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Genomic-polygenic and genomic predictions of direct and maternal effects for growth traits in a multibreed Angus-Brahman cattle population

M. A. Elzo*, M. G. Thomas‡, D. D. Johnson*, C. A. Martinez*, G. C. Lamb *, D. O. Rae *, J. G. Wasdin*, and J. D. Driver*

* University of Florida, Gainesville, FL; ‡Colorado State University, Fort Collins, CO

SUMMARY

The objectives of this research were to compare variance components, genetic parameters, and EBV rankings for birth weight (BW) direct and maternal, weaning weight (WW) direct and maternal, and postweaning gain from 205 d to 365 d (WG) direct using three genomic-polygenic and one polygenic model. In addition, trends in EBV were evaluated for each trait and model as Brahman fraction increased from 0% to 100%. The Angus-Brahman multibreed dataset included 5,264 animals born between 1987 and 2013. Genomic-polygenic models 1 (GP1; pedigree relationships for all animals; genomic relationships for genotyped animals), 2 (GP2; pedigree relationships for non-genotyped animals only; genomic relationships for genotyped animals), and 3 (GP3; no pedigree relationships; genomic relationships for genotyped animals) used actual and imputed genotypes from 46,768 SNP markers. Variance components and genetic parameters were estimated using REML procedures. Estimates of variance components and genetic parameters from GP1 were the most similar to those obtained with the polygenic model, followed by those from GP2, and the least similar (particularly for maternal traits) were those from GP3. Similarly, the highest rank correlations were those between animal EBV from the polygenic model and GP1, followed by those from GP1 and GP2 and lastly by those from the polygenic model and GP2. Model GP3 performed poorly for maternal traits due to ignoring calf-dam relationships. *These results indicated that the polygenic model and genomic-polygenic model 1 should be preferred. High genotyping costs could still make the polygenic model preferable for commercial beef cattle operations. Brahman animals tended to have higher EBV for BW direct and WW direct, and lower EBV for WG direct, BW maternal, and WW maternal. However, low regression coefficients for EBV on Brahman fraction ensured that high, medium, and low EBV animals from all breed compositions existed for all growth traits in this multibreed population.*

INTRODUCTION

Utilization of genotype information for genetic evaluation of cattle has become widespread in cattle. Implementation of genomic evaluation methodology was greatly facilitated by the development of the single-step genomic evaluation procedure and its associated software (Aguilar et al., 2010). This unified procedure made possible to extend the application of genomic procedures to traits with complex models such as preweaning weights in beef cattle that require the inclusion of direct and maternal effects. Considering the current beef cattle national genetic evaluation system in the US, genomic and polygenic models for growth traits need to be compared using information from multibreed populations. *Thus, the objectives of this research were: 1) to compare variance components and genetic parameters (heritabilities, correlations) for birth weight direct and maternal, weaning weight direct and maternal, and postweaning gain direct using genomic-polygenic and polygenic models; 2) to compare rankings of animals for birth weight direct and maternal, weaning weight direct and maternal, and postweaning gain direct using genomic-polygenic and polygenic models; and 3) to evaluate EBV trends for each trait computed using genomic-polygenic and polygenic models as Brahman fraction increased from 0% to 100% in a multibreed Angus-Brahman population under subtropical environmental conditions.*

MATERIALS AND METHODS

Animals and Data. *Animals were from the multibreed Angus-Brahman (MAB) herd of the University of Florida, Gainesville.* Calves were produced by a diallel-mating plan involving 61 sires and 365 dams from 6 mating groups: BG1 = (1.0 to 0.80) A (0.0 to 0.20) B, BG2 = (0.79 to 0.60) A (0.21 to 0.40) B, BG3 = (0.625) A (0.375) B, BG4 = (0.59 to 0.40) A (0.41 to 0.60) B, BG5 = (0.39 to 0.20) A (0.61 to 0.80) B, and BG6 = (0.19 to 0.0) A (0.81 to 1.00) B. Calves (n = 5,264; 2,689 bulls and 2,575 heifers) were the progeny of 293 sires (54 BG1, 37 BG2, 60 BG3, 35 BG4, 38 BG5, and 69 BG6) and 1,725 dams (291 BG1, 249 BG2, 254 BG3, 349 BG4, 200 BG5, and 282 BG6) born from 1987 to 2013. *There were 5,264 calves with birth weights (BW, kg; 2,689 bulls and 2,575 heifers), 5,262 calves with weaning weights adjusted to 205 d of age (WW, kg; 614 bulls, 2,573 heifers, and 2,075 steers), and 3,846 calves with postweaning gains from 205 d to 365 d of age (WG, kg; 209 bulls, 1,784 heifers, and 1,853 steers).* Number of calves per breed group, means, and SD for BW, WW, and WG are presented in Table 1.

Feeding and Management. Calves stayed at the Pine Acres Research Station (1987 to 1994) and at the Beef Research Unit (1995 to 2013) of the University of Florida from birth (December to March) to weaning (August, September). Preweaning, cows and calves were kept in bahiagrass pastures (*Paspalum notatum*) with access to a complete mineral supplement (UF University Special Hi-Cu Mineral, University of Florida, Animal Science Department, Gainesville, Florida). They also received a supplement of bermudagrass (*Cynodon dactylon*) hay and cotton seed (*Gossypium spp.*) meal during winter (mid-December to mid-March). Postweaning, calves were kept in bahiagrass pastures supplemented with bahiagrass hay, concentrate (1.6 kg to 3.6 kg per day; 14.0 % CP; 488 Pellet Medicated Weaning Ration, Lakeland Animal Nutrition, Lakeland, Florida; soy hull pellets), and free access to mineral supplement. During the years (2006 to 2010) that calves were taken to the University of Florida Feed Efficiency Facility (UFFEF), they were randomly allocated to pens within sire group (BG1 to BG6) by sex category (bull, heifer, and steer). Calves at UFFEF were fed a diet of whole corn or corn gluten, cottonseed hulls, molasses, chopped grass hay, and a vitamin-mineral-protein supplement (FRM, Bainbridge, GA; mean dry matter = 12.9%, mean crude protein = 98.2%, mean net energy for maintenance = 1.6 mcal/kg DM, and mean net energy for gain = 1.0 mcal/kg DM).

Tissue Sampling and Genotyping. Tissue samples (blood, semen) from 1,232 animals from the MAB herd were collected at the Beef Research Unit of the University of Florida from 2006 to 2010. There were samples from 161 parents (20 sires and 141 dams) and 1,071 progeny (109 bulls, 613 heifers, and 349 steers). Tissue samples were processed and stored at -80 °C at New Mexico State University. Samples were centrifuged for 30 min at 1,875 g at 4°C, followed by retrieval of the white blood cell supernatant, and addition of sterile phosphate-buffered saline up to a volume of 1.0 mL (Beauchemin et al., 2006). Samples were forwarded to GeneSeek (Gene Seek, Inc., Lincoln, NE, USA) in 2010 for genotyping with the Illumina3k genotyping beadchip.

Imputation. Multibreed animals genotyped with the Illumina3k chip were imputed to Illumina50k with software findhap2 (VanRaden, 2011) using a reference population of 828 Brangus heifers previously genotyped with version 1 of the Illumina50k chip (Peters et al., 2012).

Variance Components, Variance Ratios, and EBV. Three multiple-trait genomic-polygenic models (**GPM**) and a polygenic model (**PM**) were used to obtain variance components, heritabilities, and genetic, environmental and phenotypic correlations for BW direct, BW maternal, WW direct, WW maternal, and WG direct. The three multiple-trait genomic-polygenic models were: ***1) GPM1 = single-step model (Aguilar et al., 2010) with genotypic information and pedigree relationships among all animals 2) GPM2 = single-step model with genotypic information and pedigree relationships only for animals without genotypic information;*** and ***3) GPM3 = single-step model with genotypic information and no pedigree relationships among animals.*** The fixed effects for the three genomic-polygenic models and the polygenic model were: 1) contemporary group (location-year for BW and WW direct and maternal; location-year-pen subclass for WG); 2) age of dam (all traits); 3) sex of calf (males and females for BW, and bulls, heifers, and steers for WW and WG; and 4) direct heterosis for all traits as a function of calf heterozygosity (i.e., the probability of having Angus and Brahman alleles in 1 locus); and 5) maternal heterosis for BW and WW as a function of dam heterozygosity. Random effects were direct additive genetic for BW, WW, and WG, maternal additive genetic for BW and WW, and residual for BW, WW, and WG. ***Variance components were estimated using REML procedures with an average information algorithm (Gilmour et al., 1995).*** Standard errors of covariance estimates were computed with the inverse of the average information matrix. Standard deviations of 5,000 samples were computed for functions of variance components (Meyer and Houle, 2013). ***Estimated breeding values (EBV) were computed for 5,190 animals (genotyped = 1,232, non-genotyped = 3,958) and genotyped animals using all models. Computations utilized program AIREMLF90 of the BLUPF90 family of programs (Misztal et al., 2002). Correspondence among EBV from the four models was assessed using rank correlations.***

RESULTS AND DISCUSSION

Estimates of additive genetic variances and covariances from genomic-polygenic model 1 were, on the average, slightly larger than those from the polygenic model (mean difference = 3.25 kg^2; Table 2). ***Thus, the inclusion of genotypic information had little effect on estimates of variance components for growth traits in this multibreed population. Conversely, exclusion of pedigree information from genotyped animals (genomic-polygenic model 2) and from all animals (genomic-polygenic model 3) yielded lower estimates of variance and covariance components than estimates from the polygenic model*** (mean difference = -9.15 kg2 for model 2 and -27.27 kg2 for model 3).

The opposite occurred for environmental variances and covariances across models (Table 3). Estimates of environmental variances and covariances for BW, WW, and WG were, on the average, ***slightly lower for genomic-polygenic model 1*** (mean difference = -2.32 kg2), and ***higher for genomic-polygenic models 2*** (mean difference = 12.56 kg2) ***and 3*** (mean difference = 46.33 kg2) than estimates from the polygenic model.

Estimates of phenotypic variances and covariances (Table 4) followed the same pattern across models as additive genetic variance components. Estimates of phenotypic variances and covariances for BW, WW, and GW from genomic-polygenic model 1 were slightly higher (mean difference = 4.25 kg2), whereas those from genomic-polygenic models 2 (mean difference = -11.92 kg2) and 3 (mean difference = -19.92 kg2) were lower than those from the polygenic model. ***Thus, ignoring pedigree relationships among genotyped animals (model 2) or all pedigree relationships (model 3) resulted in underestimation of phenotypic variances and covariances.***

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

	Trait[1]								
	BW, kg			WW, kg			WG, kg		
Breed Group	N	Mean	SD	N	Mean	SD	N	Mean	SD
BG1	764	31.6	5.6	764	210.5	32.5	576	75.2	62.7
BG2	792	31.9	5.5	792	221.1	30.6	625	83.1	61.2
BG3	730	33.7	6.1	728	217.2	33.3	531	83.1	62.5
BG4	1,338	33.8	6.4	1,338	223.8	29.1	944	79.9	58.9
BG5	722	34.6	6.4	722	221.3	31.5	574	71.4	54.2
BG6	918	33.7	6.1	918	207.6	30.5	596	72.3	53.0
Total	5,264	33.3	6.1	5,262	217.4	31.6	3,846	77.7	59.0

[1]BW = Birth weight; WW = Weaning weight adjusted to 205 d of age; WG = Postweaning gain from 205 d to 365 d of age.

Variance Ratios. ***The pattern for estimates of variance ratios mimicked the one for estimates of variance components.*** **Heritabilities and genetic correlations** (Table 5) from genomic-polygenic model 1 and the polygenic model were very similar (mean difference = 0.01), while mostly lower estimates were obtained with genomic-polygenic models 2 (mean difference = -0.04) and 3 (mean difference = -0.06). **Environmental correlations** (Table 6) from genomic-polygenic model 1 were nearly identical to those of the polygenic model (mean difference = -0.003), whereas those from genomic-polygenic models 2 (mean difference = 0.05) and 3 (mean difference = 0.18) tended to be somewhat higher than estimates from the polygenic model. **Phenotypic correlations** (Table 7) from genomic-polygenic model 1 and the polygenic model were nearly identical (mean difference = 0.003), but slightly lower estimates were computed with genomic-polygenic models 2 (mean difference = -0.013) and 3 (mean difference = -0.020) than with the polygenic model.

Table 2. REML estimates of direct and maternal additive genetic variance and covariance components for growth traits

	Additive genetic covariances, kg^2							
Trait pair	GPM1	SE	GPM2	SE	GPM3	SE	PM	SE
BWD, BWD	17.90	1.92	20.93	2.20	10.42	0.14	19.56	2.03
BWD,WWD	42.25	6.36	48.06	6.94	18.50	0.45	45.60	5.72
BWD, WGD	2.47	7.81	-3.23	9.47	-9.85	0.43	0.75	7.86
BWD, BWM	-4.49	1.08	-6.19	1.30	-1.40	0.11	-5.64	1.14
BWD, WWM	-5.64	4.50	-11.07	5.25	5.79	0.29	-8.83	4.38
WWD, WWD	266.10	33.53	246.83	33.52	173.35	2.39	259.32	20.37
WWD, WGD	139.91	35.35	49.01	39.33	49.76	1.78	132.31	33.89
WWD, BWM	0.63	4.10	-2.22	4.54	15.43	0.48	-1.65	4.00
WWD, WWM	11.02	20.08	-21.18	21.97	-2.00	1.18	11.40	17.22
WGD, WGD	274.86	52.77	243.31	55.04	178.72	2.46	266.95	49.58
WGD, BWM	19.27	5.87	9.06	8.13	-2.39	0.47	19.09	5.65
WGD, WWM	56.11	28.36	75.07	36.02	9.71	1.20	43.04	26.61
BWM, BWM	8.21	0.92	8.45	1.07	12.72	0.18	8.63	0.93
BWM, WWM	12.41	3.17	12.88	3.61	4.97	0.32	13.47	3.10
WWM, WWM	164.92	19.34	150.16	21.35	84.42	1.16	153.17	17.83

Table 3. REML estimates of environmental variance and covariance components

	Environmental variances and covariances, kg^2							
Trait pair	GPM1	SE	GPM2	SE	GPM3	SE	PM	SE
BWE, BWE	12.00	1.07	10.308	1.26	10.32	0.20	11.21	1.11
BWE,WWE	19.19	3.61	15.334	4.09	31.72	1.08	17.63	3.03
BWE, WGE	8.50	5.43	15.314	6.54	26.62	5.68	9.56	5.22
WWE, WWE	300.95	19.88	320.53	21.41	411.40	5.70	307.84	6.59
WWE, WGE	-38.67	25.05	12.291	28.76	33.10	7.00	-33.02	24.08
WGE, WGE	542.96	42.87	560.41	50.18	623.62	12.15	545.61	40.63

Table 4. REML estimates of phenotypic variance and covariance components

	Phenotypic variances and covariances, kg^2							
Trait pair	GPM1	SE	GPM2	SE	GPM3	SE	PM	SE
BWP, BWP	33.62	0.86	33.50	0.82	32.06	0.30	33.75	0.87
BWP,WWP	71.34	3.21	69.63	2.84	65.81	1.26	71.46	3.12
BWP, WGP	20.61	4.90	16.62	4.74	15.57	5.77	19.86	4.86
WWP, WWP	742.99	20.28	696.34	16.47	667.17	6.37	731.73	19.37
WWP, WGP	129.30	24.31	98.83	22.16	87.72	7.23	120.81	23.79
WGP, WGP	817.82	35.31	803.72	32.94	802.34	12.32	812.56	34.34

Table 5. REML estimates of direct and maternal heritabilities and additive genetic correlations for growth traits

	Heritabilities and Additive Genetic Correlations							
Trait pair	GPM1	SD	GPM2	SD	GPM3	SD	PM	SD
BWD, BWD	0.53	0.05	0.62	0.06	0.32	0.004	0.58	0.05
BWD,WWD	0.61	0.06	0.67	0.06	0.44	0.008	0.64	0.05
BWD, WGD	0.04	0.11	-0.05	0.14	-0.23	0.009	0.01	0.11
BWD, BWM	-0.37	0.07	-0.47	0.06	-0.12	0.01	-0.43	0.06
BWD, WWM	-0.10	0.08	-0.20	0.09	0.20	0.009	-0.16	0.08
WWD, WWD	0.36	0.04	0.35	0.04	0.26	0.004	0.35	0.02
WWD, WGD	0.52	0.12	0.20	0.16	0.28	0.009	0.50	0.11
WWD, BWM	0.01	0.09	-0.05	0.10	0.33	0.009	-0.03	0.09
WWD, WWM	0.05	0.10	-0.11	0.11	-0.02	0.01	0.06	0.09
WGD, WGD	0.34	0.06	0.30	0.06	0.22	0.004	0.33	0.05
WGD, BWM	0.41	0.13	0.20	0.19	-0.05	0.01	0.40	0.12
WGD, WWM	0.26	0.14	0.39	0.20	0.08	0.01	0.21	0.13
BWM, BWM	0.24	0.03	0.25	0.03	0.40	0.005	0.26	0.03
BWM, WWM	0.34	0.07	0.36	0.08	0.15	0.01	0.37	0.07
WWM, WWM	0.22	0.02	0.22	0.03	0.13	0.002	0.21	0.02

Table 6. REML estimates of environmental correlations for growth traits

	Environmental correlations							
Trait pair	GPM1	SD	GPM2	SD	GPM3	SD	PM	SD
BWE,WWE	0.32	0.05	0.27	0.06	0.49	0.01	0.30	0.04
BWE, WGE	0.11	0.07	0.20	0.09	0.33	0.07	0.12	0.07
WWE, WGE	-0.10	0.06	0.03	0.09	0.07	0.01	-0.08	0.06

Table 7. REML estimates of phenotypic correlations for growth traits

	Phenotypic correlations							
Trait pair	GPM1	SD	GPM2	SD	GPM3	SD	PM	SD
BWP,WWP	0.45	0.01	0.46	0.01	0.45	0.007	0.45	0.01
BWP, WGP	0.12	0.03	0.10	0.03	0.10	0.04	0.12	0.03
WWP, WGP	0.17	0.05	0.13	0.03	0.12	0.01	0.16	0.03

Rank Correlations. ***Rank correlations clearly showed a high degree of agreement between animal rankings from the polygenic model and genomic-polygenic model 1. This indicated that these two models not only accounted for direct and maternal additive genetic variation for growth traits similarly, but that they also yielded predicted values that ranked animals similarly.*** Genomic-polygenic model 2 was a close second, and genomic-polygenic model 3 showed a lower level of agreement for additive direct genetic effects and a dismal performance for maternal effects likely due to assuming calves and dams to be pedigree unrelated.

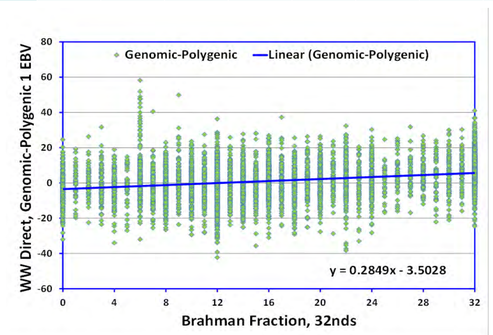
EBV Trends from Angus to Brahman. ***Regression coefficients indicated that Brahman animals tended to have higher EBV for BW direct and WW direct, and lower EBV for WG direct, BW maternal, and WW maternal.*** However, although significant (P < 0.0001), ***all regressions were low with all models indicating that animals with high, medium, and low EBV existed in this multibreed population.***

Table 8. Rank correlations between animal EBV from polygenic and genomic-polygenic models for the top 5%, 10%, 25%, and all evaluated animals

		Rank correlations					
Trait	Top	GPM1, GPM2	GPM1, GPM3	GPM1, PM	GPM2, GPM3	GPM2, PM	GPM3, PM
BWD	5%	0.61	0.40	0.90	0.73	0.66	0.47
	10%	0.69	0.54	0.93	0.75	0.74	0.59
	25%	0.78	0.58	0.96	0.64	0.82	0.59
	100%	0.93	0.78	0.99	0.87	0.94	0.80
WWD	5%	0.72	0.49	0.95	0.47	0.76	0.51
	10%	0.72	0.48	0.96	0.54	0.74	0.49
	25%	0.77	0.57	0.96	0.64	0.79	0.59
	100%	0.94	0.85	0.99	0.87	0.94	0.85
WGD	5%	0.46	0.35	0.88	0.68	0.47	0.36
	10%	0.55	0.36	0.90	0.67	0.55	0.40
	25%	0.58	0.38	0.91	0.59	0.56	0.41
	100%	0.82	0.56	0.98	0.67	0.81	0.56
BWM	5%	0.45	0.04ns	0.83	-0.08ns	0.46	-0.04ns
	10%	0.38	0.03ns	0.86	-0.11*	0.45	-0.04ns
	25%	0.50	0.06*	0.90	-0.13	0.53	-0.04ns
	100%	0.85	-0.08	0.98	-0.19	0.84	-0.12
WWM	5%	0.38	0.11ns	0.88	-0.04ns	0.28	0.06ns
	10%	0.40	0.15	0.89	-0.01ns	0.34	0.10*
	25%	0.53	0.13	0.92	-0.01ns	0.47	0.06*
	100%	0.83	0.26	0.98	0.15	0.82	0.23

Table 9. Linear regression coefficients of EBV from genomic-polygenic and polygenic models on Brahman fraction of animal

	Linear regression coefficient, kg/32nds Brahman fraction							
Trait	GPM1	SE	GPM2	SE	GPM3	SE	PM	SE
BWD	0.18	0.004	0.15	0.005	0.04	0.003	0.17	0.005
WWD	0.29	0.017	0.25	0.016	0.08	0.011	0.27	0.017
WGD	-0.29	0.014	-0.13	0.011	-0.09	0.008	-0.25	0.014
BWM	-0.12	0.002	-0.10	0.002	0.02	0.002	-0.12	0.002
WWM	-0.13	0.010	-0.09	0.010	0.03	0.003	-0.14	0.010



FINAL REMARKS

- Genomic-polygenic model 1 and the polygenic model yielded similar estimates of variance components and genetic parameters for all growth traits.
- High rank correlations existed between EBV from genomic-polygenic model 1 and the polygenic model .
- Brahman animals tended to have higher EBV for BW direct and WW direct, and lower EBV for WG direct, BW maternal, and WW maternal.

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