GENETIC CORRELATIONS BETWEEN PRODUCTION TRAITS AND COMPONENTS OF REPRODUCTION IN MERINO SHEEP

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SUMMARY

Data from the Sheep Genetics database was used in investigation of the genetic relationships between components of reproduction and traits which may be useful indirect selection criteria for reproduction rate in Merino sheep. Pre-joining weight as well as fat and eye muscle depth were favourably genetically correlated with all reproduction traits except ewe rearing ability, as were more favourable scores for maternal behaviour, wrinkle and face cover. Correlations with pre-joining condition score were only significant when unadjusted for live weight. Maternal behaviour score was favourably correlated with all reproduction traits except ewe rearing ability but the standard errors were large, and more data are required to improve the precision of estimates. These results suggest that these traits could be recorded by breeders and included in the genetic evaluation system to improve the accuracy of selection for reproduction rate in Merino sheep.

INTRODUCTION

The Sheep Genetics (SG) genetic evaluation system produces Australian Sheep Breeding Values (ASBVs) for net reproduction rate with two trait definitions, number of lambs born or weaned per ewe joined (nlb and nlw respectively). While this has worked adequately in the past there are a number of key benefits from moving towards component trait analyses, including the ability to fit different models to each trait, allowing targeted selection for components and optimal use of the data available from industry.

As reproduction traits are lowly heritable, sex-linked and expressed later in life, the accuracy of ASBVs, particularly in young animals, can be increased through the use of information on correlated traits. To make use of such correlated information, accurate estimates of the genetic and phenotypic correlations between key traits are required, many of which are not currently available in the literature. Based on the estimates presented by Hatcher *et al*. (2015), Brown and Swan (2016), Brown *et al*. (2015) and many earlier publications, important relationships exist between production and reproduction traits which could contribute to the estimation of breeding values, and the development of selection indexes.

The aim of this paper is to estimate the correlations between some key production traits and reproduction traits in Merino sheep.

MATERIALS AND METHODS

Data. Pedigree and performance data were extracted from the Sheep Genetics MERINOSELECT database (Brown *et al*. 2007). This database consists of pedigree and performance records submitted by Australian and New Zealand Merino ram breeders, and is used for genetic evaluation purposes. The database also contains information from the Sheep CRC Information Nucleus Flock (INF) and the Resource Flock. From these data all animals with at least sire known, born 2000 and later, and from flocks with a history of recording reproduction traits were included. Data were extracted for all animals with early breech wrinkle (ebwr), late body wrinkle (lbdwr), late face cover (lface), post-weaning fat and eye muscle depth (pfat and pemd) and yearling fat and eye muscle depth (yfat and yemd). Annual ewe records were also extracted for pre-joining weight (pjwt), pre-joining condition score (pjcs), number of lambs born and weaned per ewe joined (nlb and nlw), maternal behaviour

of the ewe at lambing (mbs, 1 to 6, with 1 being best), ewe fertility (fert, dry or pregnant), litter size defined as the number of lambs born per ewe lambing (ls) and ewe rearing ability defined as the proportion of lambs weaned to lambs born per ewe lambing (era).

The pedigree was built using all ancestral information available. This resulted in pedigree files comprising between 78,563 and 191,392 animals for the combined dataset depending on the trait combination being analysed. A summary of the number of records available for each trait in each data set is shown in Table 1. The number of animals with records for two traits ranged from 1479 for yfat and era to 20,847 for pjwt and nlb. At the sire level, this range corresponded to 226 common sires for lface and era to 891 for pjwt and nlb.

Table 1: Summary of raw data used for each trait

Trait	Records	Animals	Sires	Flocks	Mean	SD	Min	Max
pjwt	20,847	13,315	891	27	49.97	9.21	24.00	105.50
pjcs	8,298	4,433	388	17	3.03	0.53	1.00	5.00
pfat	22,088	22,088	912	46	2.25	0.51	0.60	5.20
yfat	59,488	59,488	1,919	71	2.50	0.57	0.50	7.60
yemd	61,986	61,986	2,046	75	23.60	4.32	10.00	45.00
pemd	22,293	22,293	924	47	22.82	3.82	10.00	41.00
ebwr	85,779	85,779	1,509	55	2.27	0.99	1.00	5.00
lbdwr	35,627	35,627	928	28	2.01	0.87	1.00	5.00
lface	26,572	26,572	776	27	2.52	0.87	1.00	5.00
mbs	4,769	3,218	333	10	2.19	1.01	1.00	6.00
nlb	73,227	34,840	2,180	53	1.18	0.65	0.00	4.00
nlw	60,639	29,693	1,925	49	1.02	0.68	0.00	4.00
fert	73,227	34,840	2,180	53	0.87	0.33	0.00	1.00
ls	63,918	31,565	2,113	53	1.35	0.51	1.00	4.00
era	52,872	26,942	1,851	49	0.87	0.32	0.00	1.00

Models of analysis. Parameters were estimated in bivariate sire model analyses for each trait combination using ASReml (Gilmour *et al.* 2009). For wrinkle, weight, and condition score traits the fixed effects of contemporary group, birth type, rearing type, age of dam, and animal's age at measurement were fitted. For the body composition traits the fixed effects of contemporary group and the regression on an animal's live weight at measurement (linear and quadratic) were fitted. Contemporary group was defined as flock, year of birth, sex, date of measurement and management group subclass. For the reproduction traits the only effect fitted was the reproduction contemporary group, based on combinations of flock and year of lambing, management group, conception method (AI and Natural) and ewe age class (1, 2, and 3+ years). A random sire term for the direct genetic effects was modelled for all traits, including ancestral sire pedigree relationships. A sire model was chosen as the data structure did not support the estimation of all parameters using an animal model. An additional random term for maternal permanent environment effects was included for ebwr and pjwt. For pjcs, pjwt, mbs, and the reproduction traits repeated records were accounted for by including an additional random term to model the permanent environment of the animal. Sire by flock-year interactions were also fitted as an additional random term for all traits. Genetic groups were specified by flock of origin and fitted as random effects (Swan *et al.* 2014). As genetic groups did not significantly improve the fit of the model for mbs and the reproduction traits they were only fitted for production traits. As pre-joining weight and condition score are related an additional pre-joining condition score trait was created which included adjustment for weight at joining (pjcs2) by fitting pjwt as an additional covariate in the model.

RESULTS AND DISCUSSION

Large numbers of records were available for most traits (Table 1). The mean of 0.87 for era is slightly higher than the value of 0.81 reported by Bunter *et al.* (2016) derived from three well-recorded industry Merino flocks, suggesting that the lamb survival data may be biased upwards in this study due to incomplete recording. Heritability estimates (Table 2) for most traits were consistent with earlier publications based on MERINOSELECT data estimated predominantly using animal models. The heritabilities for pjcs and fat depth were slightly lower than previously observed as were those for most reproduction traits compared to the earlier estimates reported by Bunter *et al.* (2016).

Table 2: Phenotypic variance (σ^2_p), heritability (h^2), repeatability (r), permanent environment due to dam (dam PE), and sire by flock interaction (s^2) for each trait

Trait	σ^2_p	h^2	r	dam PE	s^2
pjwt	31.31 (2.10)	0.39 (0.11)	0.80 (0.11)	0.10 (0.11)	0.11 (0.11)
pjcs	0.12 (0.01)	0.11 (0.03)	0.22 (0.03)		0.07 (0.03)
pjcs2	0.10 (0.01)	0.11 (0.04)	0.22 (0.04)		0.06 (0.04)
pfat	0.22 (0.04)	0.12 (0.04)	.		0.03 (0.04)
yfat	0.28 (0.02)	0.10 (0.01)	.	.	0.03 (0.01)
pemd	3.68 (0.01)	0.21 (0.02)	.	.	0.04 (0.02)
yemd	3.98 (0.01)	0.22 (0.01)	.	.	0.03 (0.01)
ebwr	0.64 (0.01)	0.35 (0.03)	.	0.12 (0.03)	0.05 (0.03)
lbdwr	0.40 (0.01)	0.37 (0.05)	.	.	0.03 (0.05)
lface	0.50 (0.01)	0.35 (0.01)	.	.	0.04 (0.01)
mbs	0.81 (0.01)	0.09 (0.02)	0.22 (0.02)		0.05 (0.02)
nlb	0.33 (0.01)	0.07 (0.01)	0.16 (0.01)	.	0.01 (0.01)
nlw	0.38 (0.01)	0.04 (0.01)	0.12 (0.01)	.	0.01 (0.01)
fert	0.09 (0.01)	0.06 (0.01)	0.16 (0.01)	.	0.02 (0.01)
ls	0.21 (0.01)	0.07 (0.01)	0.16 (0.01)	.	0.01 (0.01)
era	0.09 (0.01)	0.02 (0.01)	0.11 (0.01)	.	0.01 (0.01)

Pre-joining weight and condition score were moderately correlated genetically (0.50±0.09) and phenotypically (0.29±0.02). Pre-joining weight, early in life fat and eye muscle depth were favourably correlated with all reproduction traits except ewe rearing ability (Table 3). These results generally agree with the earlier work of Brown and Swan (2016). However, the inconsistent correlations of body composition traits with ewe rearing ability are at odds with earlier work and may be a reflection of the incomplete recording of lamb survival, as mentioned above. Further studies with high quality data to study relationships with era are certainly warranted. Better scores for wrinkle and face cover were generally favourably associated with reproduction traits. The lack of a correlation between wrinkle and ewe rearing ability is inconsistent with results of Hatcher *et al.* (2015) who estimated significant favourable relationships between these traits in both industry and INF data. Correlations of pre-joining condition score with nlb, nlw or fert were only significant when unadjusted for live weight. Walkom and Brown (2016) estimated the correlations between these traits using just the INF data and found no significant relationship between condition score and reproduction traits unless condition score was adjusted for previous reproduction status. These results are also at odds with those observed for the fat and eye muscle depth traits which were highly genetically correlated with condition score in these data (rg between 0.68 and 0.98 across the 4

ultrasound traits) and demonstrated by earlier work of Walkom and Brown (2016). As the results for condition score appear quite inconsistent across analyses and data sets more industry data are clearly required to confirm the relationships between body composition and reproductive traits.

Maternal behaviour score was favourably correlated with all reproduction traits in absolute terms, except for ewe rearing ability. However, standard errors were large and the number of ewes recorded for mbs was relatively low, suggesting that more data are required to confirm these results.

While this study has not included other weight and wool traits, it is known that significant relationships exist between live weight, scrotal circumference, fleece weight, fibre diameter, fibre curvature and staple length with the reproductive traits and these should also be considered.

Table 3: Genetic correlations between reproduction traits, and production and visual traits

	pjwt	pjcs	pjcs2	ebwr	lbdwr	lface	pfat	yfat	pemd	yemd	mbs
nlb	0.51	0.40	-0.01	-0.32	-0.46	-0.44	0.42	0.40	0.38	0.42	-0.16
	(0.09)	(0.16)	(0.17)	(0.09)	(0.10)	(0.12)	(0.14)	(0.10)	(0.12)	(0.09)	(0.23)
nlw	0.50	0.41	-0.04	-0.43	-0.50	-0.48	0.40	0.41	0.34	0.50	-0.17
	(0.11)	(0.19)	(0.19)	(0.10)	(0.12)	(0.14)	(0.16)	(0.13)	(0.15)	(0.11)	(0.26)
fert	0.20	0.42	0.28	-0.31	-0.54	-0.09	0.59	0.34	0.45	0.37	-0.22
	(0.11)	(0.18)	(0.18)	(0.10)	(0.11)	(0.14)	(0.15)	(0.12)	(0.13)	(0.10)	(0.26)
ls	0.56	0.27	-0.25	-0.22	-0.28	-0.52	0.15	0.32	0.22	0.32	-0.06
	(0.08)	(0.17)	(0.17)	(0.09)	(0.10)	(0.11)	(0.15)	(0.10)	(0.13)	(0.09)	(0.22)
Era	0.07	0.14	0.01	-0.10	-0.09	0.04	-0.27	-0.00	-0.16	0.14	0.12
	(0.15)	(0.28)	(0.27)	(0.15)	(0.18)	(0.21)	(0.24)	(0.00)	(0.21)	(0.15)	(0.33)

CONCLUSION

These results suggest that these traits could usefully be recorded more by breeders and included in the genetic evaluation system to improve the accuracy of selection for reproduction rate in Merino sheep. More high quality data are required for maternal behaviour score, condition score and ewe rearing ability to confirm associations between these traits.

ACKNOWLEDGEMENTS

REFERENCES

Brown D.J., Huisman A.E., Swan A.A., Graser H.-U., Woolaston R.R., *et al.* (2007) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **17:** 187.

Brown D.J., Fogarty N.M., Iker C.L., Ferguson D.M., Blache D., *et al.* (2015) *Anim. Prod. Sci.* **56**: 767.

Brown D.J. and Swan A.A. (2016) *Anim. Prod. Sci.* **56**: 690.

Bunter K.L., Swan A.A., Purvis, I.W. and Brown D.J. (2016) *Anim. Prod. Sci.* **56**: 679.

Gilmour A.R., Gogel B.J., Cullis B.R. and Thompson R. (2009) '*ASREML user Guide Release 3.0*' VSN International Ltd, Hemel Hempstead, UK.

Hatcher S., Brown D.J., Brien F.D. and Hebart M.L. (2015) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **21:** 354.

Swan A.A., Brown D.J. and van der Werf J.H.J (2016) *Anim. Prod. Sci.* **56:** 87.

Walkom S.F. and Brown D.J. (2016) *Anim. Prod. Sci.* **57**: 20.