# 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:

- 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 April29, 2017 (Danny Driver, M. A. Elzo). Discussed the Brahman genomics project with John Traxler, JaySizemore, 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, 2107) 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. Barthles'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 (**ABBAData**) 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 ABBAData. 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				
<b>Reproduction Set</b>	N	Mean	SD	Heritability
YW, kg	2709	342.3	56.1	0.48 ± 0.05
RTS, units	664	3.0	1.2	$0.28 \pm 0.08$
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	Ν	Mean	SD	Heritability
UW, kg	2709	353.0	70.7	$0.44 \pm 0.03$
UREA, cm <sup>2</sup>	2709	56.1	12.2	0.35 ± 0.02
UBF, cm	2715	1.1	1.7	$0.16 \pm 0.01$
UPIMF, %	2698	2.9	1.2	$0.34 \pm 0.02$
SLA, d	2040	557.8	53.1	0.70 ± 0.02
HCW, kg	2027	334.4	45.8	0.70 ± 0.02
REA, cm <sup>2</sup>	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	$0.54 \pm 0.03$
Tenderness Set	Ν	Mean	SD	Heritability
WBSF, kg	1291	4.0	1.1	0.17 ± 0.03
TEND, units	824	5.4	0.9	$0.47 \pm 0.06$

**Table 2** presents numbers of animals, means, standard deviations, minimum, and maximum values ofgenomic 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	Ν	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	Ν	Mean	SD	Min	Max
UW, kg	23750	-2.3	9.3	-59.2	66.5
UREA, cm2	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, cm2	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	Ν	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)





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. 11<sup>th</sup> World Conf. Gen. Appl. Livest. Prod., Auckland, New Zealand, February 11-16, 2018 (Submitted). [Appendix 5]

Manhattan Plot SNP Solution - Trait: 1 Effect: 6



#### Manhattan Plot SNP Solution - Trait: 2 Effect: 6



Manhattan Plot SNP Solution - Trait: 3 Effect: 6



Manhattan Plot SNP Solution - Trait: 4 Effect: 6



Manhattan Plot SNP Variance explained by 1adjacents SNP window - Trait: 1 Effect: 6



Manhattan Plot SNP Variance explained by 1adjacents SNP window - Trait: 2 Effect: 6



Manhattan Plot SNP Variance explained by 1adjacents SNP window - Trait: 3 Effect: 6



Manhattan Plot SNP Variance explained by 1adjacents SNP window - Trait: 4 Effect: 6



Manhattan Flot SNF Variance explained by faujacents SNF whittow - frait. 4 Effect

Manhattan Plot SNP Solution - Trait: 1 Effect: 5



Manhattan Plot SNP Solution - Trait: 2 Effect: 5



Manhattan Plot SNP Solution - Trait: 3 Effect: 5



#### Manhattan Plot SNP Solution - Trait: 4 Effect: 5



Manhattan Plot SNP Solution - Trait: 5 Effect: 5



Manhattan Plot SNP Solution - Trait: 6 Effect: 5



Manhattan Plot SNP Solution - Trait: 7 Effect: 5



Manhattan Plot SNP Solution - Trait: 8 Effect: 5



#### Manhattan Plot SNP Solution - Trait: 9 Effect: 5



#### Manhattan Plot SNP Variance explained by 1adjacents SNP window - Trait: 1 Effect: 5



Manhattan Plot SNP Variance explained by 1adjacents SNP window - Trait: 2 Effect: 5



Manhattan Plot SNP Variance explained by 1adjacents SNP window - Trait: 3 Effect: 5



Manhattan Plot SNP Variance explained by 1adjacents SNP window - Trait: 4 Effect: 5



Manhattan Plot SNP Variance explained by 1adjacents SNP window - Trait: 5 Effect: 5



Manhattan Plot SNP Variance explained by 1adjacents SNP window - Trait: 6 Effect: 5



Manhattan Plot SNP Variance explained by 1adjacents SNP window - Trait: 7 Effect: 5



Manhattan Plot SNP Variance explained by 1adjacents SNP window - Trait: 8 Effect: 5



Manhattan Plot SNP Variance explained by 1adjacents SNP window - Trait: 9 Effect: 5



Manhattan Plot SNP Solution - Trait: 1 Effect: 5



Manhattan Plot SNP Solution - Trait: 2 Effect: 5







Manhattan Plot SNP Variance explained by 1adjacents SNP window - Trait: 2 Effect: 5

Manhattan Plot SNP Variance explained by 1adjacents SNP window - Trait: 1 Effect: 5

# **UF-Gainesville Beef Cattle News Corner**

# The Florida Brahman Genomic Selection Project: Initial Steps

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# Introduction

Brahman is an essential component of crossbred beef production systems in Florida because of its great adaptability and endurance under the hot and humid conditions of this subtropical region. However, Brahman cattle are frequently criticized for the level of tenderness and marbling of their meat as well as their lower fertility relative to Bos taurus breeds and Brahman-Bos taurus crossbred cattle. Nevertheless, our research at the University of Florida (UF) has shown that Brahman animals display a range of EPD (expected progeny differences) for fertility, growth, ultrasound, and carcass traits comparable to that of Angus, Brangus, and Brahman × Angus crossbreds. The substantial genetic diversity among Brahman cattle observed in the UF cattle herds indicated that genetic improvement for these traits in Florida could be achieved through a concerted long-term selection effort. To maximize genetic progress throughout Florida, all available private Florida Brahman herds and the UF herds should participate in this endeavor. This was the original idea behind the Florida Brahman Genomic Selection Project. 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 of high economic importance: meat tenderness, marbling, and reproductive tract score, a trait closely associated with fertility and age at first calving. The Florida Brahman project will generate genomic EPD for the three target traits as well as for various supporting traits (e.g., weaning and yearling weights, ultrasound traits, other carcass traits) utilizing pedigree, phenotypes, and genotypes. Genomic EPD for several traits would later be combined using relative economic weights to construct selection indexes for use within and across herds. Although this project was funded by the Florida Cattle Enhancement Board for 2 years (January 2017 to December 2018), it is actually a long-term project that should continue uninterrupted over the coming years to accomplish the intended goals and to appropriately assess its impact on the Florida Brahman population.

# **Research and Outreach Activities**

The Florida Brahman Genomic Selection Project depends on pedigree, phenotypes, and genotypes from Florida Brahman private herds and UF herds. *In fact, Florida Brahman breeders* 

are an integral part of this project; their participation is crucial to achieve the statewide goals specified for this project (pedigree and phenotype database, tissue sample and DNA repository, genomic EPD summary). Consequently, our first task was to contact all Brahman breeders in Florida through email and telephone calls informing them of the project, goals, anticipated outcomes, and expected benefits. A meeting at the Florida Cattlemen's Association in February of 2017 was a turning point. Currently, eight Brahman breeders have confirmed their participation in the project. Their contribution consists of pedigree records (animals, sires, dams), phenotypic records (reproductive tract scores, growth, ultrasound, and carcass), and tissue samples for genotyping with a high-density chip (GeneSeek GGP250k). In addition, Mr. Chris Shivers, Executive Vice-President of the American Brahman Breeders Association (ABBA) provided us with the historical pedigree and phenotype files from all Florida Brahman breeders that submitted information from 1976 to 2016. We are currently constructing the accumulated pedigree and phenotype files needed for the Florida Brahman genomic evaluation using information supplied by contributing Florida Brahman breeders, ABBA, and UF Brahman and Brahman-Angus multibreed herds. Table 1 shows the current number of animals in the pedigree and phenotype files.

Table 1. Numbers of pedigree and phenotype records as of April 2017			
Dataset	Pedigree file	Phenotype file	
Florida Brahman breeders (April 2017)	198	115	
ABBA (All years; Unedited files)	15,844	7,358	
UF Brahman herd	673	446	
UF Brahman-Angus Multibreed herd	8,302	6,755	

It should be emphasized that these numbers of animals and records correspond to unedited files; numbers of animals and records in the 2017 genomic evaluation will be smaller. However, the information from these four sources of data gives this project an excellent starting point. We are currently in the process of collecting tissue samples from a large number of animals from participating Brahman breeders and UF herds (calves, yearlings, 2-year olds, cows, and sires) that will be genotyped with high (GeneSeek GGP250k) and medium density chips (GeneSeek GGP 50k) in 2017. Genotypes from these animals will be added to the existing Illumina 3k from 1,300 animals, GGP150k from 120 animals, and GGP250k from 800 animals to be used in the first statewide Brahman genomic evaluation in 2017. The resulting edited pedigree, phenotype, and genotype files will be used to compute genomic EPD for the three target traits (meat tenderness, marbling, and reproductive tract score) as well as supporting traits (growth, ultrasound, and carcass) in the second semester of 2017. Substantial amount of information from Brahman breeders exist for growth and ultrasound traits; however, most of the information for meat tenderness, marbling, reproductive tract scores, and carcass traits will come from the UF

Brahman-Angus and Brahman herds. Thus, we will likely see a large variation among genomic EPD from Brahman animals in the complete Florida Brahman population similar to that observed in our research with UF Brahman and Brahman-Angus multibreed animals. Examples of this variation in genomic EPD from UF cattle herds are shown for ribeye area and marbling in Figure 1 below. Red diamonds represent EBV for individual animals. Brahman animals are those with Brahman fraction = 32, Angus are those with Brahman fraction = 0, and Brahman-Angus crossbreds have Brahman fractions ranging from 1/32nds to 31/32nds.



This variability among Brahman genomic EPD will greatly facilitate the identification of superior animals for meat tenderness, marbling, and reproductive tract scores to be used as parents of the next generation within and across Brahman herds. Continued genomic evaluation and selection of animals in the Florida Brahman population over the coming years should yield measurable progress for the three target as well as supporting traits. *The larger the participation of private Brahman breeders in this program, the larger the chances of identifying individual animals with uniquely favorable meat tenderness, marbling, and reproductive tract scores.* Hence the importance of the continued participation of the largest possible number of private Brahman breeders in the Florida Brahman genomic selection program.

For more information on this project or interest in joining the project, please contact Dr. Mauricio Elzo (maelzo@ufl.edu or 352-392-7564).

# Genomic-polygenic EBV for reproduction, ultrasound-carcass, and tenderness traits in the Florida multibreed Brahman-Angus population

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# Summary

The objectives of this research were to estimate genomic-polygenic parameters and EBV for sets of reproduction, ultrasound-carcass, and tenderness traits as well as to assess EBV trends as Brahman percentage increased from 0% to 100% percent in the state-wide Florida multibreed Brahman-Angus population. Reproduction set heritabilities were high for yearling weight adjusted to 365 d ( $0.53 \pm 0.05$ ), moderate for reproductive tract score  $(0.26 \pm 0.04)$ , and low for age at first calving  $(0.17 \pm 0.04)$  and first calving interval (0.09) $\pm$  0.02). Ultrasound-carcass set heritabilities were high for ultrasound weight (0.57  $\pm$ 0.05), slaughter age (0.57  $\pm$  0.04), hot carcass weight (0.57  $\pm$  0.04), ribeye area (0.55  $\pm$ 0.03), and marbling (0.50  $\pm$  0.05), moderate for ultrasound ribeye area (0.35  $\pm$  0.03), ultrasound intramuscular fat  $(0.33 \pm 0.03)$ , and backfat thickness  $(0.32 \pm 0.03)$ , and low for ultrasound backfat (0.07  $\pm$  0.01). Tenderness set heritabilities were low for Warner-Bratzler shear force  $(0.17 \pm 0.03)$  and moderate for tenderness score  $(0.47 \pm 0.06)$ . Heritability estimates indicated that genomic-polygenic selection for the target traits of the Florida Enhancement Fund project currently underway (reproductive tract score, marbling, and tenderness) should be feasible. The wide range of EBV among animals of all breed compositions indicated that the best animals regardless of their breed composition should be chosen as replacements if genetic progress is to be optimized in this multibreed population.

Key words: beef, cattle, genomic, evaluation, multibreed

# Introduction

Brahman is a key component of the Brahman-*Bos taurus* 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 (Johnson *et al.*, 1990; Wheeler *et al.*, 2010; Elzo *et al.*, 2012). 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 × Angus crossbreds (Elzo *et al.*, 2015a, b, 2016). These studies led to a Florida state-wide project initiated in 2017 with the aim of developing a selection and mating program for Brahman and Brahman crossbred cattle focused on genomic selection and assortative mating to improve tenderness, marbling, and reproductive tract score. This project required estimation of genomic-polygenic variance and covariance components for reproduction, ultrasound, and carcass traits to obtain genomic-polygenic EBV for all Florida Brahman, Angus, and Brahman-Angus animals using all available information from Brahman breeders as well as the UF Brahman and multibreed Brahman-Angus herds. Thus, the objectives of this research were: 1) to estimate genomic-polygenic parameters for sets of reproduction, ultrasound-carcass, and tenderness traits; 2) to obtain genomic-polygenic EBV for all these traits; and 3) to assess genomic-polygenic EBV trends as Brahman percentage increased from 0% to 100% percent in the state-wide Florida multibreed Brahman-Angus population.

# **Materials and Methods**

#### Animals, feeding, and management

The research protocol was approved by the University of Florida Institutional Animal Care and Use Committee (IACUC protocol number 201003744). Animals were from four private Florida Brahman herds plus animals from the multibreed Angus-Brahman (MAB) and Brahman herds of the University of Florida (UF), Gainesville. The dataset contained 2,739 calves born from 2005 to 2016 with phenotypic data for various traits (637 bulls, 1,083 heifers, and 1,019 steers). Calves were the progeny of 218 sires and 1,170 dams. Matings in private herds were Brahman-Brahman only. Mating in the MAB herd followed a diallel design where sires from six breed groups were mated to dams of these same six breed groups (Elzo & Wakeman, 1998). These six breed groups were: BG1 = (1.0 to 0.80) A (0.0 to 0.20) B, BG2 = (0.79 to 0.60) A (0.21 to 0.40) B,BG3 = (0.625) A (0.375) B, BG4 = (0.59 to 0.40) A (0.41 to 0.60) B, BG5 = (0.39 to 0.40) A (0.41 to 0.40.20) A (0.61 to 0.80) B, and BG6 = (0.19 to 0.0) A (0.81 to 1.00) B, where A = Angus and B = Brahman. Number of calves were 790 in BG1, 363 in BG2, 304 in BG3, 482 in BG4, 245 in BG5, and 550 in BG6. Calves were raised with their dams on bahiagrass pastures (Paspalum notatum) at the four private herds and at the UF Beef Research Unit (UFBRU) from birth to weaning. Calves remained in their herds on bahiagrass pastures from weaning to yearling. During this period, calves at UFBRU were supplemented with bahiagrass hay, concentrate (1.6 kg to 3.6 kg of soy hull pellets per day; 14.0 % CP; 488 Pellet Medicated Weaning Ration, Lakeland Animal Nutrition, Lakeland, Florida), and a mineral supplement. Then, yearling steers were taken to a contract feeder where they were fed a standard feedlot diet comprised of corn, protein, vitamins, and minerals until their subcutaneous fat thickness over the ribeye reached 1.27 cm approximately.

## Traits

The traits in the reproduction set included yearling weight adjusted to 365 d of age (YW), reproductive tract score (RTS, units; n = 516; Andersen *et al.*, 1991), age at first calving (AFC, d; n = 909), and first calving intervals (FCI, d; n = 447). The ultrasound and carcass set of traits comprised ultrasound weight (UW, kg; n = 2,734); ultrasound ribeye area (UREA, cm<sup>2</sup>; n = 2,694), ultrasound backfat (UBF, cm; n = 2,698), ultrasound percent intramuscular fat (UPIMF, %; n = 2,680), slaughter age (SLA, d; n = 815), hot carcass weight (HCW, kg; n = 803), ribeye area (REA, cm<sup>2</sup>; n = 803), backfat thickness (FAT, cm; n = 803), and marbling score (MAR, units; n = 802; 100 to 199 = practically devoid, 200 to 299 = traces, 300 to 399 = slight, 400 to 499 = small, 500 to 599 = modest, 600 to 699 = moderate, 700 to 799 = slightly abundant, 800 to 899 = moderately abundant, and 900 to 999 = abundant). The tenderness score (TEND, units; n = 576; 1 = extremely tough, 2 = very tough, 3 = moderately tough; 4 = slightly tough; 5 = slightly tender; 6 = moderately tender; 7 = very tender; 8 = extremely tender).

#### **Tissue sampling and genotyping**

Tissue samples (blood, semen) from 782 animals (70 sires, 696 steers, and 16 heifers) were collected and stored at -80 °C between 2006 and 2015. The distribution of samples per breed group were: BG1 = 126, BG2 = 120, BG3 = 123, BG4 = 159, BG5 = 83, and BG6 = 171. DNA from blood and semen samples was extracted with a commercial kit (QIAamp DNA mini kit, Qiagen, Valencia, CA). Genotyping was done at Neogen with GeneSeek Genomic Profiler F250 (number of SNP in autosomes and X chromosome = 221,049; Neogen, 2016). Each animal in the genotype file had 127,016 SNP autosomal and X chromosome markers after discarding SNP with minor allele frequencies below 0.05 (n = 94,033).

#### **Genomic-Polygenic Variance Components, Parameters, and Predictions**

Three separate single-step genomic-polygenic multiple-trait mixed model analyses (Aguilar et al., 2010) were conducted to estimate variance components and genetic parameters. The 4-trait model for the reproduction set (YW, RTS, AFC, and FCI) contained yearling contemporary group (herd-year-season-management group), age of dam (YW only), sex of calf (YW only), direct heterosis as a function of calf heterozygosity (probability of one Angus and one Brahman allele in 1 locus), and maternal heterosis (YW only) as fixed effects. Fixed effects for the 9-trait model for the ultrasound-carcass set (UW, UREA, UFAT, UPIMF, SLA, HCW, REA, FAT, and MAR) were yearling contemporary group (herd-year-season-management group), sex of calf, ultrasound age (ultrasound traits only), and heterosis. Fixed effects for the 2-trait model for the tenderness set (WBSF, TEND) contained the fixed effects of yearling contemporary group (herd-year-season-management group), sex of calf, heterosis, and slaughter age. Random effects were animal direct genetic and residual for all models. The mean for random additive direct genetic effects was equal to zero, and the variance was equal to  $H \otimes V_a$ , where H was the combined pedigree-genotype relationship matrix among animals with and without genotypes (Legarra et al., 2009), and Va was the direct additive genetic variance-covariance matrix of the 4 traits in the reproduction set, 9 traits in the ultrasound-carcass set, and 2 traits in the tenderness set. Similarly, the mean of the residual effects was zero and its variance was equal to  $I \otimes V_e$ , where I was an identity matrix, and Ve was the environmental variance-covariance matrix for each of the three trait sets.

REML estimates of variance components and genetic parameters (Corbeil & Searle, 1971; Patterson & Thompson, 1971) were obtained using an average information algorithm (Gilmour *et al.*, 1995) with the BLUPF90 family of programs (Misztal *et al.*, 2002; Tsuruta, 2017). Standard errors of variance components were obtained as square roots of the diagonals of the inverse of the information matrix, whereas SE of heritabilities and correlations (genetic, environmental, phenotypic) were computed using a repeated sampling procedure (Meyer & Houle, 2013).

Genomic-polygenic predictions were computed for each set of traits using estimates of variance components at convergence. Genomic-polygenic EBV for each trait were plotted against Brahman fraction to visualize EBV variation among animals and EBV trends as animal Brahman fraction increased from 0% to 100%.

# **Results and Discussion**

### Heritabilities and genetic correlations

Estimates of heritability for the reproduction trait set were high for YW (0.53  $\pm$ 0.05), moderate for RTS (0.26  $\pm$  0.04), and low for AFC (0.17  $\pm$  0.04) and FCI (0.09  $\pm$ 0.02). Additive genetic correlations among these traits were low and with high SE. Heritability estimates for the ultrasound-carcass trait set were high for UW ( $0.57 \pm 0.05$ ), SLA (0.57  $\pm$  0.04), HCW (0.57  $\pm$  0.04), REA (0.55  $\pm$  0.03), and MAR (0.50  $\pm$  0.05), moderate for UREA ( $0.35 \pm 0.03$ ), UPIMF ( $0.33 \pm 0.03$ ), and FAT ( $0.32 \pm 0.03$ ), and low for UFAT ( $0.07 \pm 0.01$ ). Additive genetic correlations between ultrasound-carcass traits ranged between -0.47 to 0.81. The highest positive additive genetic correlations were between UW and HCW (0.81  $\pm$  0.08), HCW and REA (0.80  $\pm$  0.07), UW and UREA  $(0.64 \pm 0.06)$ , UREA and REA  $(0.63 \pm 0.07)$ , and UREA and HCW  $(0.3 \pm 0.09)$ . The largest negative additive genetic correlations were between UFAT and SLA (-0.47  $\pm$ 0.08), UFAT and HCW ( $-0.34 \pm 0.09$ ), and UREA and UPIMF ( $-0.25 \pm 0.07$ ). Heritability estimates for the tenderness trait set were low for WBSF ( $0.17 \pm 0.03$ ) and moderate for TEND (0.47  $\pm$  0.06). The additive genetic correlation between WBSF and TEND was negative and high (-0.97  $\pm$  0.01). The heritabilities obtained for RTS, MAR, UPIMF, WBSF, and TEND indicated that genomic selection for the target traits (reproductive tract score, marbling, and tenderness) of the Florida Enhancement Fund project currently underway would be feasible in the statewide Florida Brahman-Angus multibreed population. Noticeably, carcass information in this population originates primarily from Brahman crossbred steers. Thus, the multibreed structure of the Florida beef population will play a major role in the Brahman genetic improvement for marbling and tenderness because the number of Brahman steers with carcass information is likely to remain low in the near future. Further, the number of animals genotyped (GeneSeek Genomic Profiler F250) in the Florida Brahman-Angus multibreed population will increase dramatically in the next couple of years as a result of the Florida Enhancement Fund project. These newly genotyped animals will provide additional ties among Brahman and Brahman crossbred animals, increasing the accuracy of animal genomic-polygenic evaluation and selection for both target and associated traits.

# Genomic-polygenic EBV and trends from Angus to Brahman

High degree of variation among genomic-polygenic EBV existed for the sets of reproduction, ultrasound-carcass, and tenderness sets of traits across the spectrum of Brahman breed percentages in the statewide Florida Brahman-Angus multibreed population. Figure 1 presents graphs of genomic-polygenic EBV for two traits in the reproduction set (RTS and AFC), Figure 2 for four traits in the ultrasound-carcass set (UREA, REA, UPIMF and MAR), and Figure 3 for the two traits in the tenderness set (WBSF and TEND). These graphs show a wide range of genomic-polygenic EBV among animals of all Brahman percentages. No Brahman 32nds group was overwhelmingly better than any other one, including Angus (group with 0% Brahman). The most visible trend from Angus to Brahman occurred for RTS, where genomic-polygenic EBV tended to decrease as Brahman fraction increased. This indicated that heifers with higher Brahman fractions tended to be less mature as yearlings than heifers with higher Angus fractions.

# Conclusion

Estimates of genetic parameters in the statewide Brahman-Angus multibreed population were large enough for genomic-polygenic selection for these traits to be feasible. In particular, selection for the three target traits (reproductive tract score, marbling, and tenderness) in the Florida Enhancement Fund project is expected to be successful. The wide range of EBV among animals of all breed compositions indicated that the best animals regardless of their breed composition should be chosen as replacements if genetic progress is to be optimized in this multibreed population.



Figure 1. Genomic-polygenic EBV for two traits in the reproduction set.



Figure 2. Genomic-polygenic EBV for four traits in the ultrasound-carcass set.



Figure 3. Genomic-polygenic EBV for the two traits in the tenderness set.

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BUDGET FOR FLORIDA CATTLE ENHANCEMEN			
PROJECT TITLE: Florida Brahman: Genomic selection fo	or tenderness,	marbling, an	d reproductive ti
DETAILED LINE ITEM DESCRIPTION	QTY	% Complete	TOTAL
Materials and supplies for collection of tissue samples	2600	100%	\$ 7,750.00
DNA Extraction and Processing	2177	100%	\$ 17,214.00
DNA Genotyping	2177	100%	\$ 167,545.00
Equipment	2	100%	\$ 26,170.00
Research animal incentives and collection of reproductive, ultrasound and carcass data	2177	100%	\$ 20,200.00
UF Indirect Costs	1	100%	\$ 29,505.00
Final Research Project Report			
GRAND TOTAL: (equal to percentage of completion)			\$268,384.00

T FUND APPLICATION

act score; FCEB #: P0038402

EXPLANATION/JUSTIFICATION OF DELIVERABLE	COMPLETION DATE
Materials and supplies for collection of tissue samples (ear notch kits, applicators, FedEx delivery to farms)	9/01/2017
Costs associated with tissue sample DNA extraction and processing including materials and supplies (personnel, tissue collectors, DNA extraction kits)	9/01/2017
Genotyping at Geneseek with the Bovine GGP F250k & 50k chips	9/01/2017
Dell workstation, peripherals, Fortran compiler, and ultralow temperature freezer	9/01/2017
Costs associated with incentives for animal use and collection of reproductive, ultrasound and carcass data	9/01/2017
UF indirect costs (12%)	9/01/2017
Project report detailing accomplishments, ongoing research, and next steps of the project.	9/01/2017
Total Grant = \$208,384 + \$60,000 = \$268384	