Abstract W64

Genomic-polygenic evaluation of Angus-Brahman cattle for carcass traits with the Illumina3K chip

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SUMMARY

The objective of this research was to assess the impact of including genotypic information from the Illumina3k chip on the genetic evaluation of animals for 5 carcass traits in an Angus-Brahman multibreed population using genomic-polygenic (GP), genomic (G), and polygenic (P) models. Fractions of additive genetic variances associated with markers in the Illumina3k chip were computed, and animal EBV rankings and EBV trends as calf Brahman percent increased from 0 to 100% were compared across models. Traits were hot carcass weight (HCW), dressing percent (DP), ribeye area (REA), fat over the ribeye (FOE), and marbling (MAB). Phenotypic and genotypic data were from 202 steers born from 2006 to 2010. Data were analyzed with single-trait models. All models had contemporary group (year-pen), Brahman fraction of calf, heterozygosity of calf, and slaughter age as fixed effects. Random effects were additive SNP (GP and G models), additive polygenic (GP and P models), and residual. Program GS3 was used to compute variance components and heritabilities with option VCE (Markov Chain Monte Carlo), and EBV using option BLUP. ***Heritabilities were 0.72 for HCW, 0.25 for DP, 0.53 for REA, 0.44 for FOE, and 0.23 for MAB. Fractions of additive genetic variance explained by Illumina3k SNP were 0.08 for HCW, 0.47 for DP, 0.19 for REA, 0.27 for FOE, and 0.23 for MAB.*** Higher rank correlations existed between EBV from GP and P models (0.94 to 0.99; P < 0.0001) than between EBV from G and P models (0.78 to 0.84; P < 0.0001). Regressions of calf EBV on Brahman fractions were non-significant for all traits indicating that calves of comparable EBV for carcass traits existed across all breed compositions. ***The low fractions of additive genetic variances accounted for by the Illumina3k chip indicated that GP models would need to be used to compute EBV if this chip is used to help predict animal EBV, and that higher density chips would be needed to better account for additive genetic variation in multibreed populations.***

INTRODUCTION

Carcass traits are essential for the continued success of the beef cattle industry. Beef cattle must produce carcasses of high yield and desirable degrees of marbling, tenderness, juiciness, and flavor. Cattle producers in the Southern region of the US must not only meet these challenges, but also have cattle that can reproduce and thrive under hot and humid subtropical environments. Consequently, most cattle in the Southern region contain Brahman, the premier breed of Bos indicus adapted cattle in the US. Extensive use of crossbreeding of Bos taurus breeds with Brahman has generated a large multibreed population that needs to be accurately evaluated to identify animals that are both adapted and productive under subtropical conditions. Decreasing costs of genotyping chips has permitted the use of genotypic information to evaluate animals for a variety of economically important traits. A reasonably priced commercial chip available for cattle was the GoldenGate Bovine3K BeadChip. ***Thus, The objective of this research was to assess the impact of including genotypic information from the Illumina3k chip on the genetic evaluation of animals for 5 carcass traits in an Angus-Brahman multibreed population using genomic-polygenic (GP), genomic (G), and polygenic (P) models.***

MATERIALS AND METHODS

Animals and Data. Cattle were from the Angus (A)-Brahman (B) multibreed herd of the University of Florida (UF). Mating in this herd was diallel, i.e., sires from 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. Mating breed groups were constructed using breed composition ranges as follows: Angus = (1.0 to 0.80) A (0.0 to 0.20) B, ¾ A ½ 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. **A total of 202 steers born from 2006 to 2010 with phenotypic and genotypic information were used in this study *(31 Angus, 29 ¾ A ¼ B, 48 Brangus, 51 ½A ½B, 14 ¼ A ¾ B, and 29 Brahman).*** These steers were the offspring of 45 sires (10 Angus, 7 ¾ A ¼ B, 11 Brangus, 4 ½ A ½ B, 5 ¼ A ¾ B, and 8 Brahman) and 167 dams (28 Angus, 29 ¾ A ¼ B, 26 Brangus, 33 ½ A ½ B, 24 ¼ A ¾ B, and 27 Brahman). Table 1 presents 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	19	3	6	1	2	4	35
¾ A ¼ B	6	2	9	11	4	3	35
Brangus	1	2	22	3	4	2	34
½ A ½ B	8	12	9	7	3	1	40
¼ A ¾ B	6	8	8	1	4	2	29
Brahman	0	2	0	0	0	27	29
All	40	29	54	23	17	39	202

Feeding and Management. Cows and calves were kept on bahiagrass (*Paspalum notatum*) preweaning with access to a complete mineral supplement (Lakeland Animal Nutrition, Lakeland, FL). Winter supplementation consisted of bermudagrass (*Cylodon dactylon*) hay and cottonseed meal. After weaning, steers were transported to the UF GrowSafe Feed Efficiency Facility (UFFEF) in Marianna, Florida, where they were placed in pens and fed a concentrate diet composed of whole corn, cottonseed hulls, and a protein, vitamin, and mineral supplement (FRM, Bainbridge, Georgia, US). The concentrate diet at UFFEF had, on the average, 89.7 % of DM, 14.4 % of CP, 1.5 Mcal/kg DM of NEm, and 1.1 Mcal/kg DM of NEg. Subsequently, steers were taken to a contract feeder and fed a standard commercial corn-protein diet with vitamins and minerals until they reached a subcutaneous fat thickness of approximately 1.27 cm. Then, steers were transported to a commercial packing plant (Sam Kane Beef Processors, Corpus Christi, Texas), and harvested in a conventional manner under USDA, FSIS inspection. After 24 h postmortem, carcasses were ribbed and carcass trait data were collected (USDA, 1997).

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 at the laboratory of Dr. Milton Thomas (Garrett et al., 2008). Subsequently, DNA samples were sent to GeneSeek for genotyping with the Illumina GoldenGate Bovine3K BeadChip.

Traits. Traits were hot carcass weight (**HCW, kg**), dressing percent (**DP, %**), ribeye area (**REA, cm²**), fat over the ribeye (**FOE, cm**), and marbling (**MAB, units**). Marbling scores were: 100 to 199 = practically devoid, 200 to 299 = traces, 300 to 399 = slight, 400 to 499 = small, 500 to 599 = modest, 600 to 699 = moderate, 700 to 799 = slightly abundant, 800 to 899 = moderately abundant, and 900 to 999 = abundant.

Statistical Analysis. Data were analyzed using single-trait genomic-polygenic (**GP**), genomic (**G**), and polygenic (**P**) models. All models had contemporary group (year-pen), Brahman fraction of calf, heterozygosity of calf, and slaughter age as fixed effects. Random effects were additive SNP (mean zero; variance = additive SNP variance; **GP** and **G** models), additive polygenic (mean zero; variance = A*Vg; A = additive relationship matrix, Vg = additive polygenic variance; **GP** and **P** models), and residual. Program GS3 (Legarra, 2009) was used to compute variance components and heritabilities with option VCE (Markov Chain Monte Carlo; Number of iterations = 120,000; Burn-in = 20,000; Thinning = 100; Correction = 10000) using a GP model. ***Additive genetic (AGVar) variance was computed as the sum of the additive genomic (AGOVar) and the additive polygenic (APOVar) variances, where additive genomic variance = 2*[sum($p_i q_i$), I = 1, …, 2899)]*additive SNP variance (Gianola et al., 2009).*** Subsequently, EBV were computed using option BLUP (Gauss-Seidel iteration; Convergence Criterion = 10^{-4}) from program GS3. ***Calf EBV were computed as the sum of their breed effect (calf Brahman fraction * solution (Brahman – Angus) + calf genomic value (GP and G models) + calf polygenic value (GP and P models), where calf genomic value = sum (number of "2" alleles * SNP value)$_i$ for i = 1, …, 2899).***

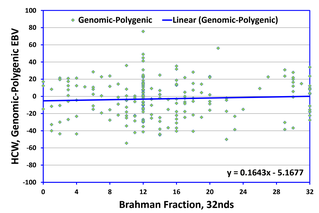
RESULTS AND DISCUSSION

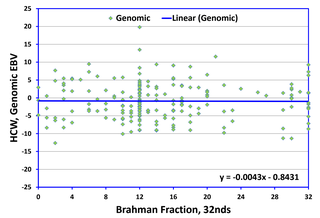
Table 2 shows estimates of additive genetic variances, phenotypic variances, heritabilities, and ratios of additive genomic to additive genetic variances for **HCW**, **DP**, **REA**, **FOE**, and **MAB**. Heritabilities ranged from 0,25 for DP to 0.72 for HCW, and r***atios of additive genomic to total additive genetic variance (AGOVar/AGVar) ranged from 0.08 for HCW to 0.47 for DP. Except for DP, AGOVar/AGVar ratios were similar to those obtained for feed efficiency (Elzo et al., 2011) and ultrasound traits (Elzo et al., 2012) in this multibreed herd.*** Thus, markers from the Illumina Bovine3K chip accounted for less than 50% and, for most traits, for less than 25% of the additive genetic variance for growth, ultrasound, and carcass traits in the UF Angus-Brahman multibreed population.

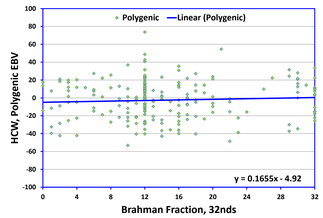
EBV Correlations and Trends. Figures show genomic-polygenic, genomic, and polygenic EBV for all calves ordered by their Brahman fraction (in 32nds) from 0 (100% Angus) to 32 (100% Brahman). ***Higher rank correlations existed between EBV from GP and P models (0.94 to 0.99; P < 0.0001) than between EBV from G and P models (0.78 to 0.84; P < 0.0001). Regressions of calf EBV on Brahman fractions were non-significant for all traits indicating that calves of comparable EBV for carcass traits existed across all breed compositions.***

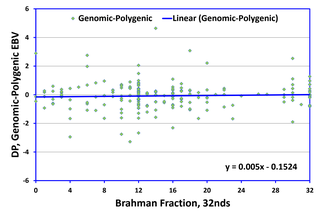
Table 2. Additive Genetic and Genomic Variation in the MAB population

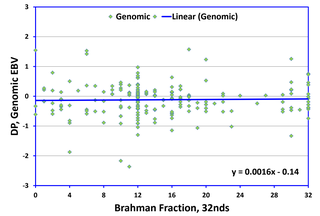
Trait	Parameter	AGVar	PhenVar	Heritability	AGOVar/AGVar
HCW	Mean	895.88	1232.48	0.72	0.08
(kg)²	SD	270.57	150.59	0.18	0.09
DP	Mean	5.03	19.24	0.25	0.47
(%)²	SD	3.89	2.39	0.17	0.26
REA	Mean	39.02	71.73	0.53	0.19
(cm)⁴	SD	18.74	9.17	0.22	0.16
FOE	Mean	0.11	0.23	0.44	0.27
(cm)²	SD	0.06	0.03	0.20	0.21
MAB	Mean	3580.57	4739.93	0.75	0.23
(unit)²	SD	980.23	572.93	0.16	0.16

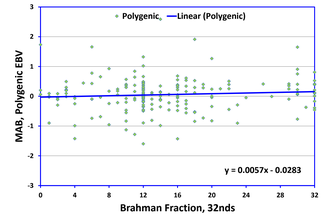


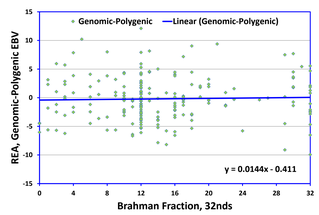


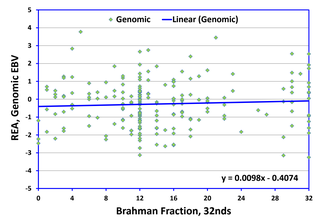


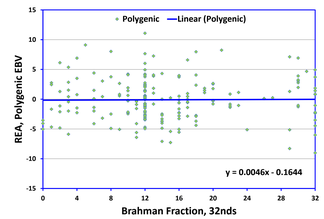


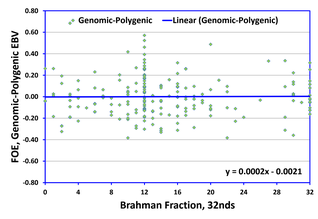


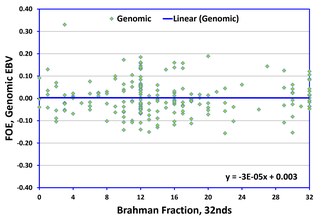


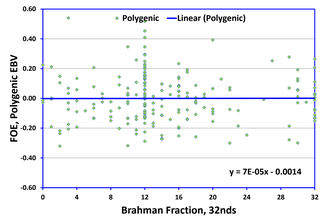


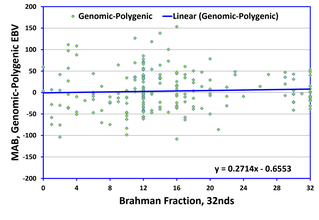


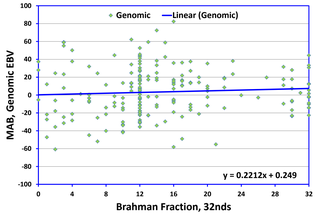


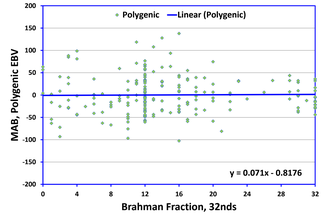












FINAL REMARKS

The low fractions of additive genetic variances accounted for by the Illumina3k chip indicated that GP models would need to be used to compute EBV if this chip were used to help predict animal EBV, and that higher density chips would be needed to more thoroughly account for additive genetic variation in Angus-Brahman multibreed populations.

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