194: Multibreed Angus-Brahman genetic parameters and predictions for nine ultrasound and carcass traits using three genomic-polygenic models and one polygenic model

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ABSTRACT

Objectives were to estimate variance components, genetic parameters, EBV, accuracies, and rankings for nine ultrasound and carcass traits in a multibreed Angus-Brahman population using three genomic-polygenic models and one polygenic model (PM). The genomic-polygenic models used the complete GeneSeek GPF250k SNP set (GPM), top 5% SNP (GPMR1), and 5% SNP evenly spread across the genome (GPMR2). Yearling ultrasound traits were weight (UW), ribeye area (UREA), backfat (UFAT), and percent intramuscular fat (UPIMF). Carcass traits were slaughter age (SLA), hot carcass weight (HCW), ribeye area (REA), backfat thickness (FAT), and marbling score (MAR). The 9-trait GPM, GPMR1, GPMR2, and PM contained fixed contemporary group, age of calf (ultrasound traits only), sex of calf, and direct heterosis effects, and random animal and residual effects. Variance components and genetic parameters were computed using AIREMLF90. ***Comparable heritabilities were obtained with GPM and PM for UW (GPM: 0.54 ± 0.05; PM: 0.51 ± 0.05), UREA (GPM: 0.36 ± 0.03; PM: 0.34 ± 0.03), UFAT (GPM: 0.12 ± 0.02; PM: 0.11 ± 0.02), UMPIMF (GPM: 0.34 ± 0.03; PM: 0.30 ± 0.03), SLA (GPM: 0.59 ± 0.07, PM: 0.61 ± 0.06), HCW (GPM: 0.58 ± 0.06, PM: 0.52 ± 0.07), REA (GPM: 0.48 ± 0.04, PM: 0.45 ± 0.05), FAT (GPM: 0.41 ± 0.05, PM: 0.30 ± 0.05), and MAR (GPM: 0.56 ± 0.07, PM: 0.51 ± 0.08). Additive genetic correlations between pairs of ultrasound and carcass traits were all between -0.31 and 0.81. The highest positive additive genetic correlations were between UW and UREA, UW and HCW, UW and REA, UREA and HCW, UREA and REA, UFAT and FAT, and between HCW and REA. The largest negative additive genetic correlations were between UREA and UPIMF, UFAT and SLA, UFAT and HCW, UPIMF and REA, and between REA and MAR. High similarity existed among EBV and accuracies from GPM, GPMR1, and GPMR2. This indicated that the two reduced genotype sets were appropriate alternatives to the complete GPF250k set for genomic-polygenic evaluation and selection in this population.***

INTRODUCTION

Carcass traits constitute a major set of target traits for genetic evaluation and selection in beef cattle. Yearling ultrasound carcass traits have been found to have high genetic correlations with carcass traits, thus they have been used to increase the accuracy and lower the cost of national genetic evaluations for slaughterhouse carcass traits (Crews et al., 2004; MacNeil et al., 2010). Genomic information has been used to further increase the accuracy of both ultrasound and carcass traits while simultaneously reducing generation interval (Fernandes Junior et al., 2016; MacNeil et al., 2010; Magnabosco et al., 2016). Large variation in genomic-polygenic and polygenic EBV for yearling ultrasound traits (ribeye area, fat over the ribeye, marbling) existed in an Angus-Brahman multibreed population containing animals ranging from 100% Angus to 100% Brahman (Elzo et al., 2013, 2015). High-accuracy animal EBV could conceivably be obtained for carcass traits by utilizing all available ultrasound and carcass phenotypic data, pedigree, and genotypic information traits in Brahman-Bos taurus multibreed populations prevalent in subtropical and tropical areas. ***Thus, the objectives of this research were: 1) To estimate heritabilities for and genetic correlations between nine ultrasound and carcass traits using multiple-trait single-step genomic-polygenic and polygenic models; 2) To assess values, accuracies, and rankings of animal genomic-polygenic EBV computed using the complete set of SNP and two small SNP subsets from GeneSeek GGPHD250k as well as animal polygenic EBV in a multibreed Angus-Brahman cattle population from subtropical US.***

MATERIALS AND METHODS

Animals. ***Animals were from the multibreed Angus-Brahman (MAB) herd of the University of Florida, Gainesville.*** Mating in the MAB herd followed a diallel design where sires from six breed groups were mated to dams of these same breed groups (Elzo and Wakeman, 1998). The Angus (A) and Brahman (B) composition of the six breed groups was as follows: BG1 = 100% A to (80% A 20% B), BG2 = (60% A 40% B) to (79% A 21% B), BG3 = Brangus = (62.5% A 37.5% B), BG4 = (40% A 60% B) to (59% A 41% B), BG5 = (20% A 80% B) to (39% A 61%B), and BG6 = (19% A 81% B) to 100% B. ***Calves (n = 1,981; 285 BG1, 316 BG2, 271 BG3, 426 BG4, 216 BG5, and 467 BG6) were born at the UF Beef Unit between 2006 and 2015. They were the offspring of 125 sires (21 BG1, 16 BG2, 22 BG3, 16 BG4, 14 BG5, and 36 BG6) and 691 dams (101 BG1, 106 BG2, 87 BG3, 135 BG4, 75 BG5, and 181 BG6).***

Traits. ***Traits were yearling ultrasound weight (UW, kg), yearling ultrasound ribeye area (UREA, cm2), yearling ultrasound backfat (UFAT, cm), yearling ultrasound percent intramuscular fat (UPIMF, %), slaughter age (SLA, d), hot carcass weight (HCW, kg), ribeye area (REA, cm2), backfat thickness (FAT, cm), and marbling score (MAR, units; 100 to 199 = practically devoid, 200 to 299 = traces, 69 300 to 399 = slight, 400 to 499 = small, 500 to 599 = modest, 600 to 699 = moderate, 700 to 799 70 = slightly abundant, 800 to 899 = moderately abundant, and 900 to 999 = abundant).*** A certified technician recorded ultrasound images from yearling male and female calves using an Aloka 500 ultrasound system (Hitachi Aloka Medical, Ltd., Wallinford, Connecticut, USA) in December. Yearling weights (UWT) were collected prior to acquiring ultrasound images. Analysis of the ultrasonic images with UICS Scanning Software by Walter and Associates, LLC (Ames, 106 Iowa, USA) yielded UREA, UBF, and UPIMF phenotypes. Steers at the contract feeder were transported to a commercial packing plant after approximately reaching 1.27 cm over the ribeye (2006 to 2010; Sam Kane Beef Processors, Corpus Christi, Texas; 2011 to 2012: FPL Food, LLC, Augusta, Georgia; 2013 to 2014: Central Beef Industries, Bushnell, Florida; 2015: Adena Meat Products, Fort McCoy, Florida, and UF Meats Laboratory, Gainesville, Florida) and harvested using established USDA-FSIS procedures. Carcass data (HCW, REA, FAT, and MAR) were collected 24 hr postmortem. Slaughter age (SLA) was computed as the number of days between birth and slaughter.

Tissue Sampling and Genotyping. ***Tissue samples (blood, semen) from 782 animals were collected for this study between 2006 and 2015 and stored at -80 °C. There were 70 sires, 696 steers, and 16 heifers (BG1 = 126, BG2 = 120, BG3 = 123, BG4 = 159, BG5 = 83, and BG6 =171) represented in these samples.*** A commercial kit (QIAamp DNA mini kit, Qiagen, Valencia, CA) was used to extract DNA from blood and semen samples. ***The DNA samples were sent to Neogen for genotyping with GeneSeek Genomic Profiler F250 (number of SNP in autosomes and X chromosome = 221,049). All SNP with minor allele frequencies lower than 0.05 were discarded (n = 94,033). Thus, the genotype files contained 127,016 SNP autosomal and X chromosome markers for each genotyped animal.***

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MATERIALS AND METHODS (Continued)

Variance Components, Heritabilities, and Correlations. ***A 9-trait single-step genomic-polygenic model (GPM; Aguilar et al., 2010) and a 9-trait polygenic model (PM) were used to obtain variance components, heritabilities, and genetic, environmental and phenotypic correlations for UW, UREA, UFAT, UPIMF, SLA, HCW, REA, FAT, and MAR .*** Fixed effects for GPM and PM were contemporary group (location-year), age of calf (ultrasound traits only), sex of calf, and direct heterosis as a function of calf heterozygosity (i.e., the probability of one Angus and one Brahman allele in 1 locus). Random effects for all traits in GPM and PM were animal direct additive genetic and residual. ***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).***

Genomic-polygenic and polygenic EBV, accuracies, and rankings. ***Genomic-polygenic estimated breeding values (GPEBV) and polygenic EBV (PEBV) for UW, UREA, UFAT, UPIMF, SLA, HCW, REA, FAT, and MAR using GPM and PM models that contained the same fixed and random effects as those used for variance component estimation.*** Genomic-polygenic EBV were also computed with GPM that used genotype files containing two reduced SNP sets of GeneSeek Genomic Profiler F250. ***The first GPM (GPMR1) utilized a reduced SNP set (R1) that contained only SNP in the top 5% by absolute value of their Best Predictor across all nine traits (n = 24,761) computed with POSTGSF90 (Aguilar and Misztal, 2014). The second GPM (GPMR2) used a reduced SNP set (R2) that was constructed using 24,761 SNP (5%) chosen evenly across the genome regardless of their predicted value.*** Genomic-polygenic EBV for all traits were computed using GPMR1 (GPEBVR1) and GPMR2 (GPEBVR2). Accuracies of GPEBV, GPEBVR1, GPEBVR2, and PEBV for all animals and traits were computed using the expression [1-PEV_ij/AGV_j]^(1/2)*100, where PEV_ij is the prediction error variance for trait j within animal i, and AGV_j is the additive genetic variance for trait j. Means and SD of accuracies for GPEBV, GPEBVR1, GPEBVR2, and PEBV were computed for sires, dams, progenies, and all animals using the TABULATE procedure of SAS. Rankings of sires (n = 292), dams (n = 1,238), progeny (n = 2,103), and all animals (n = 3,633) with GPEBV, GPEBVR1, GPEBVR2, and PEBV were compared using Spearman rank correlations computed using the CORR procedure of SAS. The GPEBV from all evaluated animals (n = 3,633) were also plotted against Brahman fraction to visualize variation and trends in EBV in animals ranging in Brahman fraction from 0% (Angus) to 100% (Brahman).

Table 1. Direct additive genetic and environmental variances for yearling ultrasound and carcass traits using GPM and PM

	Genetic variances				Environmental variances			
Trait	GPM	SE	PM	SE	GPM	SE	PM	SE
UW; kg^2	723.4	88.9	655.2	82.0	621.9	55.9	627.9	56.2
UREA; cm^4	22.1	2.6	19.7	2.4	38.5	1.3	39.0	1.4
UFAT; cm^2	0.0	0.0	0.0	0.0	0.1	0.0	0.1	0.0
UPIMF; %^{2}	0.3	0.0	0.2	0.0	0.5	0.0	0.5	0.0
SLA; d^2	587.3	97.6	565.9	73.8	404.5	60.0	351.9	43.6
HCW; kg^2	622.8	90.7	524.3	82.1	446.1	54.3	480.0	61.5
REA; cm^4	34.8	5.0	30.7	4.4	37.1	2.0	36.8	2.2
FAT; cm^2	0.1	0.0	0.1	0.0	0.1	0.0	0.2	0.0
MAR; units^2	3753.5	640.8	3270.8	628.5	2898.5	415.3	3101.9	475.0

RESULTS AND DISCUSSION

Variance Components. On the average, GPM additive genetic variances were 11.4% higher, additive genetic covariances were 25.6% higher, environmental variances were 2.3% lower, environmental covariances were 11.3% higher, phenotypic variances 4.5% higher, and phenotypic covariances were 8.5% higher than those from PM (**Tables 1 & 2**). This resemblance resulted in similar average values of heritabilities (GPM values were 9.4% higher than PM values), genetic correlations (18.4% smaller for GPM than for PM), environmental correlations (13.3% smaller for GPM than for PM), and phenotypic correlations (0.03% higher for GPM than for PM). ***Consequently, the information from the 127,016 SNP markers from the 782 animals genotyped with GeneSeek Genomic Profiler 250F had little impact on the estimates of variance components and variance ratios for these nine ultrasound and carcass traits in this population.***

Heritabilities and Correlations. Yearling ultrasound trait heritabilities were moderate for UW (GPM: 0.54 ± 0.05; PM: 0.51 ± 0.05); UREA (GPM: 0.36 ± 0.03; PM: 0.34 ± 0.03), and UMPIMF (GPM: 0.34 ± 0.03; PM: 0.30 ± 0.03) and low for UFAT (GPM: 0.12 ± 0.02; PM: 0.11 ± 0.02). Conversely, all carcass traits had moderate heritabilities (SLA, GPM: 0.59 ± 0.07, PM: 0.61 ± 0.06; HCW, GPM: 0.58 ± 0.06, PM: 0.52 ± 0.07; REA, GPM: 0.48 ± 0.04, PM: 0.45 ± 0.05; FAT, GPM: 0.41 ± 0.05, PM: 0.30 ± 0.05; MAR, GPM: 0.56 ± 0.07, PM: 0.51 ± 0.08; **Table 2**). Additive genetic correlation estimates between pairs of ultrasound and(or) carcass traits were all between -0.31 and 0.81.

Table 2. Phenotypic variances and heritabilities for yearling ultrasound and carcass traits using GPM and PM

	Phenotypic variances				Heritabilities			
Trait	GPM	SE	PM	SE	GPM	SE	PM	SE
UW; kg^2	1345.3	56.5	1283.1	51.0	0.54	0.05	0.51	0.05
UREA; cm^4	60.7	2.3	58.6	2.2	0.36	0.03	0.34	0.03
UFAT; cm^2	0.1	0.0	0.1	0.0	0.12	0.02	0.11	0.02
UPIMF; %^{2}	0.7	0.0	0.7	0.0	0.34	0.03	0.30	0.03
SLA; d^2	991.8	63.0	917.8	54.0	0.59	0.07	0.61	0.06
HCW; kg^2	1068.9	65.3	1004.3	56.0	0.58	0.06	0.52	0.07
REA; cm^4	71.9	4.4	67.5	3.8	0.48	0.04	0.45	0.05
FAT; cm^2	0.2	0.0	0.2	0.0	0.41	0.05	0.30	0.05
MAR; units^2	6651.9	414.8	6372.7	369.0	0.56	0.07	0.51	0.08

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RESULTS AND DISCUSSION (Continued)

Genomic-polygenic and polygenic EBV, accuracies, and rankings. ***Utilization of the top 5% of SNP markers across the nine ultrasound and carcass traits (n = 24,761) yielded genomic-polygenic EBV that were close to those obtained with 24,761 SNP markers spread across the genome, and to those from the full set of SNP markers.*** Accuracies of EBV for all traits differed little among the three GPM and PM for sires, dams, progenies, and all animals. Rank correlations between GPEBVR1 & GPEBVR2, GPEBV & GPEBVR1, and GPEBV & GPEBVR2 were above 0.99 for sires (all traits, except for SLA; mean = 0.994; range = 0.982 to 0.998; P < 0.0001), dams (all traits; mean = 0.998; range = 0.993 to 0.999; P < 0.0001), progenies (all traits; mean = 0.997; range = 0.992 to 0.999; P < 0.0001), and all animals (all traits; mean = 0.997; range = 0.992 to 0.999; P < 0.0001) indicating a high degree of agreement among EBV from these models.

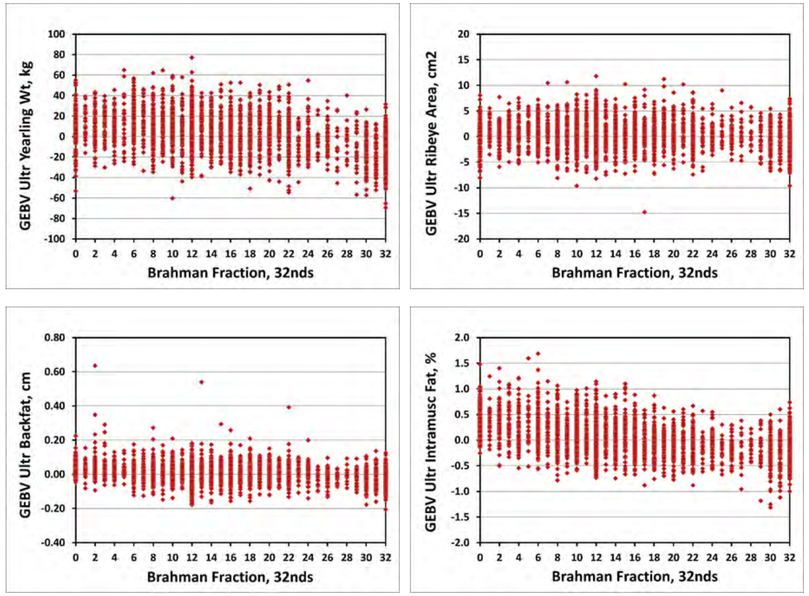

Figure 1. Genomic-Polygenic EBV for UW, UREA, UFAT, and UPIMF

Table 3. Means and SD of GPEBVR1, GPEBVR1, and PEBV differences from GPEBV for yearling ultrasound and carcass traits

			GPEBVR1		GPEBVR2		PEBV	
Trait	Animals	N	Mean	SD	Mean	SD	Mean	SD
UW	Sires	292	-0.09	0.95	0.05	0.56	-0.14	3.59
	Dams	1,238	0.04	0.69	0.06	0.38	-0.43	2.53
	Progeny	2,103	-0.03	1.13	0.05	0.68	-0.24	3.98
UREA	Sires	292	0.00	0.15	0.00	0.09	-0.06	0.49
	Dams	1,238	0.00	0.13	0.00	0.07	-0.06	0.40
	Progeny	2,103	0.01	0.21	0.01	0.12	-0.08	0.64
UFAT	Sires	292	0.00	0.00	0.00	0.00	0.00	0.01
	Dams	1,238	0.00	0.00	0.00	0.00	0.00	0.01
	Progeny	2,103	0.00	0.01	0.00	0.00	0.00	0.02
UPIMF	Sires	292	0.00	0.02	0.00	0.01	0.02	0.07
	Dams	1,238	0.00	0.02	0.00	0.01	0.01	0.05
	Progeny	2,103	0.00	0.02	0.00	0.01	0.02	0.07
SLA	Sires	292	-0.06	1.34	0.02	0.64	-0.69	3.30
	Dams	1,238	0.15	0.91	0.04	0.49	-0.96	2.62
	Progeny	2,103	-0.07	1.41	0.02	0.69	-1.37	3.48
HCW	Sires	292	-0.13	1.13	0.01	0.60	-0.60	4.43
	Dams	1,238	0.10	0.86	0.04	0.47	-0.89	3.31
	Progeny	2,103	-0.09	1.32	0.02	0.68	-1.48	4.57
REA	Sires	292	-0.01	0.25	0.00	0.14	-0.24	1.11
	Dams	1,238	0.03	0.20	0.01	0.10	-0.21	0.98
	Progeny	2,103	-0.01	0.29	0.01	0.15	-0.38	1.27
FAT	Sires	292	0.00	0.02	0.00	0.01	0.00	0.06
	Dams	1,238	0.00	0.01	0.00	0.00	0.00	0.05
	Progeny	2,103	0.00	0.02	0.00	0.01	0.00	0.07
MAR	Sires	292	-0.47	3.34	-0.05	1.61	2.68	16.63
	Dams	1,238	-0.03	2.26	0.05	1.14	1.42	10.55
	Progeny	2,103	-0.49	3.46	-0.02	1.64	4.12	15.12

FINAL REMARKS

- Comparable variance components and genetic parameters were estimated with genomic-polygenic models using a complete high-density set and two reduced sets of SNP, and a polygenic model

- Similar EBV, accuracies, and rankings among genomic-polygenic models indicated that these reduced SNP sets were appropriate alternatives to the complete high-density SNP set in this population

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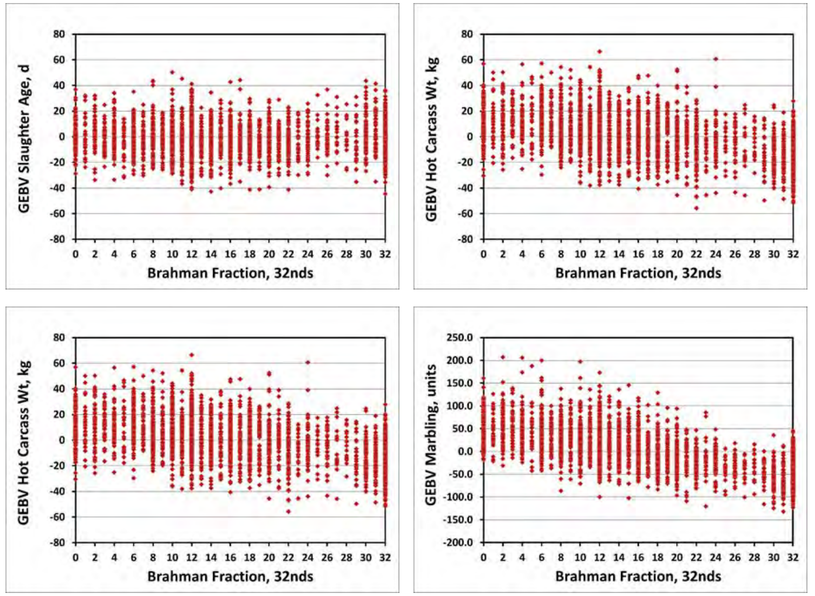

Figure 2. Genomic-Polygenic EBV for SLA, CWT, REA, and MAR