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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 = caesarean 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.

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

Data Collection

Multibreed Angus Brahman (MAB) and Brahman (BRA) herds
(2017: Number of Cows = 244; MAB = 275; BRA = 69)

1) Objectives 2 and 4 suggested phenotypic data
2) Expected breed composition of all MAB animals (calves, sires, dams)
3) Pedigree file (MAB + BRA; nanim = 8,302)
4) Phenotypic data (MAB + BRA; 1987 – Present; Unequal number of years of data per trait; nanim = 6,755)
5) Genotypic data (Illumina3k = 1,292; GeneSeek GGP150k = 238;GeneSeek GGP250k = 785)

Tissue Sample Collection

1) Blood samples from all calves & natural service sires; Semen from all AI sires (-80° Celsius; n = 3,276)

Brahman Herd [1]

Brahman Herd [3]

Brahman Herd [2]

Udder & Teat Score: Birth, Mid-Lactation, Post-Weaning

Research

1) Genomic-polygenic and polygenic predictions for nine ultrasound and carcass traits in Angus-Brahman multibreed cattle using three sets of genotypes.
2) Development of a statewide Brahman and Brahman-Angus database that includes pedigree and phenotypic information for fertility, growth, ultrasound, carcass, and meat palatability traits from private Brahman and UF herds.
3) Development of a statewide Brahman and Brahman-Angus tissue sample repository with blood, ear-notches, and semen samples from private Brahman and UF herds.
4) FORTRAN software for editing of phenotypes, genotypes, and pedigree data and construction of input data files for imputation (Findhap; FImpute) and for genomic-polygenic evaluation (BLUPF90, GS3, QXPAK).
5) 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 and polygenic predictions for nine ultrasound and carcass traits in Angus-Brahman multibreed cattle using three sets of genotypes

Heritabilities
UYW = 0.54; UREA = 0.36; UFAT = 0.12; UMAR = 0.34
SLA = 0.59; HCW = 0.58; REA = 0.48; FAT =0.41; MAR = 0.56

Additive Genetic Correlations
UYW positively correlated with UREA, HCW, REA (medium; 0.4 to 0.8)
UREA positively correlated with HCW, REA (medium)
REA positively correlated with HCW (medium)

UREA negatively correlated with UMAR (low; >-0.2 to -0.3)
UFAT negatively correlated with SLA, HCW (low)
REA negatively correlated with UMAR, MAR (low)

Other correlations either zero or below ± 0.20

Genomic-polygenic and polygenic predictions for nine ultrasound and carcass traits in Angus-Brahman multibreed cattle using three sets of genotypes

UF Multibreed Angus-Brahman & Brahman Herds
[1,981 calves, 125 sires, 691 dams]
[nSNP = 127,016; nSNP = 24,761: 1) top 5%; 2) 5% evenly spread]

Similar estimates of genetic parameters (GPM h^2 somewhat higher than PM's)
[GPM = Genomic-Polygenic Model; PM = Polygenic Model]

High similarity among predicted EBV and accuracies from GPM, GPMR1 (top 5% SNP), and GPMR2 (5% SNP across genome) as well as high-rank correlations for sires, dams, and progenies

The two reduced genotype sets were appropriate alternatives to the complete GPF250k set for genomic-polygenic evaluation and selection in this multibreed Angus-Brahman population

High EBV variability existed among animals of all Angus and Brahman percentages and no specific breed composition was overwhelmingly better or worse for any of the nine traits

Selection in multibreed Angus-Brahman populations should be based solely on genetic merit regardless of breed composition

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Genomic-Polygenic EBV Ultrasound and Carcass Traits
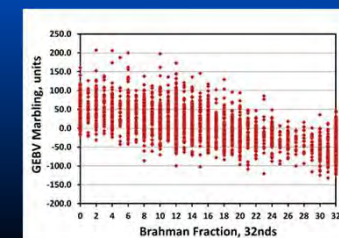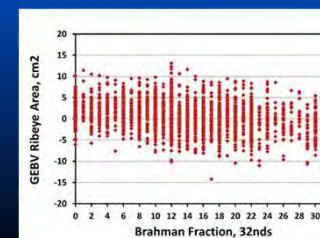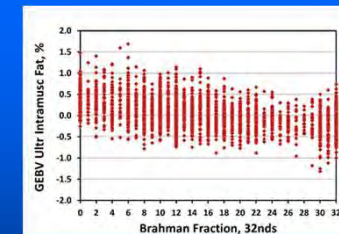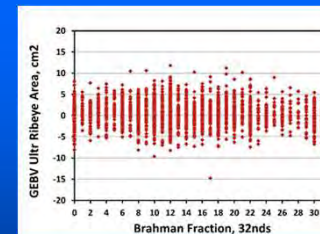
Florida Brahman: Genomic selection for tenderness, marbling, and reproductive tract score

Goals

Develop a **statewide database** with genotypes, pedigree, and phenotypes for all recorded traits (reproduction, growth, ultrasound, carcass, meat palatability) in the Florida Brahman population

Increase the size of the UF Brahman herd to 260 cows

Establish a **statewide repository** of Brahman tissue samples and DNA

Conduct **annual genomic evaluations** for tenderness, marbling, and reproductive tract score using information from phenotypes, pedigree, and genotypes

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

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

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Florida Brahman Genomic Evaluation

- Data Collection System
  - Phenotypes (ABBA, Breeders, UF)
  - Pedigree (ABBA, Breeders, UF)
- Tissue Collection System
  - Semen, Blood, Ear Notches (Breeders, UF)
- Genotyping System
  - SNP Genotypes (GeneSeek: GGPHD, GGPLD)
- Genomic-Polygenic System
  - Data Editing (UF; Edped_LD_HD)
  - Construction of Input Files (UF; BRA-MAB_Impute)
  - Imputation (Findhap)
  - Covariance Components (AIREMLF90)
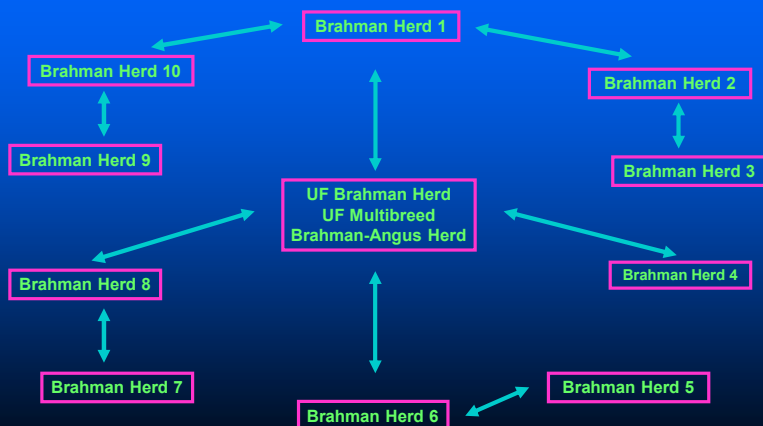 - Genomic-Polygenic Predictions (AIREMLF90, BLUPF90)
- Publication System
  - Animal EBV (UF; Online, Paper)

Population: Connected Herds {Sires, Pedigree}

Brahman Herd 1
Brahman Herd 2
Brahman Herd 3
Brahman Herd 4
Brahman Herd 5
Brahman Herd 6
Brahman Herd 7
Brahman Herd 8
Brahman Herd 9
Brahman Herd 10

UF Brahman Herd
UF Multibreed Brahman-Angus Herd

Current Work

Invitation to Florida Brahman breeders to participate in the project (emails, telephone calls, meetings)

Group and individual meetings with Brahman breeders to discuss goals, expectations, database development, tissue sample collection and repository, genomic evaluation and selection

Database (pedigree & phenotypes)
1) **Florida Brahman breeders:** pedigree & phenotypes [reproductive tract score, weights, yearling ultrasound, carcass (primarily from crossbred animals)]
2) **ABBA:** pedigree and phenotypes [birth weight, weaning weight, yearling weight, ultrasound ribeye, back fat, rump fat, intramuscular fat]
3) **UF multibreed Angus-Brahman & Brahman herds :** pedigree & phenotypes [reproduction, growth, ultrasound, carcass, meat palatability]

Repository (tissue samples & DNA)
1) **Florida Brahman breeders** (blood, ear notches, semen)
2) **UF multibreed Angus-Brahman & Brahman herds** (blood, semen)

Incentives:
$5 per animal with records or tissue sample; $12 per ultrasound; $40 per carcass record; free ear-notch kits and applicators.

Records, Tissue Samples, and Genotypes (April 2017)

Dataset	Pedigree Records	Phenotype Records	Tissue Samples	GeneSeek GGP250k
Florida Brahman breeders	198	115	1,400	0
ABBA (All years; Unedited files)	15,844	7,358	0	0
UF Brahman herd	673	446	475	47
UF Brahman-Angus Multibreed herd	8,302	6,755	2,801	738

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

Association of SNPs and haplotypes in µ-calpain and calpastatin genes with Warner-Bratzler Shear Force in multibreed Brahman-Angus cattle
(R. Mateescu)

Influence of Brahman genetics on muscle fiber properties, protein degradation, and tenderness in the Angus-Brahman multibreed herd
(T. Scheffler, J. Scheffler)

Colonization dynamics of Cefotaxime resistant bacteria in beef cattle raised without Cephalosporin antibiotics
(K. C. Jeong)

Influence and regulation of vitamin D on the immune system, health, and growth of beef calves
(C. D. Nelson)