GENETIC RELATIONSHIPS BETWEEN BREECH COVER, WRINKLE AND LAMB SURVIVAL IN MERINO SHEEP

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SUMMARY

Phenotypic and genetic correlations (r_g) between breech cover and wrinkle scores with lamb survival were estimated from research (Cooperative Research Centre for Sheep Industry Innovation (Sheep CRC) Information Nucleus (IN)) and industry data (Sheep Genetics (SG) MERINOSELECT). Breech cover had low to moderate antagonistic r_g (0.24 to 0.53) with direct lamb survival, despite favourable r_g with some lamb survival indicator traits. While there was some inconsistency in the direction of r_g at the various age expressions of wrinkle and direct lamb survival, the r_g between wrinkle and lamb survival tended to be negative and favourable.

INTRODUCTION

High wrinkle scores are related to poorer reproductive outcomes (Turner and Young 1969). Folds$^+$ ewes, selected on total fold score at four months of age, weaned half as many lambs during their lifetime as Folds$^-$ ewes (Dun 1964). Folds$^+$ rams were less fertile and sired fewer lambs than Folds$^-$ rams irrespective of whether they were mated to Folds$^+$ or Folds$^-$ ewes (Dun and Hamilton 1965). In addition, more Folds$^+$ single-born lambs died compared with Folds$^-$ singletons due to dystocia resulting from increased birthweight together with the smaller size of the Folds$^+$ ewe (Dun and Hamilton 1965). While these early studies provided insight into the relationship between wrinkle and reproduction, few studies since have reported phenotypic and genetic correlations between these traits and none have included breech cover. The recent focus by some Merino breeders to genetically reduce wrinkle, to decrease flystrike and the need for mulesing (James 2006), is likely to generate correlated improvements in Merino reproductive performance. This paper reports estimates of phenotypic and genetic correlations between wrinkle and breech cover with lamb survival to weaning (a key component of reproductive performance), assessed as a trait of both the ewe and the lamb, using a combination of industry and research data.

MATERIALS AND METHODS

Research data. Data from Merino progeny born into the Sheep CRC's IN (van der Werf *et al.* 2010) between 2007 and 2011 were used. Twice daily lambing rounds were conducted from the start of lambing in each year to uniquely identify each lamb, designate a dam, confirm birth status (alive or dead, LS0), collect early life information (sex and type of birth) and record birth weight (BWT), birth coat score (BCS), overall birth vigour (OBV), lambing ease (LE), rectal temperature (RT), three skeletal measures (crown rump length CRL, metacarpal length ML and thorax circumference THO) and a suite of timed lamb behaviours (time taken from lamb release after tagging to bleat BLT, stand STD, contact the ewe CONT, contact the udder UDD and follow the ewe FOLL) as described by Brien *et al.* (2015). Identities of all surviving lambs were confirmed at 3 (LS3) and 7 days of age (LS7) and at weaning (approx. 91 days of age, LSURV). Breech cover

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(BCOV), breech (BRWR), body (BDWR) and neck (NKWR) wrinkle were scored according to industry standards (AWI Ltd and MLA Ltd 2013) at marking (7-43 days, BCOV and BRWR only) as yearlings (11 months) and adults (23 months). Variance components were estimated using ASReml (Gilmour *et al.* 2009) from a series of univariate animal models (see Brien *et al.* (2015) for the lamb survival traits and Hatcher and Preston (2015) for BCOV and wrinkle traits). Phenotypic and genetic correlations between the lamb survival, BCOV and wrinkle traits were estimated from appropriate covariances using a series of bivariate analyses with the residual covariance with the direct lamb survival traits set to 0.

Industry data. Pedigree and performance data were extracted from the SG MERINOSELECT database (Brown *et al.* 2007). A subset of 29 flocks was selected based on their recording of wrinkle and reproduction traits and were a mix of industry ram breeders, research and sire evaluation flocks. From within these flocks all animals with both sire and dam pedigree, and born since 1990 were included. Data were extracted for all early breech wrinkle (EBWR, marking to weaning), late body wrinkle (LBDWR, yearling to adult), lamb survival as a trait of the lamb (LSURV) and lamb survival as a trait of the ewe (SURV) (Table 2). The pedigree was built using all available ancestral information. For the bivariate analyses there was between 270 and 607 sires with records for both traits depending on the trait combination. Parameters were estimated in bivariate animal model analyses in ASReml (Gilmour *et al.* 2009). For EBWR and LBDWR fixed effects of contemporary group (defined as flock, year of birth, sex, date of measurement, management group subclass), birth type, rearing type, age of dam, and animal's age at measurement were fitted. For LSURV and SURV contemporary group (defined as flock, year of lambing, ewe age class (1, 2 and 3+) and management group) was the only fixed effect fitted. Random terms for direct genetic effects and sire by flock-year were fitted for all traits. Maternal permanent environment was included for wrinkle and LSURV and a repeated record term added for SURV. For correlations involving LSURV, the residual covariance was fixed to zero as only surviving lambs had records for both traits. Genetic groups were fitted in all analyses and allocated on a flock basis for linked flocks with sufficient data (Swan *et al*. 2015).

RESULTS AND DISCUSSION

Research data. Some of the r_g, particularly those involving direct lamb survival, had large standard errors (Table 1). This may be due to the dataset size, the number of sire families represented or the low additive variation for the direct lamb survival traits ($h^2<0.01$, Brien *et al.* 2015). Nevertheless, until such time as lamb survival records become more widely represented in industry data or further analysis is done on pooled resource flock data, these results are likely to remain the only available estimates.

There were unfavourable r_g between marking, yearling and adult BCOV and direct lamb survival (Table 1), such that selection for increased bare area around the perineum and breech will generate correlated decreases in lamb survival. The low negative r_g between BWT and marking BCOV implies that selection for bare breeches is genetically associated with higher BWT, while the low positive r_g of yearling and adult BCOV with RT may be indicative of decreased thermoregulation capacity. There were favourable r_g between BCOV and LE as well as some timed lamb behaviours, no significant r_g between BCOV and any of the skeletal measurements and the direction of the r_g with BCS, OBV and the timed lamb behaviours varied with age. However, as RT had the strongest r_g with LSURV among the suite of indicator traits (Brien *et al*. 2015), it is likely to dominate the genetic relationships with lamb survival despite the favourable relationships between BCOV and the other indicator traits.

The medium to high negative rg between the marking and yearling expressions of BRWR with direct lamb survival were indicative of a favourable relationship. So selection for plainer breeches will generate correlated improvements in lamb survival. Plainer breeches were also genetically associated with lower BWT, smaller skeletal measurements and higher RT. However, the r_g between the age expressions of BRWR with OBV and the timed lamb behaviours varied in direction. The r_g between the various lamb survival traits and yearling BRWR and BDWR were similar as were those between adult NKWR and BRWR. Due to the nature of the IN data set, our ability to fully account for across flock differences via fitting genetic groups was limited. As a result, the r_g may be inflated compared to what would be observed within other flocks.

Table 1. Genetic correlations between a) marking and yearling and b) adult of breech cover (BCOV), breech (BRWR), body (BDWR) and neck (NKWR) wrinkle with lamb survival and various indirect selection criteria for lamb survival in the Sheep CRC IN

High r_g (≥0.6) are highlighted in **bold** and medium r_g are underlined. The r_g for LS0, BWT, CRL and BLT have been omitted from 1b) as they were all negligible (|r|<0.2).

a)	Marking		Yearling			
	BCOV	BRWR	BCOV	BRWR	BDWR	NKWR
LS0	-0.30±0.08	-0.03±0.05	0.53±0.13	-0.20±0.06	-0.37±0.06	0.16±0.07
LS3	0.24±0.22	-0.42±0.14	0.34±0.30	-0.41±0.17	-0.59±0.16	-0.06±0.18
LS7	0.49±0.25	-0.48±0.16	0.43±0.31	-0.49±0.18	-0.59±0.16	-0.16±0.18
LSURV	0.49±0.68	**-0.99±0.71**	0.21±0.63	**-0.98±0.87**	**-0.82±0.63**	-0.39±0.47
BWT	-0.27±0.12	0.38±0.08	-0.06±0.19	0.12±0.10	0.29±0.10	-0.01±0.11
BCS	-0.37±0.13	**-0.60±0.08**	0.32±0.21	-0.08±0.11	-0.11±0.11	-0.11±0.12
OBV	0.38±0.16	-0.30±0.11	-0.38±0.27	0.10±0.14	0.06±0.14	-0.28±0.15
LE	0.26±0.26	-0.38±0.19	-0.08±0.38	-0.17±0.22	-0.32±0.22	-0.48±0.23
RT	0.13±0.26	-0.36±0.18	0.35±0.36	-0.08±0.22	0.14±0.22	0.17±0.23
CRL	0.04±0.13	0.20±0.08	-0.04±0.19	0.11±0.10	0.18±0.09	-0.02±0.11
ML	0.12±0.19	0.32±0.13	0.16±0.26	0.33±0.14	0.39±0.13	0.27±0.15
THO	-0.13±0.16	0.31±0.09	0.10±0.22	0.22±0.11	0.38±0.11	0.32±0.13
BLT	-0.05±0.21	-0.21±0.15	0.57±0.30	-0.08±0.17	0.01±0.17	0.10±0.19
STD	0.01±0.31	-0.36±0.23	**0.73±0.37**	0.09±0.23	-0.10±0.22	0.05±0.25
CONT	-0.25±0.22	-0.22±0.14	-0.08±0.28	-0.11±0.15	-0.15±0.15	-0.19±0.17
UDD	-0.03±0.51	-0.00±0.39	0.46±0.61	-0.11±0.41	-0.37±0.44	**-0.69±0.48**
FOLL	-0.52±0.28	-0.37±0.22	0.23±0.39	-0.09±0.23	-0.22±0.24	-0.08±0.26

b)	Adult			
	BCOV	BRWR	BDWR	NKWR
LS3	0.17±0.36	0.04±0.19	0.06±0.23	0.44±0.28
LS7	0.34±0.37	0.03±0.20	-0.01±0.23	0.44±0.28
LSURV	-0.14±0.72	0.10±0.39	-0.07±0.46	**0.64±0.66**
BCS	0.44±0.23	-0.09±0.13	0.00±0.15	0.06±0.18
OBV	0.39±0.25	0.15±0.15	-0.38±0.28	-0.05±0.22
LE	**0.71±0.46**	-0.03±0.04	-0.30±0.28	**-0.71±0.32**
RT	0.22±0.40	-0.09±0.23	0.03±0.29	0.12±0.33
ML	-0.06±0.27	0.10±0.17	0.02±0.19	0.01±0.22
THO	0.01±0.22	0.46±0.14	0.29±0.16	0.57±0.18
STD	**0.66±0.35**	0.32±0.32	0.11±0.30	-0.03±0.32
CONT	0.07±0.27	0.23±0.18	0.10±0.20	0.06±0.23
UDD	**0.64±0.73**	-0.38±0.49	0.13±0.48	-0.24±0.53
FOLL	0.58±0.34	0.09±0.27	0.05±0.28	-0.30±0.31

Industry data. EBWR and LBDWR were moderately heritable and had small but significant maternal effects (Table 2) consistent with IN estimates (Hatcher and Preston 2015). The heritability of LSURV was low (0.02) with a significant maternal effect (0.14) which agreed with IN estimates (Brien *et al.* 2015). The r_g between LSURV and wrinkle were small and negative but not significantly different from zero (Table 2). The IN results were generally stronger negative, but also often not significantly different to zero. However, SURV was more negatively correlated with wrinkle both at the genetic and maternal permanent environment levels than LSURV.

Table 2. Phenotypic variance (σ^2_p), maternal permanent environment (PE), direct heritability (diagonal bold type), genetic correlations (below diagonal), maternal permanent environmental correlation (above diagonal) between wrinkle and lamb survival traits

	EBWR	LBDWR	LSURV	SURV
Records	80,467	38,348	46,826	11,957
σ^2_p	0.59±0.00	0.51±0.00	0.11±0.00	0.09±0.00
PE	0.04±0.01	0.00±0.01	0.14±0.01	NE
EBWR	**0.32±0.01**	NE	-0.14±0.06	NE
LBDWR	NE	**0.40±0.01**	0.99±0.79	NE
LSURV	-0.05±0.10	-0.24±0.20	**0.02±0.01**	NE
SURV	-0.17±0.11	-0.28±0.18	NE	**0.03±0.01**

NE: not estimated or not estimable

CONCLUSIONS

Merino breeding programs with an emphasis on reducing wrinkle are likely to generate correlated improvements in reproduction both as a trait of the ewe and the lamb. While breeders using BCOV as an indirect selection criterion for flystrike could expect correlated decreases in direct lamb survival despite favourable genetic relationships with some lamb survival indicator traits. However the inconsistency between age expressions of the wrinkle and BCOV traits due to low precision of the genetic correlations does add some uncertainty to these conclusions. The inaccurate parameter estimates are due to some animals not having both records, as dead lambs were not scored for BCOV or wrinkle and we therefore rely on the genetic relationships between animals via the pedigree to estimate these genetic correlations. Accurate parameters and multiple trait index predictions are required to properly quantify the impact of these relationships for Merino breeding programs.

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