

BREEDPLAN MULTI-BREED EBVS FOR GROWTH TRAITS IN ANGUS, HEREFORD, SIMMENTAL AND LIMOUSIN BREEDS

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SUMMARY

Data from over 3000 animals from two large sire breed comparison studies were used to estimate breed differences and adjustment factors necessary for the development of multi-breed BREEDPLAN estimated breeding values (EBV) for Angus, Hereford, Limousin and Simmental breeds for several growth traits. These included gestation length, birth weight, 200d weight, 400d weight, 600d weight and carcass weight. The adjustment factors can be used by industry to construct a conversion table that can be used to directly compare the EBVs of animals across the four breeds. This table should enhance the use of both between and within breed genetic variation, however all traits affecting profit will need to be considered, not just growth trait comparisons. Further research is underway to add more traits and breeds.

Keywords: BREEDPLAN, Multi-breed EBV, Genetic evaluation

INTRODUCTION

Australian beef producers have had BREEDPLAN EBVs available since 1985 however they are only comparable for animals within a breed. More effective use of across breed differences, as well as within breed genetic differences, could be achieved if EBVs were directly comparable both across and within breeds. The objective of this study was to use breed comparison data to estimate sire breed differences for weight traits and use these to compute BREEDPLAN adjustment factors that allow comparisons of EBVs on animals across breeds and hence the development of multi-breed EBVs.

MATERIALS AND METHODS

Animals. Performance records from the Victorian Multi-breed EBV project (VMB) and the Beef CRC Northern Crossbreeding project (CRCX) were used to estimate conversion factors to allow the adjustment of each breed's BREEDPLAN EBVs to a common base. For complete description of the VMB project see Graham *et al.* (1999). In brief, a total of 22 sires of each of Angus (AA), Hereford (HH), Limousin (LL) and Simmental (SI) breeds were mated to Angus and Hereford cows in Southern Australia in 1997 and 1998 in 19 herds. All sires had BREEDPLAN EBVs and were chosen to represent a spread in the 400d weight EBV. However sires with extreme birth weight were not used. A total of 2566 calves were generated and their complete management recorded.

The design of the CRCX is described in Upton *et al.* (2001). This study used progeny data on 8 sire breeds with BREEDPLAN analyses and comprised: Brahman (BB), Belmont Red (BR), Santa Gertrudis (SG), Angus (AA), Hereford (HH), Shorthorn (SH), Charolais (CC) and Limousin (LL). Sires were joined by AI or natural service to Brahman cows in 1993, 1994 and 1995 in 2 herds in subtropical central Queensland. At weaning the calves were allocated to a number of growout treatment groups, comprising

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market weight and finishing regimes. The number of sires were as follows BB = 13, BR = 14; SG = 8; AA = 9; HH = 8; SH = 8; CC = 15; LL = 14. There were 7 sires in common across the 2 projects.

Traits. For this study the traits included were: gestation length (GL), birth weight (BWT), 200d weight (W200), 400d weight (W400), 600d weight (W600) and carcass weight (CWT). In both projects these traits were defined and adjusted using the procedures of BREEDPLAN (Schneeberger *et al.* 1991 and Johnston *et al.* 1999).

Statistical methods. Initial analyses were performed using REML procedures in SAS (SAS 1988) on the VMB data to estimate the amount of heterosis being expressed for each trait. This was achievable because in 2 of the herds a complete diallel of the Angus and Hereford breeds was employed (N = 470). The model for each trait included a fixed effect of contemporary group (CG), sex, sire breed, dam breed, heterosis and sire as a random effect nested within breed. Heterosis was simply defined as 0 = straightbred and 1 = crossbred. The components of CG changed slightly for each trait but generally included terms for herd, year, birth month and user defined group. For post-birth weight, weigh date was also included in the CG definition. CG for all post-weaning weights included sex in the definition because the sexes were managed separately.

The CRCX top-cross design meant that an estimate of heterosis in the F1 progeny was not possible, therefore to control the contribution of non-additive effects the breeds were grouped into 3 breed types where the expression of heterosis was assumed to be the same for the sire breeds in each group. The breed types were: BA = tropically adapted breeds (BR, SG); BT = *Bos Taurus* breeds (AA, HH, SH, CC, LL); BB = straightbred Brahmans. For CRCX the model used changed for each trait. All analyses included a base model that consisted of herd, breed type, CG nested within herd, sire breed nested within breed type, and sire nested within breed as random. For BWT the model also included cow herd of origin, sex and all first order interactions and CG = year. For GL, sex was included in the model and CG = year, AI group and AI month. For W200, additional effects included cow herd of origin and sex, CG = weight date, weaning date and previous lactation status of the dam. For W400, CG = sex, weight date, weaning date, HGP treatment and geographic location. For W600, CG = sex, weight date, 400d weight date, weaning date, HGP treatment and geographic location. For CWT, CG = kill group, sex, market and finishing regime. Kill group was the combined effect of slaughter date and abattoir.

To estimate sire breed effects, separate SAS analyses were performed for the VMB and CRCX data to adjust for fixed effects specific to each project (as described above) and then the adjusted phenotypes were combined. For VMB estimates of heterosis were used to pre-adjust the data on all crossbreds using a multiplicative adjustment prior to running the same model (defined previously) with the only difference that the heterosis term was removed. Adjusted phenotypes for each trait from the 2 projects were combined and analysed in the model that included a fixed effect of project, sire breed and sire within breed as random. The sire breed solution was doubled to produce an estimate of the breed effect. The next step involved calculating the average sire BREEDPLAN EBV for the sires used for each trait. Note, the performance data on the progeny of the sires from either project were not used in the computation of the BREEDPLAN EBVs.

Table 1. Estimated breed differences and BREEDPLAN adjustment factors for growth traits

Trait	Dataset	Variable	ANGUS	HEREFORD	LIMOUSIN	SIMMENTAL
GL	CRC	N. records	139	137	145	-
		Sire breed diff.	0	0.53	6.53	-
	VMB	N. records	672	613	670	611
		Sire breed diff.	0	1.45	5.04	4.13
	COMBINED	BREED diff.	0	2.49	10.77	8.39
		SE of the diff.*		(0.93)	(0.93)	(1.00)
		Average sire EBV	-1.92	-0.50	-0.33	0.06
		ADJUSTMENT	0	1.07	9.18	6.41
BWT	CRC	N. records	89	90	218	-
		Sire breed diff.	0	2.29	2.54	-
	VMB	N. records	649	580	630	587
		Sire breed diff.	0	1.23	2.03	3.12
	COMBINED	BREED diff.	0	2.79	4.28	6.43
		SE of the diff.*		(0.80)	(0.78)	(0.85)
		Average sire EBV	3.92	3.89	1.85	1.63
		ADJUSTMENT	0	2.8	6.4	8.7
200d	CRC	N. records	138	138	294	-
		Sire breed diff.	0	3.40	-3.13	-
	VMB	N. records	623	577	622	559
		Sire breed diff.	0	-0.30	-0.19	8.00
	COMBINED	BREED diff.	0	1.02	-2.65	16.00
		SE of the diff.*		(3.2)	(3.1)	(3.5)
		Average sire EBV	28.3	20.0	13.1	13.0
		ADJUSTMENT	0	9.3	12.5	31.3
400d	CRC	N. records	135	136	292	-
		Sire breed diff.	0	7.92	-0.87	-
	VMB	N. records	425	398	423	397
		Sire breed diff.	0	-2.9	-6.2	11.0
	COMBINED	BREED diff.	0	-0.5	-9.9	24.8
		SE of the diff.*		(4.8)	(4.6)	(5.2)
		Average sire EBV	54.9	33.1	20.4	17.2
		ADJUSTMENT	0	21.2	24.6	62.5
600d	CRC	N. records	131	128	277	-
		Sire breed diff.	0	7.79	-12.32	-
	VMB	N. records	277	233	259	251
		Sire breed diff.	0	-5.43	-13.44	8.27
	COMBINED	BREED diff.	0	-2.90	-26.14	18.72
		SE of the diff.*		(7.3)	(6.9)	(8.1)
		Average sire EBV	70.1	51.0	26.7	17.5
		ADJUSTMENT	0	16.3	17.3	71.4
CWT	CRC	N. records	137	136	291	-
		Sire breed diff.	0	1.99	-0.86	-
	VMB	N. records	-	-	-	-
		Sire breed diff.	-	-	-	-
	COMBINED	BREED diff.	0	3.99	-1.72	-
		SE of the diff.*		(7.8)	(6.9)	-
		Average sire EBV	36.1	32.1	14.6	-
		ADJUSTMENT	0	8.0	19.7	-

* relative to Angus

To derive the adjustment, such that the BREEDPLAN EBVs to be directly compared across breeds, the difference in EBV between pairs of breeds was added to the estimated difference between those breeds. For convenience all differences and adjustments are reported relative to Angus. Although this may seem logical it is not necessarily the way results will be transferred to industry. Only the results for Angus, Hereford, Limousin and Simmental breeds are presented in this paper.

RESULTS AND DISCUSSION

Breed differences. The breed differences in Table 1 show that differences existed between the breeds for all traits, although the breed differences are affected by the sample of sires used in each project the differences are reasonably consistent across the projects. The results for BWT and GL are generally in agreement with those presented by Graham *et al.* (1999) on a subset of the data. For W400 and CWT the breed differences for AA and HH are similar to the CRCX results presented by Newman *et al.* (2002).

Adjustment factors. The adjustment factors are the amount that must be added to the BREEDPLAN EBVs of each breed to allow the EBVs of animals in those breeds to be directly compared. For example an Angus bull with an EBV of +4.0 could be directly compared with a Limousin bull with an EBV of 1.2 by adding 6.4 to the Limousin EBV to give a multi-breed EBV of +7.6 (i.e. $7.6 = 1.2 + 6.4$). However to correctly interpret the EBVs of these 2 bulls requires knowledge of the dam breed intended to be used. In some cases this may be important because different levels of expression of heterosis for birth weight (and other traits) may need to be taken into account when using the multi-breed EBV.

CONCLUSIONS

The estimated breed differences have been estimated with sufficient precision in this study to use the data to produce BREEDPLAN adjustment tables that allow comparisons across these 4 breeds. More data is required for other breeds and traits, particularly calving ease, carcass and fertility. Work is underway to estimate more adjustments and to compute accuracies of the adjustment factors. However the likely future direction of research is the computation of multi-breed EBV from combined data and analyses of several breeds.

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