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# GENETIC VARIATION OF WEANER SURVIVAL IN MERINO SHEEP AND ITS RELATIONSHIPS WITH GROWTH AND WOOL

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## SUMMARY

There is little evidence that mortality rates in Australian sheep during the period after weaning are improving over time. This paper explores the potential for producers to select to improve survival rates and the potential impact this may have on key production traits. A total of 114,272 weaner survival records were obtained from a wide variety of Australian Merino sheep types and production systems. Weaner survival, a binary dependent variable, was analysed as a continuous trait using a sire model. The heritability of weaner survival was estimated at 0.05 ± 0.01, significantly greater than zero. The survival of weaned lambs to yearling age was influenced by weaning weight with higher survival rates observed in heavier lambs ($r_g$ = 0.14). Weaner survival adjusted for weaning weight was found to be antagonistically genetically correlated with fleece weight ($r_g$ = -0.12 to -0.24). Due to antagonistic genetic correlations with greasy fleece weight and other production traits, producers should record weaner survival which will assist Sheep Genetics to produce breeding values and incorporate weaner survival in future indexes.

## INTRODUCTION

The Australian sheep flock includes a significant proportion of young Merino sheep that are often characterised by poor growth, slower development and high mortality in the period follow weaning (Hatcher *et al.* 2008). There is little evidence to show that survival of Merino sheep for the post-weaning period have improved since the 1950's (Hatcher *et al.* 2008) with weaner mortality rates in Australian Merino flocks at a constant 5.2% (Campbell *et al.* 2014). Current management protocols to improve weaner survival are based on providing adequate nutrition and controlling worm burdens and fly strike to enable weaners to achieve live weight targets by weaning and maintain positive growth rates in the period following weaning (Hatcher *et al.* 2008, Campbell *et al.* 2014). It has been reported that lighter weaners were less able to cope with nutritional and or other stresses owing to lower energy reserves than heavier weaners and to improve post-weaning survival, Merinos should be managed to achieve approximately 45% of mature liveweight at weaning (Thompson *et al.* 2011). However, genetic parameters for weaner survival in sheep have not been estimated and the capacity to select for improved survival rates is unknown. The aims of this paper were to quantify the genetic variation in the Australian Merino population for survival from weaning to the yearling stage (7 to 9 months after weaning) and to estimate the genetic relationships between survival and key growth, carcass and wool traits.

## MATERIALS AND METHODS

Data were obtained from 18 Merino flocks with lambs born from 1990 to 2014. The flocks included ram breeding, sire evaluation and research flocks from across Australia contributing to the MERINOSELECT database (Brown *et al.* 2007). Weaner survival was analysed as a binary trait of the lamb with animals assigned a value of 1 if alive or 0 if dead at the yearling stage. Weaner survival was verified by the presence of weight or production records provided to Sheep Genetics at or after

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the yearling stage (7 - 9 month period after weaning). Only animals with a known sire (syndicate sires removed) and a weaning weight record were included in the analyses. Contemporary groups (flock x location x year x sex) with a large number of animals which could not be assigned as dead or alive were excluded from the study. After data cleaning and the removal of uninformative contemporary groups, 104,557 weaner survival records were available for analysis with an average survival rate of 93%.

The growth and wool traits analysed included weaning, post-weaning and yearling liveweight (kg), ultrasound fat and muscle depth (mm), greasy fleece weight (kg), fibre diameter (µm), coefficient of variation (cv) in fibre diameter (%), curvature, staple length (mm), and staple strength (N/ktex). All scan and fleece traits were recorded at the yearling stage.

**Statistical analysis.** Genetic parameter estimates were calculated using a sire model in ASReml (Gilmour *et al.* 2009). The models fitted to the data were developed and described by Brown and Swan (2016) and was based on the linear mixed model:

$$y = X\hat{\beta} + Z_1 s + Z_2 m + Z_2 mp + sxf + e$$

where, $y$ is a vector of observations for the trait; $\hat{\beta}$ is a vector of the fixed effects including birth type (1,2,3,4+), rearing type (1,2,3+), age of dam (as a linear and quadratic term) (mean 4.5 years of age), age of the animal (linear) and contemporary group. Contemporary group for the production traits described flock, management group, sex, and date of measurement (Brown and Swan 2016). All contemporary groups were transformed to a common mean as done routinely for Sheep Genetic analyses (Brown *et al.* 2007). The vectors $s$, $m$, and $mp$ are the sire genetic effects, maternal genetic effects, and permanent environment due to dam effects, respectively. The incidence matrices $X$, $Z_1$, and $Z_2$ relate the respective effects to $y$; and $e$ is a vector of random error effects. A sire by flock ($sxf$) term was also fitted as random for the production traits.

Weaner survival was recorded as a binary trait (0/1) but analysed as a continuous trait. A logit function was also tested, but for computational ease was not used in the bi-variate analysis. The fixed effect models fitted for weaner survival were based on the terms normally fitted for weaning weight in Sheep Genetics analyses. Data limitations (unavailable for a large proportion of individuals) meant that the contemporary group structure could not include weaning date, age at weaning or weaning management groups, all of which are fitted in the routine genetic evaluation of weaning weight (Brown and Swan 2016). Thus, contemporary groups for weaner survival described flock, flock location, year of birth and sex (male or female). The analysis was repeated with weaning weight fitted as a covariate for survival, in part to help account for the influence of weaning date, age at weaning, weaning management groups and maternal effects. The influence of weaning weight was tested by fitting weaning weight, first, as a covariate (linear effect) across the population and also as a nested covariate within contemporary group.

## RESULTS AND DISCUSSION

**The association of weaner weight with survival.** Weaning weight exerted a strong, positive and highly significant effect on weaner survival, which is consistent with other reports in the literature (Hatcher *et al.* 2008, Thompson *et al.* 2011). In the current study, the regression of weaner survival on weaning weight predicted that on average, an 0.006 ± 0.001 (0.6%) improvement in weaner survival for every 1 kilogram increase in weaning weight, assuming a linear relationship (weaning weight; mean of 25kg, range of 6 - 49kg). However, the influence of weaning weight on weaner survival was not uniform across contemporary groups with the nested effect of weaning weight was highly significant and ranging from -0.078 to +0.050 weaner survival / kg of weaning weight. Some of the variation in survival responses to weaning weight between contemporary groups observed in the current study was likely to be due to interactions between weaning weight and post-weaning growth rate. Although not tested in this study, Thompson *et al.* (2011) concluded that post-weaning growth rates should exceed 30 g/day, and that growth rates below this level resulted in a decline in survival rates. Overall, the results suggest that the optimum weaning weight in pertaining to weaner survival is likely to differ across production systems, breeds and environments.

**Variance components.** Heritability of weaner survival in Merinos was low but significantly greater than zero and estimated at 0.05 ± 0.01 (Table 1) when analysed from a sire model. An animal model was also tested and estimated a heritability of 0.13 ± 0.01. Maternal genetic and permanent environmental effects were minimal and not significant whether an animal or sire model was fitted but were in part limited, since the structure of the survival trait means that all dams will have to have survived to the yearling stage. However, the significant effect of weaning weight on weaner survival is likely to be capturing some of the maternal environmental influence. Fitting weaning weight as a covariate had a small but not significant effect on the heritability and additive variance of weaner survival. Analysing weaner survival as a binary trait using a sire model with the logit-link function produced a heritability on the underlying scale of 0.19 which when transformed using the average frequency (incidence) equated to an approximate estimate of 0.01 on the observed scale.

**Table 1: Heritability of weaner survival and genetic correlations for weaner survival with production traits when weaner survival is unadjusted for weaning weight, adjusted for average weaning weight (adjusted) or within each contemporary group (nested)**

| Trait | Records | unadjusted | adjusted | nested |
|---|---|---|---|---|
| Heritability of weaner survival | 104,557 | 0.055 ± 0.005 | 0.053 ± 0.005 | 0.052 ± 0.005 |
| Genetic correlations with: | | | | |
| Weaning weight | 193,784 | 0.14 ± 0.06 | - | - |
| Post-weaning weight | 106,968 | 0.30 ± 0.06 | - | - |
| Yearling weight | 110,023 | 0.24 ± 0.06 | - | - |
| Yearling fat depth | 39,318 | 0.34 ± 0.11 | 0.35 ± 0.10 | 0.36 ± 0.10 |
| Yearling eye muscle depth | 39,968 | 0.35 ± 0.09 | 0.13 ± 0.14 | 0.31 ± 0.09 |
| Yearling greasy fleece weight | 78,079 | -0.12 ± 0.08 | -0.22 ± 0.08 | -0.24 ± 0.08 |
| Yearling fibre diameter | 82,293 | 0.16 ± 0.07 | 0.07 ± 0.08 | 0.07 ± 0.08 |
| Yearling fibre diameter cv | 81,687 | -0.09 ± 0.08 | -0.07 ± 0.08 | -0.07 ± 0.08 |
| Yearling curvature | 74,575 | 0.05 ± 0.07 | 0.08 ± 0.07 | 0.07 ± 0.07 |
| Yearling staple strength | 31,131 | 0.10 ± 0.10 | 0.11 ± 0.10 | 0.10 ± 0.10 |
| Yearling staple length | 54,069 | 0.15 ± 0.08 | 0.10 ± 0.08 | 0.10 ± 0.08 |

**Genetic relationship of weaner survival with production traits.** Weaner survival (unadjusted for weaning weight) was moderately positively genetically correlated with liveweight (Table 1). This was consistent with the significant phenotypic influence of weaning weight on weaner survival observed in this study and in the literature (Hatcher *et al.* 2008, Thompson *et al.* 2011).

The genetic correlations of weaner survival with ultrasound fat depth was moderate and positive at 0.34 (Table 1). The genetic correlation for lamb survival with fat depth of the carcase at the GR site and the 5th rib has been reported as 0.34 and 0.00, respectively (Brien *et al.* 2013). These results suggest that high "genetic fat" was favourably associated with survival in lambs prior to and following weaning, and this is independent of any effect of weaning weight *per se*. The genetic correlations for weaner survival with ultrasound muscle depth were positive and ranged from 0.13 to 0.35 (Table 1). Lamb survival to weaning was lowly positively correlated with carcase eye muscle depth and area with Brien *et al.* (2013) reporting estimates of 0.17 and 0.04, respectively. Low to moderate positive correlations observed in this study suggest that weaner survival rates to the post-weaning stage will improve with selection for increased fat and muscle depth.

The genetic correlation of greasy fleece weight with weaner survival was -0.12, suggesting a weak genetic relationship (Table 1). After adjusting weaner survival for the effect of weaning weight this genetic correlation was slightly stronger at -0.24 (Table 1). These low negative genetic correlations suggest that high genetic fleece weight is associated with poorer survival rates from weaning to post-weaning at a standardised weaning weight (weight corrected). Previous research by Ferguson *et al.* (2007) and Hatcher and Atkins (2007) have both indicated unfavourable phenotypic associations of fleece weight with lamb survival. Adams *et al.* (2006) proposed that Merinos genetically superior for fleece weights have relatively smaller energy reserves which could contribute to the unfavourable genetic correlations observed in this study.

The genetic correlations for weaner survival and fleece quality traits, including mean and coefficient of variation in fibre diameter, curvature, staple length and staple strength were all low and generally not significantly different from zero (Table 1). Adjusting weaner survival for weaning weight had no significant impact on the genetic correlations between survival and wool quality traits.

## CONCLUSION

Survival in Merinos from weaning to the yearling stage is lowly heritable but not zero, indicating that genetic variation exists which could be exploited. The survival of lambs from weaning to yearling was significantly influenced by weaning weight, with higher survival rates observed in genetically heavier lambs. The relationship with weight indicated that selection for heavier weaning and post-weaning weights, and in turn higher growth rates, will improve weaner survival. However, there remains genetic variation in weaner survival unrelated to weaning weight which can be selected for, and which is antagonistically associated with fleece weight. Due to antagonistic genetic correlations with key production traits, recording weaner survival would enable Sheep Genetics to calculate breeding values, and allow more balanced selection for improved survival and production traits.

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## REFERENCES

Adams N.R., Briegel J.R., Greeff J.C., and Bermingham E.N. (2006) *Aus. J. Ag. Res.* **57**: 27.

Brien F.D., Rutley D.L., Mortimer S.I., and Edwards J.E. (2013) *Proc. Assoc. Adv. Anim. Breed. Genet.* **20**: 237.

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

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

Campbell A.J.D., Broekhuizen A., Curtis K., Croker K.P., Behrendt R., *et al.* (2014) *Anim. Prod. Sci.* **54**: 783.

Ferguson M.B., Adams N.R., and Robertson I.R.D. (2007) *Proc. Assoc. Adv. Anim. Breed. Genet.* **17**: 195.

Hatcher S. and Atkins K.D. (2007). *Proc. Assoc. Adv. Anim. Breed. Genet.* **17**: 260.

Hatcher S., Eppleston J., Graham R.P., McDonald J., Schlunke S., *et al.* (2008). *Aus. J. Exp. Ag.* **48**: 966.

Gilmour A.R., Gogel B.J., Cullis B.R. and Thompson R. (2009) 'ASReml User Guide Release 3.0.' (VSN International Ltd: Hemel Hempstead).

Thompson A.N., Ferguson M.B., Campbell A., Gordon D.J., *et al.* (2011) *Anim. Prod. Sci.* **51**: 784.