Abstract T202

Genomic-polygenic evaluation of multibreed Angus-Brahman cattle for feed efficiency and postweaning growth using actual and imputed Illumina50k SNP genotypes

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SUMMARY

The objectives were to estimate the fractions of additive genetic variances for 4 postweaning feed efficiency and growth traits explained by 46,909 actual and imputed SNP genotypes, to compare EBV rankings from genomic-polygenic (GP), genomic (G), and polygenic (P) models, and to determine EBV trends from Angus to Brahman in a multibreed population. Traits were residual feed intake (RFI), daily feed intake (DFI), feed conversion ratio (FCR), and weight gain (PWG). Phenotypes were from 807 bull, heifer, and steer calves measured at the Feed Efficiency Facility of the University of Florida from 2006 to 2010. Imputation from 2,899 SNP (Illumina3k) to 46,909 SNP (Illumina50k) was done with program findhap2 using a reference population of 828 Brangus heifers. Fixed effects for all models 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 (GP and G models), additive polygenic (GP and P models), and residual. Software GS3 was used to compute variance components and heritabilities (option VCE; Markov Chain Monte Carlo), and EBV (option BLUP). ***Heritabilities were 0.31 for RFI, 0.38 for DFI, 0.25 for FCR, and 0.34 for PWG. The fractions of additive genetic variances explained by the 46,909 actual and imputed SNP were 0.46 for RFI, 0.36 for DFI, 0.47 for FCR, and 0.28 for PWG. These fractions were 3.0, 3.2, 1.9, and 1.8 times larger than those obtained for these 4 traits using the 2,899 SNP from the Illumina3k chip. Rank correlations between EBV from GP and P and from GP and G models were high (0.89 to 0.98; P < 0.0001). Lower rank correlations existed between EBV from G and P models (0.69 to 0.81; P < 0.0001). Regressions of EBV on Brahman fraction were negative with the G model for DFI (P < 0.0344) and with all models for PWG (P < 0.0171 to P < 0.0001). This suggested that calves of similar EBV for RFI, DFI and FCR existed in all breed compositions, but EBV for PWG tended to decrease as Brahman fraction increased.***

INTRODUCTION

Utilization of chips with SNP markers evenly distributed across the genome to aid genetic evaluation of beef and dairy cattle has increased substantially in recent years. However, high-density (e.g., Illumina50k, Illumina90k, IlluminaHD) chip costs have remained high limiting its widespread utilization by the cattle industry. Another option is to use less expensive low density chips (e.g., Illumina3k, Illumina7k, Illumina9k). However, the amount of additive genetic variation for postweaning feed efficiency, growth, and ultrasound carcass traits explained by the Illumina3k chip in an Angus-Brahman multibreed population was found to be lower than that explained by the Illumina50k chip in other beef cattle populations (Elzo et al., 2012a, b). An alternative to increase the fraction of additive genetic variation as well as the accuracy of genomic and genomic-polygenic EBV is imputation of SNP from low density to higher density chips. Thus, ***the objectives of this research were: 1) to estimate the fractions of additive genetic variances for 4 postweaning feed efficiency and growth traits explained by 46,909 actual and imputed SNP genotypes, 2) to compare EBV rankings from genomic-polygenic (GP), genomic (G), and polygenic (P) models, and 3) to determine GP, G, and P EBV trends from Angus to Brahman in a multibreed population under subtropical conditions.***

MATERIALS AND METHODS

Animals and Data. Calves (n = 807) belonged to the multibreed Angus-Brahman (MAB) herd of the University of Florida, Gainesville. They were produced by a diallel-mating plan involving 61 sires and 365 dams from 6 mating groups: 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. Calves were born from 2006 to 2010 (65 bulls, 409 heifers, and 333 steers). Calf numbers by breed group of calf were: 123 Angus, 164 ¾ A ¼ B, 141 Brangus, 190 ⅛A ⅛B, 86 ¼ A ¾ B, and 103 Brahman (Table 1). ***Traits were postweaning phenotypic residual feed intake (RFI, kg DM*day^{-1}), daily feed intake (DFI, kg DM*day^{-1}), feed conversion ratio (FCR, kg DM*day^{-1}/kg weight gain*day^{-1}), and postweaning weight gain (PWG, kg).*** Feed intake and weights were recorded at the UF Feed Efficiency Facility. Postweaning phenotypic residual feed intake was computed as the difference between expected and actual average DFI during a 70-day feeding trial (Koch et al., 1963; Arthur et al., 2001; Archer et al., 1997).

Feeding and Management. Calves were born and kept at the Beef Research Unit of the University of Florida (UF) until were moved to the UF Feed Efficiency Facility (UFFEF, Marianna, Florida). They received a preconditioning diet for 3 to 4 weeks before transportation to the UFFEF. The preconditioning diet included 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. The feed efficiency trial at UFFEF had an adjustment period of 21 d and a trial period of 70 d. Calves were allocated to pens at UFFEF (108 m^2/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) by sex (bull, heifer, and steer) subclasses (mean stocking rate = 15 calves/pen and 7.5 calves/GrowSafe node). Calves were identified using half-duplex passive transponder ear tags (Allflex USA Inc., Dallas-Fort Worth, TX). The UFFEF ration was offered ad libitum and contained whole corn or corn gluten, cottonseed hulls, molasses, chopped grass hay, and a vitamin-mineral-protein supplement. The UFFEF ration supplied from 2006 to 2010 had a mean of 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 using EDTA vacutainer tubes at weaning. Samples were kept at 4°C before shipping to Dr. M. Thomas laboratory at New Mexico State University for processing and storage (-80 °C). Tubes were centrifuged (1,875 x g at 4°C for 30 min) to get the white blood cell supernatant (buffy coat) and PBS added up to a volume of 1.0 mL. A volume of 0.05 mL of each sample was forwarded to GeneSeek (GeneSeek, Lincoln, NE, USA) for DNA extraction and genotyping with the Illumina Bovine3K BeadChip (Illumina, 2011).

Imputation and Datasets. Imputation of SNP from the Illumina3k to the Illumina50k chip was done using program findhap2 (VanRaden, 2011) and a reference population of 828 Brangus heifers. This resulted in ***807 calves with phenotypic data for RFI, DFI, FCR, and PWG (Table 1) and genotypic information for 46,909 actual and imputed genotypes.*** The pedigree file had 5,864 animals.

Variance Components. Estimates of variance components for RFI, DFI, FCR, and PWG were obtained using ***genomic-polygenic models.*** 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), calf additive polygenic (AP; mean zero; variance = A*Vg; A = additive relationship matrix, Vg = additive polygenic variance), and residual (mean zero, common variance). *Variance components and heritabilities were estimated using Markov Chain Monte Carlo with option VCE of program GS3 (Legarra, 2009; Number of iterations = 120,000; Burn-in = 20,000; Thinning = 100; Correction = 10,000). Total additive genetic variances (**VGTot**) were computed as the sum of additive genomic (**VAGO**) and additive polygenic (**VAPO**) variances, where **VAGO** = 2*[sum(p$_i$q$_i$), i = 1,…, 46,909)] times additive SNP variance (Gianola et al., 2009).*

EBV. Program GS3 was used to compute calf EBV using genomic-polygenic, genomic, and polygenic models with option BLUP (Gauss-Seidel iteration; convergence criterion = 10^{-4}). Genomic models ignored additive polygenic effects, and polygenic models omitted additive SNP effects. *Calf EBV were: 1) calf breed effect + calf genomic value + calf polygenic value from genomic-polygenic models, where calf breed effect = calf Brahman fraction * solution (Brahman – Angus), calf genomic value = sum (number of "2" alleles x SNP value), for i = 1, …, 46,909); 2) calf breed effect + calf genomic value from genomic models; and 3) calf breed effect + calf polygenic value from polygenic models.* Calf rankings across models were compared using Spearman's rank correlations. Calf EBV trends from Angus to Brahman were evaluated using linear regressions of genomic-polygenic, genomic, and polygenic EBV on Brahman fraction.

RESULTS AND DISCUSSION

Table 1 shows means and SD by calf breed group and all calves. Table 2 presents posterior means and SD for additive genomic (VAGO), additive polygenic (VAPO), total additive (VGTot) and phenotypic variances (PhenVar) from ***genomic-polygenic models*** for RFI, DFI, FCR, and PWG. ***For comparison purposes, the last 2 rows of*** Table 2 contain additive polygenic (VGPO) and phenotypic variances from ***polygenic models*** for these 4 traits. Estimates for VAGO were 1.7 (PWG) to 5.2 times (RFI) those obtained with the Illumina3k chip in a previous analysis (Elzo et al., 2012), whereas VAPO and PhenVar estimates were similar. Thus, ***imputation from the Illumina3k to the Illumina50k increased the fraction of additive genetic variation explained by SNP in this multibreed population.***

Table 1. Number of calves, means and SD by breed group of calf

Breed Group Of Calf	N	Trait[1] RFI Mean	RFI SD	DFI Mean	DFI SD	FCR Mean	FCR SD	PWG Mean	PWG SD
Angus	123	-0.24	1.25	8.26	2.08	7.78	2.18	78.19	22.64
¾ A ¼ B	164	0.04	1.45	8.68	2.19	8.29	2.70	78.21	22.46
Brangus	141	0.10	1.48	8.57	2.08	8.23	2.60	77.57	20.67
½ A ½ B	190	0.10	1.50	8.60	2.21	8.41	2.89	73.41	22.10
¼ A ¾ B	86	0.15	1.13	8.80	1.81	8.65	2.41	75.14	18.22
Brahman	103	-0.25	1.17	7.74	2.04	9.36	3.04	62.18	17.85
All	807	-0.00	1.38	8.47	2.12	8.41	2.70	74.59	21.68

[1]RFI, kg DM*d^{-1} = residual feed intake; DFI, kg DM*d^{-1} = mean daily feed intake; FCR, kg DM*d^{-1}/kg gain*d^{-1} = mean daily feed conversion ratio; PWG, kg = postweaning gain.

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

Variance[2]	Trait[1] RFI	DFI	FCR	PWG
VAGO	0.27 ± 0.18	0.32 ± 0.21	0.81 ± 0.48	23.9 ± 17.9
VAPO	0.28 ± 0.13	0.54 ± 0.19	0.89 ± 0.44	59.2 ± 20.3
VGTot	0.55 ± 0.19	0.86 ± 0.25	1.69 ± 0.60	83.1 ± 25.0
PhenVar	1.79 ± 0.10	2.29 ± 0.13	6.60 ± 0.47	246.3 ± 14.0
VGPO	0.31 ± 0.14	0.58 ± 0.19	0.93 ± 0.45	62.1 ± 20.3
PhenVarPO	1.75 ± 0.09	2.25 ± 0.12	6.37 ± 0.34	241.9 ± 13.2

[1]RFI, (kg DM*d^{-1})^2 = residual feed intake; DFI, (kg DM*d^{1})^2 = mean daily feed intake; FCR, (kg DM*d^{-1}/kg gain*d^{1})^2 = mean daily feed conversion ratio; PWG, kg^2 = postweaning gain.
[2]VAGO = additive genomic variance; VAPO = additive polygenic variance; VGTot = VAGO + VAPO; PhenVar = phenotypic variance; VGPO = additive genetic variance from a polygenic model; PhenVarPO = phenotypic variance from a polygenic model.

Variance Ratios. Table 3 shows posterior means and SD for additive genomic and additive genetic variance ratios. ***Ratios of VAGO to VGTot for RFI, DFI, FCR, and PWG were 3.0, 3.2, 1.9, and 1.8 times larger than those obtained using 2,899 SNP from the Illumina3k chip*** (Elzo et al., 2012). The additional additive genetic variation accounted for by imputed SNP for RFI and DFI was 1.5 times larger than for FCR and PWG. This resulted in heritabilities that were either similar (PWG) or between 20% (DFI and FCR) and 60% larger (RFI) with 46,909 actual and imputed 50k genotypes. ***Heritabilities from genomic-polygenic models were 2.07 (RFI), 1.46 (DFI), 1.67 (FCR), and 1.31 times (PWG) larger than those from polygenic models. This suggested that a larger amount of genetic variation was explained by genomic-polygenic model than by the polygenic model. Thus, utilization of EBV from genomic-polygenic models using actual and 3k to 50k imputed SNP may result in higher selection responses for feed efficiency and growth traits in this multibreed population.***

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

Variance Ratios[2]	Trait[1] RFI	DFI	FCR	PWG
VAGO/VGTot	0.46 ± 0.20	0.36 ± 0.18	0.47 ± 0.18	0.28 ± 0.17
VAGO/PhenVar	0.15 ± 0.09	0.14 ± 0.09	0.12 ± 0.07	0.10 ± 0.07
Heritability	0.31 ± 0.10	0.38 ± 0.10	0.25 ± 0.08	0.34 ± 0.09
HeritabilityPO	0.18 ± 0.07	0.26 ± 0.08	0.15 ± 0.07	0.26 ± 0.08

[1]RFI = residual feed intake; DFI = mean daily feed intake; FCR = mean daily feed conversion ratio; PWG = postweaning gain.
[2]VAGO = additive genomic variance; VAPO = additive polygenic variance; VGTot = VAGO + VAPO; PhenVar = phenotypic variance; HeritabilityPO = heritability from a polygenic model.

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

Correlation[2]	Trait[1] RFI	DFI	FCR	PWG
GP Model, G Model	0.93	0.91	0.89	0.89
GP Model, P Model	0.94	0.97	0.93	0.98
G Model, P Model	0.77	0.80	0.69	0.81

[1]RFI = residual feed intake; DFI = mean daily feed intake; FCR = mean daily feed conversion ratio; PWG = postweaning gain.
[2]GP Model = genomic-polygenic model; G Model = genomic model; P Model = polygenic model. All rank correlations were significant (P < 0.0001).

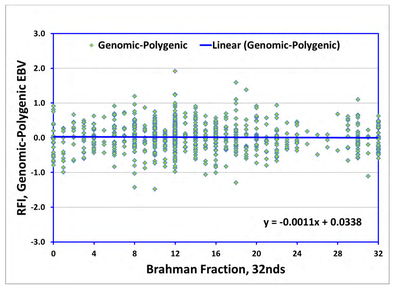
Table 5. Linear regression coefficients for genomic-polygenic, genomic, and polygenic EBV on Brahman fraction of calf

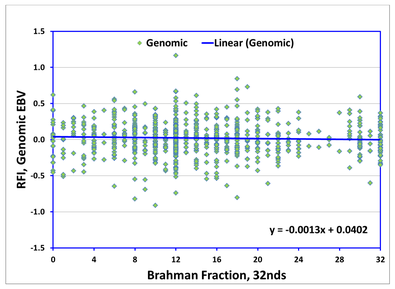
Prediction	Trait[1] RFI	DFI	FCR	PWG
Genomic-Polygenic	-0.0011	-0.0035	0.0010	-0.0748
	P < 0.5453	P < 0.1513	P < 0.7199	P < 0.0012
Genomic	-0.0013	-0.0025	-0.0004	-0.0203
	P < 0.1967	P < 0. 0344	P < 0.7761	P < 0.0171
Polygenic	0.0005	-0.0016	0.0025	-0.0769
	P < 0.6814	P < 0.4259	P < 0.1985	P < 0.0001

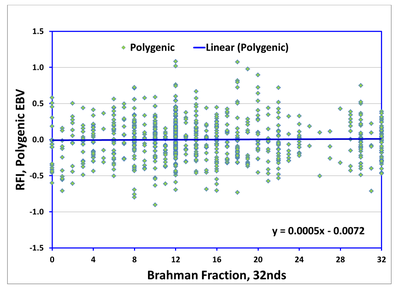
[1]RFI = residual feed intake; DFI = mean daily feed intake; FCR = mean daily feed conversion ratio; PWG = postweaning gain.

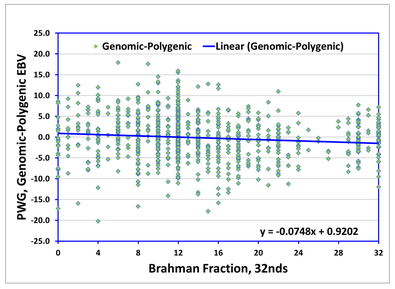
Rank Correlations. Table 4 contains Spearman's rank correlations between calf EBV rankings from GP and G models, GP and P models, and G and P models for RFI, DFI, FCR, and PWG. Rank correlations between calf EBV from the GP and P models had the highest values (0.93 to 0.98; P < 0.0001), those between calf EBV from GP and G models were somewhat lower (0.89 to 0.93; P < 0.0001), and the lowest ones were between calf EBV from the G and P models (0.69 to 0.81; P < 0.0001). *Rank correlations between GP and P models were similar to but those from the GP and G models were from 20% (PWG) to 47% (DFI) higher and those between G and P models were from 25% (PWG) to 64% (FCR) higher than rank correlations between calf EBV from the Illumina3k (Elzo et al., 2012). The average increment in rank correlation values was twice as large for RFI, DFI, and FCR as for PWG.* Thus, ***imputation from Illumina3k to 50k substantially increased rank correlations between calf EBV from GP and G and from G and P models for all traits.***

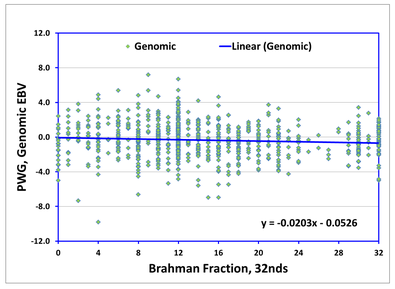
EBV Trends from Angus to Brahman. Regressions of EBV on Brahman fraction were negative with the G model for DFI (P < 0.0344) and with all models for PWG (P < 0.0171 to P < 0.0001) and non-significant for all other model by trait combinations (Table 5). ***This suggested that calves of similar EBV for RFI, DFI and FCR existed in all breed compositions, but EBV for PWG tended to decrease as Brahman fraction increased.***

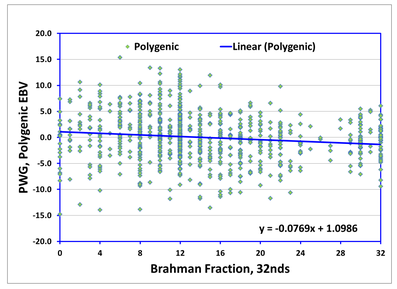












FINAL REMARKS

Imputation from the Illumina3k to 50k with SNP information from Brangus cattle increased both the explained fraction of additive genetic variation and the predictive ability of genomic models in this Angus-Brahman multibreed population.

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