Proc. Assoc. Advmt. Anim. Breed. Genet. 22:27-30

GENETIC CORRELATION BETWEEN PUREBRED AND CROSSBRED PERFORMANCE OF MERINO SHEEP FOR THREE WEIGHT TRAITS USING A GENOMIC RELATIONSHIP MATRIX.

N. Duijvesteijn[1,2] and J.H.J. van der Werf[1,2]

[1]School of Environmental and Rural Science, Univ. of New England, Armidale, NSW, Australia
[2]Cooperative Research Centre for Sheep Industry Innovation, Armidale, Australia 2351

SUMMARY

In sheep, genetic correlations between purebred and crossbred performance have not been studied extensively. The availability of genomic data on both purebreds and crossbreds makes it possible to estimate these genetic correlations for Merinos. Data of ~5000 purebred Merinos and ~ 5000 crossbred Merinos (sired by White Suffolk, Poll Dorset or Border Leicester) was used and the animals were genotyped with the Ovine 50K and phenotyped for three weight traits; weaning weight (WWT), post-weaning weight (PWWT) and carcass weight (CWT). Results showed a significant deviation from 1 for PWWT namely 0.61. While the correlation for WWT and CWT were not significant at 0.96 and 0.69 respectively. For a Merino breeding programs where emphasize is on increasing crossbred performance for PWWT (and CWT), purebred and crossbred performance should be combined in the genetic evaluation to achieve a good response to selection.

INTRODUCTION

Routine genetic evaluation of sheep in Australia is generally based on purebred performance. However, most lambs are produced as crossbreds For optimal ranking of breeding animals it is important to know whether breeding values predicted based on purebred performance, are also good predictors for crossbred performance. For example, a genetic correlation between purebred and crossbred performance (r_{pc}) of 0.8 (accurately estimated) will result in a loss in response of 20% in crossbreds when selection is based on purebred performance (Bijma *et al.* 2014). Some studies have identified moderate to high estimates for r_{pc} in Australian sheep (Ingham *et al.* 2005, Banks *et al.* 2009, Brown *et al.* 2015). These studies were all based on terminal sires having both purebred and crossbred offspring. The estimate of r_{pc} could in these cases be confounded with a potential genotype-by-environment interaction effect. It has been hard to estimate r_{pc} for Merinos as Merinos rams are rarely mated to other breeds. However, since the availability of genomic data, new opportunities arise as genetic parameters can be estimated even without structured family designs. For example, r_{pc} can be estimated through genomic relationships between purebred Merinos and crossbreds where the dam is a Merino. Such data exists abundantly in the Sheep CRC information Nucleus.

The aim of our study is to estimate r_{pc} for three weight traits, using genomic and phenotypic data on purebred Merinos and crosses between sires from terminal and maternal breeds and Merino dams.

MATERIALS AND METHODS

Animals, phenotypic and genotypic data. Data was extracted from two research datasets known as the Information Nucleus Flock (INF, (Van der Werf *et al.* 2010)) and the Sheep Genomics Flock (SGF, (White *et al.* 2012)). The data consisted of purebred Merinos (~40%) and crosses of terminal and maternal sires with Merino dams. Assigned genetic groups of base animals alongside pedigree information was used to determine the breed proportion. The sum of all Merino strains (Ultra/Superfine, Fine/Fine-medium, Medium/Strong, or undefined) was used to determine the percentage of purebred Merino. For this study, the crossbred animals should be at least 45% Merino and 45% from either Border Leicester (BL), Poll Dorset (PD) or White Suffolk (WS). The purebred

Merino were >95% Merino. Animals were genotyped using the 50k Illumina-Ovine SNP chip and 48,371 SNPs were used. Further quality control included Mendelian inconsistencies, plotting of the principal components to visually check breed assignment and removal of duplicate samples (off-diagonal relationship >0.9). To avoid that the covariance between purebred and crossbred offspring is confounded with some maternal effects, we randomly removed one of the offspring. In total the dataset consisted of 9,126 animals with 5,066 purebred Merino, 1,489 BL x Merino, 1,407 PD x Merino and 1,164 White Suffolk x Merino.

Recorded phenotypes for this study were weaning weight (WWT), post-weaning weight (PWWT) and carcass weight (CWT). Table 1 shows the number of phenotypic records for the Merino and their crosses with phenotypic information on the weight traits.

Table 1. Number of observation and phenotypic mean for purebred Merinos and their crosses.

Breed[1]	**N WWT**[2]	**Mean WWT**	**N PWWT**[3]	**Mean PWWT**	**N CWT**[4]	**Mean CWT**
Merino	5066	24.43	4623	38.67	1925	21.39
BL x Merino	1489	27.39	1095	44.24	729	22.07
PD x Merino	1407	28.47	739	45.85	1361	23.00
WS x Merino	1164	28.53	613	46.11	1128	22.89

[1]BL=Border Leicester, PD=Poll Dorset, WS=White Suffolk. [2]WWT=weaning weight. [3]PWWT=Post-weaning weight. [4]CWT=carcass weight.

Statistical analysis. Fixed effects fitted were derived from previous studies using similar data (Moghaddar *et al.* 2014) and were; birth type, rearing type, gender, age at measurement, breed and contemporary group defines as flock, birth year and management group.

The relationship matrix was constructed using genotypes to derive the genomic relationship matrix (Yang *et al.* 2010).

Linear mixed models were used to estimate the variance components and the data was fitted in the program MTG2 (Lee *et al.* 2016). Depending on the trait different random effects were fitted. The simplest model was chosen where the Likelihood Ratio Test showed no significant difference between including an extra random effect or not (results not shown).

Model 1 for WWT: $Y = Xb + Z_1a + Z_2m + e$

Model 2 for PWWT: $Y = Xb + Z_1a + Z_2m + Z_3sf + e$

Model 3 for CWT: $Y = Xb + Z_1a + Z_3sf + e$

Where **Y** is the vector with phenotypes, **b** is a vector of fixed effects, **a** is a vector of random additive genetic effects, **m** is the effect the dam, **sf** is a sire by flock interaction effects and **e** is a vector of random residual effects.

Bivariate analyses was used for all three traits, where the traits were defined by being measured either in purebred or crossbred animals, with the resulting correlation between additive genetic effects representing a correlation between purebred and crossbred performance (r_{pc}). Covariance between maternal effects in the purebred and crossbred dataset was set to zero, as dams were not allowed to have both crossbred and purebred offspring. Similarly, the covariance of the sire by flock interaction for purebred and crossbred performance was set to zero.

RESULTS

In Figure 1 the first two principle components (PC) are shown to indicate breed content of the dataset. The first PC explained 25.6 % of the genetic variance and the 2nd PC explained 19.7%. The first PC separates the Merinos from BL and the second PC separates WS and PD.

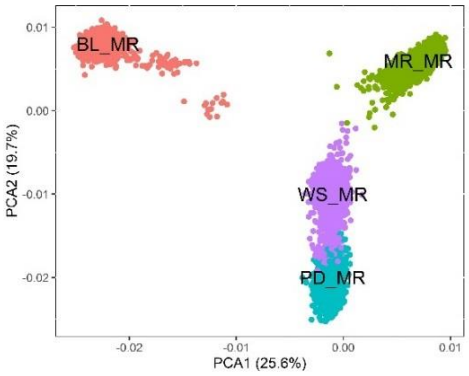

Figure 1. Plot of principal components (PC) 1 and 2 with the percentage of variance explained in brackets, where MR=Merino, BL=Border Leicester, PD=Poll Dorset, and WS=White Suffolk.

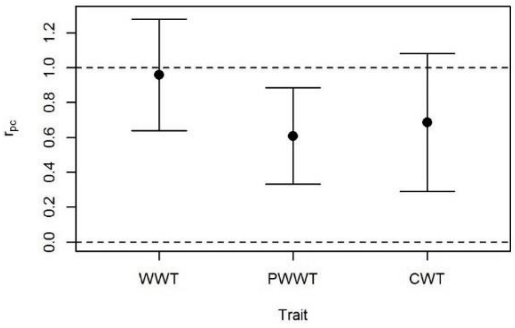

Figure 2. The genetic correlation between purebred (Merino) and crossbred performance for three weight traits. WWT= Weaning weight, PWWT=Post-weaning weight, and CWT=Carcass weight.

Table 2. Additive genetic variance (σ_a^2), maternal (σ_m^2), sire by flock interaction (σ_{sf}^2) and h^2 for each trait for purebred (PB) and crossbred (XB) performance.

		σ_a^2		σ_m^2		σ_{sf}^2		h^2	
Trait[1]	**PB/XB**	**comp[2]**	**se[3]**	**comp**	**Se**	**comp**	**se**	**comp**	**se**
WWT	PB	2.22	0.27	2.02	0.25			0.22	0.03
	XB	2.42	0.44	3.53	0.37			0.19	0.03
PWWT	PB	9.65	0.86	1.57	0.58	1.65	0.34	0.38	0.03
	XB	7.79	1.69	2.44	1.10	3.30	0.73	0.28	0.06
CWT	PB	2.65	0.41			0.60	0.20	0.38	0.05
	XB	1.16	0.24			0.37	0.11	0.20	0.04

[1]WWT=weaning weight; PWWT=Post-weaning weight; CWT=carcass weight. [2]Estimate of the variance component or ratio.[3]Approximate standard error on the estimate.

The results of the bivariate analyses are shown in Table 2 and the genetic correlation between purebred and crossbred performance (r_{pc}) with a 95% confidence interval is shown in Figure 2. The trait PWWT had the lowest r_{pc} which was 0.61 and was significantly different from one, while WWT was the highest (0.96). The trait CWT had a genetic correlation similar to PWWT (0.69), but due to lower number of records, the standard error on the estimate is larger. Results by breed group (WS X MR, BL X MR and PD X MR) showed similar trends (r_{pc} high for WWT and more variable for PWWT and CWT). In general, the r_{pc} for WS X MR and MR where lower than PD X MR or BL X MR, but due to the limited size of the data sets, standard errors were large (>0.20) and clear conclusions could not be drawn (results not shown).

DISCUSSION AND CONCLUSION

Results from the bivariate analysis show similar or slightly lower heritabilities based on genomic relationships compared to previous studies (Daetwyler *et al.* 2012, Moghaddar *et al.* 2014) ranging between 0.2 and 0.3. When the genetic correlation between purebred and crossbred performance (r_{pc}) was lower (i.e. for PWWT and CWT), the genetic variance as well as the heritability was larger in purebred animals than in crossbred animals. Brown et al (2015) found genetic correlations, which were not significantly deviating from one for similar weight traits. Their results were based on purebred Poll Dorset and their crosses. The current study focussed on a maternal contribution to crossbred performance, while other studies have often focussed on the paternal contribution to crossbred performance. A study by Moghaddar et al (2014) found a lower prediction accuracy for crossbreds for the trait PWWT for a similar dataset (genotyped Merinos including their crossbreds), lower than what was expected also after accounting for the number of haplotypes, i.e. twice the number of crossbreds gave lower accuracy than purebreds. This result could be partly explained by the r_{pc} being lower than 1. The number of studies calculating r_{pc} in sheep are limited. Other studies have mainly focused on performance traits in pigs and poultry where results seem to be very diverse in estimated r_{pc} also due to a lack of power in the datasets used (personal communication Y.C.J. Wientjes).

Generally the SE on the estimated genetic correlations were large in the current study. The SE was larger than expected when using the same size of dataset, but with paternal half sib groups (Falconer *et al.* 1996). This is likely a reflection of the smaller degree of relationship between the dam contributions and sire contributions.

To conclude, both crossbred performance and purebred performance need to be included in the estimation of the breeding values to increase crossbred performance of Merino crosses, especially for PWWT and CWT. In a Merino breeding program where both wool and meat production are selected for, the crossbred performance for production traits is relevant. If selection will be only based on purebred performance, a reduced selection response of around 40% can be expected for PWWT and CWT in the crossbreds. Therefore, genetic evaluation on traits such as PWWT and CWT should be based on both purebred and crossbred performance.

ACKNOWLEGEMENTS

The authors acknowledge the contributions of people from breeders and many CRC participant that contributed to the Sheep CRC Information Nucleus flocks. Also Nasir Moghaddar is acknowledged for his help retrieving data and helpful discussions.

REFERENCES

Banks, R., Brown, D. and Field, S. (2009) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **18**: 480.
Bijma, P. and Bastiaansen, J. W. (2014) *Genet. Sel. Evol.* **46**: 1.
Brown, D. and van der Werf, J.H. (2015) *Proc. Assoc. Advmt. Anim. Breed. Genet*. **21**: 177.
Daetwyler, H. D., Swan, A.A., van der Werf, J.H. *et al.* (2012) *Genet. Sel. Evol*. **44**: 1.
Falconer, D.S. and Mackay, T.F. (1996) In 'Introduction to quantitative genetics'. Longman, Essex United Kingdom.
Ingham, V., Fogarty, N., Gilmour, A., *et al.* (2005) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **16**: 227.
Lee, S.H. and Van Der Werf, J.H. (2016) *Bioinf.* **32**: 1420.
Moghaddar, N., Swan, A.A. and van der Werf, J.H. (2014) *Anim. Prod. Sci.* **54**: 544.
Moghaddar, N., Swan, A.A. and van der Werf, J.H. (2014) *Genet. Sel. Evol*. **46**: 1.
Van der Werf, J.H, Kinghorn, B., and Banks, R. (2010) *Anim. Prod. Sci.* **50**: 998.
White, J.D., Allingham, P.G., Gorman, C.M. *et al.* (2012) *Anim. Prod. Sci*. **52**: 157.
Yang, J., Benyamin, B., McEvoy, B.P. *et al.* (2010) *Nat. Genet.* **42**: 565.