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Research Areas

Objective 2: Meta-analyses of economically important traits of cow productivity and fertility to assess breed and production system combinations

Objective 4: Investigation of early cow-life performance (First four parities) affecting lifetime production in Brahman and Brahman-Angus cows

Activities

Objective 2 Suggested Data Collection

(1)Breed of cow, (2) Sire ID/sire breed and dam ID/dam breed of cow, (3) cow birth date, (4) Mating information (natural or artificial insemination; single or multiple sires; number of cows per bull; season or insemination date(s), (5) Predominant forage in pastures (fescue 0 = no; 1 = yes), (6) Sire/sire breed of calf, (7) Cow:bull ratio, (8) Body condition score (date and stage of production), (9) Palpation status (0 = non-pregnant; 1= pregnant), (10) Calving status (0 = no; 1 = yes), (11) Weaning status (0 = no; 1 = yes), (12) Calving date (calving season, spring or fall), (13) Calving difficulty (1 = normal; 2 = easy pull; 3 = hard pull; 4 = caesarian section; 5 = abnormal presentation, note the abnormal presentation of calf), (14) Calf vigor issues (1 = normal; 2 = weak but nursed without assistance; 3 = weak and assisted to nurse; add any notes), (15) Calf birth weight, (16) Calf weaning date, (17) Calf weaning weight, (18) Cow temperament at calving, (19) Date of death and reason/notes for cow or her calf, and (20) Date of culling and reason/notes for cow and/or her calf leaving herd.

Objective 4 Additional Data Collection

(1) Udder scores, (2) Ultrasound ribeye area, fat, percent intramuscular fat between 365 and 467 days of age, (3) Carcass and meat quality traits.

Activities

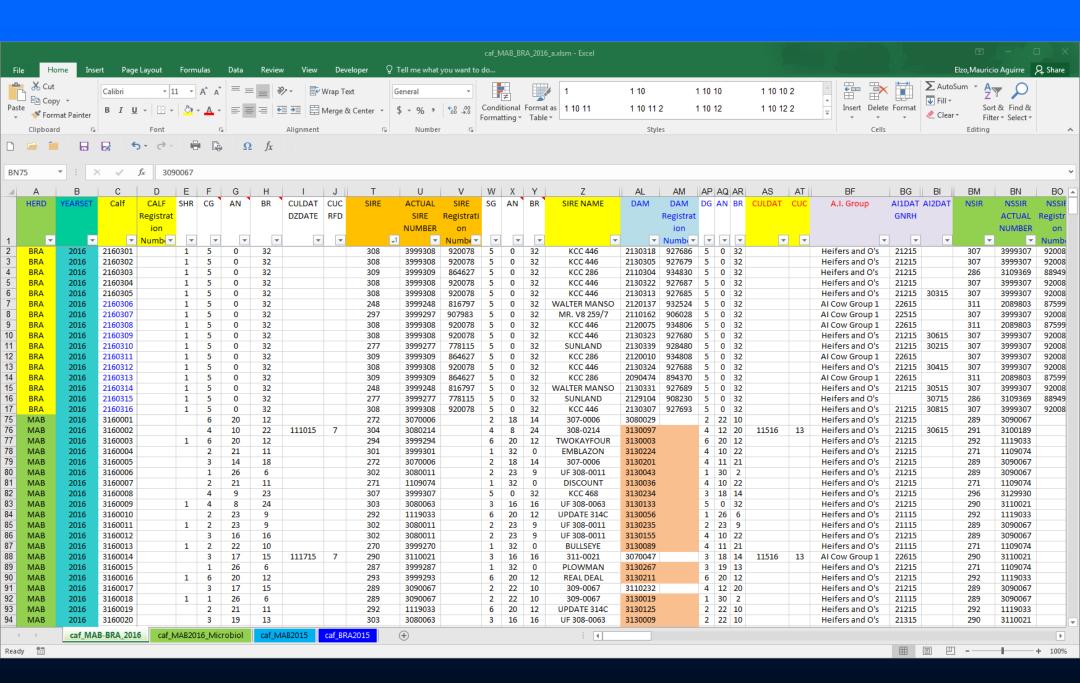
Data Collection

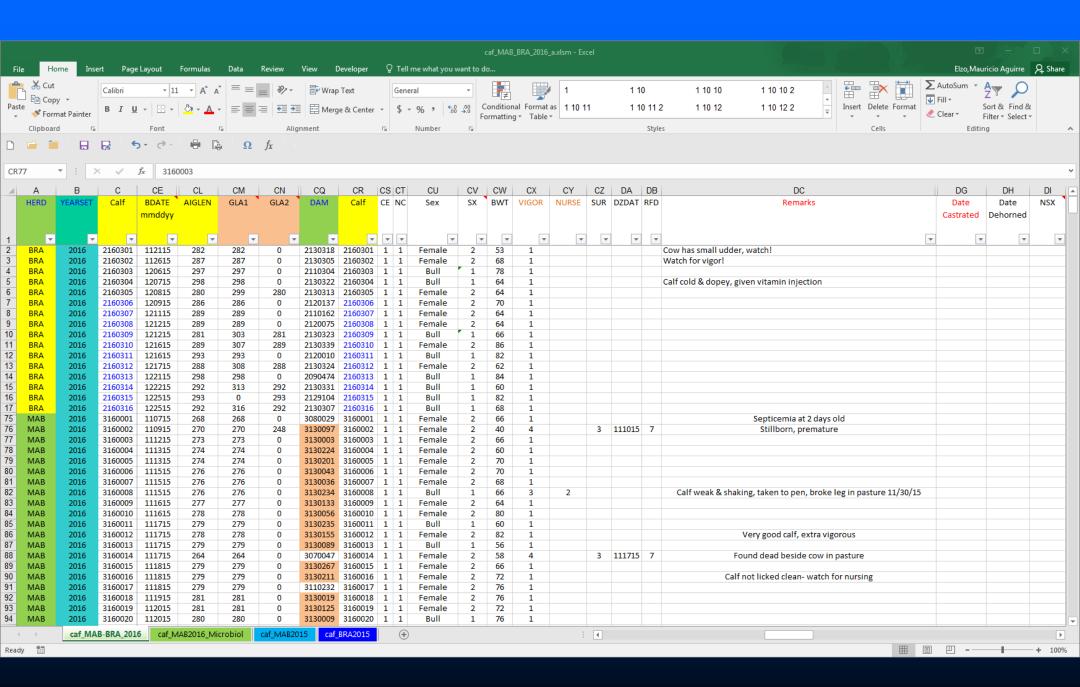
Multibreed Angus-Brahman (MAB; 270 cows) and Brahman herds (BRA; 60 cows)

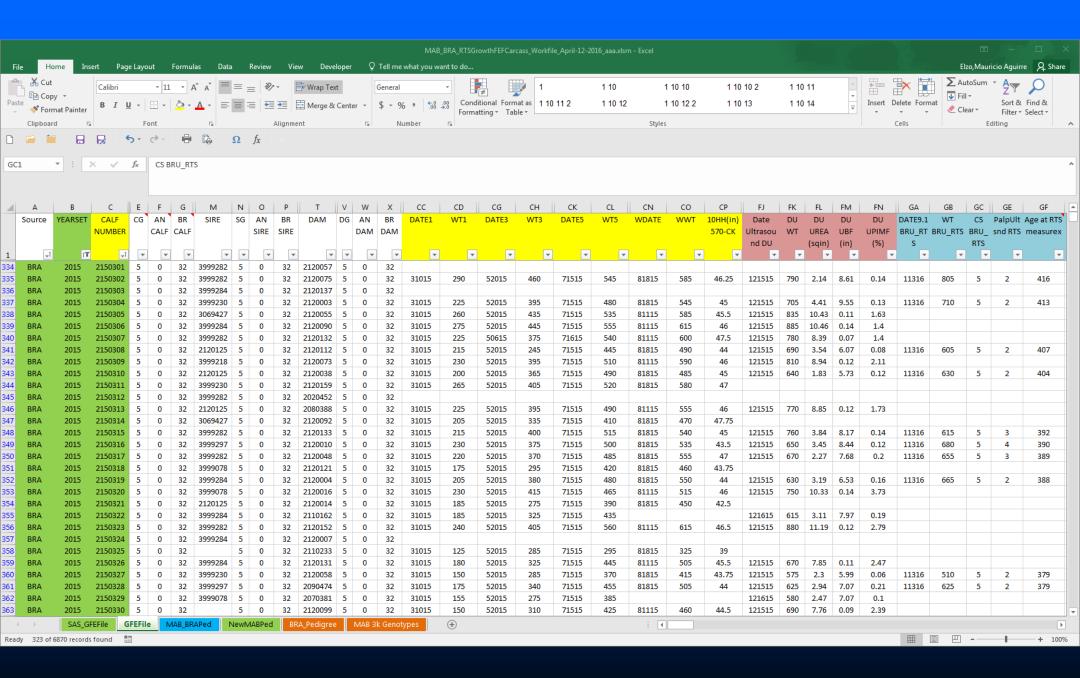
- 1) Objectives 2 and 4 suggested phenotypic data
- 2) Expected breed composition of all MAB animals (calves, sires, dams)
- 3) Pedigree file (MAB + BRA)
- 4) Accumulated phenotypic data file (MAB + BRA; 1987 Present; Unequal number of years of data per trait)
- 5) Genotypic data files (3k, 150k, 250k)

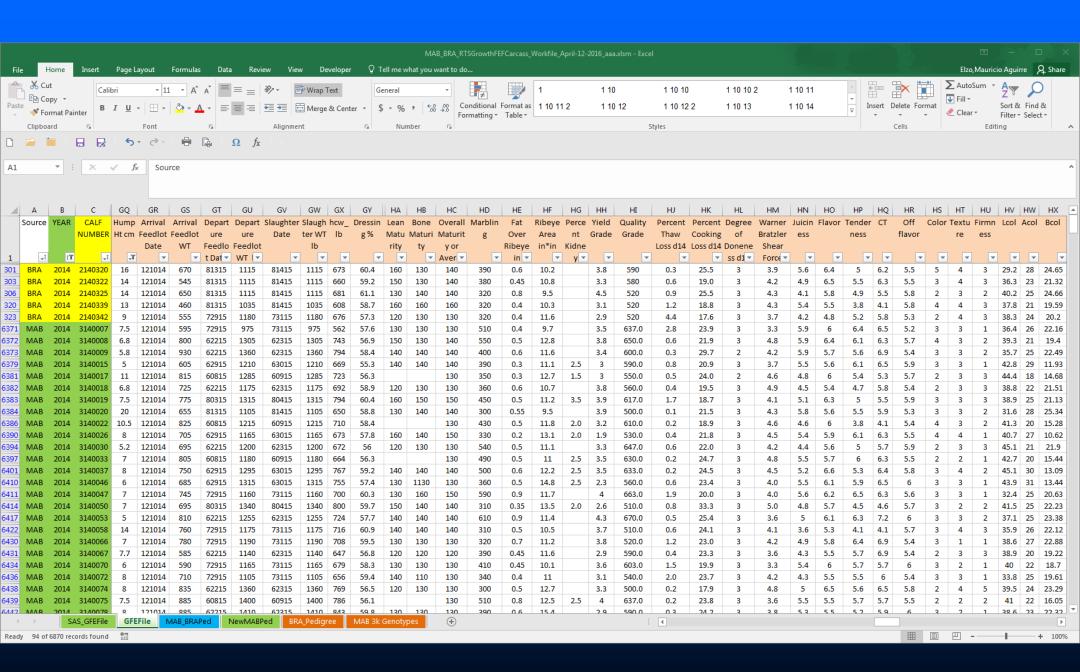
Tissue Sample Collection

- 1) Blood samples from all calves and natural service sires (-80 Celsius)
- 2) Hair samples from all calves and natural service sires (room temperature)
- 3) Semen from all Al sires (-80 Celsius)









Research

- 1) 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
- 2) 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
- 3) 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
- 4) Genomic-polygenic analysis of animals from the MAB and Brahman herds for 9
 Ultrasound and Carcass traits [UYW, UREA, UBF, UMAR, SLW, HCW, REA, FAT, and MAR]
- 5) FORTRAN software for editing of phenotypes, genotypes, and pedigree data and construction of input data files for imputation (Findhap2, 3, 4; FImpute) and for genomic-polygenic evaluation (BLUPF90, GS3, QXPAK)
- 6) 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

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

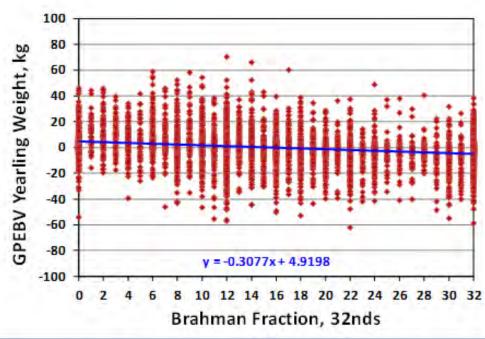
UF Multibreed Angus-Brahman & Brahman Herds

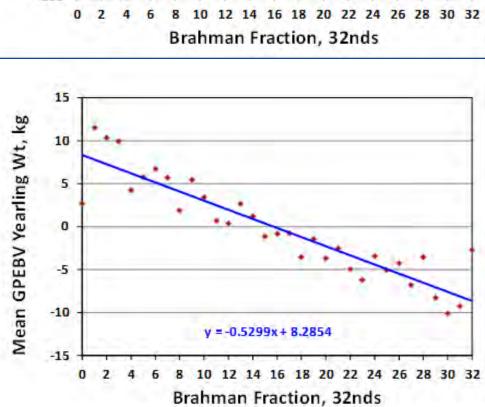
[1,758 calves, 125 sires, 701 dams] BLUPF90

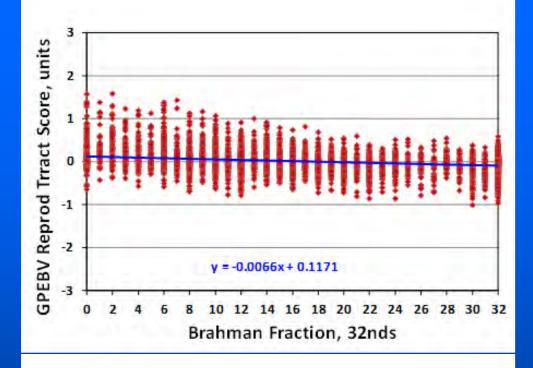
Genomic-polygenic (GPM) and Polygenic models (PM)
Similar estimates of genetic parameters (GPM somewhat higher than PM)
Similar rankings (rank correlations = 0.91 to 0.95)

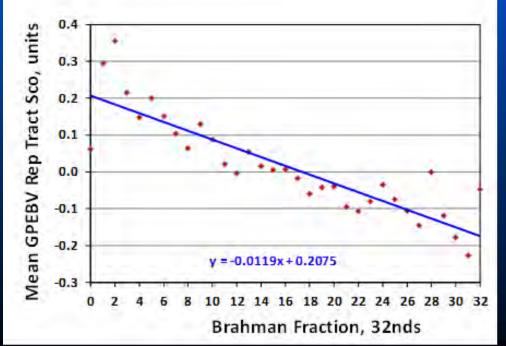
In general, Brahman had
Lower EBV for Yearling Wt
Lower EBV for Reproductive Tract Score
Higher EBV for Age at First Calving
Lower EBV for First Calving Interval
Than Angus

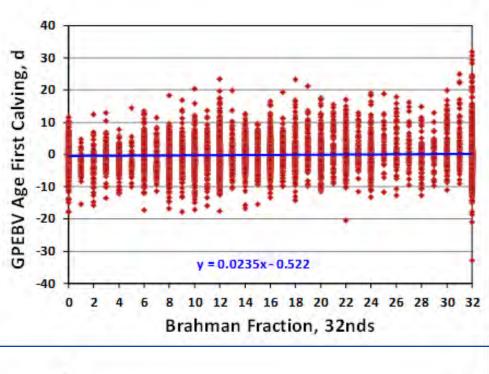
Heifers with higher Brahman percentages tended to be lighter and less mature as yearlings, older at first calving, and have shorter FCI than heifers with higher Angus percentages (Perhaps due to estrous synchronization, AI, and 60 d NS period)

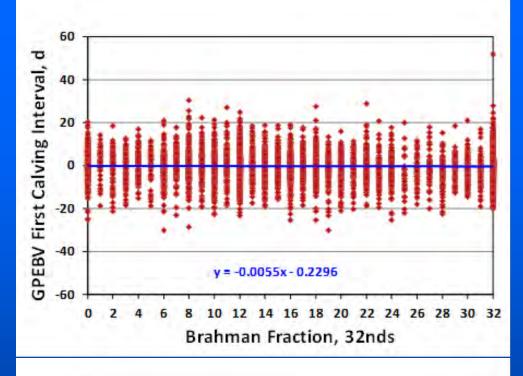


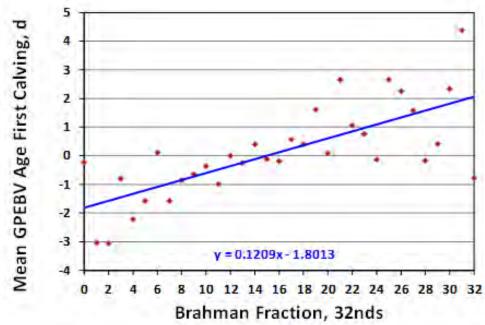


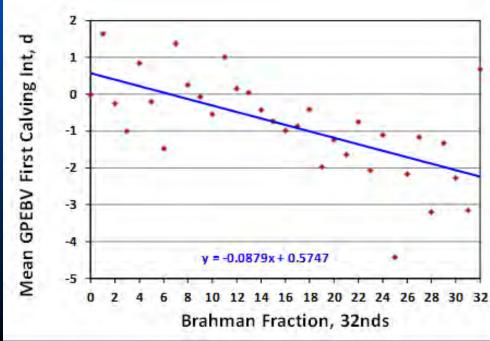












Genomic-polygenic analysis of animals from the MAB and Brahman herds for BW and WW Direct and Maternal, GW Direct, and Ultrasound Ribeye area, Backfat, and Marbling

UF Multibreed Angus-Brahman & Brahman Herds

[1,758 calves, 125 sires, 701 dams]

Genomic-polygenic (GPM) and Polygenic models (PM)
Similar estimates of genetic parameters (GPM h² somewhat higher than PM h²)

Heritabilities

BWD = 0.19; WWD = 0.61; GWD = 0.31; BWM = 0.12; WWM = 0.13 UREA = 0.50; UFAT = 0.04; UMAR = 0.05

Additive Genetic Correlations

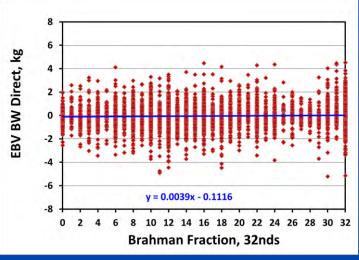
BWD positively correlated with WWD (med high)

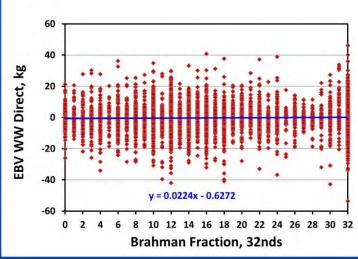
BWD, WWD negatively correlated with BWM, WWM, GWD (med high)

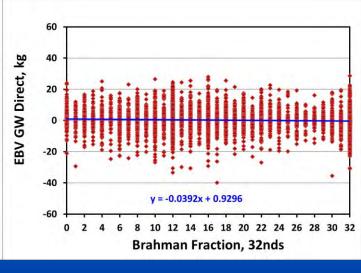
BWD, WWD, GWD positively correlated with UREA and UFAT (med high)
BWD, WWD, GWD negatively correlated with UMAR (med)
BWM, WWM negatively correlated with UREA and UFAT (low med)
BWM, WWM positively correlated with UMAR (low)

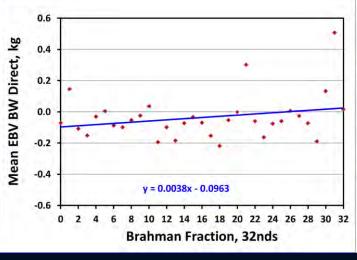
UREA positively correlated with UFAT (med high)
UREA, UFAT negatively correlated with UMAR (med high)

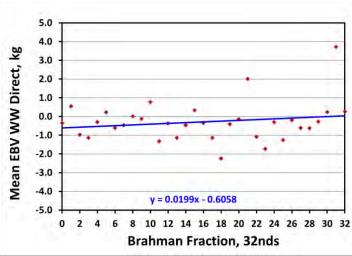
GPEBV Direct Growth Traits

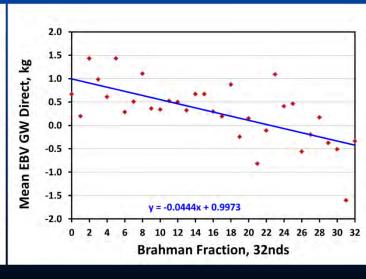




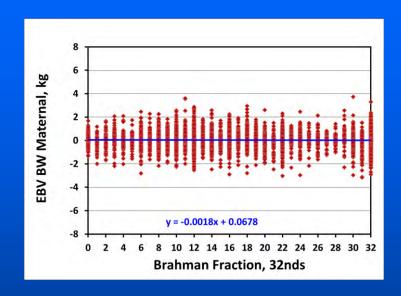


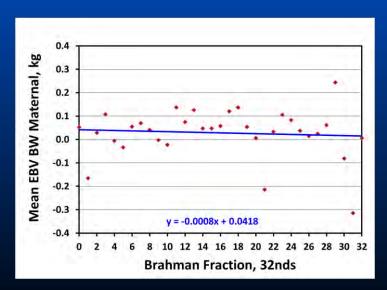


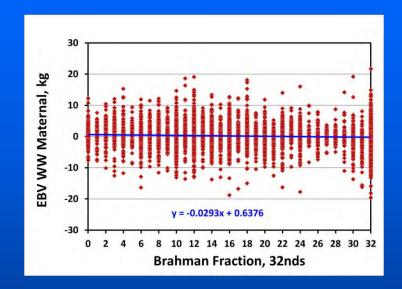


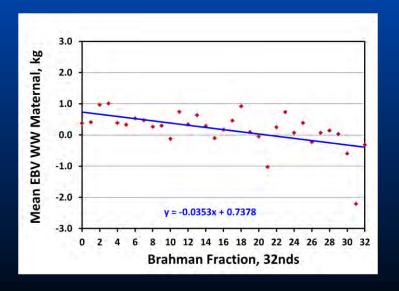


GPEBV Maternal Growth Traits

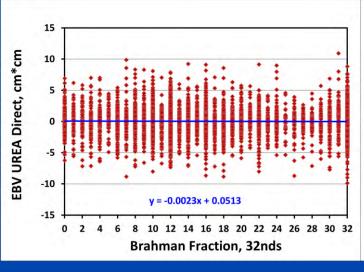


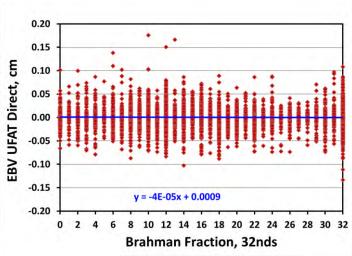


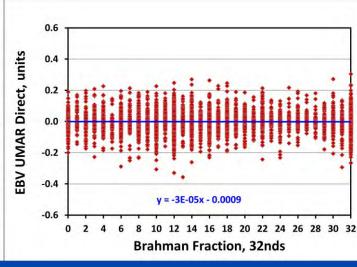


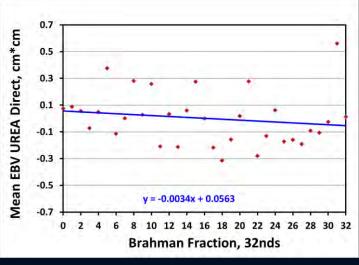


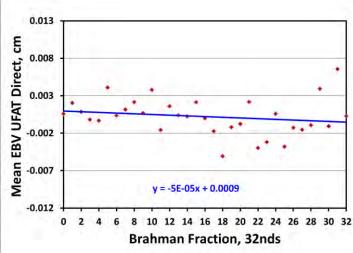
GPEBV Direct Ultrasound Traits

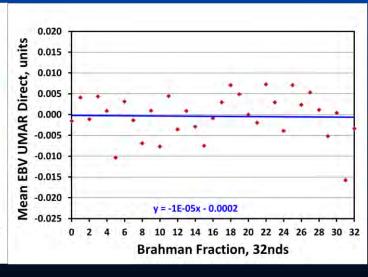












Genomic-polygenic analysis of animals from the MAB and Brahman herds for 9 Ultrasound and Carcass traits [UYW, UREA, UBF, UMAR, SLW, HCW, REA, FAT, and MAR]

UF Multibreed Angus-Brahman & Brahman Herds

[1,758 calves, 125 sires, 701 dams]

Genomic-polygenic (GPM) and Polygenic models (PM)
Similar estimates of genetic parameters (GPM h² somewhat higher than PM h²)

Heritabilities

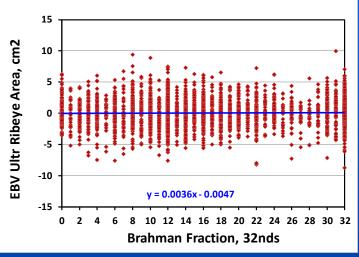
UYW = 0.23; UREA = 0.35; UFAT = 0.04; UMAR = 0.08 SLW = 0.44; HCW = 0.55; REA = 0.55; FAT =0.18; MAR = 0.31

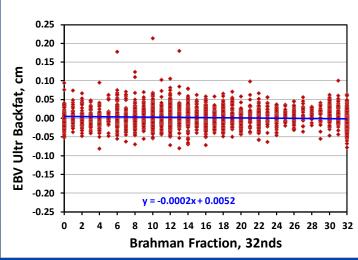
Additive Genetic Correlations

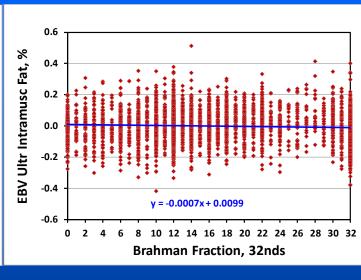
UYW, UREA positively correlated with all traits, except UMAR (med high)
UFAT positively correlated with all traits (low high)
UMAR negatively correlated with all traits except FAT, MAR (low high)

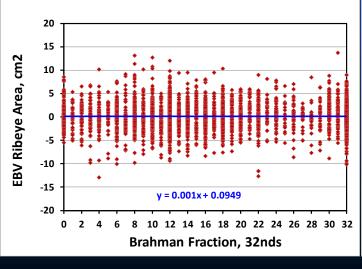
UYW, UREA, UFAT positively correlated with SLW and all carcass traits (med high) SLW and all carcass traits positively correlated with each other (low high)

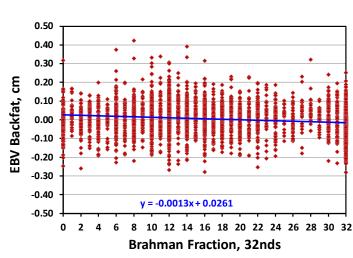
GPEBV Ultrasound and Carcass Traits

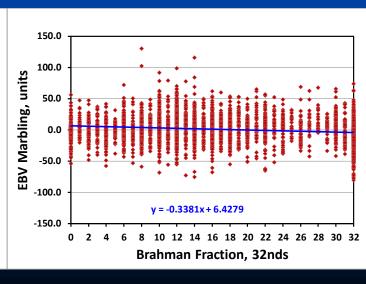




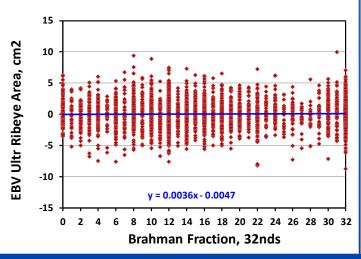


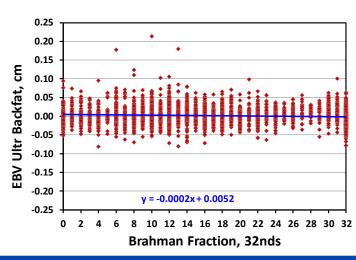


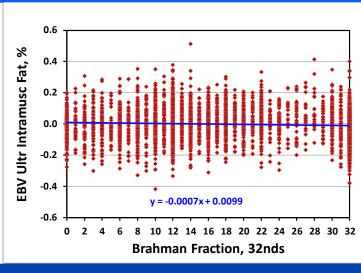


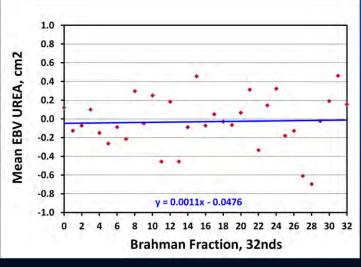


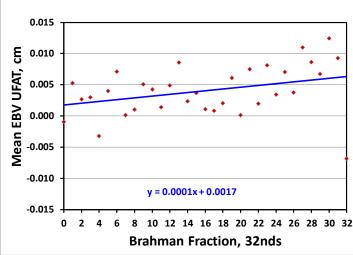
GPEBV Ultrasound Traits

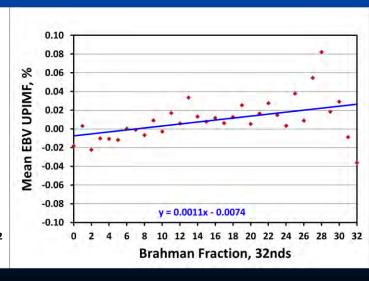




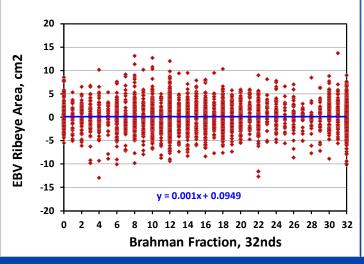


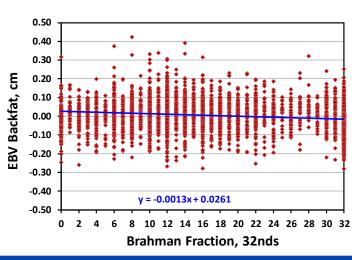


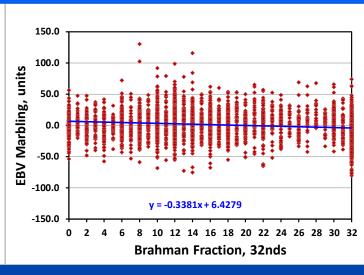


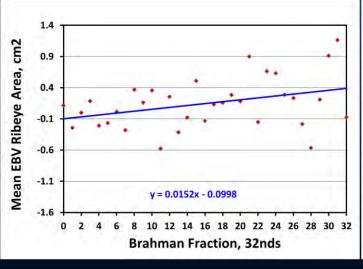


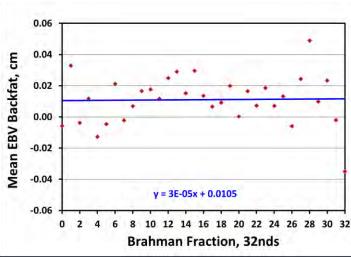
GPEBV Carcass Traits

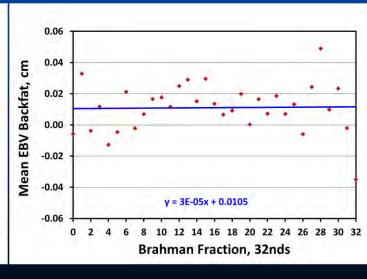




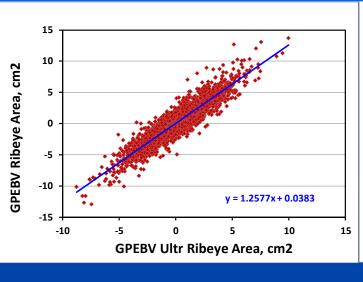


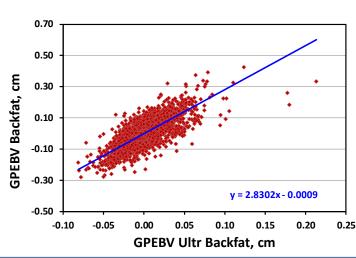


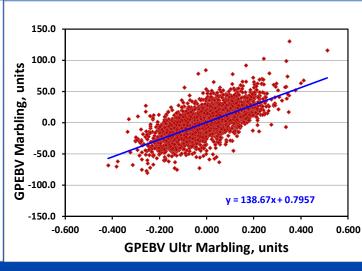


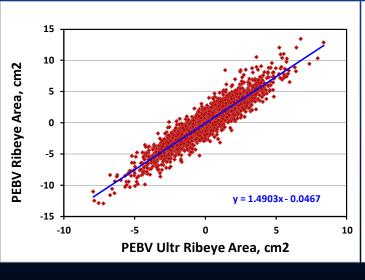


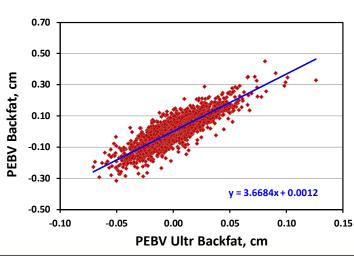
GPEBV and PEBV Ultrasound and Carcass Traits

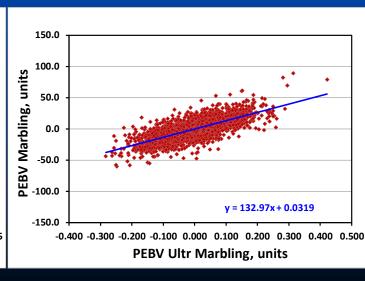












Additional Research Projects Involving the Multibreed Angus-Brahman and Brahman Herds

Identification of genetic markers associated with meat quality traits to improve prediction for tenderness in beef cattle (R. Mateescu)

Muscle metabolic phenotypes and their association with meat quality traits (T. Scheffler, J. Scheffler, J. M. Gonzalez)

Animal and microbiological factors affecting the prevalence of Shiga Toxin Producing E. coli (STEC) and Cefotaxime Resistance (CefR)

(K. C. Jeong)

Influence and regulation of vitamin D on the immune system, health, and growth of beef calves

(C. Nelson)