

NONADDITIVE GENETIC VARIABILITY IN *BOS TAURUS*-*BOS INDICUS* MULTIBREED HERDS OF BEEF CATTLE

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INTRODUCTION

Interest in genetic evaluation of crossbred animals has steadily increased in the USA in recent years. A large portion of the beef cattle records being collected in the USA for genetic evaluation comes from crossbred animals. Cornell University and the University of Georgia currently have genetic evaluation systems that account for additive and nonadditive group genetic effects, and random additive genetic effects. Multibreed genetic predictions from these systems consider only additive genetic effects. Because random nonadditive genetic effects are ignored, both systems assume that all sires within a breed group have the same level of nonadditive interbreed interaction in crossbred matings. This has been found not to be the case in small multibreed data sets (Elzo and Wakeman, 1998 ; Elzo *et al.*, 1998). A similar situation may exist in large national and international multibreed populations. Further, not only interbreed but also intrabreed random nonadditive genetic effects may be important in multibreed populations. Thus, a more complete multibreed model for beef cattle data should include intrabreed and interbreed additive and nonadditive direct and maternal genetic effects. This research reports intrabreed and interbreed additive and nonadditive direct and maternal genetic parameter estimates and genetic predictions for preweaning growth traits in two multibreed *Bos taurus* × *Bos indicus* multibreed herds of beef cattle.

MATERIAL AND METHODS

Multibreed data sets. The two multibreed data sets used here were : 1) Angus-Brahman, University of Florida, USA, and 2) Sanmartinero-Brahman, La Libertad Experiment Station, Colombia. The Angus-Brahman multibreed data set consisted of birth weight (BW) and weaning weight (WW) records from 2910 straightbred and crossbred calves born between 1989 and 2001. Calves were produced using a complete diallel mating strategy where 28 Angus (A), 44 Brahman (B), 12 $\frac{3}{4}A \frac{1}{4}B$, 16 $\frac{1}{2}A \frac{1}{2}B$, 19 $\frac{1}{4}A \frac{3}{4}B$, and 34 Brangus ($\frac{5}{8}A \frac{3}{8}B$) sires were mated to 232 A, 774 B, 265 $\frac{3}{4}A \frac{1}{4}B$, 594 $\frac{1}{2}A \frac{1}{2}B$, 282 $\frac{1}{4}A \frac{3}{4}B$, and 382 Brangus dams. Cows were kept on bahiagrass (*Paspalum notatum*) pastures. Mineral supplementation was available throughout the year. In winter, cows were provided with bermudagrass (*Cynodon dactylon*) hay, urea, and molasses. Cows were synchronized in March, artificially inseminated twice, and then exposed to a cleanup bull for 60 days. Calves were born from late December to March, and weaned in September and October. The Sanmartinero-Brahman multibreed data set contained BW and WW records from 2 756 straightbred and crossbred calves born from 1971 to 1996. Calves were the result of an incomplete diallel mating system, where 89 Sanmartinero (S), 22 B, and 10 $\frac{1}{2}S \frac{1}{2}B$ sires were mated to 477 S, 183 B, 171 $\frac{1}{2}S \frac{1}{2}B$, and 29 $\frac{1}{4}S \frac{1}{2}B$ dams. Cows were maintained in *Brachiaria* (*Brachiaria decumbens*) pastures, with free access to mineral supplementation. The breeding season was from May through July, and the calving season was from January to March.

Calves were weaned at 8 months of age.

Multibreed genetic parameters. Covariance components were estimated using Restricted Maximum Likelihood procedures (Harville 1977), applied to multibreed populations (Elzo, 1994). Estimates of base intrabreed and interbreed genetic and environmental covariances were obtained using Generalized Expectation-Maximization (GEM) algorithm (Dempster *et al.* 1977) on the Cholesky elements of the covariance matrices (Elzo, 1996). Multibreed genetic and environmental covariances were computed using linear combinations of base covariance estimates. Ratios of additive to phenotypic covariance ratios (heritabilities), nonadditive to phenotypic covariances (interactivities), and correlations (additive, nonadditive, environmental, phenotypic), were computed for all parental breed group combinations.

Multibreed model. The model was a multiple-trait multibreed sire-maternal grandsire. Fixed environmental effects were contemporary group, and age of dam \times sex of calf interaction effect as a function of the fraction of A alleles, or SM alleles, depending on the data set. Fixed regression group genetic effects were intrabreed additive (deviated from B) and interbreed nonadditive direct and maternal. Random effects were multibreed direct and maternal additive sire genetic effects, intrabreed and interbreed direct and maternal nonadditive sire \times breed-group-of-dam genetic effects, and residual. Additive and nonadditive genetic effects were assumed to be uncorrelated. Covariances among bull additive genetic effects, and among bull intrabreed, and bull interbreed nonadditive genetic effects were accounted for.

Computations. Estimates of direct and maternal additive genetic, and of environmental covariances from preliminary single-trait runs were used as priors for the two-trait (BW-WW) runs. The convergence criterion was that the difference between the sum of squares of the absolute values of covariances GEM iterations i and $i - 1$ divided by the sum of squares of covariances in GEM iteration $i - 1$ was less than 10^{-4} . Computations were performed in a DELL Precision 620 workstation, using version 2001 of the MREMLEM program.

Multibreed genetic predictions. Multibreed covariance estimates were used to obtain sire direct and maternal additive, nonadditive, and total multibreed expected progeny differences (MEPD). Sire additive MEPD were obtained directly from the mixed model equations. Sire nonadditive MEPD were computed as linear combinations of base nonadditive sire MEPD (weights = probabilities of intrabreed and interbreed intralocus interactions), assuming that sires were mated to F1 dams. Sire total MEPD were computed by adding each sire's additive and nonadditive MEPD.

RESULTS AND DISCUSSION

Estimates of covariance components and genetic parameters. The diallel design of the Angus-Brahman multibreed herd allowed the estimation of both intrabreed and interbreed additive and nonadditive genetic (table 1), and environmental covariances (table 2). The incomplete diallel design of the Sanmartinero-Brahman multibreed herd allowed the estimation of both intrabreed and interbreed nonadditive, but only intrabreed additive genetic (table 1), and environmental covariances (table 2). Estimates of covariances for all effects were within acceptable ranges, and showed similar patterns in the two multibreed herds. Remarkably, intrabreed nonadditive genetic covariances were similar to interbreed nonadditive covariances. Generalized least square means for heterosis effects in the Angus-Brahman herd were 2.6 ± 0.6 kg for BWD (D = direct), 19.2 ± 2.7

kg for WWD, $0.7 \pm .5$ for BWM (M = maternal), and 28.7 ± 2.2 kg for WWM, and 2.1 ± 0.7 kg for BWD, 18.2 ± 3.0 kg for WWD, $-.2 \pm 0.5$ kg for BWM, and 12.6 ± 2.7 kg for WWM for the Sanmartinero-Brahman herd. These results suggest that estimated mean differences between intrabreed and interbreed nonadditive genetic effects in multibreed populations may not be associated with differences in nonadditive intrabreed and interbreed variability.

Table 1. Estimates of base additive and nonadditive genetic covariances for BW and WW in two multibreed herds

Trait pair	Base genetic covariances (kg ²)										
	Angus-Brahman						Sanmartinero-Brahman				
	Additive			Nonadditive			Additive		Nonadditive		
	AA	BB	AB	AA	BB	AB	SS	BB	SS	BB	SB
BWD, BWD	5.6	5.4	4.0	5.9	5.6	5.3	3.1	6.5	3.3	4.8	4.3
BWD, WWD	1.0	1.6	7.3	0.9	1.2	1.4	0.4	1.0	0.5	0.2	0.6
BWD, BWM	-0.5	-0.3	-0.1	0.2	0.3	0.1	-0.6	-1.6	0.1	0.1	0.1
BWD, WWM	-0.1	1.8	-1.4	0.4	0.2	0.6	-0.1	-0.6	-0.3	0.0	0.0
WWD, WWD	58.4	66.6	156.3	83.5	83.0	65.8	62.6	58.8	55.9	60.2	59.3
WWD, BWM	0.3	0.9	1.9	0.7	0.1	0.8	0.1	-0.3	0.2	-0.1	-0.1
WWD, WWM	-13.5	0.5	16.4	29.4	2.4	27.3	-31.7	-33.6	-3.0	-2.6	-2.4
BWM, BWM	5.9	6.0	2.2	6.2	5.5	5.6	3.6	5.2	3.6	5.1	5.0
BWM, WWM	0.	2.9	-0.3	0.8	0.5	1.3	0.4	0.5	1.0	0.1	0.8
WWM, WWM	47.0	158.1	36.2	64.8	53.2	84.5	75.6	73.1	56.1	58.6	59.1

Table 2. Estimates of base environmental covariances for BW and WW in two multibreed herds

Trait pair	Base environmental covariances (kg ²)				
	Angus-Brahman			Sanmartinero-Brahman	
	AA	BB	AB	SS	BB
BW, BW	10.4	11.9	8.8	3.5	9.3
BW, WW	31.9	39.0	19.4	22.6	48.6
WW, WW	433.8	378.9	342.6	428.5	587.4

Estimates of intrabreed and interbreed interactibilities were larger for direct than for maternal effects, and this pattern was similar in the two herds. For example, intrabreed interactivity ratios were .16 for BWD, .11 for WWD, .16 for BWM, and .07 for WWM for BB in the USA, and .16 for BWD, .07 for WWD, .17 for BWM, and .07 for WWM for BB in Colombia. Similarly, interbreed interactivity ratios were .16 for BWD, .09 for WWD, .17 for BWM, and .12 for WWM for AB in the USA, and .18 for BWD, .08 for WWD, .21 for BWM, and .08 for WWM for SB in Colombia. Heritability ratios had values similar to interactibilities, indicating that in these

multibreed herds additive and nonadditive variation had similar importance. Also, they showed the same pattern as interactibilities (larger estimates for direct than for maternal effects).

Genetic predictions. The most salient features of the set of additive and nonadditive MEPD were : 1) Brahman sires tended to have higher MEPD for BW and WW direct additive genetic effects in both multibreed herds, 2) Sanmartinero sires had markedly higher MEPD for WW maternal direct genetic effects than Brahman, and 3) Angus and Sanmartinero sires showed less variation in nonadditive MEPD than Brahman and crossbred sires. As an illustration, figure 1 shows sire MEPD for WW direct genetic effects in both multibreed herds. Sires were ordered by year of first usage within breed group (1 = A (S), 2 = 1/4B, 3 = 1/2B, 4 = 3/4B, and 5=B). The intrabreed and interbreed nonadditive genetic variability found in these two multibreed herds indicate that nonadditive MEPD need to be included in multibreed beef cattle genetic evaluation procedures.

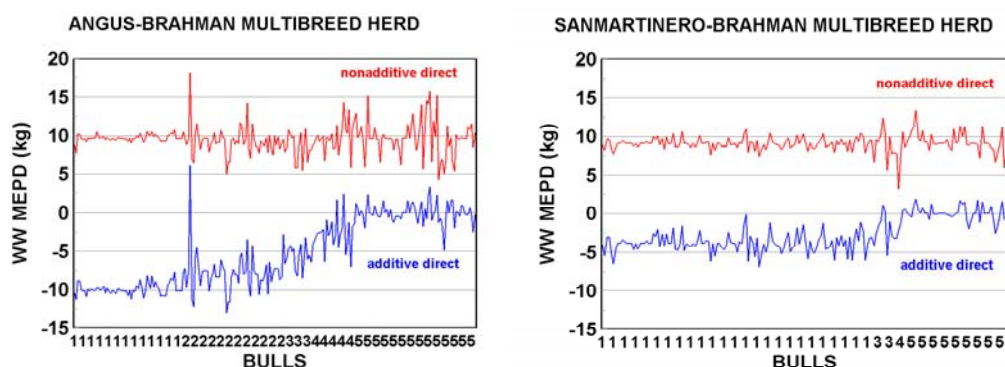


Figure 1. Additive and nonadditive MEPD for WW in two multibreed herds

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