

UF Station Report

S-1064

2017-2018

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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 3: Documentation of genetic components pertaining to heat tolerance adaptive traits in sustainable beef cattle production systems

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 = 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 and teat scores, (2) Ultrasound ribeye area, fat, percent intramuscular fat between 365 and 467 days of age, (3) Carcass and meat quality traits, (4) Thermotolerance traits.

Activities

Data Collection

Multibreed Angus-Brahman (MAB) and Brahman (BRA) herds
(2018: Number of Cows = 661; MAB = 499; BRA = 162)

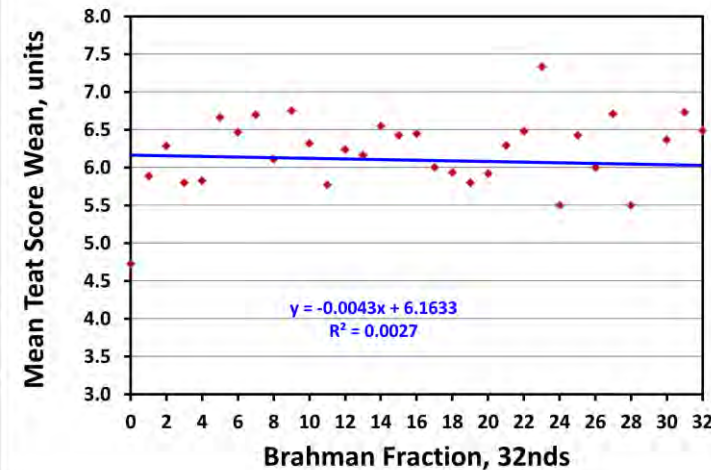
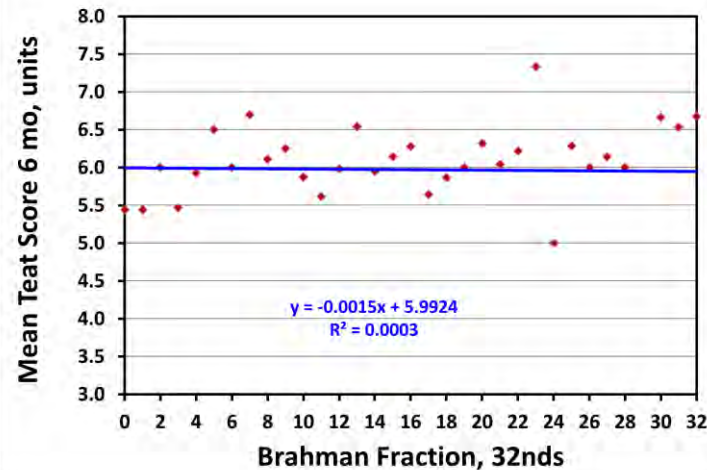
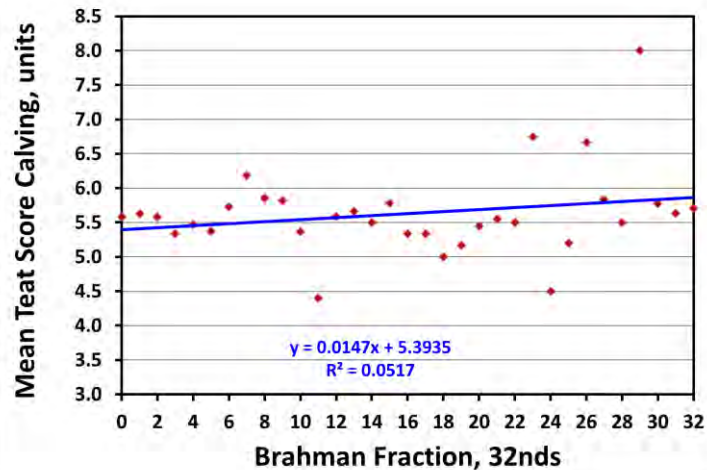
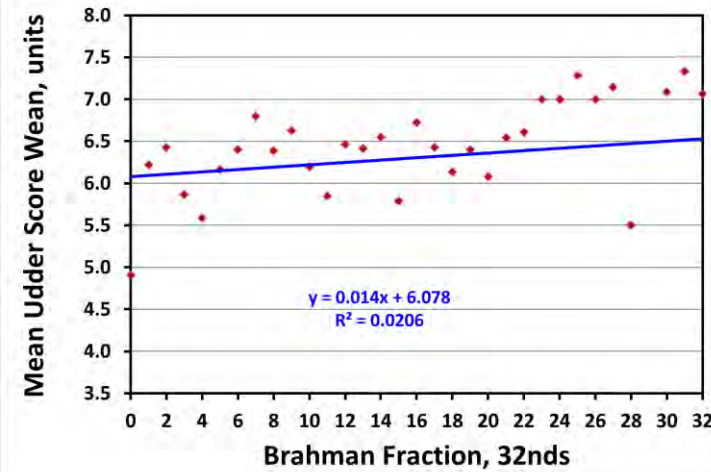
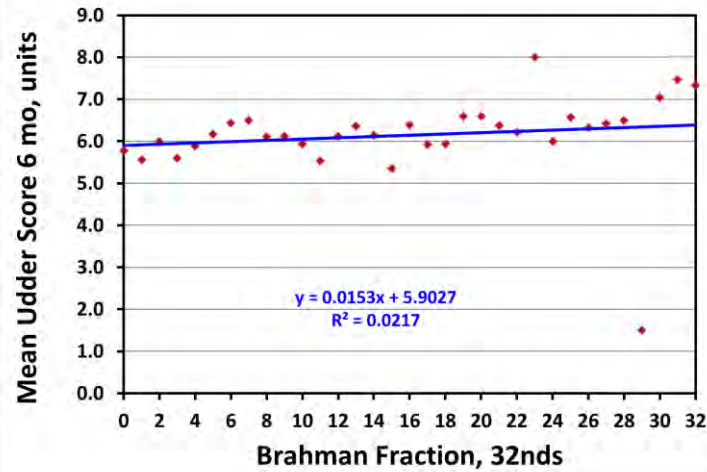
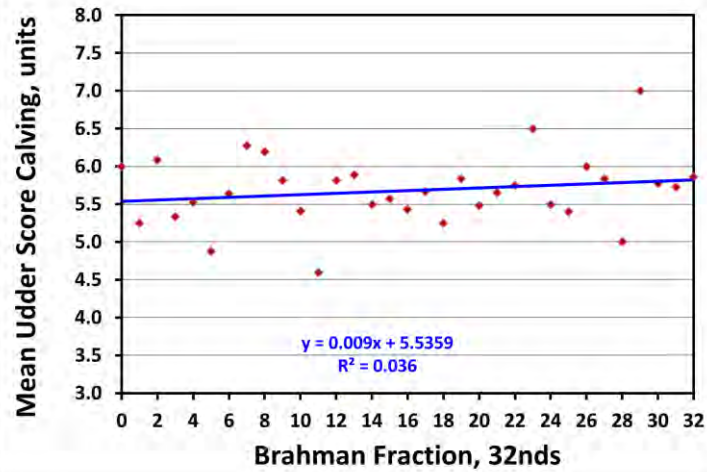
- 1) Objectives 2 and 4 suggested phenotypic data
- 2) Expected breed composition of all MAB animals (calves, sires, dams)
- 3) Pedigree file (MAB + BRA; nanim = 9,069)
- 4) Phenotypic data (MAB + BRA; 1987 – Present; Unequal number of years of data per trait; nanim = 7,960)
- 5) Genotypic data (GeneSeek GGP250k = 2,394; GeneSeek GGP50k = 1,557)

Tissue Sample Collection

- 1) Blood samples from all calves & natural service sires; Semen from all AI sires (-80° Celsius; UF Brahman & MAB herds = 3,580; FL Brahman breeders = 908)

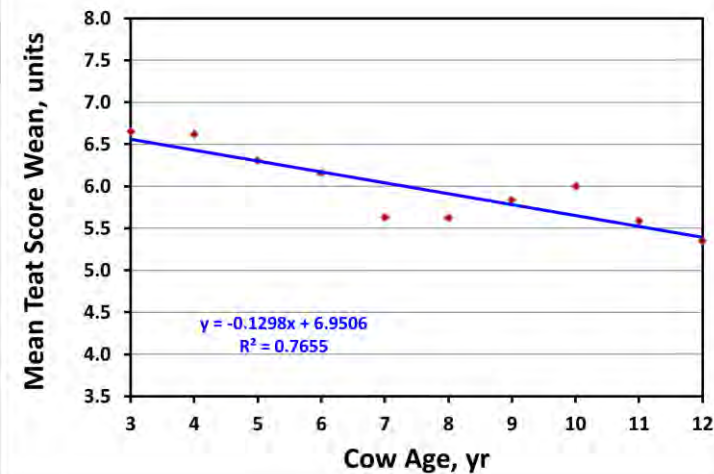
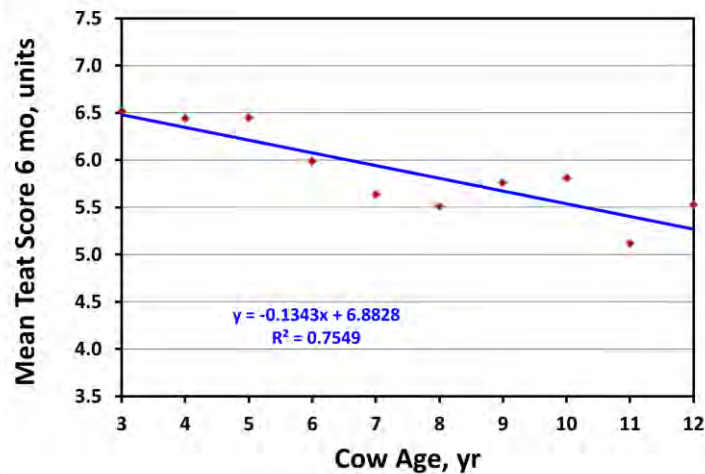
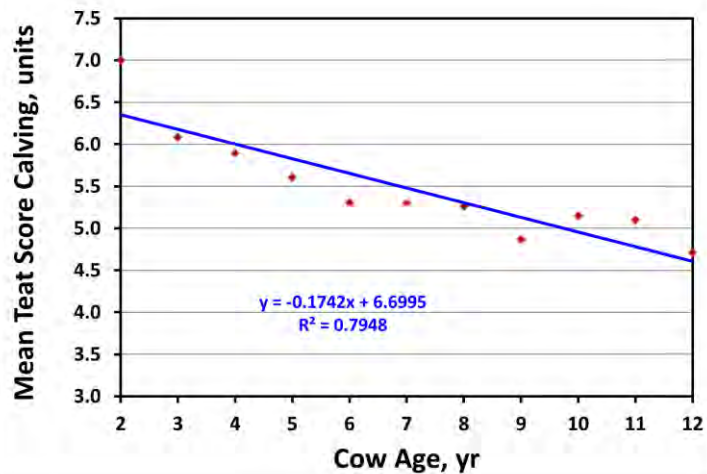
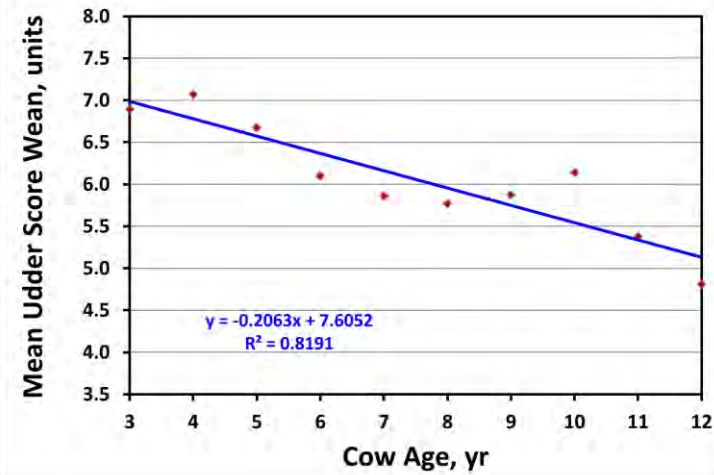
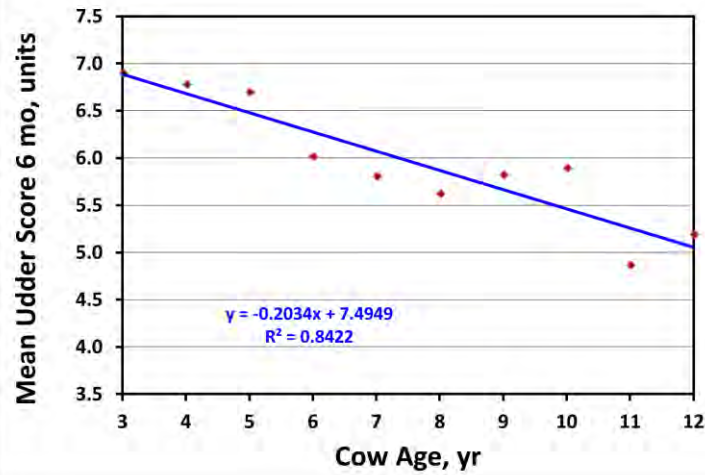
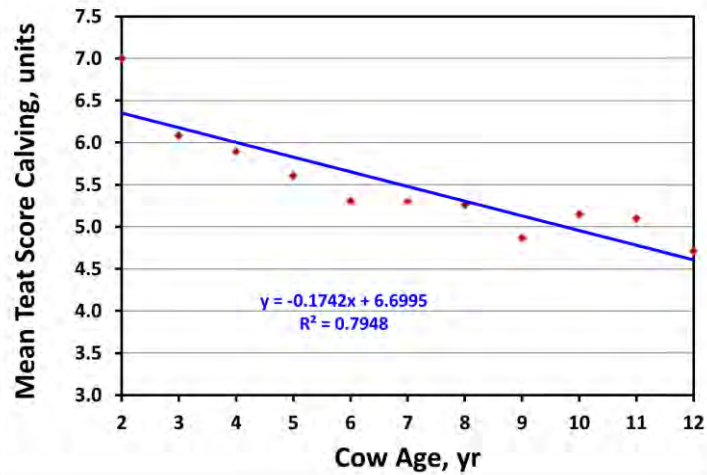
Udder & Teat Score by Brahman Fraction

(nrec = 628; ncows = 386)



Udder & Teat Score by Cow Age

(nrec = 628; ncows = 386)



Florida Brahman Genomics Project: 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

Establish a statewide repository of Brahman tissue samples and DNA

Conduct annual genomic evaluations for growth, reproduction, ultrasound-carcass, and tenderness sets of traits

Publish an annual summary with Animal Genomic EPD to aid selection and mating decisions within and across Florida Brahman herds

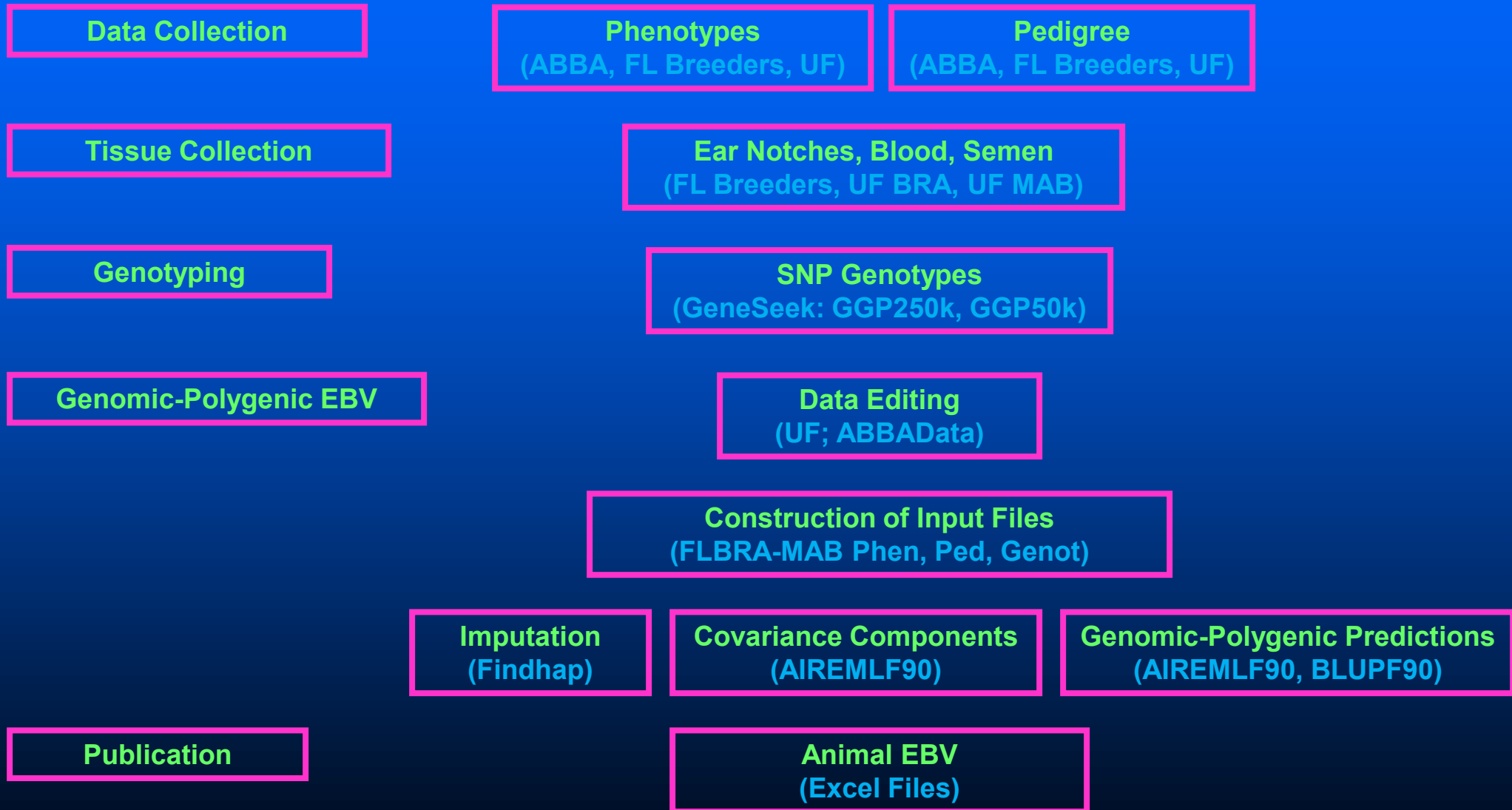
Make sires and heifers not used as replacements as well as semen and embryos from animals with favorable EPD available to Florida cattlemen

Increase the size of the UF Brahman herd to 260 cows

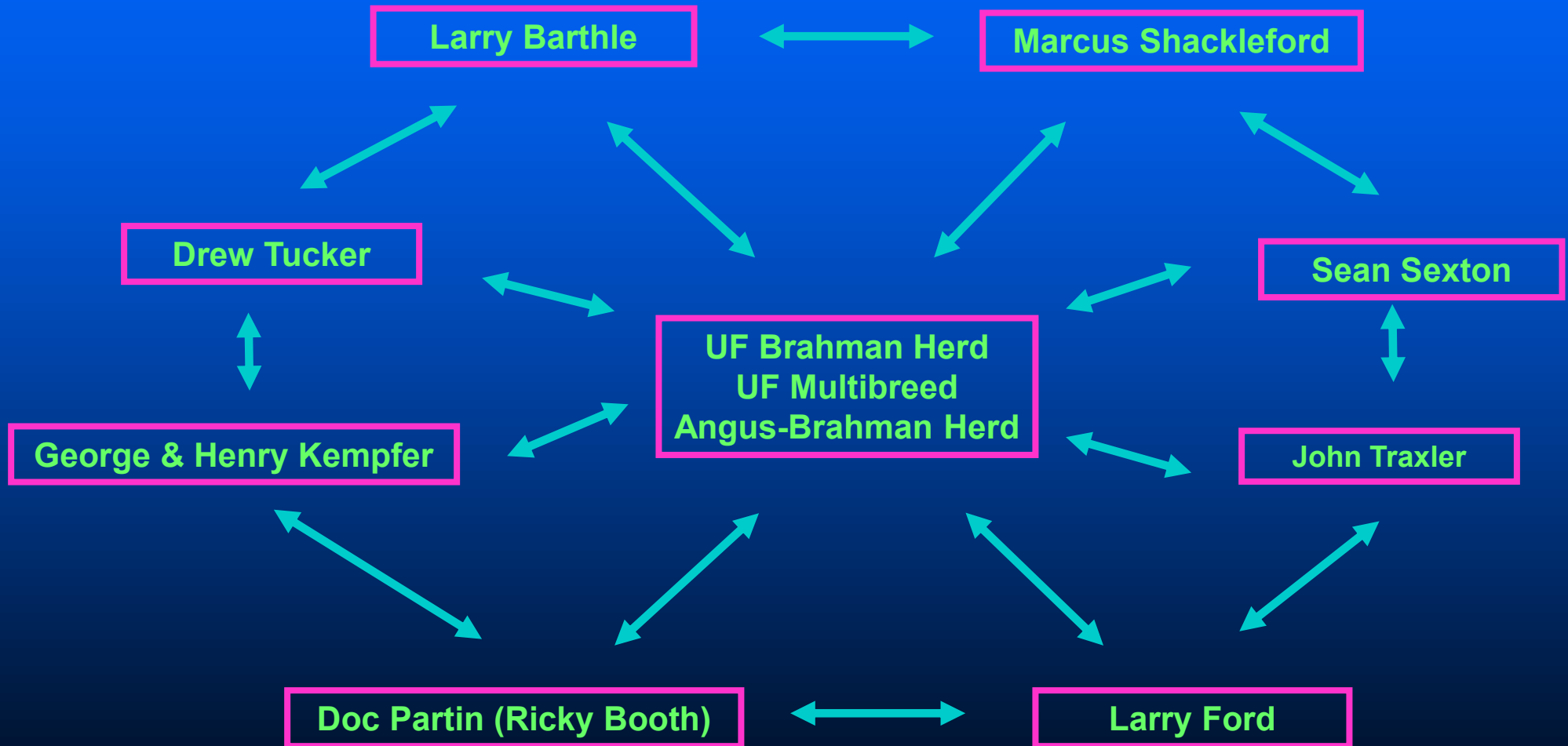
Florida Brahman Genomics Project: Accomplishments

- 1) Statewide Brahman and Multibreed Angus-Brahman (MAB) Database with phenotypes (reproduction, growth, ultrasound, carcass, meat palatability), pedigree, and genotypes from private Brahman and UF herds
- 2) Statewide Brahman and MAB Tissue Sample Repository with ear-notch, blood, and semen samples from private Brahman and UF herds
- 3) FORTRAN Software for editing of phenotypes, genotypes, and pedigree data and construction of input data files for imputation (Findhap, Flmpute) and for genomic-polygenic evaluation (BLUPF90)
- 4) SAS Programs for editing, statistical description, and mixed model analysis of phenotypic data from the Florida Brahman and MAB cattle populations
- 5) Genomic-Polygenic and Polygenic predictions for 20 reproduction, growth, ultrasound, carcass, and tenderness traits in the Florida Brahman and Multibreed Angus-Brahman cattle populations
- 6) Animal sales to Florida Brahman breeders (bulls & heifers)
- 7) Increased the size of the UF Brahman herd (n = 118 cows + 70 heifers)

FL Brahman GenomPol Evaluation System



Connectedness FL Brahman Population {Pedigree, DNA}



Genomic-Polygenic and Polygenic EBV for 20 traits

Growth Set (5 traits)

Birth Weight Direct (0.50)
Birth Weight Maternal (0.19)
Weaning Weight Direct (0.30)
Weaning Weight Maternal (0.21)
Gain Wean-to-Yearling Direct (0.33)

Reproduction Set (4 traits)

Yearling Weight (0.52)
Reproductive Track Score (0.25)
Age at First Calving (0.50)
First Calving Interval (0.06)

Ultrasound-Carcass Set (9 traits)

Ultrasound Weight (0.42)
Ultrasound Ribeye Area (0.35)
Ultrasound Backfat (0.14)
Ultrasound % Intramuscular Fat (0.33)
Slaughter Age (0.66)
Hot Carcass Weight (0.66)
Ribeye Area (0.53)
Fat over the Ribeye (0.31)
Marbling (0.49)

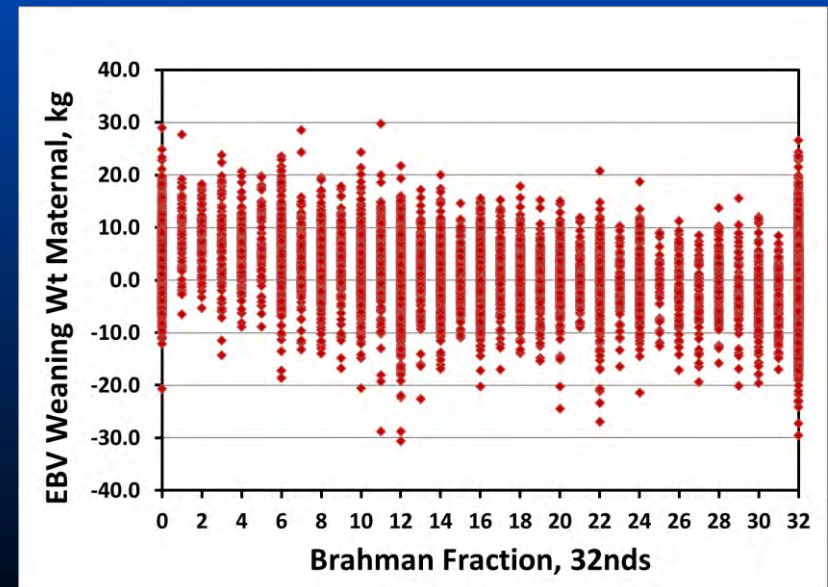
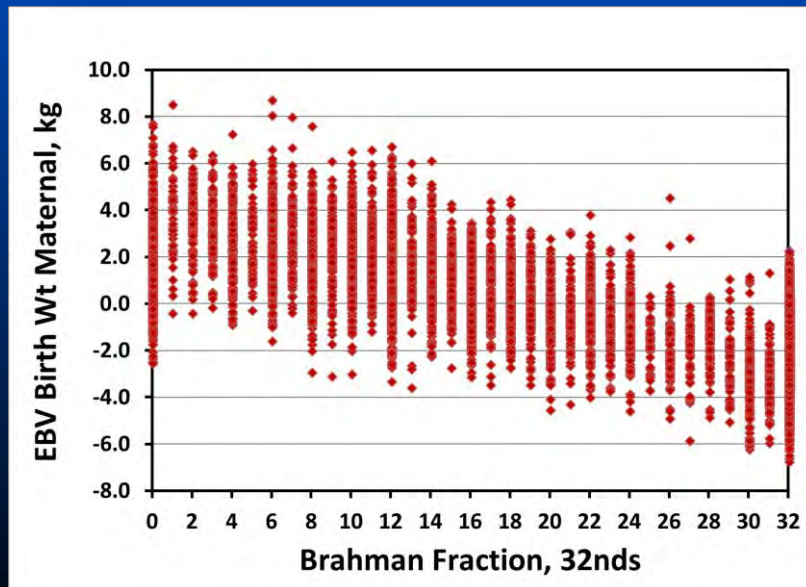
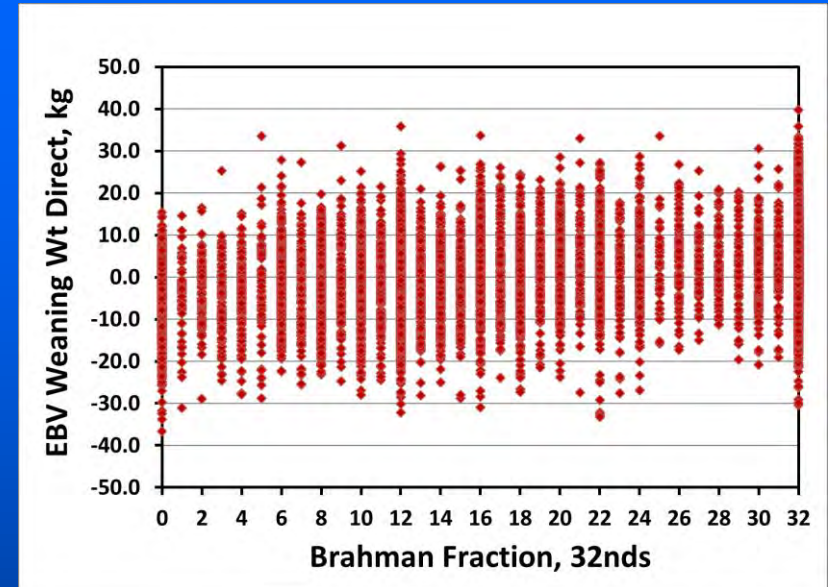
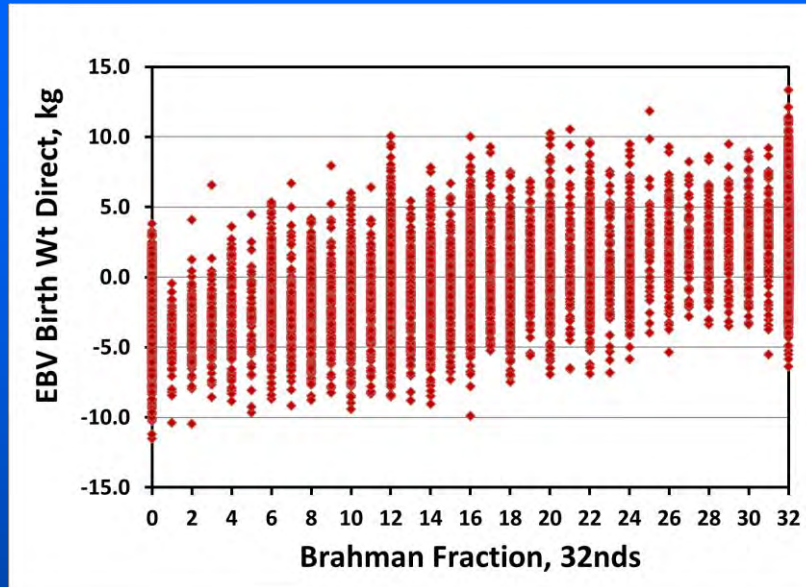
Tenderness Set (2 traits)

Warner-Bratzler Shear Force (0.16)
Tenderness Score (0.42)

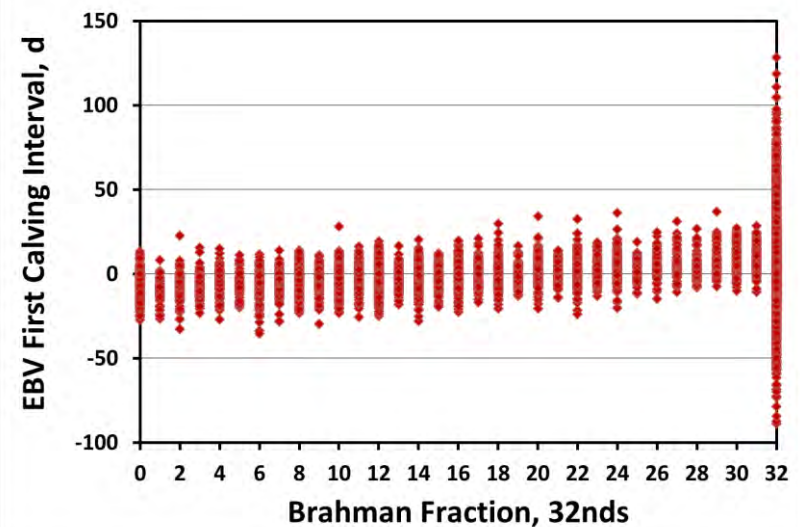
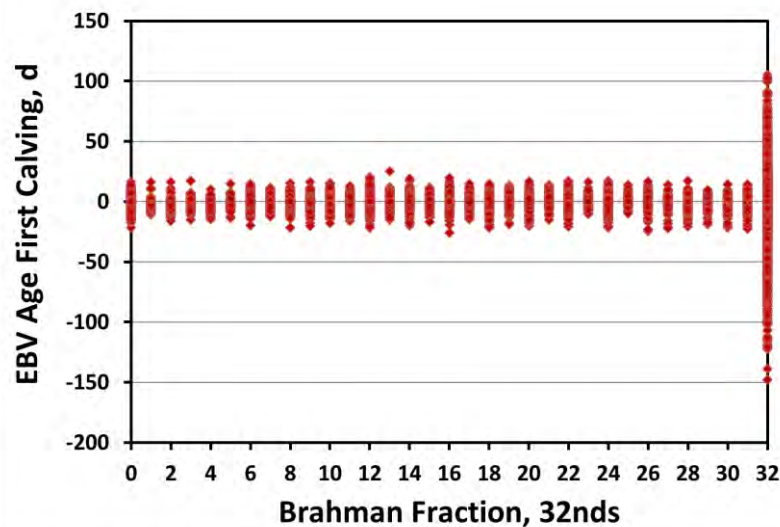
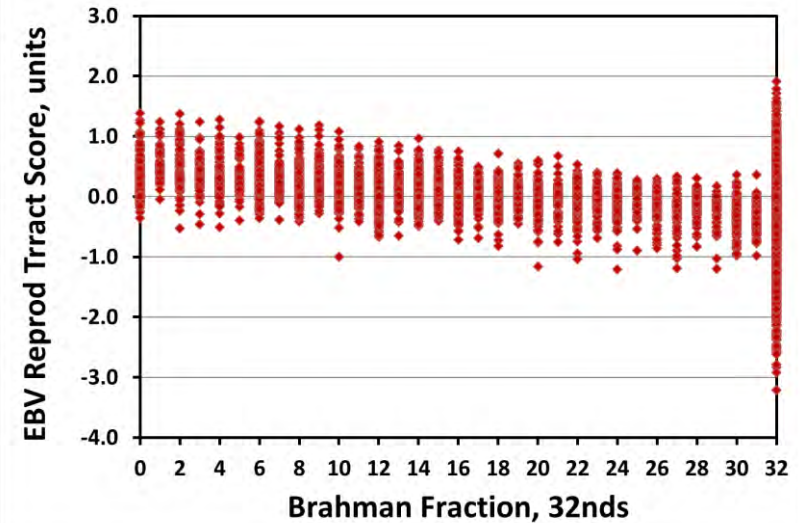
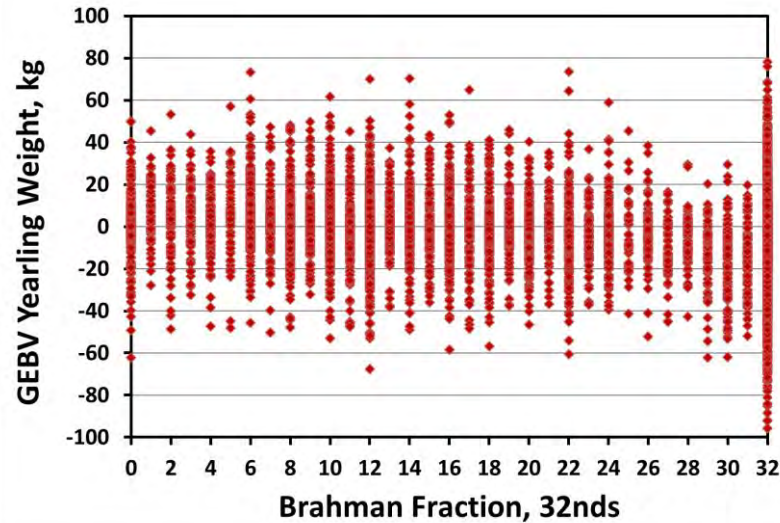
Phenotypic Data (2018 EBV)

Trait	N	Mean	SD	Min	Max
BW, kg	14635	34.0	5.6	15	62
WW, kg	12379	218.5	32.8	93	329
GW, kg	2177	114.4	46.4	-13	286
YW, kg	2620	343.2	56.1	141	571
RTS, units	664	3.0	1.2	1	5
AC1, d	3205	1065.1	84.9	626	1277
CI1, d	1594	437.8	118.7	244	790
UW, kg	2650	352.8	71.3	168	656
UREA, cm2	2735	56.1	12.1	0	961
UBF, cm	2745	1.1	1.7	0.8	2.2
UPIMF, %	2728	2.9	1.2	0.11	6.44
SLA, d	2160	558.7	52.3	324	713
HCW, kg	2146	336.3	45.9	208	489
REA, cm2	2104	80.3	10.9	47.7	129
FAT, cm	2135	1.3	0.5	1.5	9
MAR, units	2141	404.5	93.9	150	900
WBSF, kg	1398	4.0	1.1	1.5	9.4
TEND, units	931	5.4	0.9	2.4	7.6

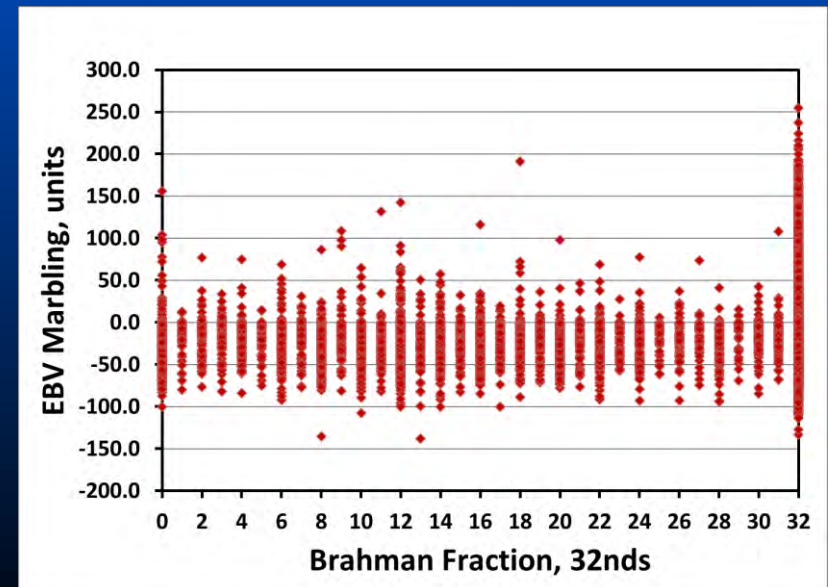
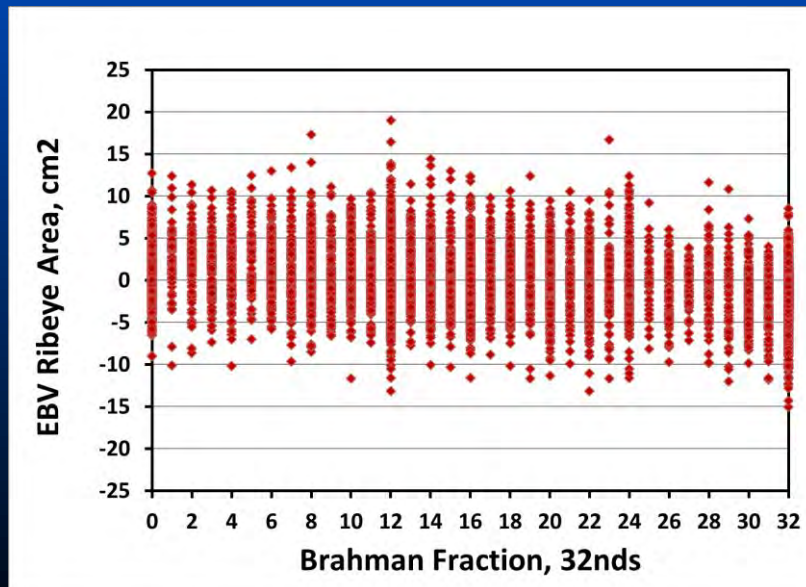
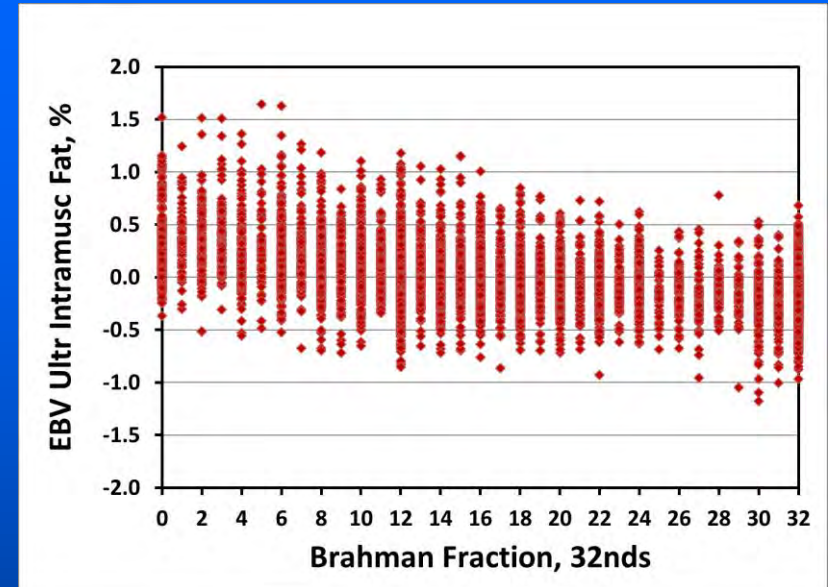
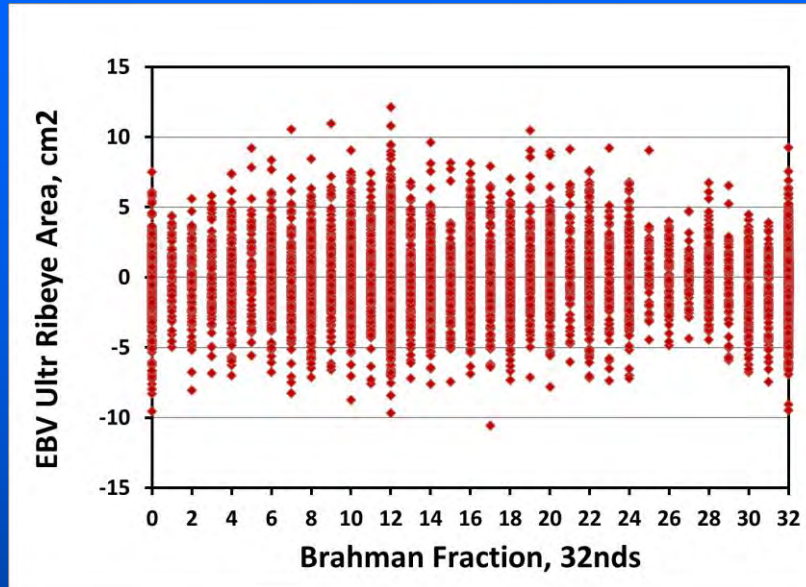
Genomic-Polygenic EBV: Growth Set



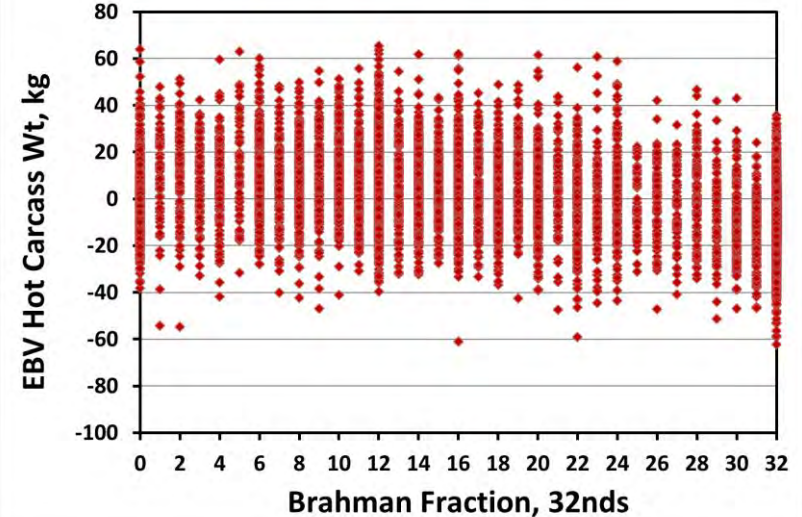
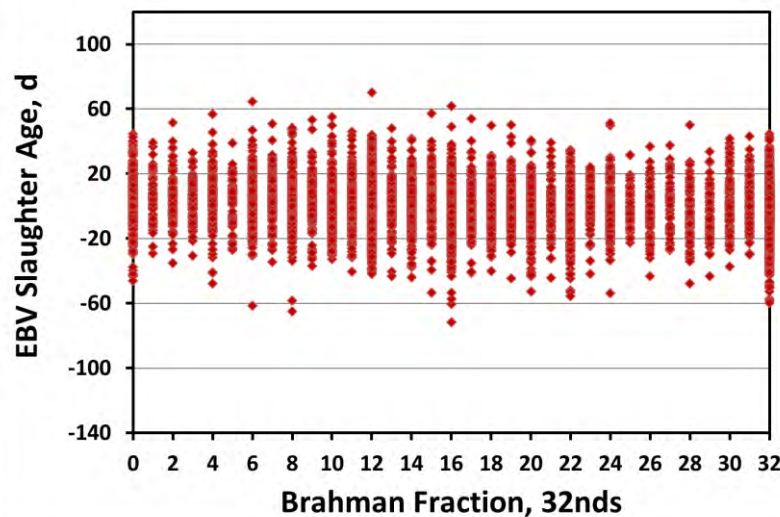
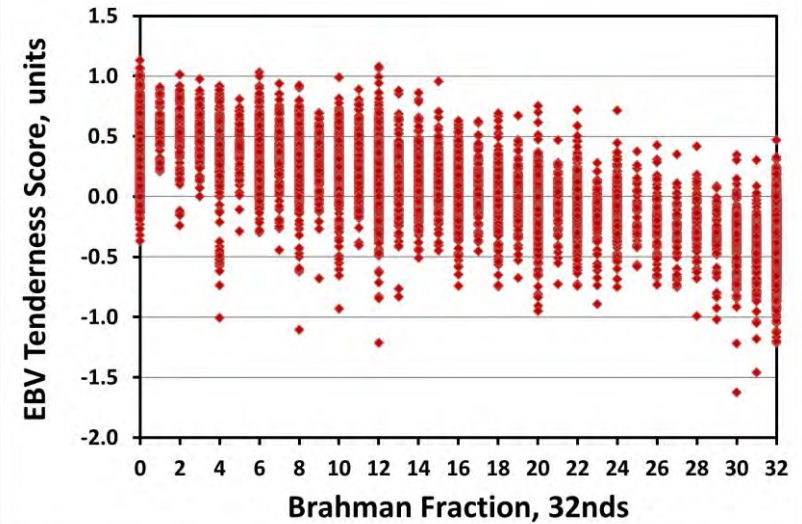
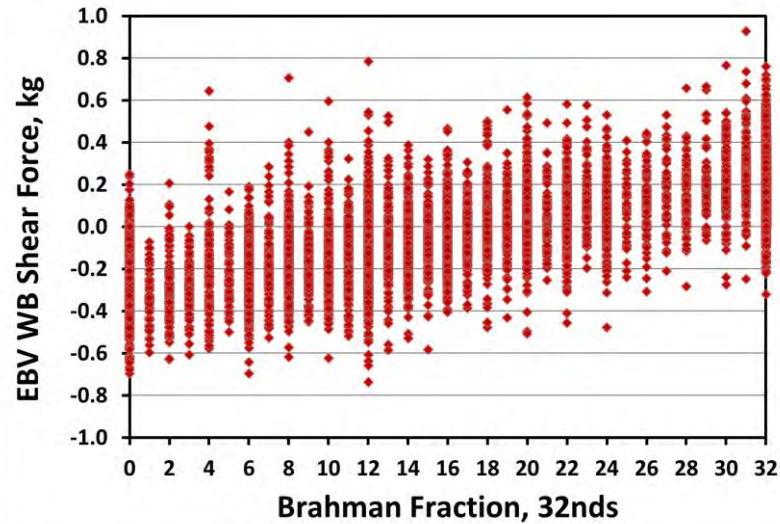
Genomic-Polygenic EBV: Reprod Set



Genomic-Polygenic EBV: UltCar Set



Genomic-Polygenic EBV: Tend Set



Future Work

Continue and Expand Current Objectives:

- 1) Database (Phenotypes, Pedigree, Genotypes)
- 2) Tissue Sample and DNA Repository
- 3) Annual Genomic-Polygenic Evaluations
- 4) Expand Florida Project to the US Southern Region
- 5) Identify a set of SNP associated with genes actually influencing traits
- 6) Obtain internal phenotype data
- 7) Construct chips with biologically meaningful SNP
- 8) Evaluate Brahman and MAB animals with chips containing biologically meaningful SNP

Genomic-Polygenic EBV

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

Genomic-Polygenic EBV

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