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GENETIC CORRELATIONS BETWEEN PUREBRED AND CROSSBRED PERFORMANCE OF POLL DORSET SHEEP

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SUMMARY

The genetic correlation between purebred and crossbred performance has implications for the utility of Australian Sheep Breeding Values (ASBVs) and the accuracy of genomic predications. The aim of this study was to estimate the genetic correlations between purebred and crossbred performance for terminal sire breeds. The genetic correlations estimated between purebred and crossbred progeny performance were all very high ranging from 0.44 to 1.00 and not significantly different from one for the weight and carcase traits examined in this study. These result support the use of the LAMBPLAN across breed ASBVs produced from animals with variable breed composition and also the use of crossbred animals in the genomic reference populations.

INTRODUCTION

Historically the LAMBPLAN genetic evaluation was based mostly on performance data from purebred flocks. The composition of ram breeding flocks is slowly changing with recent drops of rams becoming more composite in their breed makeup. In the 2014 drop of animals in the LAMBPLAN terminal sire analysis, only 24% of the animals recorded were purebred based on the pedigree information supplied.

ASBVs are used by commercial ram buyers across a wide variety of production systems but most likely these will be with the aim to produce crossbred progeny of varying breed composition. Thus it is important that the ASBVs predict sire ranking both in purebred and crossbred progeny. Ingham *et al.* (2005) demonstrated that LAMBPLAN ASBVs were moderately to highly correlated with crossbred progeny performance in maternal breeds. Banks *et al.* (2009) using data from terminal sire breeds observed similar correlations, however they highlighted the large variation in outcomes across traits and sites. Wei *et al.* (1991) pointed out that the correlation between purebred and crossbred performance (r_{PC}) depends on the amount of dominance in a trait, the distance between breeds (differences in allele frequency) and is also often confounded with genotype by environment interaction (GxE).

Furthermore most of the reference populations that underpin the Australian genomic evaluations for terminal sires are based on crossbred progeny (van der Werf *et al*. 2010). Thus an r_{PC} value of less than 1.0 could mean that the genomic breeding values derived from crossbred performance and ASBVs based on purebred performance could have different accuracies depending on what the breeding goal traits are. The aim of this study was to estimate the genetic correlations between the performance of purebred terminal sires and the performance of their crossbred progeny.

MATERIALS AND METHODS

Data. Pedigree and performance data were extracted from the Sheep Genetics LAMBPLAN terminal sire database (SG) (Brown *et al.* 2007). This database consists of pedigree and performance records submitted by Australian terminal sire ram breeders, and is used for genetic

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evaluation purposes. The database also contains information from the Sheep CRC Information Nucleus Flocks (INF) where all progeny from terminal sires have either a Merino dam (~50%) or a first cross Border Leicester x Merino dam.

From these data all animals with at least sire and dam pedigree for 2 generations and born from 2005 and later were included. Data were extracted for birth weight (Bwt), weaning weight (Wwt), post weaning weight (Pwt), post weaning fat depth (Pfat) and post weaning eye muscle depth (Pemd). All contemporary groups were transformed to a common mean within each group as is done routinely for Sheep Genetic analyses (Brown *et al.* 2007). Two analyses were undertaken using different combinations of records;

INF. Using data from all industry flocks animals with records were classified into a purebred trait if they had at least 90% breed composition of the breed of interest and animals from the Sheep CRC INF flocks into a crossbred trait if they had 50% of the breed of interest. Only the Poll Dorset breed had sufficient sires with purebred progeny in SG and first cross progeny in the INF flock to estimate the genetic correlations. The data set was reduced to all animals from the contemporary groups where the sires with progeny in both traits were represented.

SG. Using data from all flocks in Sheep Genetics, animals with records were classified into a purebred trait if they had at least 90% Poll Dorset breed composition and into a crossbred trait if they had between 25% and 75% of the Poll Dorset breed. In this dataset the breed composition of the progeny was highly variable and represented mostly crosses between terminals but also some crosses with maternal and Merino breeds.

The pedigree and breed composition was built using all ancestral information available. This resulted in pedigree files comprising between 10,835 and 132,138 animals for the INF dataset and between 379,047 and 223,424 animals for the SG dataset, depending on the trait being analysed. A summary of the number of records available for each trait in each data set is shown in Table 1.

Table 1. Summary of the number of records used for the purebred (PB) and crossbred (XB) traits, the number of sires with progeny for both traits (Sires) and the number of progeny records (Prog) from these common sires for each trait in the INF analysis (INF) and entire Sheep Genetics analysis (SG)

	Bwt		**Wwt**		**Pwt**		**Pfat**		**Pemd**	
	PB	**XB**	**PB**	**XB**	**PB**	**XB**	**PB**	**XB**	**PB**	**XB**
INF - Poll Dorset										
Rec.	117,958	3,898	120,237	3,254	107,696	3,070	91,686	2,559	90,580	2,559
Sires	118		125		126		123		123	
Prog.	27,131	3,464	28,719	3,098	25,123	2,986	21,832	2,468	21,652	2,468
SG - Poll Dorset										
Rec.	207,237	66,753	298,053	80,994	217,139	58,637	174,783	48,859	174,631	48,793
Sires	321		459		346		299		298	
Prog.	51,470	4,504	71,499	5,650	46,291	3,702	35,498	2,913	35,408	2,912

Models of analysis. Parameters were estimated in bivariate animal model analyses for each trait in ASReml (Gilmour *et al.* 2006) with purebred and crossbred performance considered as two different traits with a genetic correlation r_{PC}. For weight traits the fixed effects of contemporary group, birth type, rearing type, age of dam, and animal's age at measurement were fitted. For the carcase traits the fixed effects of contemporary group and the animal's liveweight at measurement (as quadratic) were fitted. Contemporary group was defined as flock, year of birth, sex, date of measurement, management group subclass. A random term for the direct genetic effects was modelled for all traits. An additional random term for sire by flock year interactions was fitted for all traits and maternal effects included for the weight traits.

RESULTS AND DISCUSSION

In the INF analysis the phenotypic variances and heritabilities were both significantly higher for the crossbred traits (Table 2). This might be due to the more diverse sampling of sires and also a greater genetic diversity in the dams, of which many were lacking complete pedigree with which to account for these effects. In the analyses of the entire SG datasets the phenotypic variance and heritabilities were not significantly different between the purebred performance and crossbred traits and also agreed with previously published estimates from these data (Brown *et al.* 2015).

Table 2. Phenotypic variance (σ^2_p), direct (h^2) heritability purebred (PB) and crossbred (XB) performance for each trait and breed in the INF analysis (INF) and entire Sheep Genetics analysis (SG) (s.e. in parentheses)

		Bwt		**Wwt**		**Pwt**		**Pfat**		**Pemd**	
		PB	**XB**	**PB**	**XB**	**PB**	**XB**	**PB**	**XB**	**PB**	**XB**
INF	σ^2_p	0.66 (0.00)	0.76 (0.00)	26.00 (0.14)	34.31 (1.16)	34.05 (0.19)	48.27 (1.71)	NC	NC	4.53 (0.03)	5.47 (0.16)
	h^2	0.15 (0.01)	0.07 (0.03)	0.29 (0.01)	0.82 (0.10)	0.27 (0.01)	0.64 (0.09)	NC	NC	0.27 (0.01)	0.28 (0.04)
SG	σ^2_p	0.64 (0.00)	0.60 (0.00)	25.34 (0.08)	22.59 (0.14)	32.93 (0.12)	32.08 (0.24)	0.36 (0.00)	0.40 (0.00)	4.48 (0.02)	4.41 (0.04)
	h^2	0.16 (0.00)	0.20 (0.01)	0.08 (0.00)	0.10 (0.01)	0.13 (0.00)	0.14 (0.01)	0.22 (0.01)	0.24 (0.01)	0.25 (0.01)	0.28 (0.01)

NC: Analysis did not converge

Estimates of genetic correlations between purebred and crossbred performance are shown in Table 3. Taking into account the standard errors of each estimate, all correlations were not significantly different to one. This indicates that genetically the performance of animals in purebred flocks is the same as that in crossbred flocks. This also suggests that crossbred data is just as valuable as purebred data for both estimation of breeding values and development of genomic predictions for Poll Dorsets. We expected to observe lower correlations in the INF dataset compared to the SG dataset as the INF dataset was dominated by terminal x Merino crosses which are genetically more divergent crosses than terminal x terminal crosses which dominate the SG dataset, but this was not supported by our estimates.

Table 3. Genetic correlation between purebred and crossbred performance for each trait in the INF analysis (INF) and entire Sheep Genetics analysis (SG) (s.e. in parentheses)

Dataset	**Bwt**	**Wwt**	**Pwt**	**Pfat**	**Pemd**
INF	0.97 (0.15)	0.94 (0.16)	1.00 (0.14)	0.95 (0.10)	0.99 (0.07)
SG	0.97 (0.06)	0.99 (0.06)	0.97 (0.07)	0.92 (0.07)	0.89 (0.06)

Pfec was also analysed however there were only sufficient data available for the Poll Dorset breed when using the entire SG database, There were 46 sires with both purebred and cross bred progeny and the estimated genetic correlation was 0.92 (0.40).

Our results agree with those of Nakavisut *et al*. (2005) who estimated high correlations between purebred and crossbred performance for growth and conformation traits in pigs. Wei and van der Werf (1995) estimated genetic correlations between purebred and crossbred performance for poultry egg production traits ranging between 0.56 and 0.99. Nakavisut *et al.* (2005) observed that for reproduction traits r_{PC} was lower and in some cases significantly less than one. Thus further investigation of these correlations for wool and reproduction traits is warranted in sheep, as it would be expected that such traits have more impact from dominance effects and therefore lower purebred crossbred correlations.

CONCLUSIONS

The genetic correlations estimated between purebred and crossbred progeny performance were all very high and not significantly different to one. These preliminary estimates from industry data are consistent with those in the literature and reconfirm the use of the LAMBPLAN across breed ASBVs produced from animals with variable breed composition and also the use of crossbred animals in the genomic reference populations.

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