

**University of Florida Report (2015-2016)**  
**S-1064: Genetic improvement of adaptation and reproduction to enhance sustainability of cow-calf production in the Southern United States**

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**Research Areas**

- 1) **Objective 2:** Meta-analyses of economically important traits of cow productivity and fertility to assess breed and production system combinations
- 2) **Objective 4:** Investigation of early cow-life performance (first four parities) affecting lifetime production in Brahman and Brahman-Angus cows

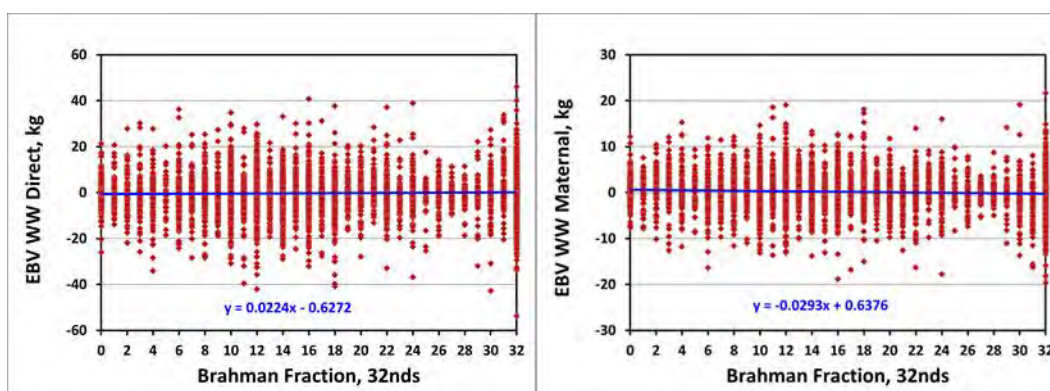
**Activities**

- 1) Collection of health, survival, fertility, growth, ultrasound, carcass, and meat palatability data from animals from the multibreed Angus-Brahman (MAB) and Brahman herds from the University of Florida (UF).
- 2) Updating and maintenance of the MAB and Brahman herd databases containing health, survival, fertility, preweaning growth, postweaning growth, carcass and meat palatability data (n=6,077).
- 3) Collection of blood and hair samples from calves (n=324), and semen from new sires (n=11) used in the MAB and Brahman herds (stored at UF).
- 4) Genotyping of 240 animals from the MAB herd with GeneSeek GGP150k and 800 animals with GeneSeek250k.
- 5) Genomic-polygenic analysis of animals in the MAB herd for direct genetic effects of postweaning ultrasound and weight data and for direct and maternal pre and postweaning growth data using actual and imputed genotypes.
- 6) Genomic-polygenic analysis of heifers from the MAB and Brahman herds for yearling weight, reproductive tract score, age at first calving, and first calving interval.
- 7) Genomic-polygenic analysis of animals from the MAB and Brahman herds for yearling weight direct and maternal, ultrasound ribeye area, ultrasound backfat, and ultrasound marbling.
- 8) Genomic-polygenic analysis of animals from the MAB and Brahman herds for birth weight direct and maternal, weaning weight direct and maternal, postweaning gain direct, ultrasound ribeye area, ultrasound backfat, and ultrasound marbling.
- 9) Genomic-polygenic analysis of animals from the MAB and Brahman herds for 9 ultrasound (yearling weight, ribeye area, fat over the ribeye, marbling) and carcass traits (slaughter weight, hot carcass weight, ribeye area, fat over the ribeye, and marbling).
- 10) Updating of FORTRAN software for editing of phenotypes, genotypes, and pedigree data and construction of input data files for imputation (Findhap2, 3, 4; Flmpute) and for genomic-polygenic evaluation (BLUPF90, GS3, QXPAK).
- 11) Updating of SAS programs for editing, statistical description, and mixed model analysis of feed intake, growth, ultrasound, carcass, and meat palatability traits in the MAB and Brahman populations.

- 12) Identification of genetic markers associated with meat quality traits to improve prediction for tenderness in beef cattle (R. Mateescu).
- 13) Muscle metabolic phenotypes and their association with meat quality traits (T. Scheffler, J. Scheffler, J. M. Gonzalez).
- 14) Animal and microbiological factors affecting the prevalence of Shiga Toxin Producing E. coli (STEC) and Cefotaxime Resistance (CefR) (K. C. Jeong).
- 15) Influence and regulation of vitamin D on the immune system, health, and growth of beef calves (C. Nelson).

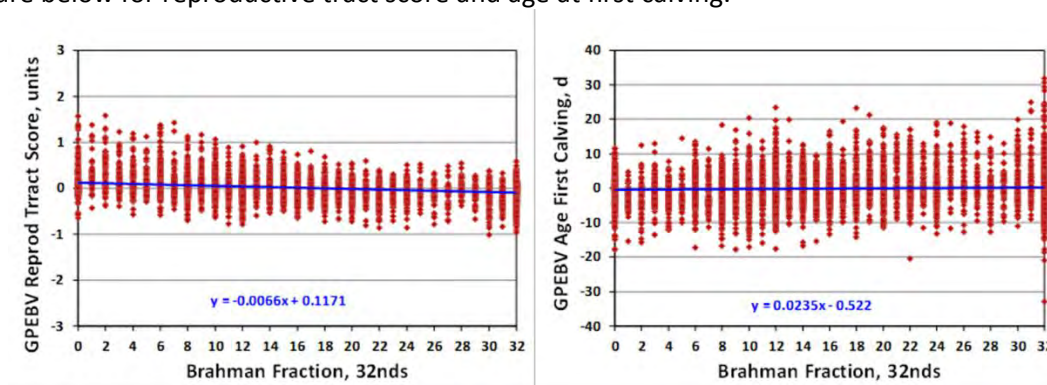
## Research Outcomes

- 1) Multibreed genomic-polygenic and polygenic evaluation of Bos taurus-Bos indicus cattle for growth traits in an Angus-Brahman multibreed population under subtropical conditions. Dataset included 5,300 calves, 293 sires, 1,725 dams. Similar estimates of variance components and genetic parameters with both models. Higher percent Brahman tended to yield higher EBV values for direct birth and weaning weight traits, but lower EBV for postweaning gain direct and birth and weaning weight maternal. Animals with high and low EBV for all traits existed across the Angus-Brahman expected composition spectrum. Genomic-polygenic values of animals ranging from 0 to 100% Brahman are shown in the Figure below for weaning weight direct and weaning weight maternal.

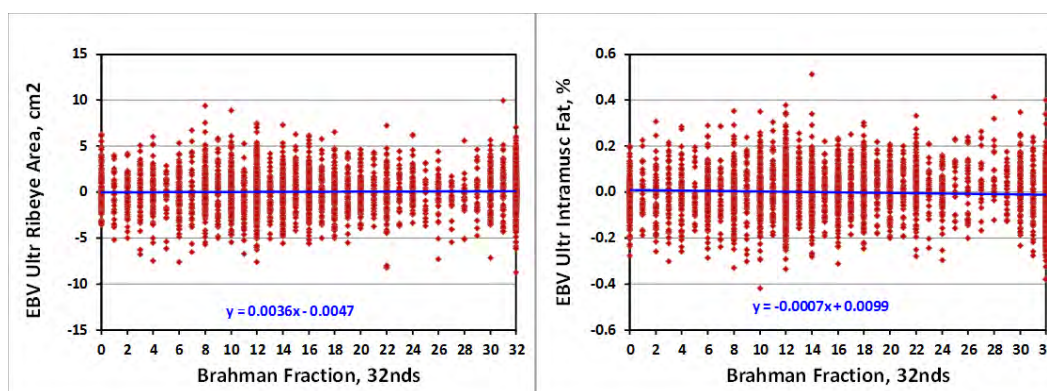


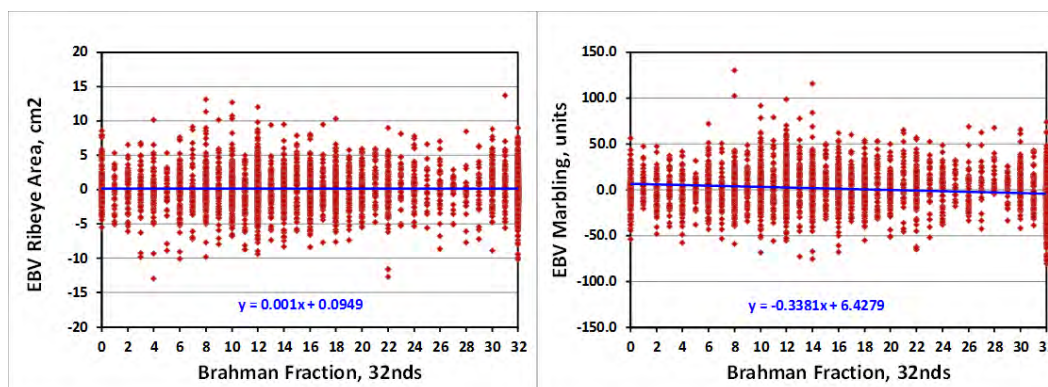
- 2) Genomic-polygenic evaluation of multibreed Angus-Brahman cattle for postweaning ultrasound and weight traits with actual and imputed Illumina50k SNP genotypes. Additive genomic to total genetic variance fractions for postweaning ultrasound traits explained by 46,909 actual and imputed Illumina50k SNP genotypes were 0.17 for ultrasound ribeye area, 0.32 for ultrasound fat thickness, 0.25 for ultrasound percent intramuscular fat, and 0.19 for postweaning weight. Rank correlations between genomic-polygenic and polygenic EBV were higher (0.93 to 0.96) than between genomic-polygenic and genomic EBV (0.81 to 0.94), and between genomic and polygenic EBV (0.66 to 0.81).
- 3) Growth and reproduction genomic-polygenic and polygenic parameters and prediction trends as Brahman fraction increases in an Angus-Brahman multibreed population. Traits were 365-d yearling weight (YW), yearling reproductive tract score (RTS), age at first calving (AFC), and first calving interval (FCI). Numbers of phenotypic records were 1,758 for YW, 381 for RTS, 1,385 for AFC, and 985 for FCI. Heritabilities were somewhat higher for GPM than PM (0.47 vs. 0.45 for YW, 0.31 vs. 0.30 for RTS, 0.14 vs. 0.12 for AFC, and 0.31 vs. 0.29 for FCI). Genetic correlations were positive between YW and RTS (GPM: 0.55; PM: 0.60), negative between RTS and AFC (GPM: -0.22; PM: -0.55) and between AFC and FCI (GPM: -0.68; PM: -0.67), and near zero for all other trait pairs. Heifers with higher Brahman percentages tended to be lighter and less mature as yearlings, older at first calving, and have shorter

FCI than heifers with higher Angus percentages under the subtropical environmental conditions of the MAB population. Animals with high, medium, and low EBV existed across all Brahman percentages, thus selection of replacement animals of all Brahman percentages could use a common set of objectives. Genomic-polygenic values of animals ranging from 0 to 100% Brahman are shown in the Figure below for reproductive tract score and age at first calving.

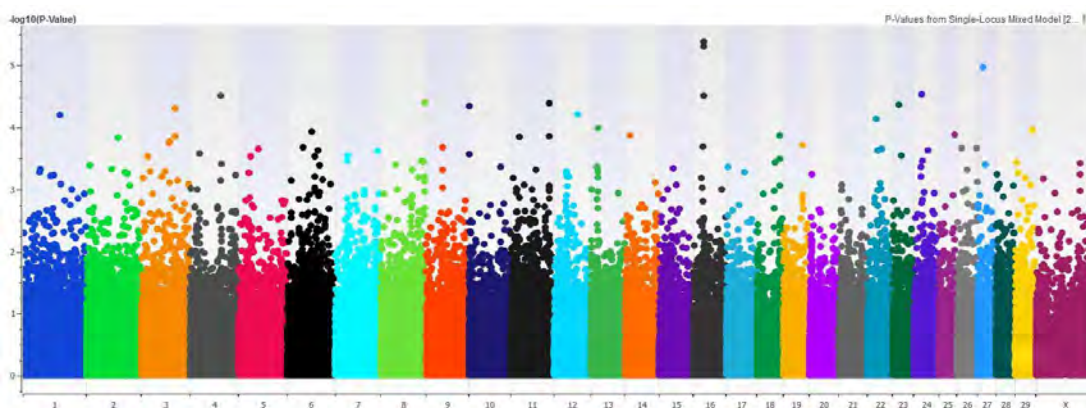


- 4) Ultrasound and carcass genomic-polygenic and polygenic parameters and prediction trends as Brahman fraction increases from 0 to 100% in an Angus-Brahman multibreed population. Ultrasound traits were weight at ultrasound measurements (UYW), ribeye area (UREA), fat over the ribeye (UFAT), and marbling (UMAR). Carcass traits were slaughter weight (SLW), hot carcass weight (HCW), ribeye area (REA), fat over the ribeye (FAT), and marbling (MAR). Numbers of phenotypic records were 1,758 for UYW, 1,748 for UREA, 1,754 for UFAT, 1,752 for UMAR, 761 for SLW, 744 for HCW, REA, and FAT, and 743 for MAR. Heritabilities were mostly higher for GPM than for PM (0.23 vs. 0.20 for UYW, 0.35 vs. 0.28 for UREA, 0.04 vs. 0.02 for UFAT, 0.08 vs. 0.05 for UMAR, 0.44 vs. 0.41 for SLW, 0.55 vs. 0.50 for HCW, 0.55 vs. 0.58 for REA, 0.18 vs. 0.20 for FAT, and 0.31 vs. 0.17 for UMAR). Genetic correlations were mostly positive among all traits with values ranging from low to high. As with reproduction and preweaning growth traits previously evaluated in this population, animals with low, medium, and high EBV existed across the spectrum of Brahman percentages indicating that a common set of selection criteria would be feasible in this multibreed population and likely in similar populations in subtropical and tropical regions. Genomic-polygenic values of animals ranging from 0 to 100% Brahman are shown in the Figure below for ultrasound ribeye area and ultrasound marbling and their corresponding carcass traits, i.e., ribeye area and marbling.





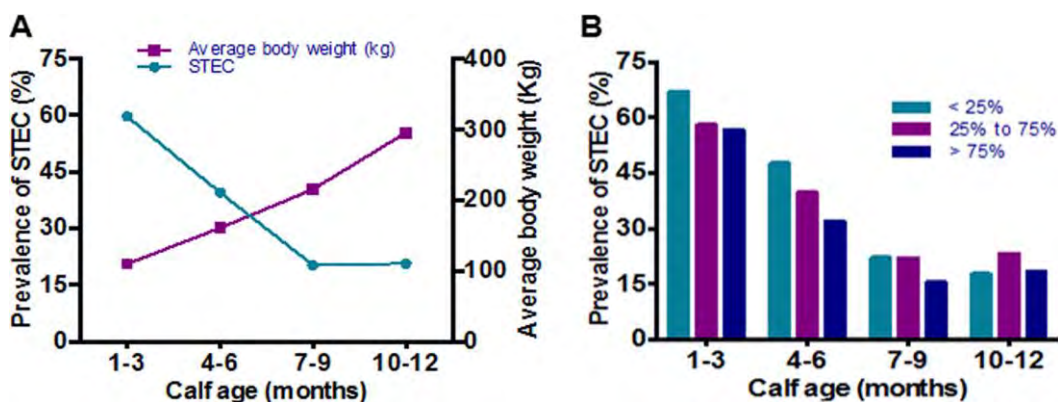
- 5) Genomic tools to improve meat quality traits in Angus-Brahman cattle. Several genomic regions were associated with tenderness of beef in a multibreed Angus-Brahman population. Investigation of several regions revealed strong candidate genes with possible direct relations to meat tenderization process. The predictive analysis revealed that opportunity existed for development and implementation of a system to communicate tenderness attributes to consumers and improve the probability that consumers' eating expectations are met. The Figure below shows the genome-wide association results with 150K genotypes for Warner-Bratzler Shear Force on 418 animals ranging from 0 to 100% Brahman.



- 6) Relating muscle fiber morphometrics and protein degradation to meat quality in a multibreed herd. Warner-Bratzler Shear Force (WBSF) increased as the percentage of Brahman increased. The degree of  $\mu$ -calpain autolysis at 24 h decreased as WBSF values increased, and autolysis decreased as the percentage of Brahman increased. Citrate synthase activity increased with greater percentage of Brahman indicating that Brahman genetics tended to influence oxidative capacity. Postmortem proteolysis and muscle fiber type will be utilized to establish predictors for the optimum breed group that provides desirable meat quality and palatability traits, while having enough Brahman influence to thrive in sub-tropical climates.
- 7) Effect of Brahman genetics on myofibrillar protein degradation, collagen crosslinking, and meat tenderness. This research showed that loin eye (*longissimus lumborum*) steaks from steers of greater percentage Brahman had reduced tenderness when measured objectively and subjectively. Additionally, trained sensory panelists detected an increase in connective tissue content as percentage Brahman increased. Decreases in tenderness from Brahman steaks were most likely due to the reduction in degradation of desmin and troponin-T proteins and not increases in hydroxylysylpyridinoline crosslinks.



- 8) Colonization of beef cattle by Shiga toxin-producing *Escherichia coli* during the first year of life: a cohort study. This study identified that beef calves were more likely to shed STEC during the first 6 months and that STEC shedding decreased as the animal matured. Animal breed group, sex of the calf, and average weight gain were not significantly associated with STEC colonization. The Figure below shows the prevalence of STEC and mean body weight of calves ranging from 0 for 100% Brahman during their first year of life.



## Publications

- Elzo, M. A., D. D. Johnson, R. Mateescu, D. O. Rae, T. Scheffler, J. Scheffler, K. C. Jeong, C. D. Nelson, J. M. Gonzalez, J. G. Wasdin, M. D. Driver, and J. D. Driver. 2016. Brahman Research Report 2016. Dept. Animal Sciences, University of Florida, Gainesville, FL, p 1-6.
- Elzo, M. A., R. Mateescu, M. G. Thomas, D. D. Johnson, C. A. Martinez, D. O. Rae, J. G. Wasdin, M. D. Driver and J. D. Driver. 2016. Growth and reproduction genomic-polygenic and polygenic parameters and prediction trends as Brahman fraction increases in an Angus-Brahman multibreed population. *Livest. Sci.* (Submitted)
- Elzo, M. A., M. G. Thomas, D. D. Johnson, C. A. Martinez, G. C. Lamb, D. O. Rae, J. G. Wasdin, and J. D. Driver. 2015. Genetic parameters and predictions for direct and maternal growth traits in a multibreed Angus-Brahman cattle population using genomic-polygenic and polygenic models. *Livest. Sci.* 178:43-51.
- Elzo, M. A., M. G. Thomas, C. A. Martinez, G. C. Lamb, D. D. Johnson, I. Misztal, D. O. Rae, J. G. Wasdin, and J. D. Driver. 2015. Genomic-polygenic evaluation of multibreed Angus-Brahman cattle for postweaning ultrasound and weight traits with actual and imputed Illumina50k SNP genotypes. *Livest. Sci.* 175:18-26.
- Elzo, M. A., M. G. Thomas, D. D. Johnson, C. A. Martinez, G. C. Lamb, D. O. Rae, J. G. Wasdin, and J. D. Driver. 2015. Genomic-polygenic and polygenic evaluation of multibreed Angus-Brahman cattle for direct and maternal growth traits under subtropical conditions. *Florida Beef Research Report*, p 7-12.
- Elzo, M. A., M. G. Thomas, C. A. Martinez, G. C. Lamb, D. D. Johnson, I. Misztal, D. O. Rae, J. G. Wasdin, and J. D. Driver. 2015. Genomic variability and predictions for postweaning ultrasound traits using actual and imputed Illumina50k SNP markers in Angus-Brahman multibreed cattle. *Florida Beef Research Report*, p 1-6.
- Leal, J., D. Johnson, M. A. Elzo, and R. Mateescu. 2016. Association of SNPs in calpain and calpastatin genes with meat tenderness in an Angus-Brahman population. *Proc. 14th Annual Res. Symp. Anim. Mol. Cell. Biol. Grad. Prog. Univ. Florida, Brooksville, FL, April 15-16, 2016*, p 22.
- Mateescu, R., M. A. Elzo, and D. D. Johnson. 2016. Genomic tools to improve meat quality traits in Angus-Brahman cattle. *Final Project Report, Florida Beef Council, Gainesville, FL*, p 1-5.

- Mir, R. A., T. A. Weppelmann, M. A. Elzo, S. Ahn, and K. C. Jeong. 2016. Colonization of beef cattle by Shiga toxin-producing *Escherichia coli* during the first year of life: a cohort study. PLoS One 12(2): e0148518.
- Mir, R., T. A. Weppelmann, M. A. Elzo, K. C. Jeong. 2015. Animal factors that influence the prevalence of Shiga toxin-producing *Escherichia coli* in beef cattle. Verocytotoxin-producing *Escherichia coli* (VTEC) Conference, Boston, MA, September 13-16, 2015 (Abstract).
- Phelps, K. J., D. D. Johnson, M. A. Elzo, C. B. Paulk, and J. M. Gonzalez. 2016. Effect of Brahman genetics on myofibrillar protein degradation, collagen crosslinking, and meat tenderness. AMSA 69<sup>th</sup> Recip. Meat Conf., Angelo State Univ., San Angelo, TX, June 19-22, 2016 (Abstract).
- Wright, S., Scheffler, T., Scheffler, J., D. Johnson, M. A. Elzo. 2016. Relating muscle fiber morphometrics and protein degradation to meat quality in a multibreed herd. AMSA 69<sup>th</sup> Recip. Meat Conf., Angelo State Univ., San Angelo, TX, June 19-22, 2016 (Abstract).

### Presentations

- Elzo, M. A., M. G. Thomas, D. D. Johnson, C. A. Martinez, G. C. Lamb, D. O. Rae, J. G. Wasdin, and J. D. Driver. 2015. Genomic-polygenic and genomic predictions of direct and maternal effects for growth traits in a multibreed Angus-Brahman cattle population. ADSA- ASAS Joint Annual Meeting, Orlando, FL, July 12-16, 2015.
- Elzo, M. A. 2015. Brahman Project Update. Florida Cattlemen Association Research Committee, Santa Fe and Beef Research Units, FL, January 06, 2015.
- Mir, R., T. A. Weppelmann, M. A. Elzo, K. C. Jeong. 2015. Animal factors that influence the prevalence of Shiga toxin-producing *Escherichia coli* in beef cattle. Verocytotoxin-producing *Escherichia coli* (VTEC) Conference, September 13-16, 2015, Boston, MA.
- Phelps, K. J., D. D. Johnson, M. A. Elzo, C. B. Paulk, and J. M. Gonzalez. 2016. Effect of Brahman genetics on myofibrillar protein degradation, collagen crosslinking, and meat tenderness. AMSA 69<sup>th</sup> Recip. Meat Conf., Angelo State Univ., San Angelo, TX, June 19-22, 2016.
- Wright, S., Scheffler, T., Scheffler, J., D. Johnson, M. A. Elzo. 2016. Relating muscle fiber morphometrics and protein degradation to meat quality in a multibreed herd. AMSA 69<sup>th</sup> Recip. Meat Conf., Angelo State Univ., San Angelo, TX, June 19-22, 2016 (Abstract).

### Research Impacts

- 1) The similarity between genomic-polygenic and genomic predictions for reproductive, pre and postweaning growth direct, preweaning growth maternal, postweaning ultrasound, and carcass traits indicated that genomic information added little information to genetic predictions for these traits.
- 2) The large variability among genomic-polygenic and genomic EBV among animals of each 32nds Brahman fraction indicated that selecting animals in this multibreed Angus-Brahman herd could be accomplished using a common set of objectives across all Angus-Brahman breed compositions.
- 3) Genome-wide association analysis with the GGPHD150k chip from GeneSeek indicated several genomic regions associated with tenderness and the predictive analysis suggested the possibility of developing a more precise system to assess tenderness and improve consumer expectations.