University of Florida Report (2017-2018)
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 3:** Documentation of genetic components pertaining to heat tolerance adaptive traits in sustainable beef cattle production systems.
3) **Objective 4:** Investigation of early cow-life performance (first four parities) affecting lifetime production in Brahman and Brahman-Angus cows

Activities

1) Collection of phenotypic data from the UF multibreed Angus-Brahman (MAB) and Brahman herds (health, survival, fertility, growth, ultrasound, carcass, meat palatability), and eight Florida Brahman herds (fertility, growth, ultrasound, and carcass). Number of animals with records = 15,642.
2) Collection of tissue samples from calves, sires, and dams from UF MAB, UF Brahman, and Florida Brahman breeders (n = 4,488).
3) Collection of phenotypic data describing thermal tolerance in *Bos Indicus* influenced populations and characterization of the genetic component underlying these traits.
4) Statewide Brahman and Brahman-Angus tissue sample (blood, ear-notches, semen) and DNA repository housed at the Animal Science Department of the University of Florida (UF MAB, UF Brahman, Florida Brahman herds).
5) Statewide Brahman and Brahman-Angus database: phenotypes, pedigree, genotypes (GeneSeek GGP50k, GGP250k). Phenotypic and pedigree data came from UF, Florida Brahman breeders, and ABBA (American Brahman Breeders Association). Number of animals with one or more phenotypic records = 15,642 (9,327 Brahman and 6,315 Angus and Brahman-Angus crossbreds). Number of animals in the pedigree file = 23,971 (16,966 Brahman and 7,005 Angus and Brahman-Angus crossbreds). Number of animals with genotypes = 3,951 (2394 GGP250k and 1,557 GGP50k).
6) Genomic-polygenic and polygenic predictions for twenty growth, fertility, ultrasound, carcass, and tenderness traits in the statewide multibreed Brahman-Angus multibreed population. Number of evaluated animals = 23,958.
7) FORTRAN and SAS software for editing of phenotypes, genotypes, and pedigree data, and construction of input files for imputation and genetic evaluations using genomic-polygenic and polygenic models.
8) Structural equation and genome wide association analyses for growth, carcass quality and meat quality in a multibreed Angus-Brahman population (R. Mateescu).
9) Association between proteolysis and tenderization and pH decline and calpain-1 autolysis in Angus, Brahman and Brangus (T. Scheffler).
10) Characterization of meconium microbiota and its association with fetal development, establishment of postnatal gut microbiota, and subsequent animal growth (K. C. Jeong).

Research Outcomes

1) Phenotypic analyses of udder and teat scores in the UF MAB and Brahman herds (2016 to 2018; number of records = 628; number of cows = 386).
   a) Udder score means by Brahman fraction at calving, 6 months, and weaning: Upward trends as Brahman fraction increased (Figure 1a; better udders towards Brahman).
   b) Teat score means by Brahman fraction: Upward trend at calving, and slightly negative trends at 6 months and at weaning (Figure 1a; better teats at calving; unclear at later stages; more data needed).
   c) Udder and teat score means by age of cow: Downward trends at calving, 6 months, and weaning (Figure 1b; better udder and teat shape in younger cows).

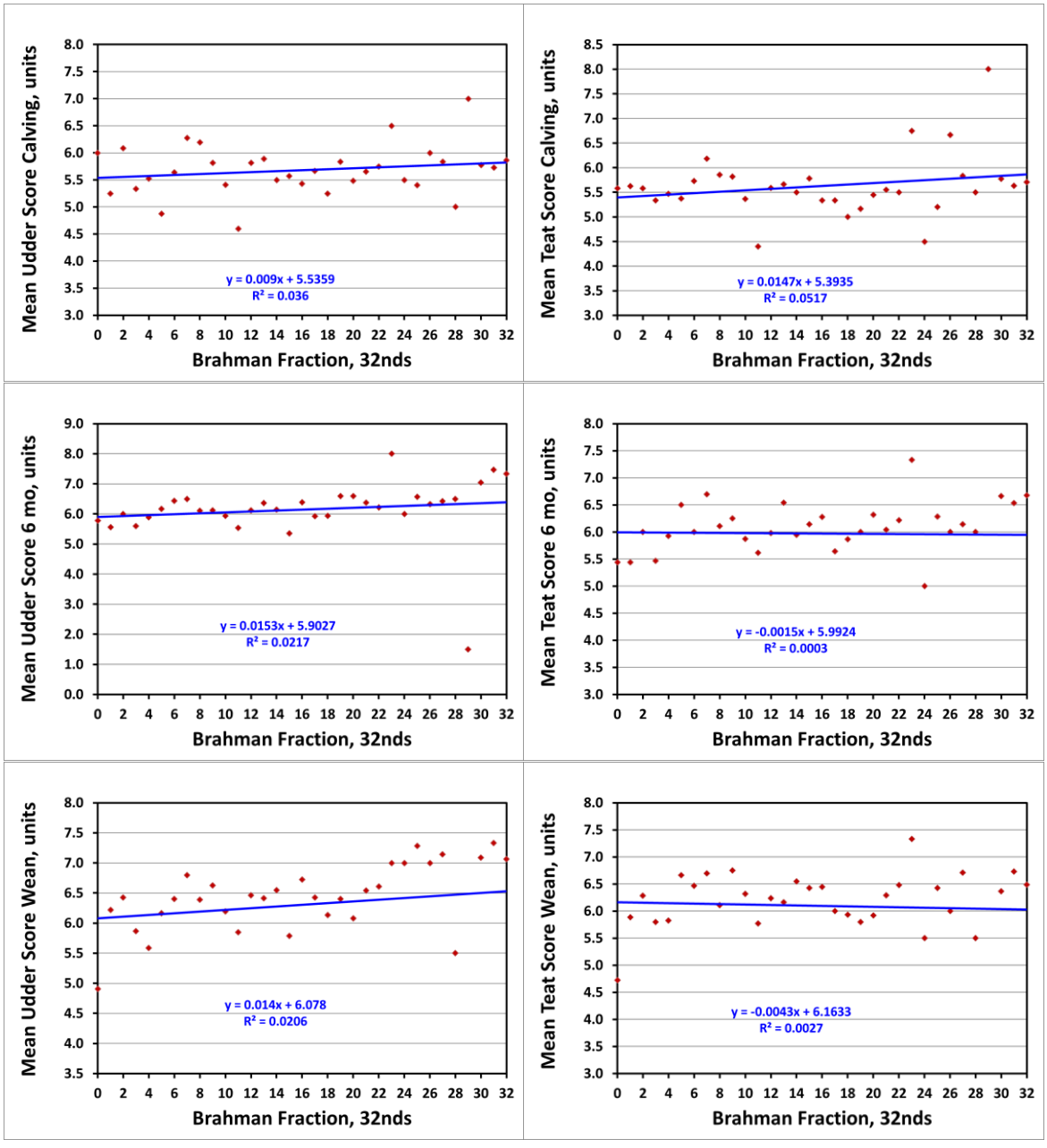


Figure 1a. Udder and teat score means by Brahman fraction

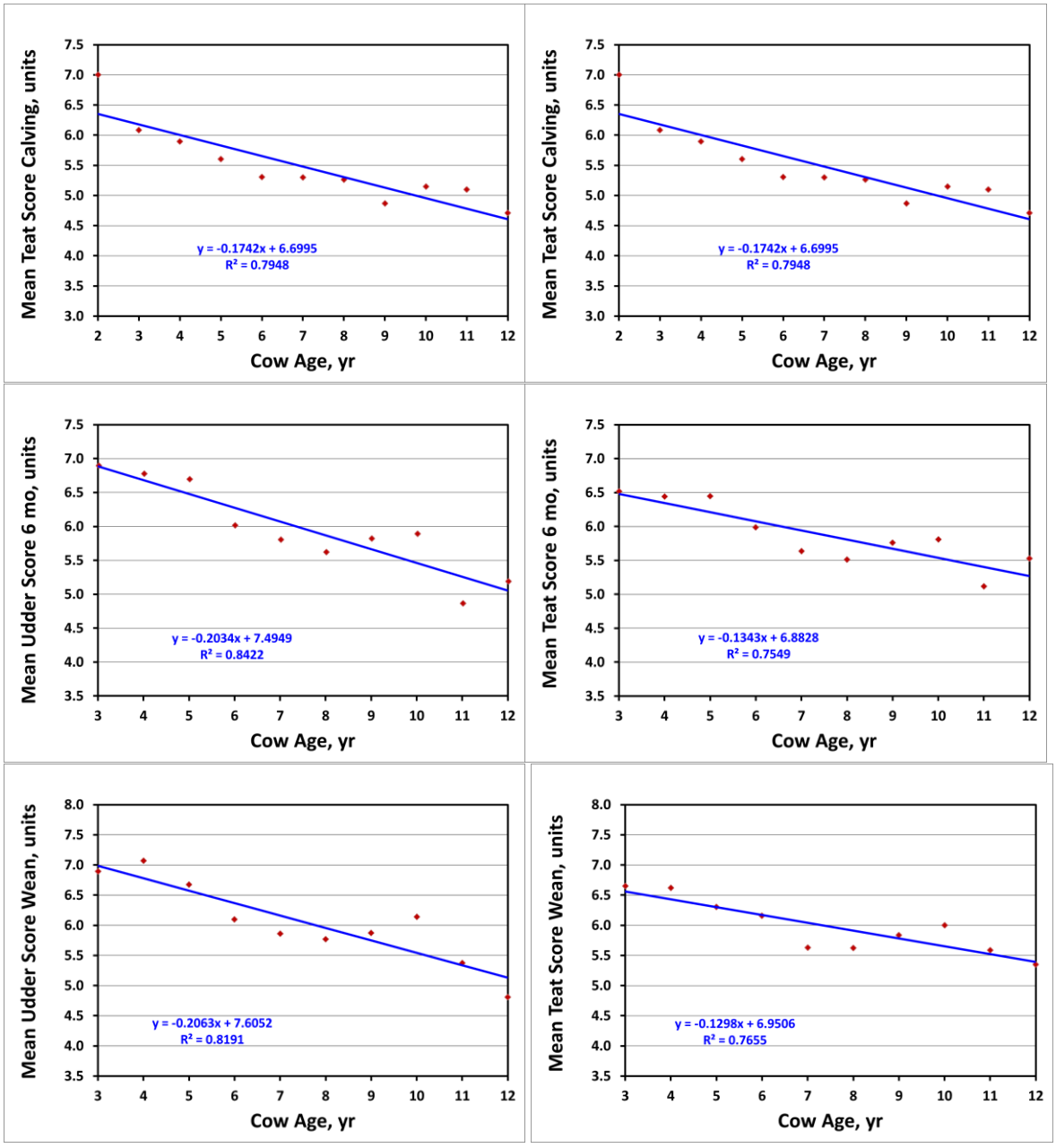


Figure 1b. Udder and teat score means by age of cow

2) Genomic-polygenic and polygenic predictions for twenty growth, fertility, ultrasound, carcass, and tenderness traits in the statewide multibreed Brahman-Angus multibreed population. Number of evaluated animals = 23,971. Phenotypic and pedigree data came from UF, Florida Brahman breeders, and ABBA. Number of animals with one or more phenotypic records = 15,642 (9,327 Brahman and 6,315 Angus and Brahman-Angus crossbreds). Number of animals in the pedigree file = 23,971 (16,966 Brahman and 7,005 Angus and Brahman-Angus crossbreds). Number of animals genotyped with GeneSeek GGP250k = 2,394. The twenty traits were analyzed in four sets: a) Growth set (birth weight

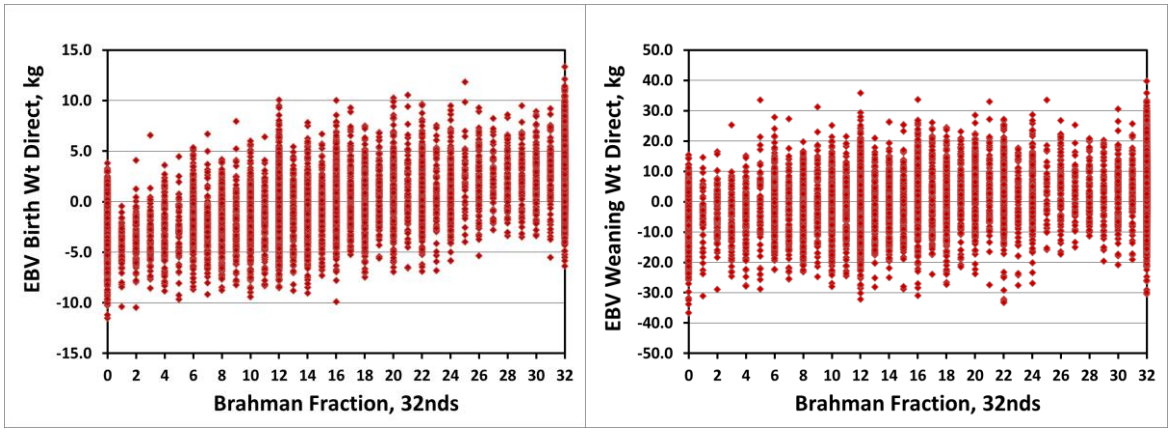
direct (BWD), weaning weight direct (WWD), weight gain from weaning to yearling direct (GWD), birth weight maternal (BWM), and weaning weight maternal (WWM)); b) Reproduction set (yearling weight adjusted to 305 days of age (YW), reproductive tract score (RTS), age at first calving (AFC), and calving interval (FCI); c) 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 d) Tenderness set (Warner-Bratzler shear force (WBSF) and tenderness score (TEND)).

Table 2a. Description of Genomic-Polygenic EBV and Accuracies for the growth and reproduction sets of traits

Trait	N	Mean	SD	Min	Max
Sol bwd	23958	1.32	2.75	-11.52	13.34
BIF Acc bwd	23958	0.22	0.14	0.00	0.74
Sol wwd	23958	3.22	7.79	-36.60	39.79
BIF Acc wwd	23958	0.19	0.12	0.00	0.71
Sol gwd	23958	-0.76	6.00	-43.09	39.47
BIF Acc gwd	23958	0.08	0.10	0.00	0.68
Sol bwm	23958	-0.81	1.89	-6.73	8.73
BIF Acc bwm	23958	0.14	0.14	0.00	0.90
Sol wwm	23958	-0.27	5.12	-30.55	29.71
BIF Acc wwm	23958	0.17	0.13	0.00	0.71
Sol yw	23958	-2.03	13.82	-107.01	78.11
BIF Acc yw	23958	0.12	0.12	0.00	0.71
Sol rts	23958	-0.11	0.41	-3.21	1.91
BIF Acc rts	23958	0.34	0.05	0.00	0.69
Sol ac1	23958	-0.30	14.53	-147.57	105.25
BIF Acc ac1	23958	0.75	0.02	0.58	0.88
Sol ci1	23958	2.58	12.93	-88.74	128.50
BIF Acc ci1	23958	0.41	0.05	0.00	0.73

Table 2b. Description of Genomic-Polygenic EBV and Accuracies for the ultrasound-carcass and tenderness sets of traits

Trait	N	Mean	SD	Min	Max
Sol uw	23958	-2.75	10.93	-69.47	78.44
BIF Acc uw	23958	0.07	0.12	0.00	0.69
Sol urea	23958	-0.06	1.55	-10.56	12.14
BIF Acc urea	23958	0.07	0.11	0.00	0.68
Sol ubf	23958	-0.01	0.05	-0.40	0.66
BIF Acc ubf	23958	0.32	0.08	0.00	0.75
Sol upimf	23958	-0.08	0.20	-1.18	1.64
BIF Acc upimf	23958	0.06	0.10	0.00	0.67
Sol slage	23958	0.77	9.49	-71.87	70.12
BIF Acc slage	23958	0.20	0.12	0.00	0.71
Sol hcw	23958	-2.54	11.88	-62.08	65.41
BIF Acc hcw	23958	0.07	0.12	0.00	0.66
Sol rea	23958	-0.41	2.38	-15.05	18.99
BIF Acc rea	23958	0.18	0.11	0.00	0.70
Sol fat	23958	-0.04	0.15	-1.07	1.96
BIF Acc fat	23958	0.04	0.08	0.00	0.61
Sol marb	23958	-19.12	37.08	-137.90	254.40
BIF Acc marb	23958	0.05	0.10	0.00	0.63
Sol wbsf	23958	0.09	0.18	-0.74	1.08
BIF Acc wbsf	23958	0.02	0.07	0.00	0.85
Sol tend	23958	-0.16	0.30	-1.62	1.13
BIF Acc tend	23958	0.03	0.08	0.00	0.85



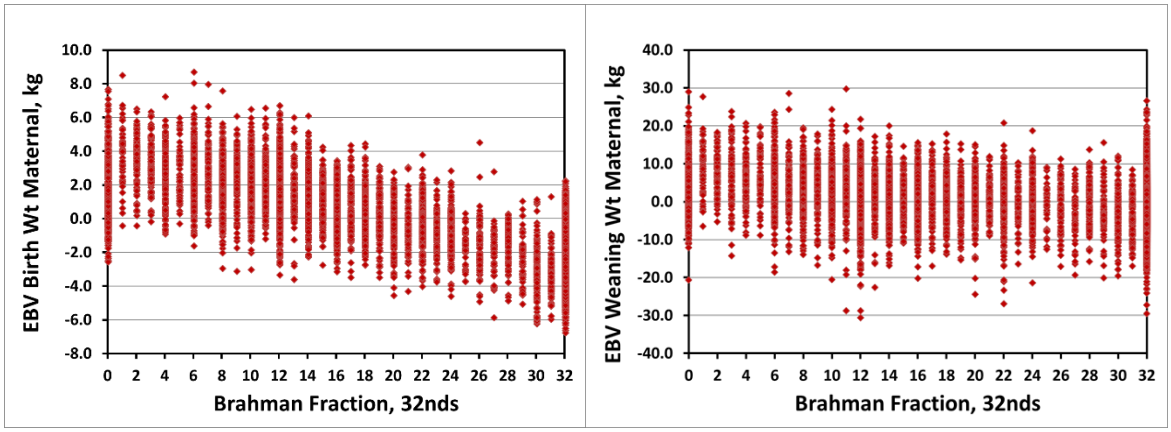


Figure 2a. Genomic-polygenic EBV (GEBV) for four traits in the growth set

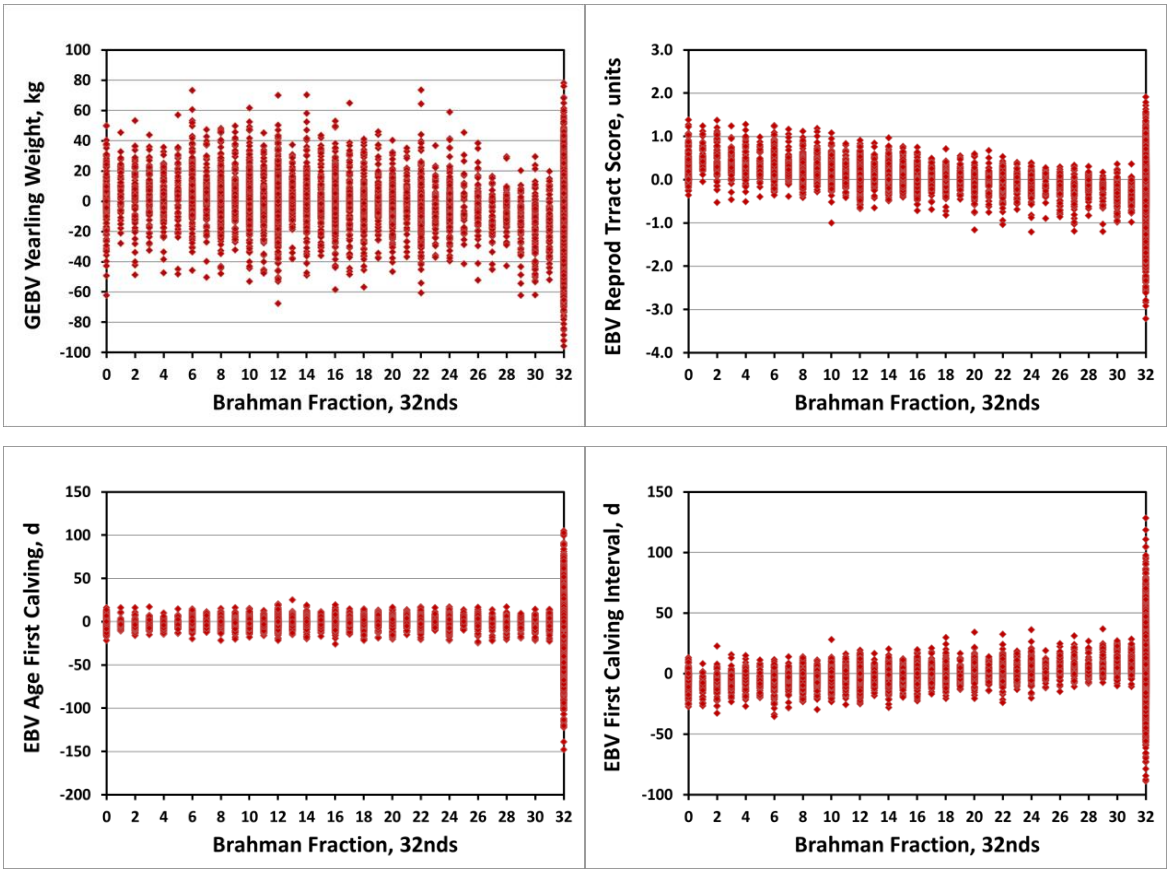


Figure 2b. Genomic-polygenic EBV (GEBV) for four traits in the reproduction set

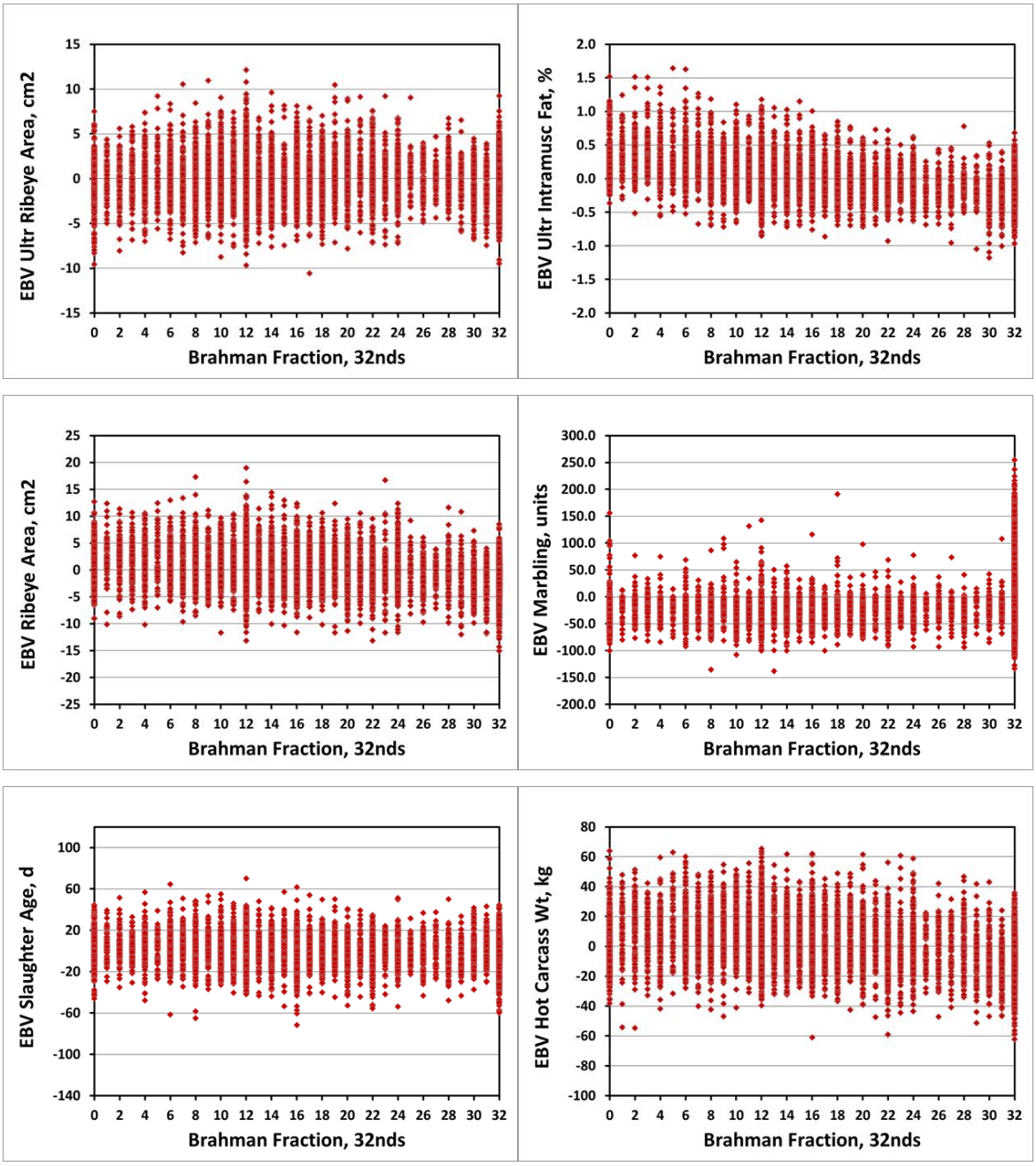


Figure 2c. Genomic-polygenic EBV (GEBV) for six traits in the ultrasound-carcass set

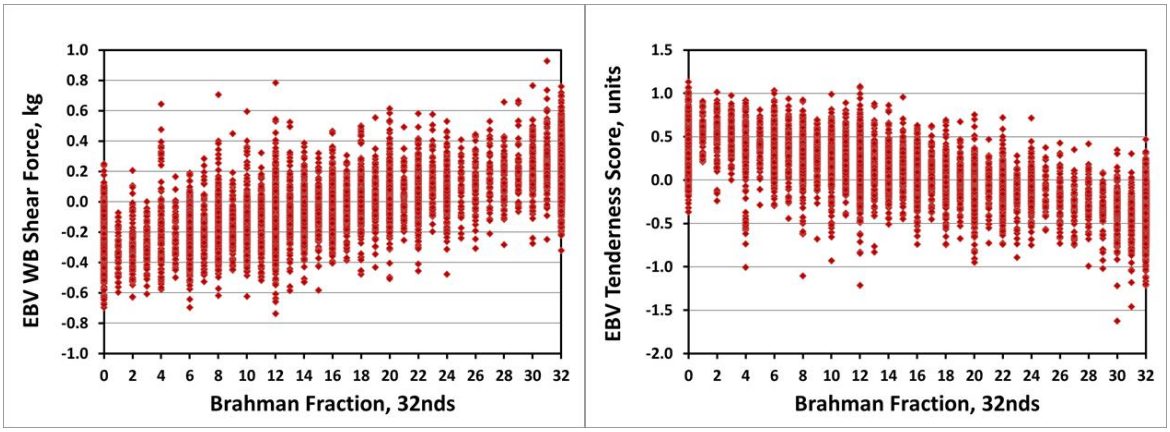


Figure 2d. Genomic-polygenic EBV (GEBV) for two traits in the tenderness set

3) Association between proteolysis and tenderization and pH decline and calpain-1 autolysis in Angus, Brahman and Brangus. Early postmortem muscle pH decline influences protease activation and therefore tenderization. Brahman often shows slower proteolysis and less extended tenderization. Thus, the objective of this study was to determine pH decline, calpain-1 autolysis and protein degradation from Angus, Brahman and Brangus beef aged to 14d. Steers were part of a long-term genetics study involving Angus, Brahman, and Angus-Brahman crossbreds. Three genetic groups were: Angus (A; 0.8-1), Brahman (B; 0.8-1) and Brangus (A 0.625; B 0.375). Steers (n = 6 per breed group) were harvested and the pH decline was assessed in the *Longissimus lumborum* at 1, 3, 6, 9 and 24h postmortem. *Longissimus lumborum* muscle samples were collected at 1, 3, 6 and 24h and 7 and 14d postmortem. Calpain-1 autolysis and troponin-T degradation (TnT) were evaluated with Western blotting. Tenderization in aged steaks was assessed using Warner-Bratzler shear force (WBSF; 7 and 14d) and sensory analysis (14d). Data were analyzed using SAS and the model included the fixed effects of breed, time and their interaction. Time was considered a repeated measure (pH, calpain-1 and troponin-T). Means were compared using Tukey-test.
   Breed affected pH decline (P = 0.049). Brahman showed higher pH than Brangus, particularly within the first 6h postmortem. Rate of autolysis tended to be different between breeds (breed x time, P = 0.06). At 24h postmortem, Brangus showed greater calpain-1 autolysis compared to Brahman. Similarly, breed influenced the rate of TnT degradation during the aging period (breed x time, P = 0.001). At 24h, Brahman had less TnT degradation compared to Brangus, but not Angus. However, after 7d aging, Brahman had less TnT degradation than Angus; and at 14d, Brahman showed less TnT degradation compared to both Angus and Brangus. No differences were found for WBSF-7d (P = 0.092) or WBSF-14d (P = 0.292) between breeds, but breed affected (P = 0.004) sensory tenderness.
   Longissimus from Brahman exhibited slower rate of pH decline that coincided with slower tenderization, evidenced by reduced calpain-1 autolysis at 24h postmortem and less troponin-T degradation. Although breed did not affect WBSF, it decreased sensory tenderness, with Brahman beef considered slightly tough after 14d aging. The slower rate of acidification in Brahman indicates ATP levels are maintained longer; this may prolong calcium uptake by the sarcoplasmic reticulum and mitochondria, thereby delaying calpain activation and tenderization.

4) Structural equation and genome wide association analyses for growth, carcass quality and meat quality in a multibreed Angus-Brahman population. Structural equation (SE) models involving latent variables are useful for formulating hypothesized models defined by theoretical causal variables and relations between these variables. The objectives of this study were: a) to identify latent variables

concerning beef growth, carcass quality and meat quality as latent phenotypes, and b) to perform a genome wide association study (GWAS) for these latent variables to identify QTLs with direct and indirect effects on them. A total of 726 steers from an Angus-Brahman multibreed population with records for 21 phenotypes were used. Genomic DNA from 480 animals was genotyped with GeneSeek GGP250k. A single-step genomic best linear unbiased prediction (ssGBLUP) model was used to estimate the amount of genetic variance explained in each latent variable by 20 adjacent-SNP windows across the genome. Three types of effects for each window were considered: a) identify a theoretical model for beef growth, carcass quality and meat quality that would closely fit the variance-covariance structure of the sample data, and b) perform a GWAS for the growth, carcass quality and meat quality latent variables to identify genomic regions with direct and indirect effects on these latent constructs. The final structural model included carcass quality as an independent latent variable and meat quality as a dependent latent variable, where carcass quality was evaluated based on quality grade (QG), fat over ribeye (FOR) and marbling (MARB), and meat quality was assessed using juiciness (JC), tenderness (TD) and connective tissue (CT). From 571 associated windows (643 genes) able to explain at least 0.05 percent of the additive variance, 159 windows (179 genes) were associated with carcass quality, 106 windows (114 genes) were associated with carcass and meat quality, 242 windows (266 genes) were associated with meat quality, and 64 windows (84 genes) were associated with carcass quality, having an indirect effect on meat quality. Three biological mechanisms can explain the association of the identified genes with the latent constructs for carcass and meat quality: a) postmortem proteolysis of structural proteins and cellular compartmentalization, b) cellular proliferation and differentiation of adipocytes, and c) fat deposition.

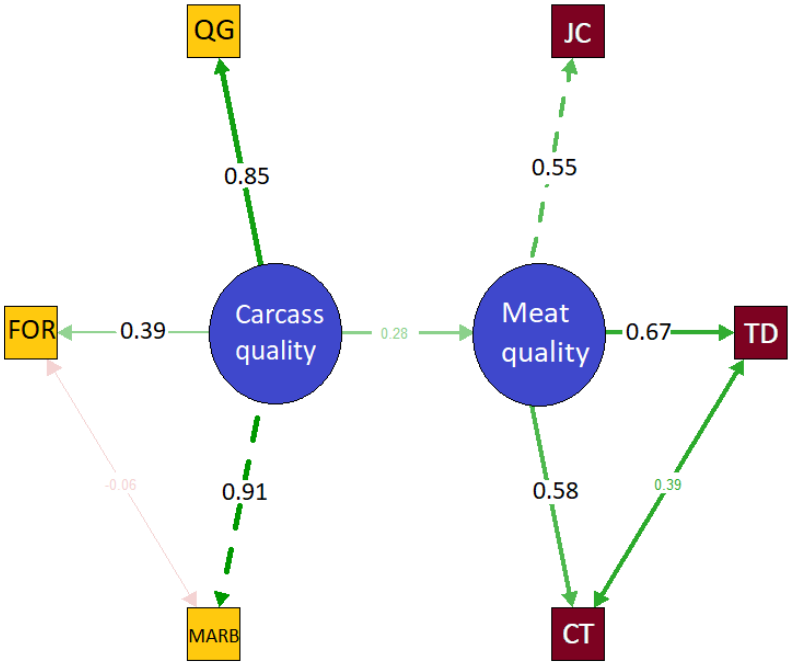


Figure 4a. Relationship between observed variables and the latent variables carcass quality and meat quality in *Longissimus dorsi* muscle from an Angus-Brahman multibreed herd in the final SE model. The estimation of unstandardized loadings is presented. Marbling (MARB), juiciness (JC); fat over ribeye (FOR); quality grade (QG); tenderness (TD); connective tissue (CT).

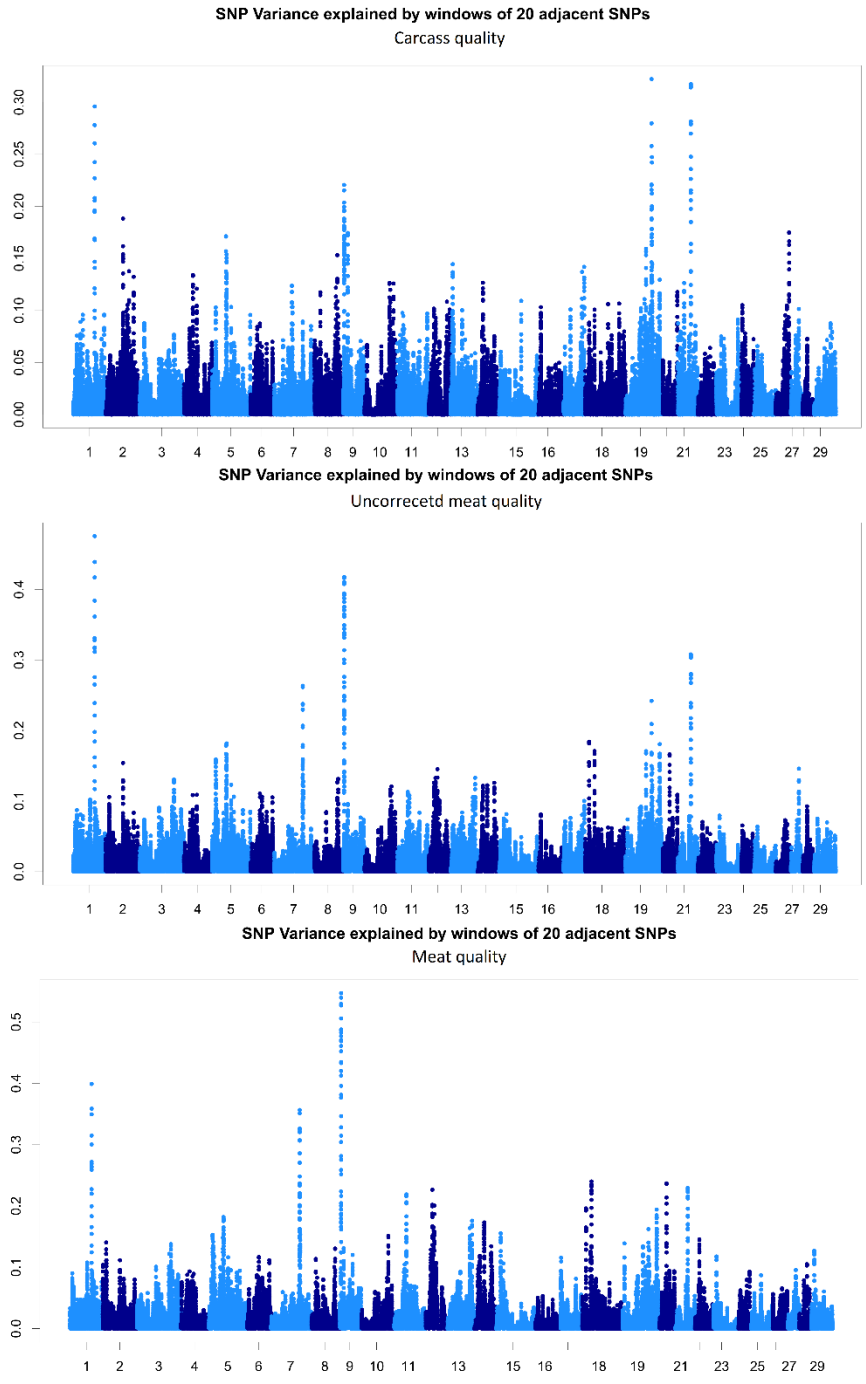


Figure 4b. Percentage of the genetic variance explained by the latent phenotypes for carcass quality (top), uncorrected meat quality (middle), and meat quality (bottom) explained by 20 adjacent-SNP windows in *Longissimus dorsi* muscle from Angus-Brahman crossbred steers. The amount of additive variance explained was 29.2% for carcass quality and 41.3 % for meat quality.

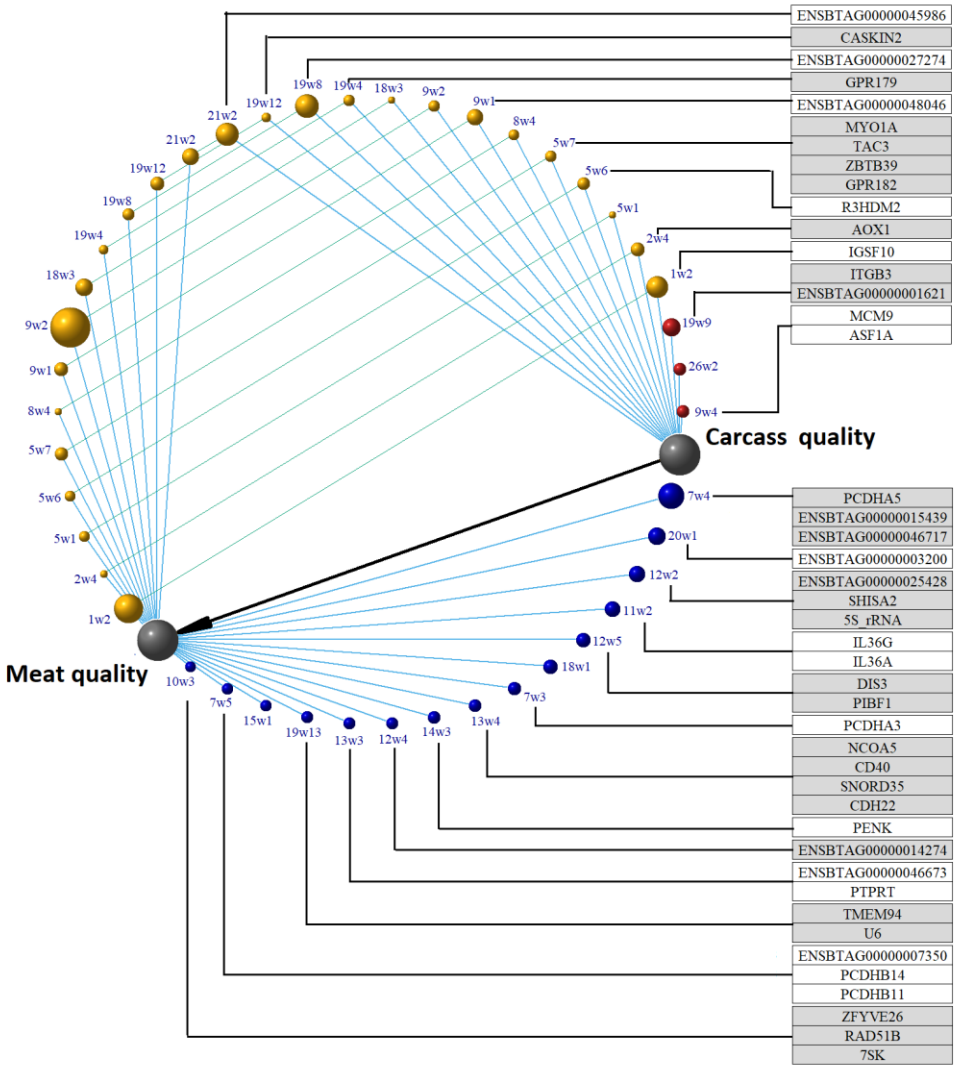


Figure 4c. Amount of additive variability of the latent variables for meat quality and carcass quality explained by 20 adjacent-SNP windows harboring genes identified in the *Longissimus dorsi* muscle from animals in an Angus-Brahman multibreed herd. Only windows that explained more than 0.15% of the additive variance are shown. Gray nodes are the latent phenotypes for carcass quality and meat quality constructed by the SE analysis. Red nodes are windows explaining variability in carcass quality; yellow nodes are windows explaining variability in carcass quality and in meat quality simultaneously; blue nodes are windows explaining variability in meat quality. The black edge shows the causal relationship between the latent variables carcass quality and meat quality; blue edges represent the relationship between a chromosomal window and a latent variable; green edges relate the effect of the window on the latent phenotypes carcass quality and meat quality. Red, yellow and blue node sizes represent the amount of genetic variability explained by the window in each latent phenotype. Seven windows had no reported gene inside them.

5) Characterization of meconium microbiota and its association with fetal development, establishment of postnatal gut microbiota, and subsequent animal growth. The sterile womb dogma has been challenged during last decade with the detection of commensals in fetal environment. There is uncertainty, however, whether microbiota in the fetus influence offspring's development. This

research showed that the establishment of microbiota starts even in the fetus and its composition is associated with birthweight in a cattle model. We collected meconium samples from 268 newborn calves and found that 182 meconium samples contained bacterial DNA. The associations among meconium microbiota and birthweight as well as gut microbiota development during preweaning (about 3 months of age) were investigated. Newborn calves were divided into 3 different groups (low, medium, and high) based on birthweight. Meconium from the low birthweight group tended to have higher microbial richness (P = 0.076) compared to meconium from the high birthweight group, including pathogens such as *Pseudomonas*, *Legionella*, and *Actinobacillus*. The relative abundance of *Bacillus* (P = 0.039) was higher in the low birthweight group. Moreover, meconium in the low birthweight group contained more genes involved in amino acid metabolism and xenobiotics biodegradation. Conversely, meconium from the high birthweight group contained more microbial genes involved in fructose/mannose and glycerolipid metabolism as well as secondary bile acid biosynthesis pathways. During the preweaning stage, calves in the low birthweight group grew more slowly (P < 0.001), and their gastrointestinal tract microbiota structure was different than calves in the high birthweight group (P = 0.013). In conclusion, microbes likely colonize the fetus and influence fetal development that may affect the establishment of the gastrointestinal tract microbiota during the early stage of life.

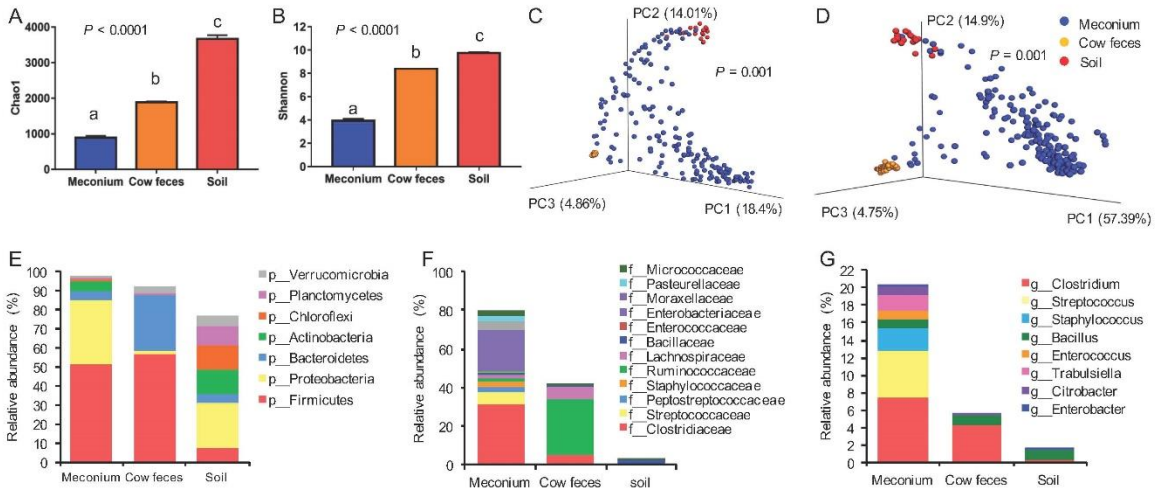


Figure 5a. Breed composition did not influence meconium microbiota. The meconium microbial richness from Chao1 index (A) and diversity from Shannon index (B) showed no significant differences among breed groups. The PcoA plot for the unweighted UniFrac distance (C) and the weighted UniFrac distance (D) showed no significant dissimilarities in meconium microbial membership and abundance among breed groups. Error bars are SEM. nBG1 = 27, nBG2 = 34, nBG3 = 21, nBG4 = 42, nBG5 = 26, nBG6 = 32.

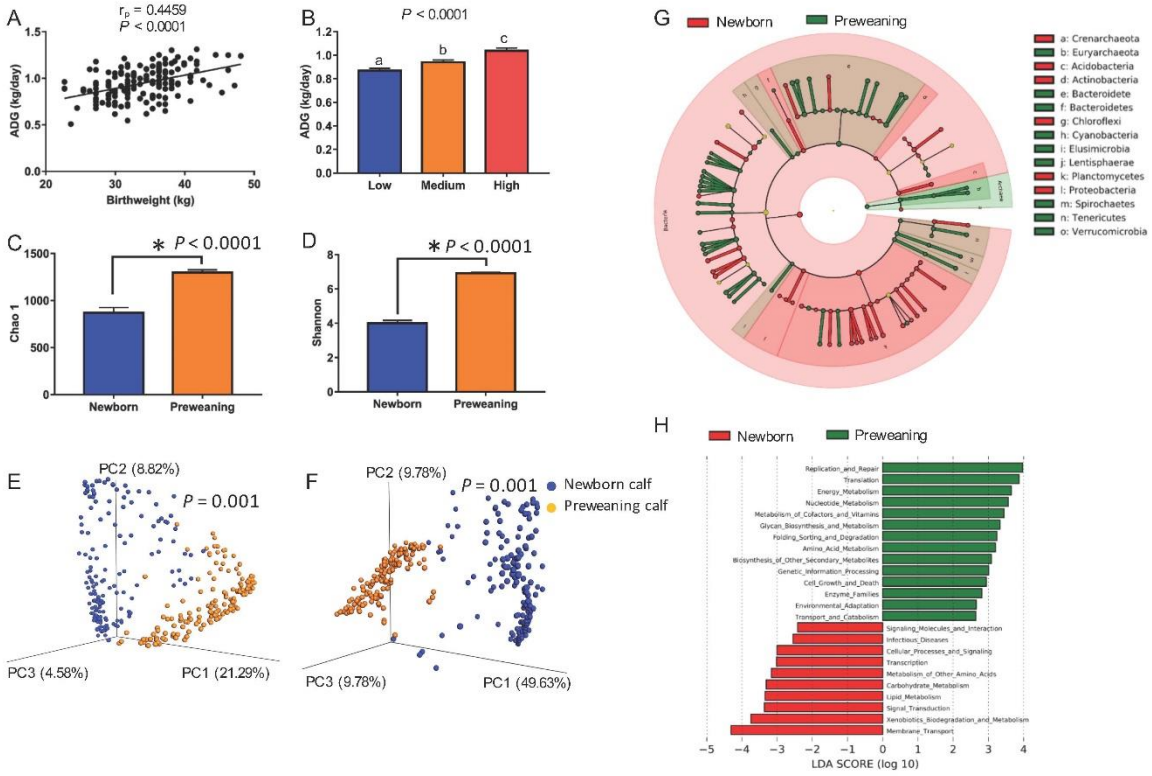


Figure 5b. Gut microbiota differed among preweaning calves from different birthweight groups. The gut microbial richness and diversity of preweaning calves in different birthweight groups were analogous according to Chao 1 Index (A) and Shannon Index (B). The PCoA plot based on unweighted UniFrac distance and ANOSIM analysis showed that gut microbial membership of preweaning calves was significantly different among birthweight groups (C), and gut microbial community structure tended to change with birth weight according to the weighted UniFrac distance (D). (E) The heatmap shows differences in microbial prevalence among birthweight groups. Only microbial taxa with variation in prevalence higher than 20% were extracted and included in the heatmap. The relative abundance of taxa changed with birth weight at both phylum (F) and genus levels (G). (H) LDA scores of the differentially abundant KEGG pathways enriched in gut microbiota of preweaning calves. Error bars are SEM. nlow = 50, nmedium = 63, nhigh = 48.

6) Collection of phenotypic data describing thermal tolerance in *Bos Indicus* influenced populations and characterization of the genetic component underlying these traits. First step in the process of revealing the genetic architecture of traits defining thermal tolerance using Bos indicus influenced cattle is to estimate the genetic parameters. Vaginal temperature was measured at 5-min intervals for 5 days in 286 cows over two years (2015 and 2017) from the multibreed herd (ranging from 100% Angus to 100% Brahman) of the University of Florida. Ambient environmental conditions were monitored using HOBO data loggers, which continuously record temperature, humidity, solar radiation, black globe temperatures, and wind speed which were used to calculate a temperature humidity index (THI). There was a breed effect on body temperature with Angus and 3/4 Angus cows had a vaginal temperature higher 39°C even during lower heat stress conditions while Brahman cattle were the only ones able to maintain a lower vaginal temperature throughout the 24h-day during high heat stress conditions (Figure 6a). Heritabilities for all different vaginal temperature measures (Table

6a) were low or medium and ranged from 0.11 to 0.27. The lowest heritability estimate is for vaginal temperature under high THI conditions (0.11), while heritability for vaginal temperature under low or average THI was slightly higher (0.25 and 0.20, respectively).

Table 6a. Genetic (σ^2_a) and residual (σ^2_e) variance and heritability (h^2) estimates for difference in vaginal temperature between the high and low THI (Temp Diff Hi-Low) , vaginal temperature under high THI (Temp High), vaginal temperature under low THI (Temp Low), and vaginal temperature under average THI (Temp Mean)

Trait	σ^2_a	σ^2_e	h^2
Temp Diff Hi-Low	0.17	0.45	0.27
Temp High	0.07	0.56	0.11
Temp Low	0.14	0.42	0.25
Temp Average	0.09	0.35	0.20

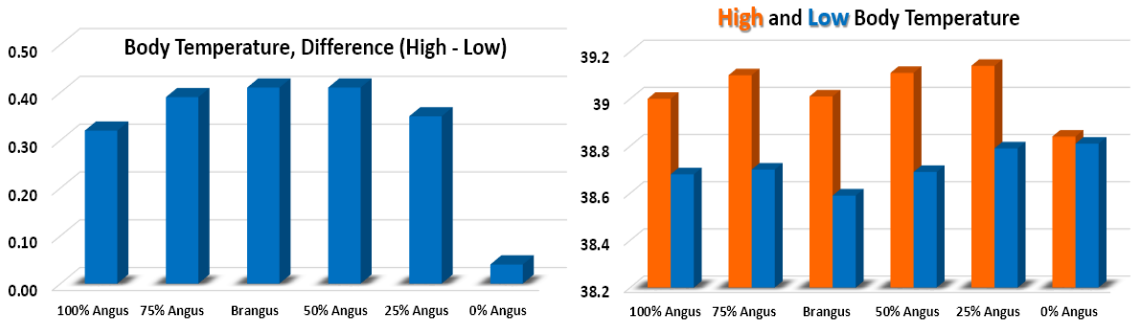


Figure 6a. Least square means for difference in vaginal temperature between the high and low THI, vaginal temperature under high THI (Temp High), vaginal temperature under low THI (Temp Low) for 6 different breed groups.

Another study assessed the phenotypic variability in core body temperature and sweating rate and to evaluate the effect of coat type, temperament, and body weight on core body temperature and sweating rate in Brangus heifers. During August and September of 2016, 725 Brangus heifers on pasture were evaluated in four separate groups (n = 200, 189, 197, and 139). Coat score, sweating rate, chute score, exit score, and live weight were recorded as the animals passed through the chute. Vaginal temperature was recorded every 5 minutes for 5 consecutive days. There was significant variation in vaginal temperature between heifers in the same environmental conditions ($\sigma^2_u = 0.049$), suggesting opportunities for selective improvements. A repeatability of 0.47 and 0.44 was estimated for sweating rate and vaginal temperature, respectively, suggesting that one measurement would be able to adequately describe the sweating capacity or ability to control the body temperature of an individual. Vaginal temperature increased as THI increased, with approximately one-hour lag time in the animal's response (Figure 6b). Vaginal temperature ($P = 0.015$) and sweating rate were lower (-5.49 ± 2.12 g/(m^2·h), $P < 0.01$) for heifers that demonstrated a calmer behavior in the chute. Animals with shorter, smoother hair coats had significantly lower vaginal temperatures when compared to animals with longer hair coats ($P < 0.01$). Heifers weighing more maintained a significantly lower vaginal temperature ($P < .0001$). Our results showed that hair coat, temperament, and weight influenced vaginal temperature regulation.

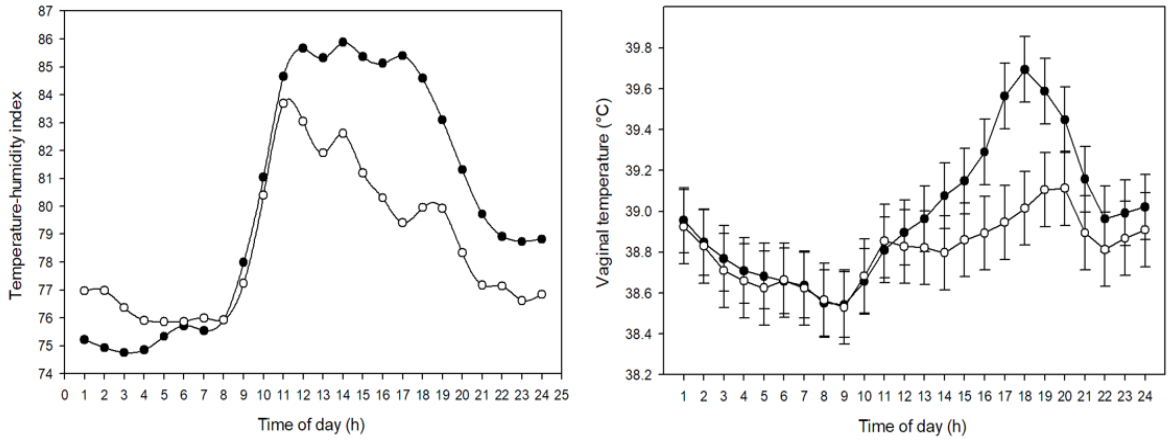


Figure 6b. Thermal environment during two extreme days in group 2 and 3 of heifers (left panel). Data represents least squares means THI during low heat stress days (open circles) and high heat stress days (closed circles). Right panel shows least squares means ± SEM for vaginal temperature of the same group of heifers during a low heat stress day (open circles) and a high heat stress day (closed circles).

Publications

Dikmen, S., R. G. Mateescu, M. A. Elzo, and P. J. Hansen. 2018. Determination of the optimum contribution of Brahman genetics in an Angus-Brahman multibreed herd for regulation of body temperature during hot weather. J. Anim. Sci. (https://doi.org/10.1093/jas/sky133).

Elzo, M. A., R. Mateescu, C. Carr, D. O. Rae, T. Scheffler, J. Scheffler, K. C. Jeong, J. D. Driver, and M. D. Driver. 2018. FCEF 2018 Report 1 for Florida Brahman: Genomic selection for tenderness, marbling, and reproductive tract score. University of Florida, Gainesville, FL, p 1- 9.

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Research Impacts

1) Udder score means by Brahman fraction at calving, 6 months, and weaning indicated that cows with higher Brahman percentages tended to have better udders. A similar trend existed for teat score means at calving (cows with higher Brahman percentages had better teats); a slightly negative trend towards Brahman occurred at 6 months and at weaning. Conversely, udder and teat score means at calving, 6 months, and weaning showed consistent downward trends as cows aged, thus younger cows tended to have better udders and teats than older cows at all lactation stages.
2) The successful completion of the first genomic-polygenic evaluation of animals in the Florida Multibreed Angus-Brahman population for twenty growth, fertility, ultrasound, carcass, and tenderness traits showed the feasibility of developing a statewide genetic evaluation system for sub-tropically adapted animals based on phenotypic, pedigree, and genotypic data from experimental and

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private herds. This system required the development of a statewide database (phenotypes, pedigree, genotypes) and a tissue sample and DNA repository. The feasibility of extending this system to the US Southern Region merits to be explored.

3) Proteolysis and tenderization in Angus, Brahman and Brangus is related to Ph decline and calpain-1 autolysis. Longissimus from Brahman exhibited slower rate of pH decline that coincided with slower tenderization, evidenced by reduced calpain-1 autolysis at 24h postmortem and less troponin-T degradation. The slower rate of acidification in Brahman indicated that ATP levels were maintained longer, prolonging calcium uptake by the sarcoplasmic reticulum and mitochondria, thereby delaying calpain activation and tenderization.
4) Structural equation analysis and genome wide association for growth, carcass quality and meat quality in an Angus-Brahman multibreed population indicated that three biological mechanisms could explain the association of identified genes with latent constructs for carcass and meat quality: postmortem proteolysis of structural proteins and cellular compartmentalization, cellular proliferation and differentiation of adipocytes, and fat deposition.
5) Meconium microbiota was associated with fetal development, establishment of postnatal gut microbiota, and subsequent animal growth. Meconium from the low birthweight group tended to have higher microbial richness compared to meconium from the high birthweight group, including pathogens such as *Pseudomonas*, *Legionella*, and *Actinobacillus*. Microbes likely colonize the fetus in its early stages influencing fetal development and affecting the establishment of gastrointestinal tract microbiota pre and postnatally.
6) Heritabilities for all different vaginal temperature measures were low or medium and ranged from 0.11 to 0.27. The lowest heritability estimate was for vaginal temperature under high THI conditions (0.11), while heritability for vaginal temperature under low or average THI was slightly higher (0.25 and 0.20, respectively). Coat score and temperament influenced vaginal temperature responses to heat stress in Brangus heifers. Vaginal temperature increased as THI increases, with a one-hour lag time in the animal's response. Temperament was important for both sweating rate and vaginal temperatures, with calm cattle having lower sweating rates and maintaining lower body temperatures, suggesting that heifers with a calmer demeanor respond better in hot conditions.