Abstract W63

Genomic-Polygenic evaluation of postweaning weight and ultrasound carcass traits in an Angus-Brahman multibreed population

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SUMMARY

The objectives of this study were to estimate the fraction of additive genetic variance explained by the SNP in the GoldenGate Bovine3K BeadChip (Illumina, Inc., 2011), to compare the ranking of animals evaluated using a genomic-polygenic model, a genomic model, and a polygenic model, and to evaluate the trends of genomic, polygenic-genomic and polygenic breeding values as Brahman fraction increased from 0 to 1 for 3 postweaning ultrasound traits and postweaning weight (UW). Ultrasound traits were ribeye area (UREA), backfat thickness (UBF), and percent of intramuscular fat (UPIMF). Data were from 623 calves from the Angus-Brahman multibreed herd of the University of Florida born from 2006 to 2010. A genomic-polygenic model was used to estimate additive SNP, polygenic, and total additive genetic variances using Markov Chain Monte Carlo procedures. Fixed effects were contemporary group (year-pen), age of dam, sex of calf, age of calf, B fraction of calf, and heterozygosity of calf. Random effects were additive SNP, additive polygenic, and residual. Estimated variance components were used to compute EBV using genomic polygenic, genomic, and polygenic models. Spearman's rank correlations among EBV from the 3 models were computed to assess the impact of including SNP information on EBV rankings. Regressions of EBV on Brahman fraction of calf were also computed to analyze EBV trends from 100% Angus to 100% Brahman calves. ***The fractions of the additive genetic variance explained by SNP in the Illumina3k chip were 0.09 for UREA, 0.38 for UBF, 0.06 for UPIMF, and 0.08 for UW. Rank correlations were high among genomic–polygenic and polygenic models (0.89 to 0.99) and moderate (0.51 to 0.65) among EBV from genomic and polygenic models. Regression coefficients for all models and traits showed that calf EBV tended to decrease as B fraction of calves increased suggesting that calves with higher B fraction were leaner, had smaller ribeye areas, and grew more slowly than calves with higher Angus fractions. The low fraction of additive genetic variances accounted for by the markers in the Illumina3k chip indicated that higher density chips would be needed to more completely account for additive genetic variation in multibreed populations.***

INTRODUCTION

Hot and humid climatic conditions in Florida and other subtropical regions of the US have required the use of cattle adapted to these tough environmental conditions that have good reproduction and are competitive in both growth and carcass characteristics with cattle from temperate regions of the country. Thus, Brahman and Brahman x temperate *Bos taurus* crossbred cattle have been extensively used. However, Brahman and high percent Brahman cattle are less tender than temperate *Bos taurus* cattle. A recent study in Florida found that Brahman-Angus crossbred steers with 50% Brahman or less showed little impact on meat quality (Elzo et al., 2011). Low numbers of cattle measured for carcass traits have resulted in increased use of ultrasound measurements as they are closely associated with carcass traits at slaughter (Houghton and Turlington, 1992; Wilson, 1992; MacNeil, 2009). Genotypes from marker chips represent another source of information that could vastly improve the accuracy of genetic predictions for carcass and meat quality traits. However, the amount of genetic information explained by these chips will have direct impact on the accuracy of genomic predictions. Thus, the objectives of this research were: 1) to estimate the fraction of the additive genetic variance explained by the SNP in the GoldenGate Bovine3K BeadChip (Illumina, Inc., 2011) for 4 ultrasound and weight traits, 2) to assess the impact of the inclusion of SNP marker information on animal rankings for these 4 traits using genomic-polygenic, genomic, and polygenic models, and 3) to evaluate trends of genomic, genomic-polygenic, and polygenic breeding values as Brahman fraction increased from 0 to 1 in an Angus-Brahman multibreed population under subtropical conditions.

MATERIALS AND METHODS

Animals and Data. Data were from calves belonging to the Angus-Brahman multibreed (MAB) herd of the University of Florida located in Gainesville, Florida. The herd mating plan was diallel where bulls from 6 breed groups were mated to dams of the same 6 breed groups. Mating groups were: Angus = (1.0 to 0.80) A (0.0 to 0.20) B, ¾ A ¼ B = (0.79 to 0.60) A (0.21 to 0.40) B, Brangus = (0.625) A (0.375) B, ½ A ½ B = (0.59 to 0.40) A (0.41 to 0.60) B, ¼ A ¾ B = (0.39 to 0.20) A (0.61 to 0.80) B, and Brahman: (0.19 to 0.0) A (0.81 to 1.00) B. There were 623 calves born between 2006 and 2010 (90 Angus, 123 ¾ A ¼ B, 114 Brangus, 154 ½A ½B, 69 ¼ A ¾ B, and 73 Brahman). Numbers of calves by sex were 56 bulls, 310 heifers, and 257 steers. Calves were the progeny of 64 sires and 330 dams. Traits were ultrasound weight (UW), ultrasound ribeye area (UREA), ultrasound percent of intramuscular fat (UPIMF), and ultrasound backfat (UBF). Live weights (UW) and ultrasound measurements were taken at the end of a 70 days feed efficiency trial by a trained technician using an Aloka 500 (Hitachi Aloka Medical, Ltd., Wallinford, Connecticut, USA). Ultrasound images were analyzed with UICS Scanning Software by Walter and Associates, LLC (Ames, Iowa, USA) to obtain UREA (cm^2), UBF (cm) and UPIMF (%) phenotypes.

Feeding and Management. Calves were born between December and March from 2006 to 2010 and kept preweaning at the Beef Unit of the University of Florida (UF). They received a preconditioning diet for 3 to 4 weeks before being moved to the UF Feed Efficiency Facility (UFEF) in Marianna, Florida, to participate in a feed efficiency trial (adjustment period = 21 d and trial period = 70 d). The preconditioning diet of calves consisted of concentrate (1.6 kg to 3.6 kg per day; 14.0 % CP; 488 Pellet, Medicated Weaning Ration, Lakeland Animal Nutrition, Lakeland, Florida; and soy hull pellets), ad libitum access to mineral supplement, and bahiagrass hay. Calves were assigned to pens at UFEF (108 m2/pen; 2 GrowSafe nodes per pen) according to sire group (A, ¾ A ¼ B, Brangus, ½ A ½ B, ¼ A ¾ B, and B) and sex (bull, heifer, and steer) subclass. The mean stocking rate was 15 animals per pen and 7.5 animals per GrowSafe node. Calves were individually identified using a half-duplex passive transponder ear tags (Allflex USA Inc., Dallas-Fort Worth, TX). The ration at UFEF was composed of various percentages of whole corn or corn gluten, cottonseed hulls, molasses, chopped grass hay, and a vitamin-mineral-protein supplement and it was offered ad libitum. The average composition of the diet from 2006 to 2010 was 89.2% of dry matter, 12.9% of crude protein, 1.6 mcal/kg DM of net energy for maintenance, and 1.0 mcal/kg DM of net energy for gain.

Tissue Sampling and Genotyping. Blood samples were collected at weaning with vacutainer tubes coated with EDTA. Samples were kept at a temperature of 4°C and sent to the New Mexico State University for DNA extraction. Tubes were centrifuged to obtain the white blood cell supernatant, then PBS was added to yield a volume of 1.0 mL. A sample of 0.05 mL of each sample was sent to GeneSeek (Gene Seek, Lincoln, NE, USA) to have DNA extracted and for genotyping with Illumina GoldenGate Bovine3K BeadChip (Illumina, Inc., 2011).

Statistical Analysis. A genomic-polygenic animal model was used to estimate variance components for UREA, UBF, UPIMF and UW. Fixed effects were contemporary group (year-pen), age of dam, sex of calf, age of calf, Brahman fraction of calf, and heterozygosity of calf. Random effects were additive SNP (AS; mean zero; variance = additive SNP variance), animal additive polygenic (AP; mean zero; variance = A*Vg; A = additive relationship matrix, Vg = additive polygenic variance), and residual (mean zero, common residual variance). Variance components and heritabilities were estimated using Markov Chain Monte Carlo (MCMC) procedures (VCE option in program GS3 of Legarra, 2009; Number of iterations = 120,000; Burn-in = 20,000; Thinning = 100; Correction = 10,000). Additive genetic variances (**VAG**) were computed as the sum of the additive genomic (**VAGO**) and the additive polygenic (**VAPO**) variances, where VAGO = 2*[sum($p_i q_i$), i = 1,…, 2899)] times additive SNP variances (Gianola et al., 2009).

Subsequently, program GS3 was used to compute BLUP of Additive Polygenic and Additive SNP effects for all traits with genomic-polygenic, genomic, and polygenic models (Gauss-Seidel iteration; convergence criterion = 10^{-4}). Genomic models excluded polygenic effects, and polygenic models excluded additive SNP effects.

Calf EBV were computed as: 1) the sum of their breed effect (calf Brahman fraction * solution (Brahman – Angus) + calf genomic value + calf polygenic value, where calf genomic value = sum (number of "2" alleles x SNP value)I, i = 1, …, 2899) for genomic-polygenic models; 2) the sum of breed effect + genomic value for genomic models; and 3) the sum of breed effect + polygenic value for polygenic models. Spearman's rank correlations were computed to compare calf rankings across models. Linear regressions of genomic-polygenic, genomic, and polygenic EBV on Brahman fraction of calves were estimated to assess EBV trends as Brahman fraction increased from 0 to 1.

RESULTS AND DISCUSSION

Number of calves, means and standard deviations by calf breed group and total are shown in **Table 1**. Ultrasound ribeye area means per breed group ranged from 55.7 cm^2 (Brahman) to 62.6 cm^2 (¼ A ¾ B), UBF means from 0.61(¾A¼B) to 0.68 cm (¼ A ¾ B), UPIMF means from 2.55 (¼ A ¾ B) to 3.3% (A) and UW means ranged from 317.9 kg (B) to 356.2 kg (¾ A ¼ B). The mean age of animals at the end of the trial was 370 days. The additive SNP variances were 1.7 x 10^{-3} cm^4 for UREA, 1.8 x 10^{-6} cm^2 for UBF, 1.5 x 10^{-5} % for UPIMF and 0.05 kg^2 for UW. Thus VAGO values were 2.06 cm^4 for UREA, 0.002 cm^2 for UBF, 0.02% for UPIMF and 56.7 kg^2 for UW. **Table 2** presents genomic, polygenic, total genetic and phenotypic estimates of variance components estimated for all traits.

Table 1. Numbers of calves, means and standard deviations per breed group and total

		Trait[1]											
		UREA, cm^2			UBF, cm			UPIMF, %			UW, kg		
Breed group	N	Mean	SD	N	Mean	SD	N	Mean	SD	N	Mean	SD
Angus	89	59.7	13.2	89	0.66	0.40	90	3.30	1.55	90	349.6	57.2
¾ A ¼ B	123	59.5	12.6	123	0.61	0.36	122	3.15	1.55	123	356.2	63.4
Brangus	114	58.1	11.0	114	0.62	0.37	114	2.87	1.43	114	344.6	50.5
½ A ½ B	154	58.4	11.8	154	0.63	0.38	153	2.74	1.53	154	351.1	57.2
¼ A ¾ B	69	62.6	12.1	69	0.68	0.41	67	2.56	1.49	69	346.9	48.9
Brahman	73	55.7	9.6	73	0.62	0.40	73	2.64	1.61	73	317.9	46.2
Total	622	58.9	11.9	622	0.63	0.38	619	2.89	1.54	623	346.3	56.2

[1]UREA = ultrasound ribeye area; UBF = ultrasound backfat; UPIMF = ultrasound percent intramuscular fat; UW = ultrasound weight.

Table 2. Posterior means for additive genomic, polygenic, total genetic, and phenotypic variances

	Trait[1]			
Variance[2]	UREA, cm^4	UBF, cm^2	UPIMF, %	UW, kg^2
VAGO	2.06	0.002	0.02	56.7
VAPO	20.14	0.004	0.29	612.2
VAG	22.20	0.006	0.31	668.9
PhenVar	56.30	0.022	0.59	1227.3

[1]UREA = ultrasound ribeye area; UBF = ultrasound backfat thickness; UPIMF = ultrasound percent intramuscular fat; UW = ultrasound weight.
[2]VAGO = additive genomic variance; VAPO = additive polygenic variance; VAG = total genetic variance = VAGO + VAPO; PhenVar = phenotypic variance.

Variance ratios. Heritabilities of UREA, UBF, UPIMF and UW ranged from moderate to high (**Table 3**). Ultrasound weight had the largest heritability (0.54) and UBF the lowest one (0.39). The heritability values for these four traits suggest that selection for them is feasible in this multibreed population, especially for UPMIF and UW.

All VAGO/VAG ratios were low, except for UBF (0.38; Table 3). On the other hand, VAGO to Phenvar ratios were low for all traits. The lowest value was for UPIMF (0.03) and the greatest for UBF (0.10). Thus, the proportion of phenotypic variance accounted for by the SNP in the Illumina Bovine3K chip suggested that only a small proportion of total variability is accounted for by this particular set of markers. ***These results suggested that the fraction of the additive genetic variance accounted by the set of markers in the Illumina3k chip was too low to permit computation of EBV with genomic information alone.*** Thus, a genomic-polygenic model would be needed to compute EBV for this multibreed population.

Table 3. Posterior means for additive genetic and genomic variance ratios

	Trait[1]			
Variance Ratios[2]	UREA	UBF	UPIMF	UW
Heritability	0.39	0.25	0.53	0.54
VAGO/VAG	0.09	0.38	0.06	0.08
VAGO/Phenvar	0.04	0.10	0.03	0.05

[1]UREA = ultrasound rib eye area; UBF = ultrasound back fat; UPIMF = ultrasound percent intramuscular fat; UW = ultrasound weight.
[2]VAGO = additive genomic variance; VAG = total additive genetic variance = VAGO + VAPO; PhenVar = phenotypic variance.

Table 4. Spearman rank correlations among calf EBV from genomic-polygenic, genomic, and polygenic models

	Trait[1]			
Correlation[2]	UREA	UBF	UPIMF	UW
P Model, GP Model	0.99	0.89	0.99	0.99
P Model, G Model	0.58	0.51	0.60	0.65
GP Model, G Model	0.65	0.79	0.64	0.70

[1]UREA = ultrasound ribeye area; UBF = ultrasound back fat thickness; UPIMF = ultrasound percent intramuscular fat; UW = ultrasound weight.
[2]GP Model = genomic-polygenic model; G Model = genomic model; P Model = polygenic model. All correlations were significant (P < 0.0001).

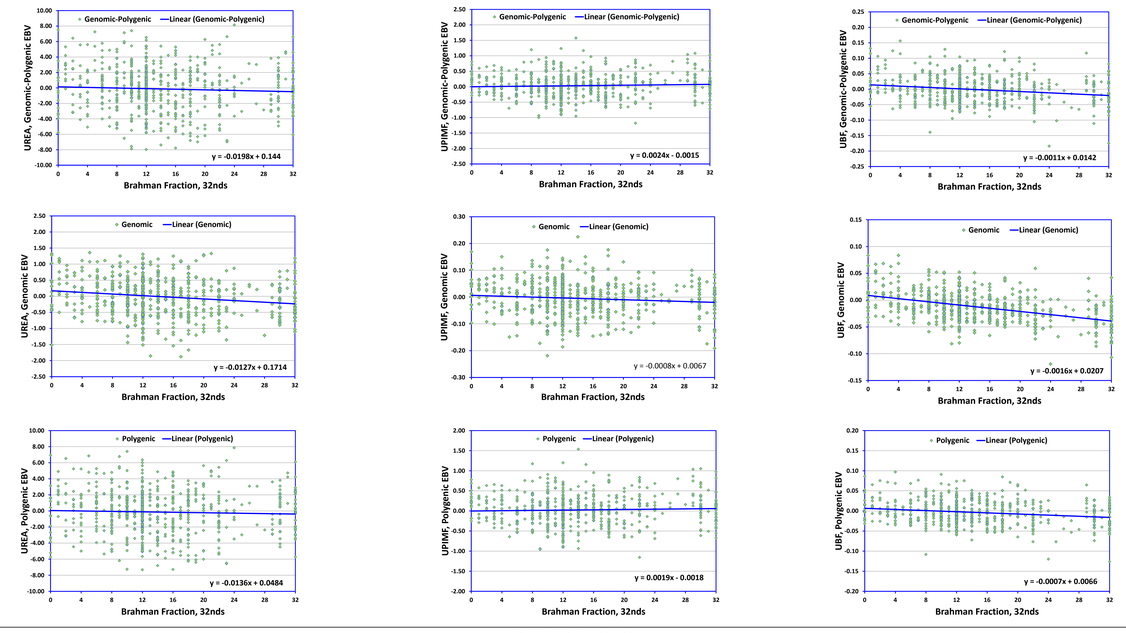
Table 5. Linear regression coefficients for genomic-polygenic, genomic, and polygenic EBV on Brahman fraction of calf

	Trait[1]			
Effect	UREA	UBF	UPIMF	UW
Genomic-Polygenic	-0.0198	-0.0011	0.0024	-0.23
	P = 0.1778	P < 0.0001	P = 0.2222	P = 0.0133
Genomic	-0.0127	-0.0015	-0.0008	-0.17
	P < 0.0001	P < 0.0001	P = 0.0107	P < 0.0001
Polygenic	-0.0136	-0.0007	0.0019	-0.20
	P = 0.3321	P < 0.0001	P = 0.3256	P = 0.0252

[1]UREA = ultrasound ribeye area; UBF = ultrasound backfat thickness; UPIMF = ultrasound percent intramuscular fat; UW = ultrasound weight.

Ranking of Animals and EBV trends from Angus to Brahman. Spearman's rank correlations among calf EBV rankings for UREA, UBF, UPIMF and UW from genomic-polygenic, genomic and polygenic models are shown in **Table 4**. All rank correlations were highly significant (P < 0.0001). The lowest correlations were those among EBV rankings from genomic and polygenic models. ***The highest correlations were between EBV rankings from the genomic-polygenic and polygenic models suggesting that the genomic information from the Illumina Bovine3k chip had little impact on animal rankings in this multibreed population.*** There were calves with high, medium, and low EBV for UREA, UBF, UPIMF and UW of all breed compositions in the MAB population. Except for predictions from the genomic-polygenic and polygenic models for UPIMF, all linear regression coefficients of breeding values on Brahman fraction calf were negative (**Table 5**).

Figures show genomic-polygenic, genomic and polygenic EBV trends for UREA by Brahman fraction of calf from 100% Angus to 100% Brahman. Genomic-polygenic regression coefficients were significant for UBF and UW, whereas genomic regression coefficients were significant for all traits, and polygenic regression coefficients were significant only for UBF and UW (**Table 5**). ***These trends suggested that as Brahman fraction increased, calves tended to have lower postweaning weights, smaller ribeye areas, and lower backfat thicknesses.***



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