

## Estimates of genetic parameters and breeding values for New Zealand and Australian Angus cattle

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### Abstract

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 indication of a genotype  $\times$  environment interaction. A joint genetic evaluation, using adjustment factors specific to each country but the same covariance matrices is recommended.

### Introduction

With widespread trade in genetic material, live animals as well as frozen semen and embryos, between countries there now exist strong genetic links between geographically distinct populations belonging to the same breed of cattle. For Angus in Australia (AU) and New Zealand (NZ) these genetic links can be attributed to two main sources : bulls of NZ origin with progeny in AU and semen of North American (USA and Canada)

bulls being imported into both countries. This has stimulated interest in international genetic evaluations, using records of relatives (e.g. progeny) of an animal (e.g. sire) in all countries in estimating its genetic merit, thus obtaining a more accurate proof or obtaining a proof exceeding a certain level of accuracy earlier. With increasing computing power and improved algorithm used to solve large sets of mixed model equations, this is becoming technically feasible for increasingly large or numerous populations.

However, such an enterprise assumes that populations in individual countries are just subgroups of the same overall population with the same or at least proportional genetic parameters and (co)variances, and that all animals rank the same in each country. The objectives of this study were to investigate these assumptions for the Angus populations in AU and NZ and examine the scope of a joint, trans-Tasman genetic evaluation for Angus.

## **Material and Methods**

### *Data*

Data consisted of the complete BREEDPLAN weight and pedigree files of the Australian (AU) and New Zealand (NZ) Angus population, containing 298,874 weight records for NZ and 329,135 records for AU, and pedigrees for 187,650 and 192,608 animals registered in NZ and AU, respectively. Records reached back as far as 1970 for NZ and 1971 for AU.

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), with permissible ages ranging from 120 to 300 days, 300 to 500 days and 500 to 700 days for WW, YW and FW, respectively. After merging of weight and pedigree information and a series of edits, involving, amongst others, checks of validity of dates and ranges for weights and ages, there were close to 150,000 animals with valid weight records in each country.

For the estimation of breeding values, all records were considered, allowing for repeated records per trait, while subsets of the data were extracted for the estimation of genetic parameters. In doing so, the weight closest to the target age of 200, 400 or 600 days was selected for animals with more than one record in the age range pertaining to a trait. For the NZ data, there were proportionally fewer BW records than for the other weights. Thus data for univariate analyses of variance components were restricted to

herds with BW recording and at least 100 animals with any valid weight. For NZ, this left 52 herds (out of 287) with a total of 63,062 animals. For AU data, BW recording was much more frequent than in NZ. Extracting a subset of AU records based on the same criterion, thus yielded a much bigger data set involving 123,071 animals in 134 (out of 443) herds. Numbers of records for each trait and further details of the data structure are summarised in Table 1.

For NZ, a further subset of these data was selected for multivariate analyses. This was necessary due to computational restraints. With numerous animals with BW and WW, WW and YW, or WW and FW recorded and comparatively few animals with BW and YW, BW and FW, or YW and FW recorded, herds were selected for which the total number of pairs of records for the latter pairs (BW+YW, BW+FW, YW+FW) divided by the number of animals in the herd was at least 0.45. This attempted to retain as many animals as possible with the three ‘rarer’ combinations of records. In total, this left 24,874 animals in 20 herds in the data set used for bivariate analyses. Numbers of records for individual weights in this subset are given in Table 2.

An additional data set was formed for a bivariate analysis treating WW in AU and NZ as different traits. For this animals with progeny in both countries were identified, counting the number of such progeny records in each herd. Considering the 6 largest herds in each country (with at least 680 progeny of common animals each) resulted in a data set consisting of 14,290 (NZ) and 13,927 (AU) WW records, 1832 and 3183 of which were progeny of 28 ‘common’ sires or dams in NZ and AU, respectively.

### *Analyses*

Estimates of genetic parameters were obtained by Restricted Maximum Likelihood (REML) using a derivative-free algorithm, fitting an animal model with 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. A previous analysis of Australian Angus data had found these to be negligible (Meyer, 1994). All calculations were performed using DFREML version 2.1 (Meyer, 1992a).

Fixed effects fitted were similar to those in BREEDPLAN, including a herd-year-management group-sex-month of weighing subclass, birth type (single vs. twin), sex and an age status of dam (heifers : 28 months or less at calving, vs. cow : older than 28

months at calving) effect. Age of dam was fitted as a linear and quadratic covariable, and age at weighing as a linear covariable for each sex separately for WW, YW and FW.

Univariate analyses were performed for each trait and both populations using large numbers of records, deriving generalised least squares solutions for fixed effects and regression coefficients fitted at convergence. Covariance components for NZ were estimated carrying out bivariate analyses for all 6 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.

Estimated Breeding values (EBVs) were obtained for each country separately using BREEDPLAN (BREEDPLAN, 1995) software (version 3.3) in a GROUPBREEDPLAN run. For AU, the current BREEDPLAN set of covariance components and adjustment factors for Angus was utilised, while for NZ estimates from the current study were substituted. Approximate accuracies of evaluation were obtained for all direct effects and the maternal genetic effect for WW (“milk” EBV).

‘Equivalent’ identities in each population were available for 1066 animals. Of these, 846 animals were found with EBVs in both data sets. Eliminating 6 animals with grossly differing birth dates, left 840 pairs of proofs and corresponding accuracies. These were correlated and correlations were contrasted to their expected values, derived as the product of the accuracies, averaged over animals, assuming a genetic correlation of unity between performance in the two countries.

## Results and Discussion

### *Genetic parameter estimates*

Results from univariate analyses for both countries are summarised in Table 3. Overall estimates showed remarkable agreement, and were well within the range of literature estimates for Angus from other countries (e.g. Skaar, 1985; Trus and Wilton, 1988; Brown *et al.*, 1990; Boldman *et al.*, 1991; Cantet *et al.*, 1993). A somewhat higher phenotypic variance for YW in AU than in NZ was accompanied by a higher mean (see Table 1), reflected, to some extent at least, a scale effect. The biggest difference occurred for BW for which the direct ( $h^2$ ) heritability was almost 0.1 lower in NZ than in AU. Repeating analyses for a subset of 7 NZ herds which were known to weigh

daily during the calving season, however, essentially did not change results, i.e. low  $\hat{h}^2$ s for BW in the NZ data could not be attributed to potentially unreliable recording. Furthermore, NZ estimates for BW agreed well with those reported by Waldron *et al.* (1993) for NZ Angus in a research herd.

The objectives of this study did not include the estimation of (co)variance components for AU Angus since previous estimates existed. However, the latter were based on data from a selection experiment (Meyer, 1992b and 1994) or on the analysis of field records but considering a number of small subsets of the data, each involving a few herds only, and pooling the resulting estimates (Robinson, 1993). In contrast, the present study considered numerous herds simultaneously and involved large numbers of records. To rule out any systematic differences associated with this, univariate analyses were performed for both populations applying the same criteria for the selection of data utilised.

To date these were the largest analyses of this kind performed for beef cattle data. The model of analysis for WW in AU, for instance, included a total 330,544 fixed and random effects levels. This showed that large scale, “whole breed” analyses are feasible and that with sufficient information, accurate and consistent results are obtained. Overall, results for AU agreed well with previous estimates, though the  $\hat{h}^2$  of 0.38 for BW was somewhat lower than values of 0.42 (Meyer, 1992b) and 0.48 (Robinson, 1993) reported previously. Thus re-estimation of covariance components for the AU data was considered unnecessary.

Table 4 gives the numbers of animals with each pair of traits recorded and the results from individual bivariate analyses of the NZ data. Again there was good agreement with previous estimates. A higher maternal genetic correlation between BW and YW than BW and WW, for instance, has been observed repeatedly in other studies, mainly in Australia (Robinson, 1993; Meyer 1994; Meyer *et al.*, 1993). For each trait, there were up to four estimates of variance components, namely from a univariate analysis and from each of the three bivariate analyses the trait was included in (not shown). On the whole, these estimates of variance components and the resulting genetic parameters ( $h^2$ ,  $m^2$ ,  $c^2$ ) agreed closely. For YW and FW though, estimates from joint analyses with WW were somewhat higher than for the other analyses. Selection for growth mainly occurs post weaning. Hence this is likely to indicate removal of selection bias in the bivariate analysis including WW.

Combined matrices of estimates were formed from correlation estimates (Table 4) and genetic parameter estimates ( $h^2$ ,  $m^2$ ,  $c^2$ ) for individual traits. For the latter estimates from univariate analyses were used for BW and WW, and from bivariate analyses together with WW for YW and FW. This choice avoided selection bias in the estimates for YW and FW. For both genetic and environmental maternal effects, the resulting matrices of co-heritabilities (or equivalent) were not positive definite and required some “bending” to force them within the bounds of the parameter space. The resulting pooled matrices of estimates are given in Table 5 as well as corresponding values currently used as input parameters in Angus BREEDPLAN analyses for comparison. Estimates of  $\sigma_p^2$  for NZ in Table 4 are, as are the genetic parameters for each trait, from univariate analyses for BW and WW and from bivariate analyses together with WW for YW and FW.

Overall, the NZ estimates agreed well with the current Australian genetic parameters for Angus, except for an assumed maternal genetic correlation of zero between BW and WW. In light of estimates from several other studies in beef cattle which consistently yielded estimates for this correlation of 0.3 or higher (Meyer *et al.*, 1993; Swalve, 1993; Robinson, 1993; Meyer, 1994), this assumption appeared disputable. Furthermore, results from univariate analyses for AU (see Table 3) suggest that current values for BW might be slightly too high for  $h^2$  and too low for  $\sigma_p^2$ . However, disregarding these minor discrepancies, the correlation matrices for AU and NZ Angus can be regarded as identical for most purposes, and the adoption of a single set of covariance matrices for genetic evaluation for growth, jointly or separately, can be recommended.

Treating WW in AU and NZ as different traits gave estimates of the direct genetic and maternal genetic correlations of 0.97 and 0.82, respectively, i.e. indicated that performance in the two countries was influenced by the same genes.

Estimates of regression coefficients on age at weighing and dam age as well as the fixed effects solutions for dams being ‘cows’, i.e. older than 28 months, (expressed as difference from ‘heifers’) are given in Table 6. Coefficients for the linear, within-sex regression of weight on age were consistently higher in NZ than in AU, especially for post-weaning weights, presumably due to more seasonal production conditions in NZ. Conversely, both linear and quadratic coefficients for age of dam were lower in NZ than AU. Differences appeared sufficiently large to suggest that adjustment factors specific to each country should be used in a joint genetic evaluation.

### *Breeding value estimates*

Summary statistics for the BREEDPLAN runs carried out for each country and means (in kg) adjusted for differences in dam age and age at weighing are shown in Table 7. 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, herds and management groups in AU than in NZ. There were a considerable number of animals appearing only in the pedigree and not weight files, resulting in the total number of animals being substantially higher than the number of animals with records. Both raw (not shown) and adjusted means in both countries were 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 EBVs, accuracies of evaluation ( $r_{TI}$ ) and observed and expected correlations between EBVs in AU and NZ are given in Table 8 for cows and bulls separately. Proofs of ‘common’ animals were more accurate and, except for BW, considerably more variable in the NZ than AU data set, with only part of the differences in variability attributable to the differences in accuracies. Coefficients for the regression 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  $r_{TI}$ , the higher variability of EBVs in NZ and, for BW, the difference in heritabilities assumed.

Observed correlations between EBVs for direct effects were consistently and substantially higher than their expected values. This might be attributed to inappropriate covariance matrices used, bad approximation of accuracies or some intangible factors making proofs more similar than expected. When calculations were repeated within years of birth of animals, observed and expected correlations for cows agreed closely, suggesting a genetic correlation of unity between performance in AU and NZ, and that inflated correlations, ignoring years, were due to genetic trend.

For bulls, however, calculations on a within year basis only reduced the discrepancy between observed and expected correlations. On closer examination, it was found that some of the bulls did not have progeny in AU but received a proof in AU only because of son(s) with progeny. This led to some ‘double-counting’ of information which made EBVs more similar than expected. As shown in Table 9, considering only bulls with actual progeny in both countries yielded correlations between EBVs which matched their expectations very closely.

Most bulls with EBVs in both countries were of either NZ (n=89) or North American (USA or Canada, n=97) origin. Figure 1 shows the distribution of EBVs for WW for these two groups, which exhibited a clear clustering around a regression line with a slope of unity and showing only very few animals deviating from it by more than 20 kg. As Table 9 shows, North American bulls had substantially higher and more accurate EBVs than NZ bulls. Bulls of NZ origin had consistently higher EBVs in AU than in NZ, suggesting some preferential treatment of their progeny in AU and thus potential bias in EBVs, or the existence of some non-additive genetic effects.

Calculating correlations for bulls of different origin separately gave somewhat lower than expected values (Table 9), in particular for NZ bulls. As discussed above, this might be due to some bias of EBVs of these bulls in AU. On the whole, however, observed correlations were consistent with a genetic correlation between performance in AU and NZ of 0.8 or higher. Robertson (1959) considered only genetic correlations between performance in different environments below 0.8 to be of biological importance.

## **Conclusions**

This study shows that genetic parameters in the NZ and AU Angus populations are virtually identical. Furthermore, correlations between direct genetic effects for growth appear be close to unity. Hence, a joint genetic evaluation as a single population, using separate adjustment factors for each country can be recommended. This would increase the accuracy of evaluation for animals with progeny in both countries and could encourage increased exchange of genetic material.

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**Table 1** : Characteristics of the data structure for univariate genetic parameter estimation.

Trait <sup>a</sup>	New Zealand				Australia				
	BW	WW	YW	FW	BW	WW	YW	FW	
No. of records	19,475	60,218	28,599	23,711	59,699	108,856	55,460	35,244	
No. of animals <sup>b</sup>	32,966	74,085	42,949	36,221	92,348	141,411	86,922	63,773	
No. of sires <sup>c</sup>	834	1938	1319	1072	2129	3403	2424	2124	
No. of dams <sup>c</sup>	8,905	20,560	13,183	10,583	26,616	40,474	25,813	19,214	
No. of HYGMS <sup>d</sup>	2055	1955	962	1152	7015	7231	3788	2461	
Weight <sup>e</sup>	$\bar{x}$	34.07	216.8	285.8	475.2	33.27	233.1	337.5	474.5
(kg)	<i>s.d.</i>	5.38	50.9	81.2	101.8	5.63	48.3	72.3	98.8
Age <sup>e</sup>	$\bar{x}$		202.0	378.8	567.3	-	214.5	401.6	580.3
(days)	<i>s.d.</i>		40.1	39.8	41.3		33.5	39.3	39.7
Dam age <sup>e</sup>	$\bar{x}$	5.54	5.40	5.06	5.71	4.81	4.91	4.99	5.10
(years)	<i>s.d.</i>	2.83	2.56	2.42	2.69	2.35	2.32	2.41	2.38

<sup>a</sup>BW : birth weight, WW : weaning weight, YW : yearling weight, FW : final weight

<sup>b</sup>In the analysis, including parents without records

<sup>c</sup>With progeny in the data

<sup>d</sup>Herd-year-(management)group-month-sex subclasses

<sup>e</sup> $\bar{x}$ , *s.d.* : raw mean and standard deviation

**Table 2** : Characteristics of the data structure for multivariate genetic parameter estimation for New Zealand Angus.

Trait <sup>a</sup>	BW	WW	YW	FW	
No. of records	14,382	23,688	10,055	12,717	
No. of animals <sup>b</sup>	21,103	29,675	16,765	18,535	
No. of sires <sup>c</sup>	644	911	599	602	
No. of dams <sup>c</sup>	5647	7700	4846	5140	
No. of HYGMS <sup>d</sup>	1429	910	490	625	
Weight <sup>e</sup>	$\bar{x}$	33.79	228.3	321.6	478.2
(kg)	<i>s.d.</i>	5.36	48.5	81.4	98.1
Age <sup>e</sup>	$\bar{x}$	-	209.8	394.8	566.2
(days)	<i>s.d.</i>	-	36.2	39.1	37.3
Dam age <sup>e</sup>	$\bar{x}$	5.55	5.63	5.39	5.79
(years)	<i>s.d.</i>	2.86	2.81	2.79	2.81

<sup>a</sup>BW : birth weight, WW : weaning weight, YW : yearling weight, FW : final weight

<sup>b</sup>In the analysis, including parents without records

<sup>c</sup>With progeny in the data

<sup>d</sup>Herd-year-(management)group-month-sex subclasses

<sup>e</sup> $\bar{x}$ , *s.d.* : raw mean and standard deviation

**Table 3 :** Estimates of the phenotypic variance ( $\sigma_P^2$ ) and genetic parameters ( $h^2$  : direct heritability,  $m^2$  : maternal heritability, and  $c^2$  : permanent environmental maternal effects) from univariate analyses of Australian and New Zealand data.

Trait <sup>a</sup>	New Zealand				Australia			
	BW	WW	YW	FW	BW	WW	YW	FW
$\sigma_P^2$	15.56	533.1	704.3	1267.7	15.44	531.1	826.7	1231.6
$h^2$	0.286	0.201	0.278	0.303	0.379	0.230	0.312	0.319
<i>s.e.</i> <sup>b</sup>	0.024	0.009	0.016	0.021	0.013	0.008	0.013	0.018
$m^2$	0.096	0.081	0.036	0.031	0.066	0.084	0.038	0.031
<i>s.e.</i> <sup>b</sup>	0.015	0.008	0.009	0.009	0.008	0.006	0.006	0.008
$c^2$	0.060	0.153	0.075	0.020	0.052	0.156	0.069	0.029
<i>s.e.</i> <sup>b</sup>	0.012	0.007	0.011	0.009	0.007	0.006	0.007	0.009

<sup>a</sup>BW : birth weight, WW : weaning weight, YW : yearling weight, FW : final weight

<sup>b</sup>Approximate sampling error

**Table 4 :** Numbers of animals in the analyses (including parents without records) and with each combination of traits recorded, together with estimates of direct genetic ( $r_A$ ), maternal genetic ( $r_M$ ), maternal permanent environmental ( $r_C$ ), residual ( $r_E$ ) and phenotypic ( $r_P$ ) correlations, for pairwise, bivariate analyses of the New Zealand data.

Trait <sup>a</sup> 1	BW	BW	BW	WW	WW	YW
Trait 2	WW	YW	FW	YW	FW	FW
No. animals	30,654	24,748	26,514	30,013	29,927	23,266
- trait 1 only	927	7,866	7,538	14,015	11,280	4,638
- trait 2 only	10,233	3,539	5,873	382	309	7,300
- both traits	13,455	6,516	6,844	9,673	12,408	5,417
$r_A$	0.65	0.59	0.60	0.89	0.86	0.88
$r_M$	0.37	0.62	0.38	1.00	0.90	1.00
$r_C$	0.43	0.51	0.85	0.93	1.00	1.00
$r_E$	0.31	0.22	0.22	0.58	0.47	0.69
$r_P$	0.40	0.36	0.36	0.71	0.62	0.77

<sup>a</sup>BW : birth weight, WW : weaning weight, YW : yearling weight, FW : final weight

**Table 5 :** Pooled correlation matrices, after 'bending' where required, for birth (BW), weaning (WW), yearling (YW) and final (FW) weight for the New Zealand data, together with current BREEDPLAN values for Angus.

		NZ estimates				BREEDPLAN values			
		BW	WW	YW	FW	BW	WW	YW	FW
A <sup>a</sup>	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 <sup>b</sup>	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 <sup>c</sup>	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 <sup>d</sup>	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

<sup>a</sup>Direct additive genetic effects : heritabilities on, correlations below the diagonal

<sup>b</sup>Maternal additive genetic effects: heritabilities on, correlations below the diagonal

<sup>c</sup>Maternal permanent environmental effects : "c-squared" effects on, correlations below the diagonal

<sup>d</sup>Phenotypic effects : variances on, correlations below the diagonal

**Table 6 :** Estimates of regression coefficients on dam age (1 : linear, 2 : quadratic; in kg/year and kg/year<sup>2</sup>, respectively) and age at weighing within sex (H : heifers, B : bulls; in kg/day), and the estimated difference in weight of calves of cows over that of calves of heifers ("heifer factor"; in kg), from univariate analyses.

Trait <sup>a</sup>		New Zealand				Australia			
		BW	WW	YW	FW	BW	WW	YW	FW
Dam age	1	0.2871	2.7363	2.6528	1.2978	0.3630	3.3015	2.7201	1.662
	2	-.05854	-.54744	-.44117	-.42622	-.06355	-.56505	-.50885	-.41025
Age	H	–	0.7883	0.7854	0.5693	–	0.7526	0.5829	0.4737
	B	–	0.8669	0.9684	0.7752	–	0.8615	0.8091	0.6967
"Heifer" factor		1.863	8.484	8.827	11.012	1.620	9.314	9.110	9.665

<sup>a</sup>BW : birth weight, WW : weaning weight, YW : yearling weight, FW : final weight

**Table 7 :** Summary statistics for the BREEDPLAN runs, together with means (in kg) for birth weight (BW), weaning weight (WW), yearling weight (YW) and final weight (FW) adjusted for differences in age at weighing and age of dam.

No. of		New Zealand	Australia
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 (kg)	BW	34.5	34.3
	WW	220	226
	YW	313	341
	FW	500	488

**Table 8 :** Mean estimated breeding values (EBV) and approximate accuracies ( $r_{TI} \times 100$ ) for birth weight (BW), weaning weight (WW), yearling weight (YW), final weight (FW) and the maternal effect on WW (Milk), for animals with proofs in Australia (AU) and New Zealand (NZ), together with observed ( $r$ ) and expected ( $E(r)$ ) correlations between EBVs, overall and calculated within year of birth (of animal) subclasses.

			BW	WW	YW	FW	Milk
			Cows				
Overall (n=459)	Mean $r_{TI}$	AU	38.4	37.8	36.9	36.3	29.5
		NZ	46.2	56.5	54.6	56.5	51.7
	Mean EBV	AU	0.1	0.4	1.7	0.5	0.2
		NZ	0.0	0.1	0.0	-0.6	0.1
	SD <sup>a</sup> EBV	AU	1.30	6.2	9.6	11.9	2.3
		NZ	1.34	9.4	14.3	19.1	3.0
			0.49	0.85	0.82	0.90	0.24
			0.47	0.56	0.55	0.56	0.19
			0.19	0.22	0.21	0.21	0.16
W/i year (n=338)	Mean $r_{TI}$	AU	38.1	37.7	36.6	36.0	30.4
		NZ	49.8	62.2	60.0	62.3	60.0
			0.23	0.25	0.22	0.26	0.09
			0.20	0.24	0.22	0.23	0.17
			Bulls				
Overall (n=381)	Mean $r_{TI}$	AU	56.6	56.6	55.7	54.7	44.0
		NZ	63.0	73.5	71.4	73.2	62.3
	Mean EBV	AU	0.8	4.6	7.4	8.4	0.8
		NZ	0.6	4.2	6.9	8.7	0.2
	SD EBV	AU	1.97	10.0	14.8	19.2	3.4
		NZ	1.95	13.3	20.2	27.0	3.6
			0.70	1.04	1.06	1.08	0.39
			0.72	0.77	0.78	0.77	0.37
			0.38	0.43	0.42	0.42	0.29
W/i year (n=301)	Mean $r_{TI}$	AU	59.4	59.9	58.8	57.9	47.1
		NZ	69.7	82.0	79.5	81.6	70.9
			0.57	0.65	0.65	0.64	0.37
			0.43	0.49	0.47	0.47	0.33

<sup>a</sup>Standard deviation

<sup>b</sup>Regression coefficient for the regression of EBV in NZ on EBV in AU

**Table 9** : Observed ( $r$ ) and expected ( $E(r)$ ) correlations between estimated breeding values (EBV) for birth weight (BW), weaning weight (WW), yearling weight (YW), final weight (FW) and the maternal effect on WW (Milk), for subsets of bulls with proofs in Australia (AU) and New Zealand (NZ), calculated within year of birth subclasses.

		BW	WW	YW	FW	Milk
		<i>Bulls with progeny in AU (n=153)</i>				
Mean $r_{TI}^a$	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>				
Mean $r_{TI}$	AU	66.1	67.2	65.8	65.1	55.5
	NZ	69.1	82.5	79.9	82.2	75.1
Mean EBV	AU	0.2	2.2	3.4	5.1	0.2
	NZ	0.0	-0.5	-0.2	0.2	1.0
SD <sup>b</sup> EBV	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>				
Mean $r_{TI}$	AU	91.3	89.1	88.5	86.7	71.3
	NZ	81.4	88.0	86.4	87.7	67.3
Mean EBV	AU	3.1	18.1	26.6	32.2	2.6
	NZ	2.7	19.0	29.1	38.9	-0.2
SD EBV	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

<sup>a</sup>Mean accuracy of evaluation  $\times 100$

<sup>b</sup>Standard deviation

**Figure 1** : Estimated breeding values (EBV) for weaning weight (in kg) in Australia and New Zealand, for bulls of NZ ( $\diamond$ ) and North American (+) origin.

