Florida Brahman: Genomic selection for tenderness, marbling, and reproductive tract score

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
Brahman is a crucial component of the Brahman-*Bos taurus* crossbred beef production system in Florida because of their high adaptability to hot and humid conditions. Although Brahman cattle are frequently criticized for the tenderness and marbling of their meat and their lower fertility compared to other breeds and crossbreds, research at the University of Florida (UF) has shown that Brahman displays a range of estimated breeding values (EBV) for fertility, growth, ultrasound, and carcass traits comparable to Angus, Brangus, and Brahman x Angus crossbreds*.* ***The aim of this project 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: tenderness, marbling, and reproductive tract score***. This project requires the utilization of as many cattle from UF and participating herds as possible to maximize genetic progress in the Florida Brahman population. We are also increasing the UF Brahman herd to 260 cows. A statewide tissue sample repository provides DNA for genotyping and a database supplies phenotypes, pedigree, and genotypes for genomic predictions in the Florida Brahman population. This information was used to compute animal genomic EBV for both target and supporting reproduction, growth, ultrasound, carcass, and meat tenderness traits.

Research and Outreach Activities
The Florida Brahman genomics project depended on phenotypic, pedigree, genotypic data from Florida Brahman and UF herds. Hence, Florida Brahman cattlemen were not only an integral part of this effort, their participation was essential to achieve the statewide goals of this project (database, tissue sample and DNA repository, animal EBV summary). Thus, we contacted all Florida Brahman breeders by email and telephone to inform them of the goals of the project, projected outcomes, and expected benefits. Eight Florida Brahman breeders agreed to contribute to this project with phenotypes, pedigree, and tissue samples for genotypes. In addition, the American Brahman Breeders Association (ABBA) provided historical phenotypic and pedigree data files until January 2017.

We conducted two rounds of estimation of variance components, heritabilities, correlations (genetic, environmental, phenotypic), and genomic EBV for three sets of traits (June 2017 and August 2017). The three sets of traits were: a) *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); b) *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 c) *Tenderness set:* Warner-Bratzler shear force (WBSF) and tenderness score (TEND). We also obtained predictions of single nucleotide polymorphism (SNP) marker effects and genomic variance accounted for by each SNP marker for each trait. Lastly, we constructed graphs of individual animal EBV for each trait as well as graphs of predicted SNP values and genomic variances accounted by each individual SNP.

The number of animals with one or more phenotypic records was 15,637 (9,327 Brahman and 6,310 Angus and Brahman-Angus crossbreds), and the number of animals in the pedigree file was 23,750 (16,818 Brahman and 6,932 Angus and Brahman-Angus crossbreds). Genotypic data were from 782 Brahman, Brahman-Angus, and Angus animals from the UF Brahman and Multibreed Brahman-Angus herds genotyped with GeneSeek GGP250k chip. Estimates of heritabilities ranged from moderate to high for all traits. In particular, the heritabilities for the three target traits were 0.47 for tenderness, 0.54 for marbling, and 0.28 for reproductive tract score. ***Heritability estimates indicated that sufficient genetic variation existed for all evaluated traits, thus selection for any of these traits would be effective in the Florida Brahman population.*** **Table 1** shows means, standard deviations (SD), minimum, and maximum values for genomic EBV from the August 2017 round of evaluations for the three sets of traits.

Table 1. Numbers of animals, means, standard deviations (SD), minimum, and maximum values of genomic EBV					
Reproduction Set	**N**	**Mean**	**SD**	**Min**	**Max**
YW, kg	23750	-0.2	9.9	-66.5	77.0
RTS, units	23750	-0.1	0.3	-1.3	1.3
AFC, d	23750	1.6	25.7	-218.9	169.8
FCI, d	23750	1.5	20.0	-102.6	161.8
Ultrasound-Carcass Set	**N**	**Mean**	**SD**	**Min**	**Max**
UW, kg	23750	-2.3	9.3	-59.2	66.5
UREA, cm^2	23750	0.0	1.4	-9.0	12.1
UBF, cm	23750	0.0	0.1	-0.5	1.0
UPIMF, %	23750	-0.1	0.2	-1.3	1.6
SLA, d	23750	0.5	11.0	-83.3	81.0
HCW, kg	23750	-1.6	10.1	-62.5	58.8
REA, cm^2	23750	-0.1	2.5	-16.2	20.3
FAT, cm	23750	0.0	0.1	-0.9	2.1
MAR, units	23750	-13.4	29.7	-127.1	234.1
Tenderness Set	**N**	**Mean**	**SD**	**Min**	**Max**
WBSF, kg	23750	0.1	0.1	-0.7	1.2
TEND, units	23750	-0.1	0.2	-1.9	1.1

We obtained DNA samples from 3,226 sires, dams, and calves (Brahman breeders = 849; UF Brahman = 404; Multibreed Brahman-Angus = 1,973). Samples were sent to GeneSeek in late November and early December of 2017 to be genotyped with either GGP250k (n = 1,771) or GGP50k (n = 1,455). We will send additional DNA samples to GeneSeek in 2018. All genotypes from 2017 and 2018 DNA samples will be used in subsequent genomic evaluations to be conducted in 2018. Outcomes of the third Florida Brahman genomic evaluation will be presented to participating Florida Brahman breeders in a group meeting scheduled for March 2018. This meeting will be followed by discussions with individual Brahman breeders on individual animal genomic EBV and implications for their individual selection and mating programs. These meetings will also help define long-term activities for the Florida Brahman Genomics Program.