

SCOPE FOR A JOINT GENETIC EVALUATION OF NEW ZEALAND AND AUSTRALIAN ANGUS CATTLE

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SUMMARY

Genetic parameters and adjustment factors for birth, weaning, yearling and final weight were estimated for the New Zealand Angus population, fitting an animal model including maternal genetic and permanent environmental effects as additional random effects. Overall, pooled covariance matrices agreed well with those for Australian Angus, though heritability estimates for birth weight were somewhat lower than in Australian Angus. BREEDPLAN estimates of breeding values and their accuracies were obtained for each population separately. Correlations between estimates for sires with accurate proofs in both countries agreed with their expectations, giving no indications of genotype \times environment interactions.

INTRODUCTION

Widespread exchange of genetic material through import/export of live animals, semen and embryos has created strong genetic links between countries. For Angus in Australia (AU) and New Zealand (NZ) these are predominantly due to NZ bulls with progeny in AU, or North American bulls (USA and Canada) or their semen being imported into both countries.

With increasing computing power, international genetic evaluations have become possible. However, such enterprise assumes that all animals belong to the same population and rank the same in each country. The objectives of this study were to investigate these issues with a view to routine joint genetic evaluation of Angus cattle in AU and NZ. This involved estimation of genetic parameters for growth traits in NZ Angus and comparison of estimated breeding values (EBVs) for animals with progeny in both countries.

MATERIAL AND METHODS

Data consisted of the complete National Beef Recording Scheme weight and pedigree files of the AU and NZ Angus populations. Traits considered were birth weight (BW), weaning or 200-day weight (WW), yearling or 400-day weight (YW), and final or 600-day weight (FW). For the estimation of genetic parameters, NZ data subsets were extracted after preliminary, basic edits. For univariate analyses this included 52 herds with BW recording and at least 100 animals. For multivariate analyses, a smaller subset of 20 herds was utilised. Characteristics of the data structure are summarised in Table 1.

Estimates of genetic parameters were obtained by Restricted Maximum Likelihood using DFREML version 2.1 (Meyer, 1992a). The model of analysis was an animal model fitting both maternal genetic and maternal permanent environmental effects as additional random effects, and incorporating all pedigree information available. Direct-maternal genetic covariances were assumed to be zero throughout. As in BREEDPLAN, analyses were carried out within herd-year-management group-sex-month of weighing subclasses. Other fixed effects were birth type (single vs. twin), sex and an age status of dam (heifer vs. cow, the distinction based on 28 months at calving) effect. Age of dam (in years) was fitted as a linear and quadratic covariable, and days of age at weighing (for WW, YW and FW) was fitted as a linear covariable for each sex separately. Univariate analyses were performed for each trait, deriving adjustment factors as generalised least squares solutions at

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Trait	Univariate				Multivariate			
	BW	WW	YW	FW	BW	WW	YW	FW
No. of records	19,475	60,218	28,599	23,711	14,382	23,688	10,055	12,717
No. of animals ^a	32,966	74,085	42,949	36,221	21,103	29,675	16,765	18,535
No. of sires ^b	834	1938	1319	1072	644	911	599	602
No. of dams ^b	8,905	20,560	13,183	10,583	5647	7700	4846	5140
No. of HYGMS ^c	2055	1955	962	1152	1429	910	490	625
Weight ^d \bar{x}	34.07	216.8	285.8	475.2	33.79	228.3	321.6	478.2
<i>s.d.</i>	5.38	50.9	81.2	101.8	5.36	48.5	81.4	98.1
Age ^d \bar{x}		202.0	378.8	567.3	-	209.8	394.8	566.2
<i>s.d.</i>		40.1	39.8	41.3	-	36.2	39.1	37.3

^aIn the analysis, including parents without records

^bwith progeny in the data

^cHerd-year-(management)group-month-sex subclasses

^d \bar{x} , *s.d.* : raw mean and standard deviation

Table 1: Characteristics of the data for REML analyses (NZ)

convergence. Covariance components were estimated carrying out bivariate analyses for all pairs of traits. Results were combined to form pooled correlation and covariance matrices, 'bending' (Hayes and Hill, 1981) them if necessary to ensure estimates within the parameter space.

EBVs and their approximate accuracies were obtained using BREEDPLAN (version 3.3) software and incorporating all available weight and pedigree records. Analyses were carried out for each country separately, using the appropriate set of covariance components and adjustment factors. Animals with EBVs in both countries were identified and correlations between proofs calculated and contrasted with their expected values, derived as the product of the respective accuracies, averaged over animals.

An analysis considering WW in NZ and WW in AU as different traits was carried out considering 6 herds from each country with the largest numbers of progeny of 'link' animals. This resulted in a data set consisting of 28,217 records and means as given in Table 2. There were 1,832 and 3,183 progeny records of 28 'link' animals in NZ and AU, respectively.

	NZ	AU
No. records	14,290	13,927
Mean	252.8	232.3
SD	48.0	45.7
Age	226.0	220.9

Table 2: WW as different trait

RESULTS AND DISCUSSION

Table 3 gives estimates of the "heifer" factor, i.e. the expected increase in the weight of a calf (in kg) due to the fact that its dam was a cow rather than a heifer, and regression coef-

	BW	WW	YW	FW
"Heifer" factor	1.863	8.484	8.827	11.012
Age H	-	0.78829	0.7854	0.56925
B	-	0.86694	0.9684	0.77516
Dam age 1	0.2871	2.7363	2.6528	1.2978
(NZ) 2	-0.0585	-0.5474	-0.4412	-0.4262
Dam age 1	0.5400	3.8098	3.4226	1.9633
(AU) 2	-0.1600	-0.6191	-0.7186	-0.5180

Table 3: Fixed effects estimates

Pooled correlation matrices in Table 4 give direct additive genetic (A), maternal genetic (M), maternal permanent environmental (C) and phenotypic (P) correlations below the diagonal, and corresponding heritabilities (A,M), "c²" effects (C) or phenotypic variances (P) on the diagonal. The latter values (diagonals) are estimates from univariate analyses for BW and WW, and from bivariate analyses together with WW for YW and FW, to avoid bias due to post-weaning selection for

ficients on age at weighing (linear, in kg/day) fitted within sex (H : heifers, B : bulls), and dam age (1 : linear, 2 : quadratic coefficient, in kg/year and kg/year², respectively). For comparison, the current adjustment factors for age of dam used in BREEDPLAN for Australian Angus are given showing increased impact of dam age in AU.

growth. For comparison, Table 4 also gives the values currently used as input parameters in Angus BREEDPLAN analyses, derived from analyses of AU Angus data (Meyer 1992b, 1994; Robinson

		NZ estimates				BREEDPLAN values			
		BW	WW	YW	FW	BW	WW	YW	FW
A	BW	0.29				0.42			
	WW	0.65	0.20			0.66	0.20		
	YW	0.59	0.89	0.28		0.53	0.84	0.30	
	FW	0.60	0.86	0.88	0.35	0.56	0.84	0.81	0.33
M	BW	0.09				0.11			
	WW	0.35	0.08			0.00	0.10		
	YW	0.58	0.94	0.05					
	FW	0.35	0.83	0.92	0.04				
C	BW	0.06				0.05			
	WW	0.41	0.15			0.54	0.11		
	YW	0.48	0.89	0.08					
	FW	0.75	0.90	0.89	0.03				
P	BW	15.6				14.3			
	WW	0.40	533			0.35	500		
	YW	0.36	0.71	844		0.32	0.59	850	
	FW	0.36	0.62	0.77	1344	0.31	0.54	0.72	1200

Table 4: Pooled correlation matrices

1993, unpublished). On the whole there was good agreement between estimates for NZ and AU Angus. For BW, both direct (A) and maternal (M) heritabilities were lower than found in AU data. Repeating analyses for a subset of 7 herds with daily weighing during the calving season, however, did not change results (not shown), i.e. lower values in the NZ data could not be attributed to unreliable recording. Furthermore, estimates agreed well with values reported by Waldron *et al.* (1993) for NZ Angus in a research herd.

Summary statistics for the BREEDPLAN runs carried out for each country together with means (in kg) adjusted for differences in dam age and age at weighing are shown in Table 5, where the number of records denotes the number of animals with at least one valid weight. Populations were of roughly equal size, while there were considerably more foster dams, sires with progeny in the data and recording of management groups in AU than in NZ. Records reached back as far as 1970 for NZ and 1971 for AU, with a considerable number of animals appearing only in the pedigree and not weight files, resulting in the number of animals being substantially higher than the number of animals with records. Both raw (not shown) and adjusted means in both countries were very similar for all four traits. A total of 840 animals, 459 cows and 381 bulls, were found with EBVs in both countries, 639 with known birth dates. Mean accuracies of evaluation ($r_{TI} \times 100$) and observed (r) and expected correlations ($E(r)$) between EBVs in AU and NZ for each sex are given in Tables 6 and 7. To eliminate an upwards bias of r due to genetic trends, (co)variances to determine r were calculated within the 29 year of birth subclasses and pooled over years. Regressions of EBVs in NZ on EBVs in AU, were on average 0.75 (0.72 to 0.80) for WW, YW and FW, and less (0.45) for BW. This deviation from unity reflected differences in r_{TI} , a higher variability of EBVs in NZ (not shown) and, for BW, the difference in heritabilities assumed.

No. of	NZ	AU
Animals	206,740	223,174
Sires	4,763	8,049
Dams	74,315	88,467
Records	157,787	150,612
Foster dams	843	4,681
Genetic groups	22	23
Subclasses	30,330	76,434
Adj. mean		
BW	34.5	34.3
WW	220	226
YW	313	341
FW	500	488

Table 5: BREEDPLAN run statistics

		BW	WW	YW	FW	Milk
r_{TI}	AU	38.1	37.7	36.6	36.0	30.4
	NZ	49.8	62.2	60.0	62.3	60.0
r		0.23	0.25	0.22	0.26	0.09
$E(r)$		0.20	0.24	0.22	0.23	0.17

Table 6: Correlation for cows (n=338)

For cows, r and $E(r)$ agreed closely. For bulls, however, observed values were consistently higher than expected, markedly so for the weight EBVs. Such discrepancy might be attributed to inappropriate covariance matrices used, poor approximation of accuracies or other, intangible factors making proofs more similar than expected.

Considering only bulls found in the AU Angus sire list, i.e. disregarding sires without progeny in AU which obtained an AU EBV only because they appeared in the pedigree of a 'link' animal, left 153 bulls. Only 90 of these had 6 or more progeny in each country, totalling 23,494 and 14,634 progeny in AU and NZ, respectively. Elimination of 'pedigree only' bulls increased the average accuracy of evaluation, markedly in AU, and r and $E(r)$ for this group of animals agreed well, i.e. the inflated observed correlations when considering all bulls were due to some "double counting" of information (sires obtaining EBVs only through their sons). Close agreement between r and its expectation for both cows and this group of bulls suggested a genetic correlation between performance in AU and NZ near unity.

		BW	WW	YW	FW	Milk
<i>All bulls (n=301)</i>						
r_{TI}	AU	59.4	59.9	58.8	57.9	47.1
	NZ	69.7	82.0	79.5	81.6	70.9
r		0.57	0.65	0.65	0.64	0.37
$E(r)$		0.43	0.49	0.47	0.47	0.33
<i>Bulls w. AU progeny (n=153)</i>						
r_{TI}	AU	76.3	76.2	75.1	74.0	62.6
	NZ	72.3	83.2	81.0	82.9	70.5
r		0.54	0.63	0.63	0.61	0.44
$E(r)$		0.56	0.64	0.61	0.62	0.45
<i>NZ bulls (n=89)</i>						
r_{TI}	AU	66.1	67.2	65.8	65.1	55.5
	NZ	69.1	82.5	79.9	82.2	75.1
\bar{x}	AU	0.2	2.2	3.4	5.1	0.2
	NZ	0.0	-0.5	-0.2	0.2	1.0
sd	AU	1.5	5.7	8.9	11.8	3.1
	NZ	1.3	6.6	10.3	15.6	3.3
r		0.26	0.40	0.39	0.41	0.32
$E(r)$		0.47	0.56	0.53	0.54	0.42
<i>USA/CAN bulls (n=55)</i>						
r_{TI}	AU	91.3	89.1	88.5	86.7	71.3
	NZ	81.4	88.0	86.4	87.7	67.3
\bar{x}	AU	3.1	18.1	26.6	32.2	2.6
	NZ	2.7	19.0	29.1	38.9	-0.2
sd	AU	1.8	9.1	14.4	20.4	5.7
	NZ	1.4	10.1	15.0	22.1	4.6
r		0.55	0.58	0.60	0.62	0.73
$E(r)$		0.74	0.78	0.77	0.76	0.51

Table 7: Correlation for bulls

Repeating calculations for bulls divided according to country of origin, gave observed correlations somewhat lower than expected, in particular for NZ bulls (second part of Table 7), but still consistent with a genetic correlation between countries of 0.8 or higher. Higher mean EBVs (\bar{x}) for WW, YW and FW for NZ bulls in AU than NZ, might indicate preferential treatment of these imported animals or their sons in AU which would reduce r . In spite of roughly equal r_{TI} for WW, YW and FW for North American bulls in both countries and about the same phenotypic variances (see Table 4), standard deviations (sd) of EBVs in NZ were about 10% higher than in AU. Similarly, higher sd of EBVs in NZ than in AU for NZ bulls could not be attributed completely to differences in r_{TI} .

Estimates from the bivariate analysis treating WW in AU and NZ as different traits were 0.97 for the direct genetic and 0.82 for the maternal genetic correlations.

CONCLUSIONS

Estimates of genetic parameters for growth traits in AU and NZ Angus have been found to be almost identical. For animals with progeny in both countries, correlations between EBVs agreed closely with their expectations, i.e. no genotype \times environment interactions were found. A joint genetic evaluation of the two populations, using the appropriate adjustment factors for each of them, can be recommended. This should lead to improved accuracies of evaluations, encourage greater trans-Tasman exchanges of genetic material, and facilitate higher genetic gains.

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