13915: Genomic-polygenic and polygenic parameters and prediction trends for growth and reproduction traits in an Angus-Brahman multibreed population

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ABSTRACT

The objectives of this research were to estimate genomic-polygenic and polygenic parameters and to evaluate prediction trends as Brahman fraction increased from 0% to 100% in an Angus-Brahman multibreed (MAB) population for 305-d yearling weight (YW), yearling reproductive tract score (RTS), age at first calving (AFC), and first calving interval (FCI) using single-step genomic-polygenic (GPM) and polygenic models (PM). Phenotype records were 1,758 for YW, 381 for RTS, 1,385 for AFC, and 985 for FCI. The pedigree file had 6,869 calves, sires, and dams, and genotype file contained 115,711 actual and imputed Illumina150k SNP markers from 1,547 animals. The 4-trait GPM and PM included contemporary group, age of dam (YW only), sex of calf (YW only), direct heterosis, maternal heterosis (YW only) as fixed effects, and animal and residual as random effects. Genetic parameters were estimated using REML procedures and computed using AIREMLF90. *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. The similarity between GPM and PM heritabilities and genetic correlations indicated that the 115,711 Illumina150k SNP markers added little additional information to that contained in the pedigree. Regression coefficients of breed group EBV means on Brahman fraction were negative (P < 0.0005) for YW, RTS, and FCI, and positive (P < 0.0001) for AFC as Brahman fraction increased. This indicated that 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 in this population. Regression coefficients of individual animal EBV on Brahman fraction showed similar trends, but were smaller, guaranteeing the existence of animals with high, medium, and low EBV across all Brahman percentages.*

INTRODUCTION

Beef cattle operations routinely perform the task of choosing replacement heifers to be added to the breeding cow herd. Identification of sexually mature heifers is particularly important for reproduction strategies involving estrous synchronization and seasonal matings that require cows to calve once a year. Reproductive tract score (RTS) is an indirect measure of sexual maturity the can be used to identify replacement heifers instead of directly measuring age at puberty (Andersen et al., 1991). This trait is favorably correlated with yearling weight (YW; 0.31; Andersen et al., 1991). In turn, YW is negatively correlated with age at first calving (AFC; -0.16; Snelling et al., 2012), and AFC is negatively correlated with rebreeding (-0.35; Cavani et al., 2015), a trait similar to first calving interval (FCI). Genetic evaluation of heifers in the Angus-Brahman multibreed (MAB) herd of the University of Florida (UF) for these four traits (YW, RTS, AFC, and FCI) would provide a reliable assessment of their reproductive ability and potential as replacement cows in Florida and the US Southern region. *Thus, the objectives of this research were to estimate genomic-polygenic and polygenic parameters and to evaluate prediction trends as Brahman fraction increased from 0% to 100% in an Angus-Brahman multibreed population for 305-d yearling weight (YW), yearling reproductive tract score (RTS), age at first calving (AFC), and first calving interval (FCI) using single-step genomic-polygenic (GPM) and polygenic models (PM).*
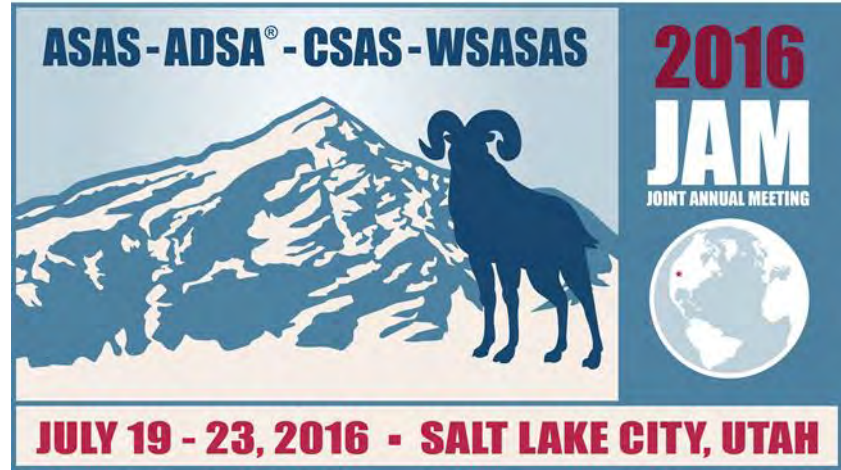
Table 1. Numbers of calves, means and SD per trait and breed group

Breed Group	YW, kg			RTS, units			AFC, d			FCI, d		
	N	Mean	SD	N	Mean	SD	N	Mean	SD	N	Mean	SD
BG1	251	354	56	62	3.6	1.3	180	1078	40	143	390	28
BG2	286	366	58	42	3.5	1.3	218	1083	41	162	388	32
BG3	250	358	58	37	2.8	1.3	164	1081	55	116	389	26
BG4	380	364	55	63	3.2	1.1	363	1084	45	263	385	31
BG5	196	355	52	46	2.7	1.1	205	1087	40	129	379	28
BG6	395	322	48	131	2.4	1.0	255	1078	46	172	390	44
Total	1758	352	57	381	2.9	1.2	1385	1082	45	985	387	33

MATERIALS AND METHODS

Animals and Data. *Animals were from the multibreed Angus-Brahman (MAB) herd of the University of Florida, Gainesville.* Calves were produced by a diallel-mating plan involving sires and dams from 6 mating groups: BG1 = (1.0 to 0.80) A (0.0 to 0.20) B, BG2 = (0.79 to 0.60) A (0.21 to 0.40) B, BG3 = (0.625) A (0.375) B, BG4 = (0.59 to 0.40) A (0.41 to 0.60) B, BG5 = (0.39 to 0.20) A (0.61 to 0.80) B, and BG6 = (0.19 to 0.0) A (0.81 to 1.00) B. Calves (n = 5,799) were the progeny of 341 sires (60 BG1, 38 BG2, 62 BG3, 37 BG4, 39 BG5, and 105 BG6) and 1,907 dams (306 BG1, 258 BG2, 265 BG3, 362 BG4, 210 BG5, and 506 BG6) born from 1987 to 2015. *There were 1,758 calves with YW (kg), 381 heifers with RTS (units; 1 to 5; Andersen et al., 1991), 1,385 heifers with AFC (d), and 985 heifers with FCI (d).* Number of calves, means, and SD for YW, RTS, AFC, and FCI per breed group are shown in Table 1.

Feeding and Management. Calves were kept at the Pine Acres Research Station (1987 to 1994) and Beef Research Unit (1995 to 2015) of the University of Florida from birth (December to March) to weaning (August, September). Preweaning, cows and calves stayed in bahiagrass pastures (*Paspalum notatum*) with access to a complete mineral supplement (University of Florida Special Hi-Cu Mineral). In winter (mid-December to mid-March), cows and calves were fed bermudagrass (*Cynodon dactylon*) hay and cotton seed (*Gossypium spp.*) meal. Postweaning, calves remained in bahiagrass pastures supplemented with bahiagrass hay, concentrate (1.6 kg to 3.6 kg per day; 14.0 % CP; 488 Pellet Medicated Weaning Ration, Lakeland Animal Nutrition, Lakeland, Florida; soy hull pellets), and mineral supplement. Calves taken to the University of Florida Feed Efficiency Facility (UFFEF; 2006 to 2010) were randomly allocated to pens within sire group (BG1 to BG6) by sex (bull, heifer, and steer). Calves at UFFEF were fed a diet of whole corn or corn gluten, cottonseed hulls, molasses, chopped grass hay, and a vitamin-mineral-protein supplement (FRM, Bainbridge, GA; mean dry matter = 12.9%, mean crude protein = 98.2%, mean net energy for maintenance = 1.6 mcal/kg DM, and mean net energy for gain = 1.0 mcal/kg DM).

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MATERIALS AND METHODS (Continued)

Tissue Sampling and Genotyping. Tissue samples (blood, semen) were from 1,514 animals from the MAB herd (108 sires, 144 dams, and 1,262 progeny) collected at the UF Beef Research Unit between 2006 to 2015. Progeny samples were from 109 bulls, 595 heifers, and 554 steers. Samples were processed and stored at -80 °C. Two sets of samples were genotyped by GeneSeek (GeneSeek, Inc., Lincoln, NE, USA). White blood cells from samples in the first set were isolated using the procedure outlined by Beauchemin et al. (2006) and sent to GeneSeek for genotyping with the Illumina3k beadchip in 2010 (n = 1289; 95 sires, 144 dams, 76 bulls, 596 heifers, and 378 steers). Genomic DNA from the second set was extracted from whole blood or semen using a commercial kit (QIAamp DNA mini kit, Qiagen, Valencia, CA) and genotyped with GeneSeek GGPHD 150k chip in 2015 (n = 238; 29 sires, 36 bulls, 173 steers).

Imputation. Animals genotyped with the 3k chip were imputed to 150k chip with findhap4 (VanRaden, 2015) using the second set of 238 animals from the MAB population genotyped with GGPHD in 2015.

Variance Components, Variance Ratios, and EBV. *A 4-trait single-step genomic-polygenic model (GPM; Aguilar et al., 2010) and a polygenic model (PM) were used to obtain variance components, heritabilities, and genetic, environmental and phenotypic correlations for YW, RTR, AFC, and FCI.* The fixed effects for GPM and PM were: 1) contemporary group (location-year; all traits); 2) age of dam (YW only); 3) sex of calf (YW only); 4) direct heterosis as a function of calf heterozygosity (i.e., the probability of having Angus and Brahman alleles in 1 locus; all traits); and 5) maternal heterosis as a function of dam heterozygosity (YW only). Random effects were direct additive genetic and residual. The pedigree file had 7,141 calves, sires, and dams, and the genotype file contained 115,711 actual and imputed Illumina150k SNP markers from 1,547 animals. Pedigree and SNP information contributed to the variance of direct additive genetic effects for GPM and only pedigree information for PM. *Variance components were estimated using REML with an average information algorithm (Gilmour et al., 1995). Standard errors of variance and covariance estimates were obtained from the inverse of the average information matrix. Standard deviations of 5,000 samples were computed for functions of variance components (Meyer and Houle, 2013). Estimated breeding values (EBV) were computed for 6,851 animals (genotyped = 1,547, non-genotyped = 5,304) and genotyped animals using GPM and PM. The AIREMLF90 program of the BLUPF90 family of programs (Misztal et al., 2002) was used to perform computations. Regressions of individual EBV and breed group mean EBV were used to assess EBV trends for YW, RTS, AFC, and FCI as Brahman fraction increased from 0% to 100%.*

RESULTS AND DISCUSSION

Variance Components and Variance Ratios. Estimates of additive genetic variances from GPM were, on the average, 9.2 % larger and covariances 23 % smaller whereas environmental variances were, on the average, 1.8 % smaller and covariances 6.9% larger than those from PM (**Table 2**). Phenotypic variances were only slightly larger (0.6 %) and phenotypic covariances slightly smaller (0.5%), heritabilities were 7.8 % larger and additive genetic correlations 116.9 % smaller for GPM than for PM (**Table 3**). Lastly, environmental correlations were 7.2 % larger and phenotypic correlations 3.3 % smaller for GPM than for PM (**Table 4**). *The similarity between additive genetic, environmental, and phenotypic variance components, heritabilities, and genetic correlations indicated that the 115,711 Illumina150k SNP markers added little additional information to that contained in the pedigree.*

Heritabilities were medium for YW (GPM: 0.47; PM: 0.45), RTS (GPM: 0.31; PM: 0.30), and FCI (GPM: 0.31; PM: 0.29), and low for AFC (GPM: 0.14; PM: 0.12). 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: -0.67; PM: -0.67), and near zero for all other trait pairs. *These estimates of heritabilities and genetic correlations indicated that selection for reproduction traits would be feasible in this multibreed population. Choosing replacement heifers based on their RTR values would lower AFC and FCI, resulting in higher reproductive efficiency and helping to lower production costs in this beef herd.*

Table 2. Direct additive genetic and environmental covariances for YW, RTR, AFC, and FCI using GPM and PM

Trait pair	Additive genetic covariances				Environmental covariances			
	GPM	SE	PM	SE	GPM	SE	PM	SE
YW, YW; kg²	761.0	112.8	729.5	107.3	872.4	81.1	886.9	78.8
YW, RTR; kg*u	9.8	4.0	10.7	3.0	2.4	3.8	2.0	3.4
YW, AFC, kg*d	18.1	82.3	-6.6	74.6	36.1	88.0	48.6	85.2
YW, FCI; kg*d	-27.1	84.5	-22.1	78.5	-104.0	83.9	-106.1	80.9
RTR, RTR; u*u	0.45	0.19	0.43	0.11	1.00	0.17	1.02	0.14
RTR, AFC; u*d	-2.1	3.5	-4.6	2.7	-7.3	4.9	-5.2	4.8
RTR, FCI; u*d	-1.9	3.8	-0.5	2.9	4.6	4.2	4.1	3.9
AFC, AFC; d²	198.6	80.6	164.6	74.0	1231.7	85.5	1264.5	83.8
AFC, FCI; d²	-170.9	70.8	-149.0	64.9	-429.1	68.9	-450.6	65.9
FCI, FCI; d²	321.6	94.0	303.9	89.0	725.3	85.0	736.8	81.4

Table 3. Phenotypic covariances, heritabilities, and additive genetic correlations for YW, RTR, AFC, and FCI using GPM and PM

Trait pair	Phenotypic covariances				Heritabilities and additive genetic correlations			
	GPM	SE	PM	SE	GPM	SE	PM	SE
YW, YW; kg²	1633.4	66.1	1616.4	64.2	0.47	0.06	0.45	0.06
YW, RTR; kg*u	12.3	3.2	12.7	2.9	0.53	0.32	0.60	0.16
YW, AFC, kg*d	54.1	76.9	42.0	74.7	0.05	0.24	-0.02	0.28
YW, FCI; kg*d	-131.1	71.6	-128.2	69.9	0.04	0.18	-0.01	0.17
RTR, RTR; u*u	1.46	0.11	1.45	0.10	0.31	0.12	0.30	0.08
RTR, AFC; u*d	-9.4	4.3	-9.9	4.2	-0.22	0.55	-0.55	0.58
RTR, FCI; u*d	2.6	3.4	3.5	3.2	-0.16	0.41	-0.05	0.29
AFC, AFC; d²	1430.3	55.8	1429.1	53.8	0.14	0.05	0.12	0.05
AFC, FCI; d²	-600.0	44.5	-599.6	42.9	-0.67	0.24	-0.67	0.32
FCI, FCI; d²	1046.9	52.3	1040.7	51.1	0.31	0.09	0.29	0.08
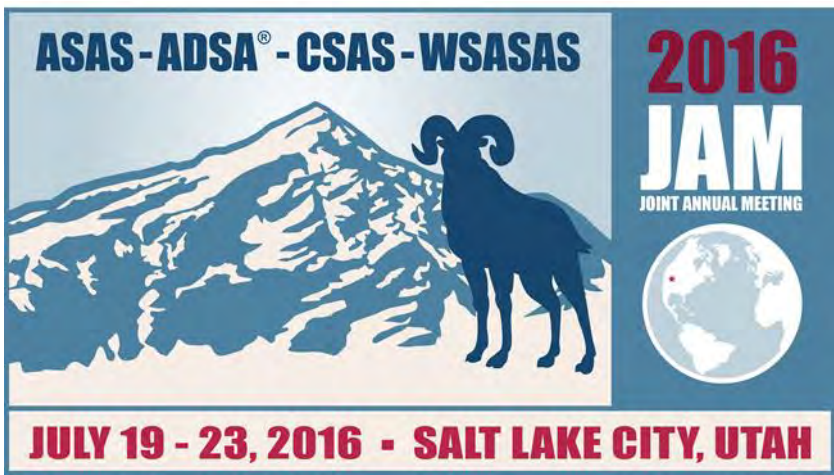
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RESULTS AND DISCUSSION (Continued)

Breed Group Mean EBV Trends. Regression coefficients of breed group EBV means on Brahman fraction from GPM and PM were negative (P < 0.0005) for YW, RTS, and FCI, and positive (P < 0.0001) for AFC as Brahman fraction increased (**Table 5**). *This indicated that 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 in this population.*

Individual Animal EBV Trends. Regression coefficients of individual animal EBV on Brahman fraction from GPM and PM showed similar trends (**Table 6**), but were smaller, guaranteeing the existence of animals with high, medium, and low EBV across all Brahman percentages (**Figures 1 and 2**).

Table 4. REML estimates of environmental and phenotypic correlations for YW, RTR, AFC, and FCI using GPM and PM

Trait pair	Environmental correlations				Phenotypic correlations			
	GPM	SE	PM	SE	GPM	SE	PM	SE
YW, RTR; kg*u	0.08	0.13	0.07	0.11	0.25	0.06	0.26	0.06
YW, AFC, kg*d	0.04	0.09	0.05	0.08	0.04	0.05	0.03	0.05
YW, FCI; kg*d	-0.13	0.11	-0.13	0.10	-0.07	0.10	-0.09	0.10
RTR, AFC; u*d	-0.21	0.14	-0.15	0.13	-0.21	0.10	-0.22	0.09
RTR, FCI; u*d	0.17	0.16	0.15	0.15	0.07	0.09	0.09	0.08
AFC, FCI; d²	-0.45	0.05	-0.47	0.05	-0.49	0.03	-0.49	0.03

FINAL REMARKS

- *The genomic-polygenic and polygenic models yielded similar estimates of variance components and genetic parameters for yearling weight, reproductive tract score, age at first calving, and first calving interval*

- *Heifers with higher Brahman fractions tended to be lighter and less mature as yearlings, older at first calving, and have shorter FCI than heifers with higher Angus fractions*

REFERENCES

Aguilar et al., 2010. J. Dairy Sci. 93:743-752; Andersen et al., 1991. Agri-Practice 12:19-26; Beauchemin et al., 2006. Genet. Mol. Res. 5:438-447; Cavani et al., 2015. J. Anim. Sci. 93:3287-3291; Gilmour et al., 1995. Biometrics 51:1440-1450; Snelling et al., 2012. J. Anim. Sci. 90:1152-1165; VanRaden, P. M. 2015. http://aipl.arsusda.gov/software/findhap.
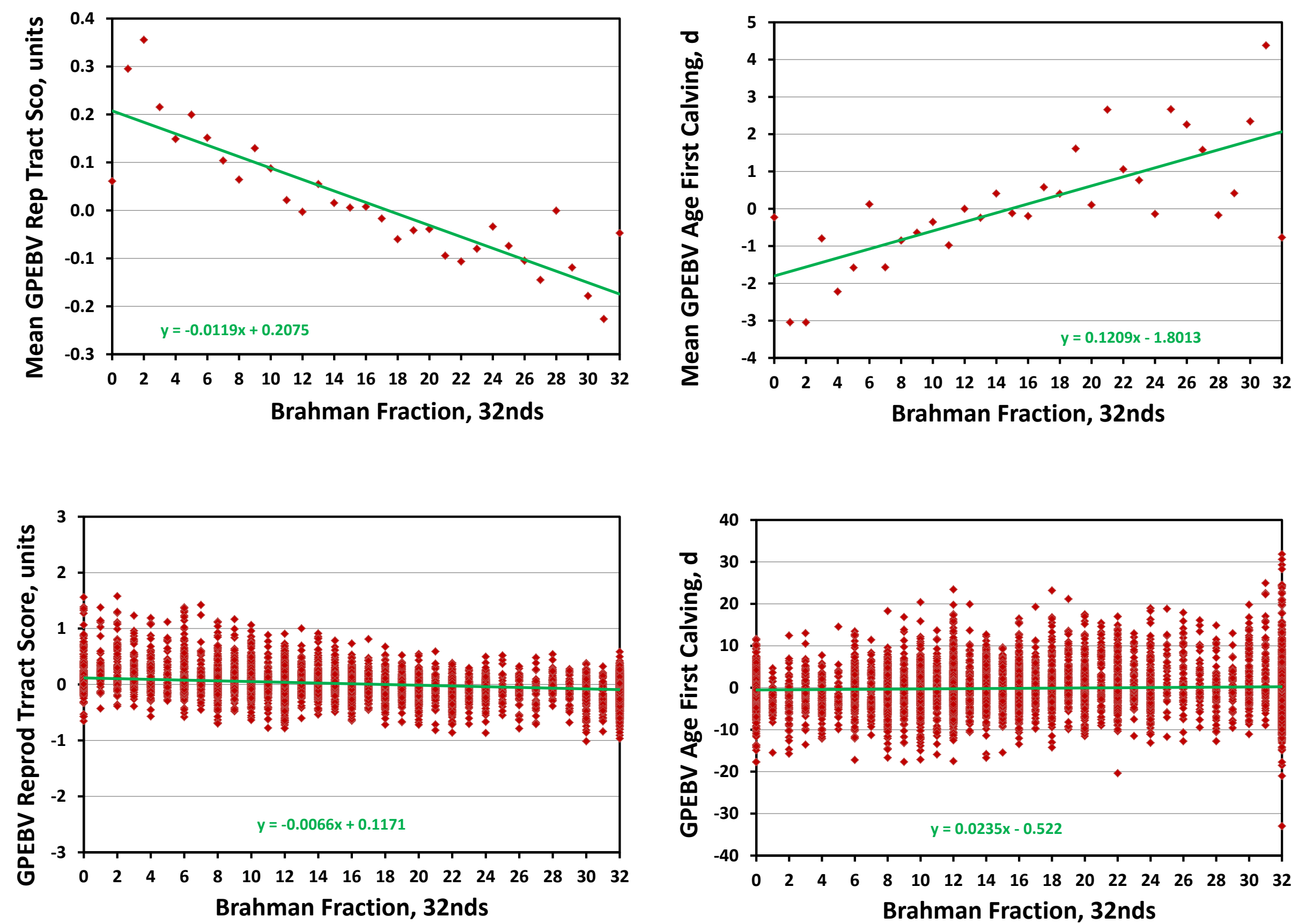
Table 5. Linear regression coefficients of breed group mean EBV on Brahman fraction for YW, RTR, AFC using GPM and P

Trait	Linear regression coefficient					
	GPM	SE	P-value	PM	SE	P-value
YW, kg/32nds	-0.5299	0.0419	P < 0.0001	-0.4378	0.0437	P < 0.0001
RTR, units/32nds	-0.0120	0.0012	P < 0.0001	-0.0099	0.0013	P < 0.0001
AFC, d/32nds	0.1209	0.0206	P < 0.0001	0.1022	0.0167	P < 0.0001
FCI, d/32nds	-0.0878	0.0191	P < 0.0001	-0.0795	0.0203	P < 0.0005

Table 6. Linear regression coefficients of individual animal EBV on Brahman fraction for YW, RTR, AFC using GPM and PM

Trait	Linear regression coefficient					
	GPM	SE	P-value	PM	SE	P-value
YW, kg/32nds	-0.3077	0.0147	P < 0.0001	-0.2205	0.0149	P < 0.0001
RTR, units/32nds	-0.0066	0.0003	P < 0.0001	-0.0041	0.0004	P < 0.0001
AFC, d/32nds	0.0235	0.0062	P < 0.0001	0.0115	0.0053	P < 0.0303
FCI, d/32nds	-0.0055	0.0081	P < 0.4993	0.0059	0.0079	P < 0.4546

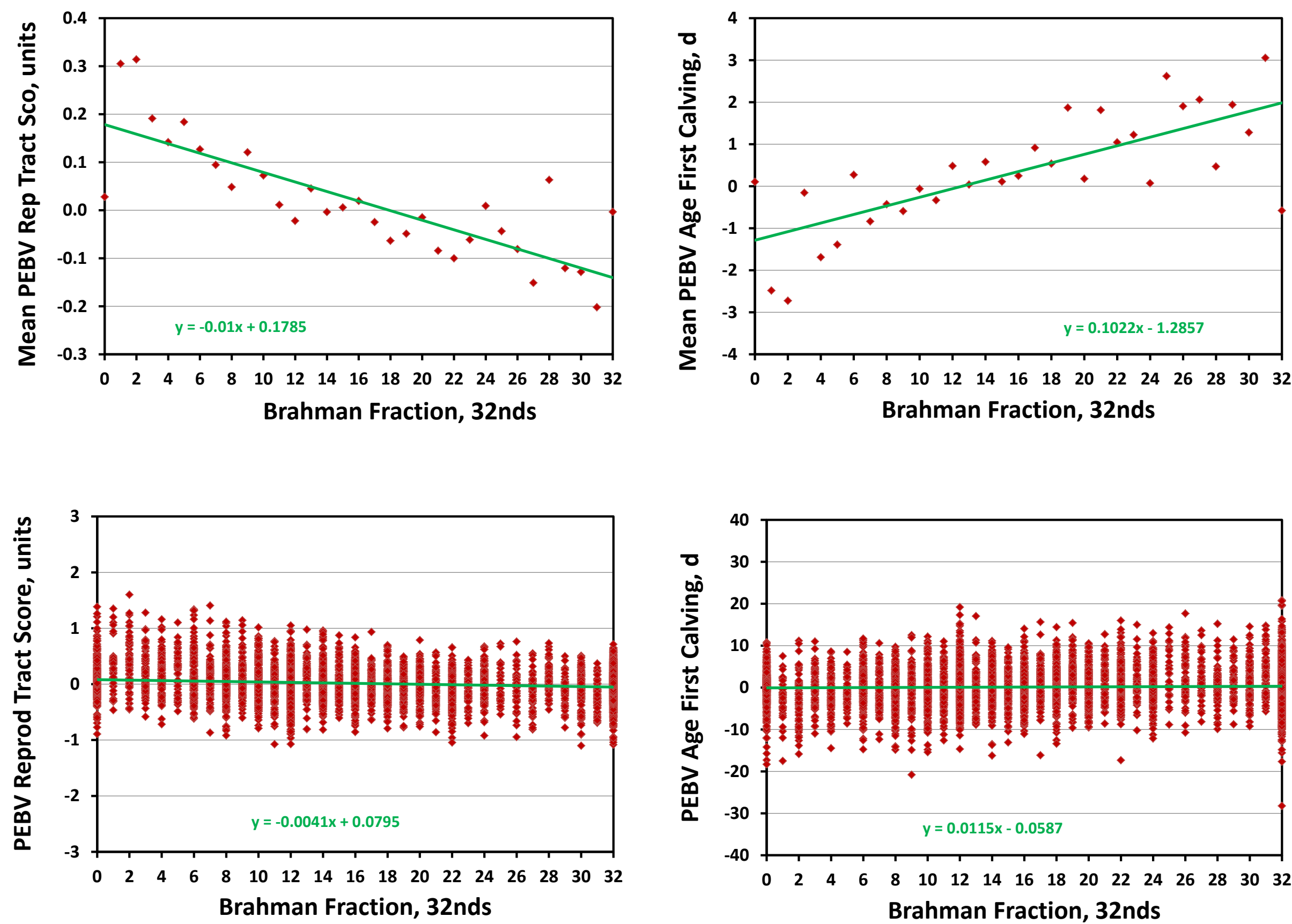Figure 1. RTR and AFC Genomic-Polygenic Breed Group Means and Animal EBV Trends

Figure 2. RTR and AFC Polygenic Breed Group Means and Animal EBV Trends