Abstract W54

Genomic evaluation of Angus-Brahman multibreed cattle for feed efficiency and postweaning growth using the Illumina3k chip

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SUMMARY

The objective of this research was to evaluate 620 bulls, steers, and heifers ranging from 100% Angus to 100% Brahman (B) using phenotypes from for 4 postweaning feed efficiency and growth traits, pedigree, and SNP genotypes from 2900 loci (Illumina3k chip). Traits were residual feed intake (RFI), daily feed intake (DFI), feed conversion ratio (FCR), and weight gain (WG). Data was collected in a GrowSafe automated feeding facility from 2006 to 2010. Calves remained in pens for the 21-d pre-trial and 70-d trial periods. Animals were assigned to pens by sire group and sex. Concentrate consisted of cottonseed hulls, corn, molasses, and a protein, vitamin, and mineral supplement. Calves were evaluated using a polygenic-genomic mixed model. 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 animal polygenic (AP; mean zero; variance = A*Vg; A = additive relationship matrix, Vg = additive polygenic variance), additive SNP (AS; mean zero; variance = additive SNP variance), and residual effects (mean zero, common residual variance). Variance components and heritabilities were estimated using option VCE (Markov Chain Monte Carlo) of program GS3. ***Heritabilities were 0.21 for RFI, 0.33 for DFI, 0.20 for FCR, and 0.37 for PWG. The fraction of the additive genetic variance explained by the 2900 markers of the Illumina3k chip was 14% for RFI, 10% for DFI, 26% for FCR, and 16% for PWG. The genomic, polygenic, and total additive EBV for all traits tended to decrease as B fraction increased, suggesting that high percent B calves were genetically more efficient (lower RFI), but had lower WG.***

INTRODUCTION

Beef cattle production in subtropical regions of the US must rely on cattle that are able to survive, reproduce, and yield meat of excellent quality under hot and humid climatic conditions. Consequently, cattle producers have made extensive use of crossbreeding *Bos taurus* breeds to Brahman to create a type of animal capable of coping with these harsh environmental conditions. This has created a large multibreed population of *Bos taurus* × *Bos indicus* cattle in which Angus has a significant proportion of the represented *Bos taurus* breeds. As in temperate regions, feed costs represent the largest single expenditure of beef cattle operations in subtropical environments. Even small genetic changes in feed efficiency will have a large impact on the profitability of cattle operations. However, the high cost of obtaining phenotypic information for feed efficiency limits the number of animals with phenotypes. Genotyping information could help improve our ability to identify animals with superior feed efficiency and growth characteristics. ***Thus, the objective of this research was to evaluate 620 bulls, steers, and heifers ranging from 100% Angus to 100% Brahman (B) using phenotypes from for 4 postweaning feed efficiency and growth traits, pedigree, and SNP genotypes from 2900 loci (Illumina3k chip) under Florida subtropical conditions.***

MATERIALS AND METHODS

Animals and Data. Cattle were from the Angus (A)-Brahman (B) multibreed herd (MAB) of the University of Florida (UF). Breed composition was used to construct six breed groups for mating purposes: 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. Mating followed a diallel design, i.e., sires from the six breed groups (Angus, ¾ A ¼ B, Brangus, ½ A ½ B, ¼ A ¾ B, and Brahman) were mated across to dams from the six breed groups. ***This research used postweaning feed consumption and growth data from 620 calves born between 2006 and 2010 (90 Angus, 122 ¾ A ¼ B, 113 Brangus, 153 ¼A ½B, 69 ¼ A ¾ B, and 73 Brahman).*** Calves were the progeny of 64 sires (12 Angus, 11 ¾ A ¼ B, 14 Brangus, 8 ½ A ½ B, 8 ¼ A ¾ B, and 11 Brahman) and 329 dams (53 Angus, 61 ¾ A ¼ B, 52 Brangus, 74 ½ A ½ B, 42 ¼ A ¾ B, and 47 Brahman). Table 1 shows numbers of calves by breed-group-of-sire × breed-group-of-dam combination.

Table 1. Number of calves by breed group of sire x breed group of dam combination

Breed group of dam	Breed group of sire						
	Angus	¾ A ¼ B	Brangus	½ A ½ B	¼ A ¾ B	Brahman	All
Angus	46	10	18	7	7	17	105
¾ A ¼ B	24	21	31	26	14	16	132
Brangus	4	10	60	9	10	7	100
½ A ½ B	30	27	21	26	22	20	146
¼ A ¾ B	13	17	11	9	11	4	65
Brahman	1	2	1	0	0	68	72
All	118	87	142	77	64	132	620

Feeding and Management. Calves from the UF Angus-Brahman herd were transported to the UF GrowSafe Feed Efficiency Facility in Marianna, Florida, and assigned to pens (108 m2/pen; 2 GrowSafe nodes per pen) by sire group (A, ¾ A ¼ B, Brangus, ½ A ½ B, ¼ A ¾ B, and B) and by sex (bull, heifer, and steer) subclass. Calves were identified with half-duplex passive transponder ear tags (Allflex USA Inc., Dallas-Fort Worth, TX). The mean stocking rate was 15 animals per pen and 7.5 animals per GrowSafe node. Animals were offered a concentrate diet composed of various percentages of whole corn or corn gluten, cottonseed hulls, molasses, chopped grass hay, and a vitamin-mineral-protein supplement (FRM, Bainbridge, GA) ad libitum. Dry matter, crude protein, net energy for maintenance, and net energy for gain averaged 12.9%, 89.2%, 1.6 mcal/kg DM, and 1.0 mcal/kg DM from 2006 to 2010. There was an adjustment period of 21 days prior to the 70-day trial period. GrowSafe software recorded feed intake information in real-time. Weights (kg) were collected every 2 weeks.

Tissue Sampling and Genotyping. Blood samples were collected using EDTA tubes, refrigerated at 4°C, and shipped to New Mexico State University for DNA extraction per procedures used in the laboratory of Dr. Milton Thomas (Garrett et al., 2008). Subsequently, DNA samples were sent to GeneSeek for genotyping with the 2,900 marker Illumina GoldenGate Bovine3K BeadChip.

Traits. Traits were **RFI (kg DM*day-1), DFI (kg DM*day-1), FCR (kg DM*day-1/kg weight gain*day-1), and PWG (kg)**. Intake traits were defined on a dry matter basis. Feed intake and growth traits were measured at the UF Feed Efficiency Facility. Phenotypic residual feed intake was obtained as the difference between expected and actual average DFI during the 70-day postweaning feeding trial (Koch et al., 1963; Arthur et al., 2001; Archer et al., 1997).

Statistical Analysis. A polygenic-genomic mixed model was used to estimate variance components and predict calf estimated breeding values (EBV) for each trait. 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 animal polygenic (AP; mean zero; variance = A*Vg; A = additive relationship matrix, Vg = additive polygenic variance), additive SNP (AS; mean zero; variance = additive SNP variance), and residual effects (mean zero, common residual variance). Variance components and heritabilities were estimated using option VCE (Markov Chain Monte Carlo (MCMC); Number of iterations = 120,000; Burn-in = 20,000; Thinning = 100; Correction = 100) of program GS3 (Legarra, 2009). ***Additive genetic (AG) variance was computed as the sum of the additive genomic (AGO) and the additive polygenic (APO) variances, where additive genomic variance = 2*[sum(p_i q_i), i = 1, …, 2900)]*additive SNP variance (Gianola et al., 2009).*** Subsequently, program GS3 was run using option BLUP (Gauss-Seidel iteration; Convergence Criterion = 10^{-4}) and the estimated variance components for additive polygenic, additive SNP, and residual effects to obtain calf polygenic-genomic predictions. ***Calf Total EBV were computed as 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 * SNP value)$_i$, i = 1, …, 2900).***

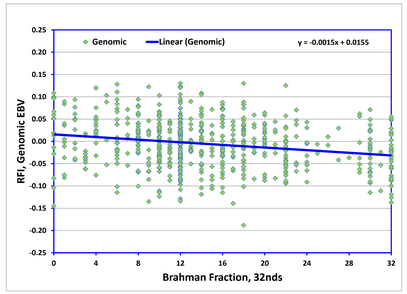
RESULTS AND DISCUSSION

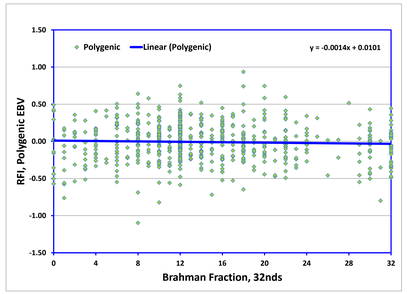
Table 2 shows estimates of additive genetic variances, phenotypic variances, heritabilities, and ratios of additive genomic variances to additive genetic variances for RFI, DFI, FCR, and PWG. Heritabilities for the 4 traits were somewhat smaller than those obtained in a 3-herd Angus-Brahman multibreed population in Florida (Elzo et al., 2009). ***Ratios of additive genomic to additive genetic variance ranged from 0.10 for DFI to 0.26 for FCR.*** Thus, the 2900 markers of the Illumina Bovine3K chip accounted for only a small fraction of the total genetic variation for these 4 traits in this multibreed population. ***The small number of markers in the chip and the high level of intermixing among Angus and Brahman genotypes may have contributed to the low level of additive genetic variation accounted for the Illumina3K chip in this Angus-Brahman multibreed population.***

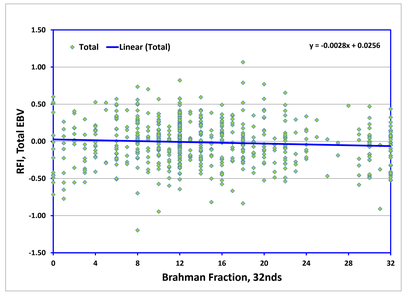
EBV Trends. Figures show genomic EBV, polygenic EBV, and calf total EBV for all calves in the multibreed population ordered by their Brahman fraction (in 32nds) from 0 (100% Angus) to 32 (100% Brahman). ***Correlations between genomic and polygenic EBV were 0.45 for RFI, 0.39 for DFI, 0.45 for FCR, and 0.56 for PWG. Genomic, polygenic, and total additive EBV values tended to decrease from Angus to Brahman. However, calves of similarly high, medium, and low EBV existed across the spectrum of Angus and Brahman fractions.***

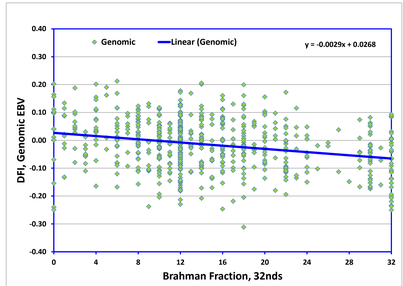
Table 2. Additive Genetic and Genomic Variation in the MAB population

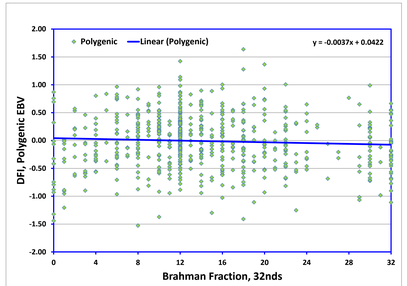
Trait	Parameter	AGVar	PhenVar	Heritability	AGOVar/AGVar
RFI	Mean	0.37	1.79	0.21	0.14
(kg/d)	SD	0.15	0.11	0.08	0.11
DFI	Mean	0.80	2.42	0.33	0.10
(kg/d)	SD	0.24	0.15	0.09	0.08
FCR	Mean	1.32	6.50	0.20	0.26
(kfd/kgd)	SD	0.56	0.40	0.08	0.17
PWG	Mean	89.74	240.97	0.37	0.16
(kg)	SD	25.85	15.09	0.10	0.11

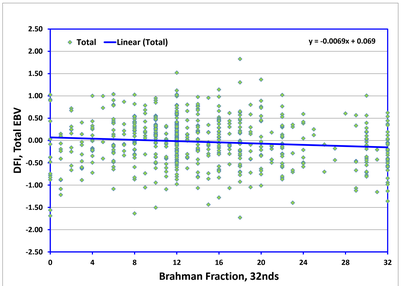


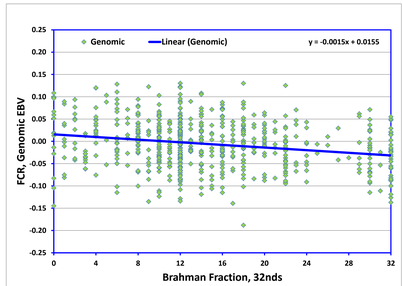


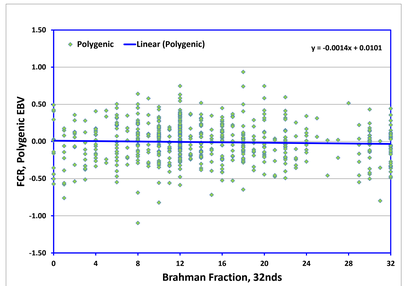


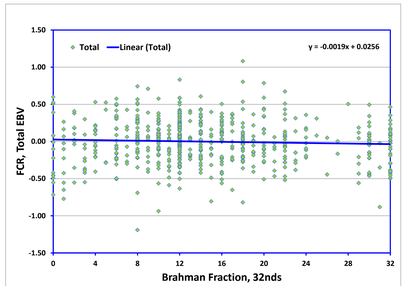


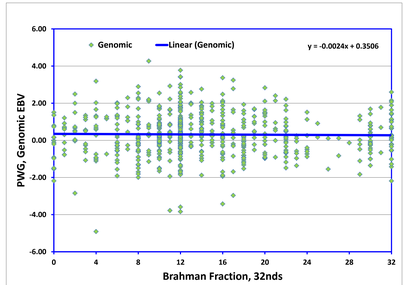


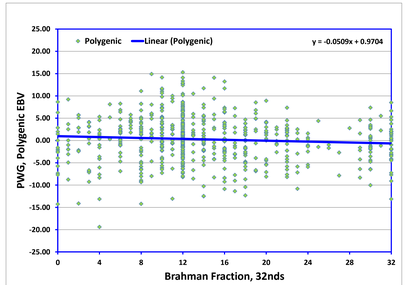


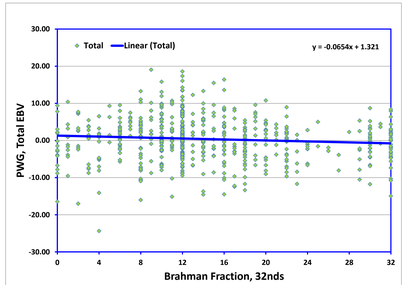












FINAL REMARKS

The Illumina3K chip accounted for only a small fraction (10% to 26%) of the genetic variation for postweaning feed consumption, feed efficiency, and growth suggesting that either the number of markers or the set of markers used in the chip were insufficient to account for the existing genetic variation in this multibreed population.

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