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

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Specific Aims

Brahman is a key component of the Brahman-*Bos taurus* crossbred beef production system in Florida. Brahman brings great adaptability to Brahman-*Bos taurus* crossbred cattle permitting them to endure adverse hot and humid conditions. Brahman cattle are frequently criticized for the tenderness and marbling of their meat and for their lower fertility relative to other breeds and crossbred cattle. However, research at the University of Florida (UF) has shown that Brahman animals exhibit a range of EPD for fertility, growth, ultrasound, and carcass traits comparable to that of Angus, Brangus, and Brahman x Angus crossbreds. This project aims at developing 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. To maximize genetic progress in the complete population, we will utilize as many cattle from UF and participating herds as possible. We will increase UF Brahman herd size to 260 cows. We will construct a statewide tissue sample repository and a database with phenotypes, pedigree, and genotypes to conduct annual genomic evaluations of all Brahman cattle in the population. Animal genomic EPD for the three target traits will be published annually.

Anticipated Outcomes and Potential Benefits

This project seeks to increase the number of Florida Brahman cattle with improved EPD for tenderness, marbling, and reproductive tract score. To achieve this goal, we will:

- 1) Develop a statewide database with genotypes, pedigree, and phenotypes for all recorded traits (reproduction, growth, ultrasound, carcass, meat palatability) in the Florida Brahman population.
- 2) Increase the size of the UF Brahman herd to 260 cows.
- 3) Establish a statewide Brahman tissue sample (blood, hair, ear notches) and DNA repository.
- 4) Conduct annual genomic evaluations for tenderness, marbling, and reproductive tract score using information from phenotypes, pedigree, and genotypes.
- 5) Publish an annual summary with animal genomic EPD to aid selection and mating decisions to increase tenderness, marbling, and reproductive tract score within and across Florida Brahman herds.
- 6) Make semen and embryos from animals with favorable EPD for the three target traits as well as sires and heifers not used as replacements available to Florida cattlemen.

Educational Products and Outreach Activities

This genomics project depends on phenotypic and pedigree data, and genotypes from herds from the University of Florida and from Florida Brahman cattlemen. In fact, Florida Brahman cattlemen are an integral component of this project, thus their participation is crucial to achieve the statewide goals specified for this project (trait database, tissue sample and DNA repository, animal EPD summary). Thus, we will involve and keep Florida Brahman cattlemen informed of the work carried out in this project from the beginning and throughout its execution. Specifically, we will carry out the following educational and outreach activities:

- 1) We will contact Brahman cattlemen (email, telephone) to request their participation in the project (our goal is to have at least 500 cows from private herds in the project) in one of the two following options:
 - 1.1) Phenotypic and pedigree information only (option 1).
 - 1.2) Phenotypic and pedigree information, and tissue samples (option 2).
- 2) We will conduct meetings to address and provide information on the following aspects:
 - 2.1) Phenotypic, pedigree, and tissue samples needed from each participating Brahman cattleman.
 - 2.2) Structure of the Florida Brahman population involved in this project including connections through the utilization of sires to connect herds.
 - 2.3) Genomics aspects of the project, i.e., the inclusion of genomic information in the unified genomic evaluation procedure, the utilization of genomic EPD computed in this project for selection within and across herds, and the relationship of these Florida Brahman EPD with national Brahman EPD.
 - 2.4) The Florida Brahman genomic animal summary (i.e., explanatory information, traits, genetic parameters, trends).
 - 2.5) Utilization of genomic EPD information to construct indices to be used for mating and selection decisions.
- 3) We will provide reports on:
 - 3.1) Statewide trait database containing phenotypic, pedigree, and genotypic information.
 - 3.2) Statewide tissue sample and DNA repository and genotyping with Gene-Seek high and low-density genotyping chips.
- 4) We will write two articles for The Florida Cattleman & Livestock Journal to provide information on the design and outcomes of this project.
- 5) We will construct an internet page containing an online version of the Florida Brahman genomic animal summary and related information.

Areas of Work (January to August 2017)

1) Collaborative work and exchange of information with Florida Brahman breeders (emails, telephone calls, meetings).

1.1) Obtained the complete list of Florida Brahman breeders from the American Brahman Breeders Association (ABBA; n = 97; January 10, 2017).

1.2) First email (January 13, 2017) to Florida Brahman breeders with ABBA member identification number (n = 93) inviting them to participate in the genomics project, requesting an answer by January 23, 2017, and indicating that a first meeting would be scheduled for late January or early February. Three attachments: a) Approach_FL Brahman Genomic Selection Project_January-11-2017.pdf: detailed approach of the genomics project; b) EducProd&OutreachActiv_January-11-2017.pdf: educational products and outreach activities; and c) Summary_FL Brahman Genomic Selection Project_January-11-2017_aaaa.pdf: summary of the genomics project.

Second email (January 23, 2017) to all Florida Brahman breeders inviting them to participate in the genomics project. Email followed by telephone calls (January 23 to 30).

Response to invitation to participate in the project (email; telephone): Yes = 12; Would think about it = 5; No or no answer = 3. Final number of participants = 9 (3 breeders decided not to participate at a later date). One Brahman breeder decided to participate in August 2017. Current number of participants = 8 (Larry Barthle; Drew Tucker; Kempfer Cattle; Doc Parting_Ricky Booth; Larry Ford; John Traxler; Sean Sexton; Markus Shakelford; August 23, 2017).

1.3) Work on setting up the first meeting with Brahman breeders (emails, telephone calls; Ricky Booth, George Kempfer, Henry Kempfer, Raluca Mateescu, Owen Rae, Danny Driver; January 13 to February 22, 2017). Preparation of PowerPoint presentation for the first meeting with Florida Brahman breeders (16 slides; February 07-09, 2017).

Meeting occurred at the Florida Cattlemen's Association headquarters (800 Shakerag Road, Kissimmee, FL 34744) on February 22, 2017 from 3:30 PM to 5:45 PM. Present at this meeting were George Kempfer, Henry Kempfer, Drew Tucker, Ricky Booth, Raluca Mateescu, and Mauricio Elzo. Meeting included a presentation on objectives, population structure, target and supporting traits, multiple-trait genomic evaluation for reproductive tract score, tenderness, and marbling, and selection indices. Discussion involved data contributions by breeders, incentives, and benefits of participation in the project. The long-term nature of the project was emphasized.

1.4) Conference call (February 28, 2017) to discuss reproductive tract score measurements. Present in the call were George Kempfer, Drew Tucker, Larry Barthle, Chad Carr, Owen Rae, and Mauricio Elzo. Items discussed were: a) Reproductive tract score description and visit schedule (March 1: Larry Barthle; March 15-16: Kempfer Cattle, Drew Tucker, Doc Partin Ranch_Ricky Booth); and b) Feedlot and carcass information data collection, contemporary groups, and schedule for groups to be sent to Quincey's Farm (Mr. Larry Barthle sent 14 bulls to Quincey's in March).

1.5) Exchanged numerous emails and telephone calls between March and August 2017 with participating Florida Brahman breeders concerning pedigree and phenotypic information as well as tissue sampling (ear notches, blood, semen) needed for the Brahman genomics project. Explained the

importance of pedigree and phenotypic information from all animals in the herd (i.e., registered and non-registered) to increase the accuracy of genomic predictions.

1.6) Attended the Florida Brahman Field Day at Kempfer Cattle Company in Saint Cloud, Florida, on April 29, 2017 (Danny Driver, M. A. Elzo). Discussed the Brahman genomics project with John Traxler, Jay Sizemore, George Kempfer, and Larry Barthle's son.

1.7) Visited Kempfer Cattle farm with attendants to the 2017 S-1064 Southern Regional Meeting organized by UF (May 26, 2017). Various aspects of the Florida Brahman genomics project were presented and discussed during the S-1064 sessions in Gainesville and at the Kempfer Cattle farm. George Kempfer explained structure, management, and selection goals of Kempfer Cattle Co.

1.8) Prepared and emailed incentive invoices for approval from all participating Florida Brahman breeders (July 20, 2017).

2) Development of the Florida Brahman database and tissue sample repository

2.1) Requested Florida Brahman breeders (email, telephone calls, and meetings) to contribute with pedigree and phenotype information on target traits (i.e., tenderness, marbling, and reproductive tract score), dates and weights (e.g., insemination, birth, weaning, yearling, other weights), ultrasound records, carcass data (e.g., hot carcass weight, ribeye area, marbling), and reproductive tract score data (collected by Dr. Owen Rae) starting in January 2017.

2.2) Emailed prototypes of Excel sheets for calves, sires, and dams (February 27, 2017) to help Florida Brahman breeders with data collection and submission to this project. Received phenotypic information (calving, preweaning, ultrasound, and reproductive tract score on March 15, 2017, and 2016 heifer ultrasound data on March 22, 2017) on ABBA pdf file reports from Mr. Larry Barthle. Converted pdf files to Excel files using a combination of Word and Adobe Acrobat Pro DC 2015.

Utilized Mr. Barthle's information to construct prototypes for pedigree and calf work files for all participating Florida Brahman breeders (emailed prototype files on March 22, 2017).

To facilitate data retrieval and additional processing by breeders and researchers, ABBA could make information on reports available both in pdf and text formats (e.g., ABBA "pipe-delimited" text files, i.e., fields separated by "|", and csv: comma separated txt files). Files formatted as text could be easily read in Excel for further processing and research.

2.3) Collection of reproductive tract scores and blood samples (Dr. Owen Rae) from four farms: a) Mr. Larry Barthle: 13 yearling heifers and scrotal circumferences on 17 yearling bulls (March 01, 2017); b) Drew Tucker: 13 heifers (March 16, 2017); c) Kempfer Cattle: 23 heifers (March 16, 2017); d) Doc Partin: 22 heifers; Ricky Booth, Manager (March 16, 2017).

2.4) Contacted Mr. Chris Shivers, Executive Vice-President of ABBA to explore the possibility of obtaining phenotypic and pedigree records from Florida Brahman breeders submitted to ABBA (emails; telephone call; January 17 to February 3, 2017). Attached a list of Florida Brahman breeders and their ABBA numbers, summary of the Brahman genomics project, and detailed explanation of phenotypic records we could use in the project.

Received the initial set of phenotypic and pedigree files from ABBA (Chris Shivers, Peter Paine) on March 27, 2017. Requested information on traits and units of measurement in the ABBA phenotype file (uncorrected weights in lb, scrotal circumference in cm*10, rump fat in cm*100, rib fat in cm*10, ribeye are in squared inches*10, intramuscular fat in %*10) and sex of animal on March 27, 2017. Received sex information for animals in the ABBA pedigree file on March 30, 2017. These files provided information on ABBA registration numbers and birth dates on sires and dams reported by Florida Brahman breeders, and provided the largest fraction of information on growth traits for cattle from participating Florida Brahman breeders.

2.5) Contacted Ms. Armelinda Ibarra requesting phenotypes and pedigree data for approximately 500 Brahman animals without information in the ABBA pedigree and data files sent on March 30, 2017 (August 10, 2017).

2.6) Received pedigree and phenotypic information from participating Brahman breeders at various times between March and August 2017. Constructed individual herd Excel files with the information received and sent these files back to Brahman breeder. The goal was to create individual herd Excel files that could be used to exchange information expeditiously over the coming years.

2.7) Sent 1,600 ear notch sample kits and 9 applicators to the eight participant Florida Brahman breeders by FedEx (May 08, May 15, and August 14, 2017).

2.8) Received 630 blood and ear notch samples from 5 participating Florida Brahman Breeders between March 01 and August 21, 2017.

2.9) Processing of ear notch, blood, and semen samples as well as extraction of DNA from Florida Brahman and UF Brahman and Brahman-Angus multibreed herds is taking place at Dr. Raluca Mateescu's laboratory prior to submission to GeneSeek for genotyping with GeneSeek 250k or 50k. Brahman animals from all herds will be genotyped with the GeneSeek 250k chip. Because there is insufficient funds to genotype all animals with GeneSeek 250k, Brahman-Angus sires and dams will be genotyped with GeneSeek 250k whereas younger animals (weanlings and some yearlings) will be genotyped with GeneSeek 50k. It should be emphasized that information from the UF Brahman-Angus Multibreed herd is providing all the information for carcass traits (including marbling, Warner-Bratzler shear force, and tenderness score), most of the information for ultrasound traits, and a large fraction of growth traits. Thus, strengthening of the connections between animals in the Brahman-Angus multibreed herd and animals from the UF and Florida Brahman breeder herds through genotype information will increase the accuracy of EBV relative to connections through pedigree alone.

2.10) Processed an invoice from GeneSeek to genotype 1,080 animals with the Bovine GGP F250K chip and 1,097 animals with the Bovine GGP 50K chip.

2.11) Received an additional \$60,000 for the Florida Genomics project on August 22, 2017. These funds (minus 12% for indirect costs = \$7,200, i.e., \$52,800) will be used for genotyping additional animals in the population.

3) Development of a statewide genomic evaluation for tenderness, marbling, and reproductive tract score

3.1) Developed a FORTRAN program (**ABBADData**) to construct joint pedigree and phenotypic files that included information from participating Florida Brahman breeders, ABBA, UF Brahman, and UF Brahman-Angus multibreed sources. Common link among datasets: registration numbers for animals. If unavailable, constructed a unique number using: a) the sequential herd number, year, and herd tag number for animals without ear notch samples; and b) the sequential herd number and the numeric part of the Allflex number for animals with ear notch samples. This program

3.2) Constructed edited pedigree, phenotype, and genotype files for genomic evaluation with the BLUPF90 Family of Programs from the University of Georgia using program ABBADData. The phenotype file contained all available reproduction, growth, ultrasound, carcass, and meat palatability traits of potential interest for genomic evaluation in the Florida Brahman population. The pedigree file included animals from the ABBA database, Florida Brahman breeders, and UF Brahman and Brahman-Angus multibreed herds. Genotypic data were from UF Brahman and Brahman-Angus multibreed herds genotyped with GeneSeek Bovine GGP F250K chip.

3.3) Conducted two rounds of estimation of variance components, heritabilities, correlations (genetic, environmental, phenotypic), and genomic-polygenic EBV for three sets of traits as data became available (the first one in June 2017, and the second one in August 2017; Only results from the second round are reported here). 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 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 files was 23,750 (16,818 Brahman and 6,932 Angus and Brahman-Angus crossbreds). Genotypic data were from 782 Brahman, Brahman-Angus, and Angus cattle from the UF Brahman and Brahman-Angus multibreed herds genotyped with GeneSeek Bovine GGP F250K chip.

Table 1 shows numbers of records, means, standard deviations, and heritabilities for traits in the three evaluation sets.

Table 1. Numbers of records, means, standard deviations, and heritabilities				
Reproduction Set	N	Mean	SD	Heritability
YW, kg	2709	342.3	56.1	0.48 ± 0.05
RTS, units	664	3.0	1.2	0.28 ± 0.08
AFC, d	3205	1065.1	84.9	0.48 ± 0.05
FCI, d	1565	438.8	118.7	0.26 ± 0.06

Ultrasound-Carcass Set	N	Mean	SD	Heritability
UW, kg	2709	353.0	70.7	0.44 ± 0.03
UREA, cm ²	2709	56.1	12.2	0.35 ± 0.02
UBF, cm	2715	1.1	1.7	0.16 ± 0.01
UPIMF, %	2698	2.9	1.2	0.34 ± 0.02
SLA, d	2040	557.8	53.1	0.70 ± 0.02
HCW, kg	2027	334.4	45.8	0.70 ± 0.02
REA, cm ²	1989	8.0	1.1	0.56 ± 0.02
FAT, cm	2019	1.3	0.5	0.36 ± 0.02
MAR, units	2024	401.5	93.1	0.54 ± 0.03
Tenderness Set	N	Mean	SD	Heritability
WBSF, kg	1291	4.0	1.1	0.17 ± 0.03
TEND, units	824	5.4	0.9	0.47 ± 0.06

Table 2 presents numbers of animals, means, standard deviations, minimum, and maximum values of genomic EBV (GEBV) for traits in the three evaluation sets.

Table 1. Numbers of animals, means, standard deviations, 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

Genomic EBV for the 16,818 evaluated Florida Brahman animals are shown as **red diamonds** in **Figure 1** for the four traits in the reproduction set, **Figure 2** for the nine traits in the ultrasound-carcass set, and **Figure 3** for the two traits in the tenderness set.

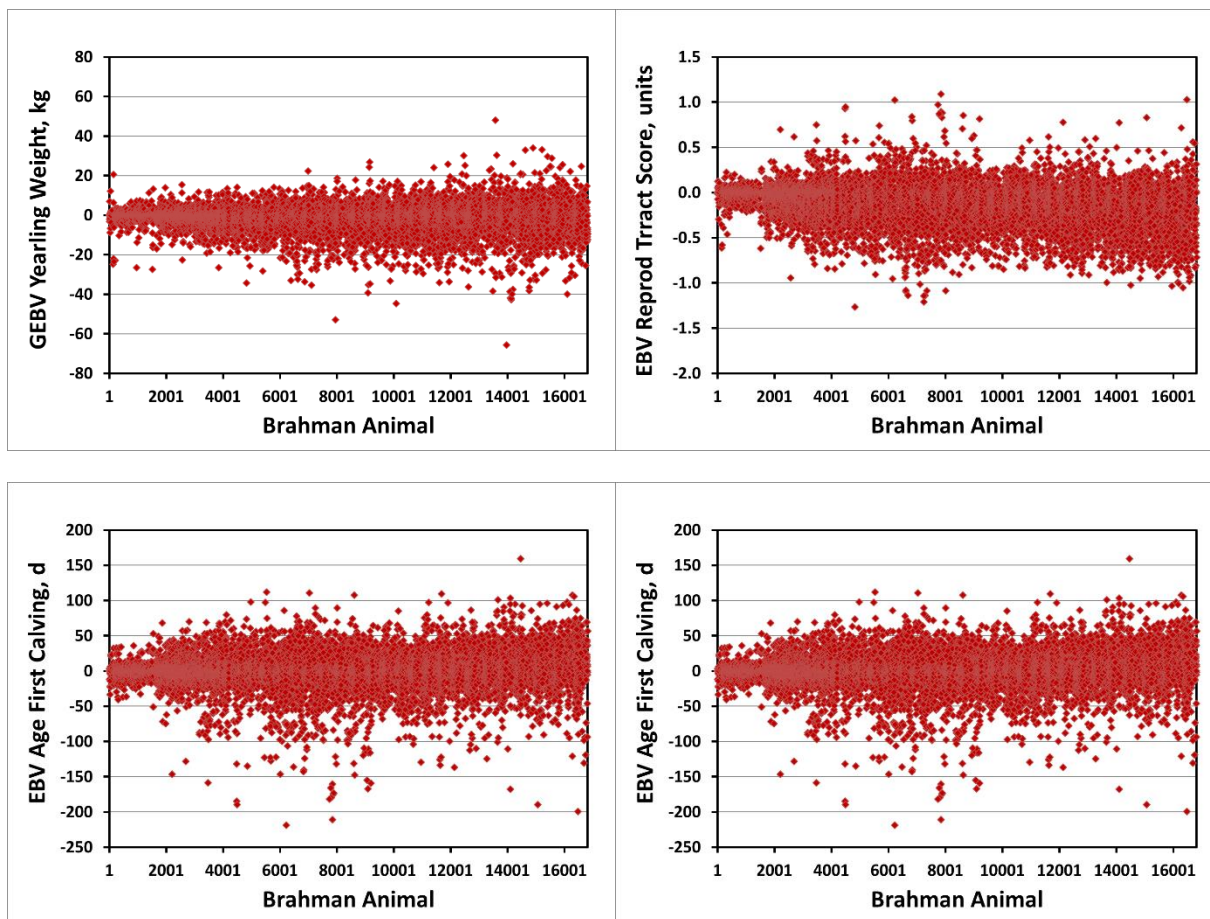
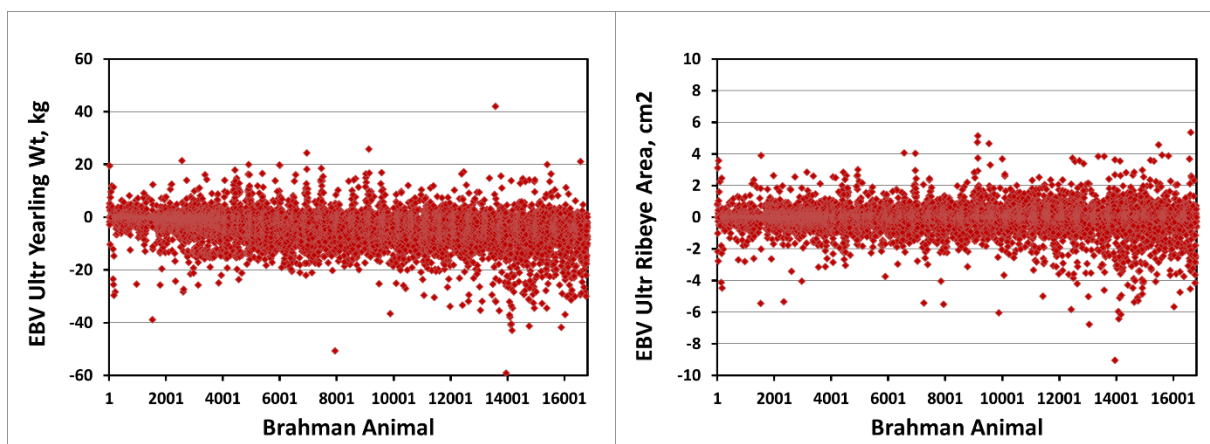
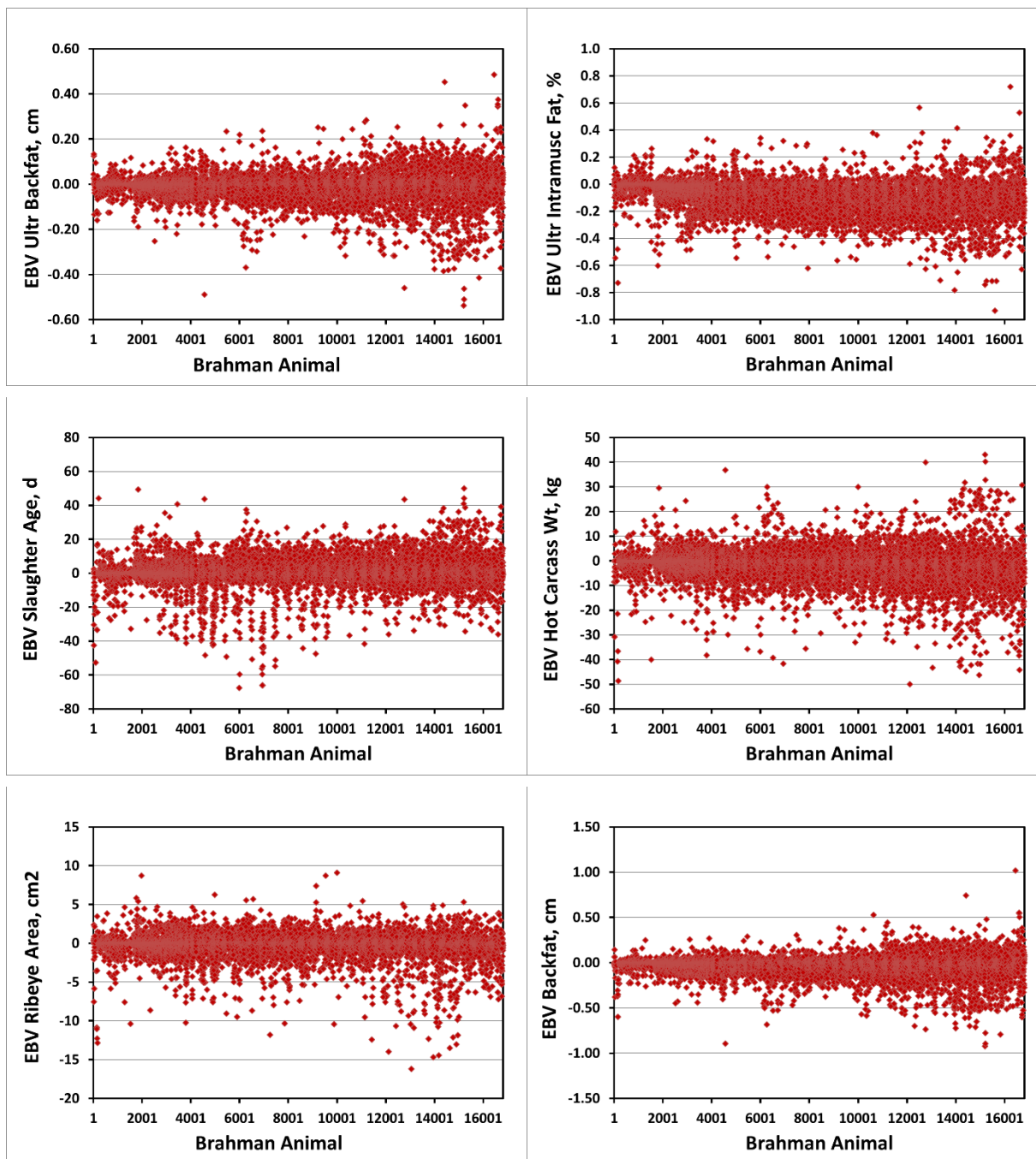


Figure 1. Florida Brahman animal genomic EBV for yearling weight adjusted to 305 days of age (YW), reproductive tract score (RTS), age at first calving (AFC), and calving interval (FCI)





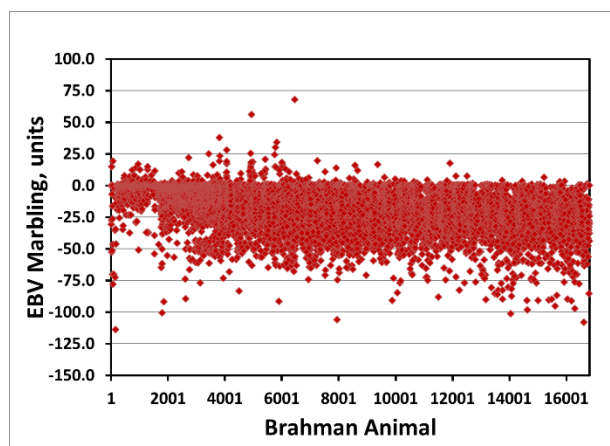


Figure 2. Florida Brahman animal genomic EBV for ultrasound weight (UW), ultrasound ribeye area (UREA), ultrasound fat (UBF), ultrasound percent intramuscular fat (UPIMF), slaughter age (SLA), hot carcass weight (HCW), ribeye area (REA), backfat thickness (FAT), and marbling score (MAR)

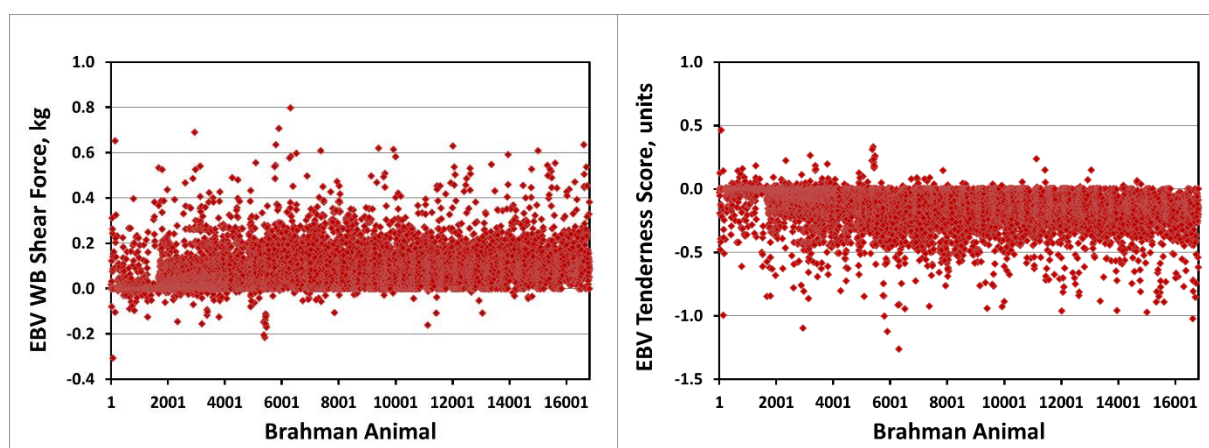


Figure 3. Florida Brahman animal genomic EBV for Warner-Bratzler shear force (WBSF) and tenderness score (TEND)

Figures 1, 2, and 3 clearly show that there is substantial genetic variation available in all traits in the Florida Brahman population for genomic selection to be effective, including the three target traits (tenderness, marbling, and reproductive tract score). Thus, implementation of a genomic selection program for the target traits and other traits in the reproduction, ultrasound-carcass, and tenderness set should yield changes in the Brahman population in the desired direction. This means a larger number of Brahman cattle with more tender meat, more marbling, and reaching puberty and having their first calf at younger ages.

Graphs of predictions of and variances accounted for single nucleotide polymorphism (SNP) marker effects are shown in **Appendix 1** for the four traits in the reproduction set, **Appendix 2** for the nine traits

in the ultrasound-carcass set, and **Appendix 3** for the two traits in the tenderness set. Predictions of SNP are shown in the first four graphs of Appendix 1, the first nine graphs of Appendix 2, and the first two graphs of Appendix 3. Markers within each chromosome are in different colors. The remaining graphs in each appendix show the percent of the genetic variance accounted for by each SNP marker. Traits in Appendix 1 are yearling weight adjusted to 305 days of age (Trait 1), reproductive tract score (Trait 2), age at first calving (Trait 3), and calving interval (Trait 4). Traits in Appendix 2 are ultrasound weight (Trait 1), ultrasound ribeye area (Trait 2), ultrasound fat (Trait 3), ultrasound percent intramuscular fat (Trait 4), slaughter age (Trait 5), hot carcass weight (Trait 6), ribeye area (Trait 7), backfat thickness (Trait 8), and marbling score (Trait 9). Traits in Appendix 3 are Warner-Bratzler shear force (Trait 1) and tenderness score (Trait 2). **As expected for quantitative traits determined by large numbers of genes, most SNP markers had small effects for all traits. This was also reflected in the genetic variance accounted for each SNP marker. However, SNP markers with bigger effects were found in chromosomes 22, 23, 27, 28, 29, and X for most traits in the reproductive, ultrasound-carcass, and tenderness sets, except for reproductive tract score and marbling that had influential SNP markers across most chromosomes.**

4) Increase the size of the UF Brahman herd

This part of the project is being developed by the concomitant FCEF project on development and expansion of the UF Brahman herd led by Dr. Geoffrey Dahl. Two rounds of in vitro fertilization and embryo transfer (IVFET) were carried out and 45 sexed female embryos were located and purchased from Southern Cattle Co. These resulted in 47 IVF pregnancies. In addition, there are 88 pregnancies in the Brahman herd by AI and natural service (62 cows, 15 2-yr old heifers, and 11 yearling heifers), for a combined total of 135 pregnancies. For details, please refer to the second report of Dr. Dahl's project.

5) Equipment purchases

3.1) Tissue sampling and DNA repository: a) Ultralow Temperature Upright Freezer, 25.6 cu ft., -86°C, to store tissue and DNA samples; b) Ear-Notch Kits for tissue sampling (n = 1,000). Requested numbers of animals to be genotyped (calves, sires, dams) from all participating Florida Brahman breeders (n = 560 for 3 herds; Need animal numbers for the other 9 participating herds); b) Allflex ear notch kits (n = 2,600) and applicators (n = 40) from Zoetis (April 24 and May 8, 2017).

3.2) Database construction and genomic evaluation: a) Dell Workstation; b) FORTRAN Compiler.

6) Next steps for Fall 2017 and 2018

5.1) Continue to collaborate and exchange information by phone, email, and in-person meetings with participating Florida Brahman breeders. Emphasize the importance of their role in pedigree, phenotype, and tissue sample collection for the continuity of the Florida statewide genomic evaluation system. In particular, highlight the importance of collecting phenotypic records on all animals in each herd at least for some traits (e.g., weaning weight) to avoid genomic selection biases due to missing records.

- 5.2) Add new information from ABBA, Florida Brahman breeders, and UF Brahman and Brahman-Angus multibreed herds to the accumulated Florida Brahman pedigree, phenotype, and genotype data files for the next series of genomic evaluations.
- 5.3) Collect tissue samples from all newborn animals and from new animals brought into the herd.
- 5.3) Conduct a third genomic evaluation of the Florida Brahman population for the three sets of traits (reproductive, ultrasound-carcass, and tenderness) utilizing all available historical information from ABBA, Florida Brahman breeders, and UF Brahman and Brahman-Angus multibreed herds and all available genotypic data.
- 5.4) Conduct periodic genomic evaluation updates for tenderness, marbling, and reproductive tract score of Florida Brahman in 2018 as new data pedigree, phenotype, and genotype data becomes available.
- 5.5) Publish one article on the Florida Cattleman & Livestock Journal providing information on current activities and outcomes of this project.

7) Publications

- Elzo, M. A., R. Mateescu, C. Carr, D. O. Rae, T. Scheffler, J. Scheffler, J. D. Driver, and M. D. Driver. 2017. The Florida Brahman Genomic Selection Project: Initial Steps. The Florida Cattleman & Livestock Journal, 81(9):46-52. [**Appendix 4**]
- Elzo, M. A., R. G. Mateescu, D. O. Rae, C. C. Carr, T. L. Scheffler, J. M. Scheffler, M. D. Driver, and J. D. Driver. 2017. Genomic-polygenic EBV for reproduction, ultrasound-carcass, and tenderness traits in the Florida multibreed Brahman-Angus population. Proc. 11th World Conf. Gen. Appl. Livest. Prod., Auckland, New Zealand, February 11-16, 2018 (Submitted). [**Appendix 5**]