% of the animals have a Genomic EBV higher than -0.2 lb in the Florida Brahman population. It also means that this animal would be expected to have tougher meat than 30% and more tender meat than 70% of animals in the Florida Brahman population. Similar information can be obtained for GEBV from any of the 20 traits evaluated per animal in the Florida Brahman population.

Percentile graphs can also be obtained for trait indexes that include all traits within each set. We used a simple index that assigned a relative weight of (+1) if a higher GEBV for a trait is favorable, and a relative weight of (-1) if a higher GEBV for a trait is unfavorable. The indexes for each trait set had the following relative weights: 1) *Growth Index (5 traits):* birth weight direct (-1), weaning weight direct (+1), postweaning weight direct (+1), birth weight maternal (+1), and weaning weight maternal (+1); 2) *Reproduction Index (4 traits):* yearling weight adjusted to 305 days of age (+1), reproductive tract score (+1), age at first calving (-1), and first calving interval (-1); 3) *Ultrasound-Carcass Index (9 traits):* ultrasound weight (+1), ultrasound ribeye area (+1), ultrasound fat (+1), ultrasound percent intramuscular fat (+1), slaughter age (-1), hot carcass weight (+1), ribeye area (+1), backfat thickness (+1), and marbling score (+1)); and 4) *Tenderness Index (2 traits):* Warner-Bratzler shear force (-1) and tenderness score (+1). Below are percentile graphs for each one of these four indexes.