ANALYSIS OF LAMB SURVIVAL IN AUSTRALIAN MERINO

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SUMMARY

Lamb survival from a Merino flock (13,163 records) and a crossbred flock (15,569 records) were analysed by both animal and sire model to estimate genetic parameters for lamb survival on the normal and logit transformed scales. Average survival rates were 77.5% in crossbred and 72.7% in Merino flock. The estimated direct heritabilities from animal model in the crossbred flock were 0.013 and 0.001 on normal and logit scales respectively and in the Merino flock 0.026 and 0.006. Maternal heritability was 0.007 and 0.013 on normal and logit scales in the crossbred flock and 0.026 and 0.031 in the Merino flock. The estimated direct and maternal heritabilities from sire model on normal and logit scales were similar within each flock, as well as and heritability estimates from animal and sire model on normal scale. However heritability estimates on the logit scale from animal model were seriously underestimated. The results suggest that selection for lamb survival will have limited impact in Merinos.

Keywords: Lamb survival, heritability, maternal effect

INTRODUCTION

Reproductive performance, the major contributor to the profitability of sheep enterprises is low in the Australian Merino in comparison with other breeds both in Australia and throughout the world (McGuirk 1982). A critical component of reproduction is lamb survival. In particular, lamb losses between birth and marking in Merino are very high with losses of more than 30 percent predicted from discrepancies between ultrasound reproductive potential and achieved marking percentages in NSW (Kilgour 1992) and South Australia (Kleeman *et al.* 1991).

The components of lamb survival can be defined as the lamb's own capacity to survive (direct genetic) and the rearing ability of the dam which has both genetic and environmental components. In determining the contribution of genetic variation to lamb survival it is necessary to consider these components to identify the possible role that genetic improvement might have in reducing lamb mortality. This study aims to identify the systematic effects influencing lamb mortality and to estimate genetic parameters using both normal and logit analyses. For the normal analysis we directly analyse survival as (0, 1) variable. For the logit analysis we assume an underlying logistic (similar to normal) variable categorised at a threshold value to generate the observed binary outcome.

MATERIALS AND METHODS

Animals. The data were collected from two different flocks. In the multiple bloodline project (Mortimer and Atkins 1989) data were collected from 15 separate sub-flocks maintained by New South Wales Department of Primary Industries at the Agricultural Research Centre, Trangie. Three rams and 100 ewes was the basic annual size of each of the 15 flocks, except for a flock derived from the Trangie Fertility flock (Atkins and Robards 1976) which had an annual size of 6 rams and 200

ewes. In the crossbred bloodline project (Mortimer *et al.* 1994) which started in 1984, 8 flocks from the multiple bloodline project (2 fine wool, 2 medium-wool non-Peppin, 3 medium-wool Peppin and one strong wool) were mated in a complete diallel design to produce both purebred progeny and two-way cross progeny derived from within and between strains crossings. From 1986, the purebred and crossbred ewe progeny of these matings were mated to purebred and a restricted range of crossbred ram genotypes to produce groups of purebred, F1, F2 interbred and backcross progeny, as well as the progeny of three-way and four-way matings.

Lambs were tagged and recorded with their dams within 12 hours of birth. Any lamb dead at tagging was recorded. All lambs and their dams were removed from the lambing paddocks between 5 and 8 days after lambing and lambs survived to this stage were recorded. At approximately one month of age (between 3 and 5 weeks), lambs were marked and the identity of all surviving lambs were recorded. Lambs were weaned on a single day in each year at an average age of 100 days. A total of 15569 lamb records (1975-1985) in the multiple bloodline flock and 13163 records (1984-1994) in the crossbred bloodline flock were available for analysis. Summary statistics and flock structure is presented in Table 1.

Data analysis. Variance components were estimated by REML (Gilmour *et al.* 2002) assuming that lamb survival was normally distributed and on a logit transformed scale. On the logit scale data was analysed by generalized linear mixed model (GLMM) using iteratively re-weighted least-squares assuming survival was binomially distributed. The model included birth type (3 levels), sex (2 levels), age of dam (6 levels) and birth year (11 levels) and bloodline (15 levels in the multiple bloodline flock, 8 levels in the crossbred flock) as fixed effects. In the animal model direct animal genetic, maternal genetic, maternal environmental effect, litter effect as well as covariance between direct and maternal genetic effects was included as random components. While in the sire model, both sire and dam direct genetic effect, maternal environmental effect and litter effect was included as random components.

RESULTS AND DISCUSSION

All fixed effects were significant (P<0.01) for lamb survival with dam age having a quadratic effect. Survival rate was highest for lambs from 4-6 years old dams, a trend also observed by Knight *et al.* (1988). Survival rate decreased from single to triplet born lambs. Male lambs had lower survival rate compared to female lambs, a pattern observed in other studies (Peterson and Danell, 1985; Knight *et al.* 1988).

The estimates of variance components and genetic parameters from the best model for the normal and the equivalent logit transformed animal model are presented in Table 2. The best model from the normal analysis was based on the likelihood ratio test. Inclusion of the covariance between direct and maternal genetic effects did not improve the log likelihood. Similar and very low heritability were observed in both flocks under the assumption of normally distributed records. These results agree with the Romney and Coopworth analyses of Amer and Jopson (2003) and the conclusion of Piper *et al* (1982) on direct heritability for lamb survival.

On the logit scale both the direct and maternal genetic variances are seriously underestimated relative to what is expected on the normal scale analyses. For example with an incidence of 0.77, heritability

on the underlying scale should be around 5.6 times that on the normal scale. This underestimation is well known for the animal model and is less severe for the maternal component which is based on an average of 4 progeny. The typical advice is that cell size (which is one under animal model) should be >10 for logit scale components to be acceptable. Lower direct heritability and higher maternal heritability were observed in both flocks compared to estimates on the normal scale. Direct heritability observed in this analysis was lower than that observed by Lopez-Villalbos and Garrick (1999) in New Zealand, who reported similar estimates of maternal heritability. Maternal environmental variance as a proportion of the phenotypic variance accounted for 6-10% of total variance with similar values in multiple bloodline flock on both scales and the higher value for logit scale in the crossbred flock. Litter component accounted for 5% of total variance in the crossbred flock only in normal scale. A significant heterosis of about 1% was observed on both scales in the crossbred flock.

Estimates of heritabilities from sire model were similar on both normal and logit scales for each flock (Table 3). This was expected since the average number of progeny per sire was high (51 and 34 in crossbred and Merino flock, respectively). The estimated maternal heritabilities were generally higher on the logit scale, which is the reflection of much smaller number of progeny from dam (average of 4 progeny).

Table 1. Summary statistics and data structure for lamb survival

	Flock	
	Crossbreed bloodline	Multiple bloodline
Number of lambs	13,163	15,569
Number of dams	3,113	3,987
Number of sires	260	454
Average lamb survival	77.5	72.9

Table 2. Estimates of genetic parameters for lamb survival from animal model†

	Flock			
	Crossbred bloodline		Multiple bloodline	
	Normal	Logit	Normal	Logit
h^2	0.013 ± 0.007	0.001 ± 0.001	0.026 ± 0.009	0.006 ± 0.010
m^2	0.007 ± 0.009	0.013 ± 0.014	0.026 ± 0.011	0.031 ± 0.020
ce^2	0.073 ± 0.011	0.101 ± 0.017	0.060 ± 0.012	0.065 ± 0.017
l^2	0.050 ± 0.016	0.000 ± 0.000	0.000	0.000
H^2	0.006 ± 0.003	0.010 ± 0.005	-	-

† h^2 direct heritability; m^2 maternal heritability; ce^2 maternal common environmental variance expressed as a proportion of the phenotypic variance; l^2 litter variance expressed as a proportion of the phenotypic variance; H^2 non-additive genetic variance expressed as a proportion of the phenotypic variance.

Table 3 Estimates of genetic parameters for lamb survival from sire model

	Flock			
	Crossbred bloodline		Multiple bloodline	
	Normal	Logit	Normal	Logit
h^2	0.015 ± 0.009	0.018 ± 0.014	0.026 ± 0.010	0.028 ± 0.014
m^2	0.004 ± 0.009	0.009 ± 0.014	0.022 ± 0.011	0.032± 0.016
ce^2	0.074 ± 0.011	0.099 ± 0.017	0.061 ± 0.012	0.065 ± 0.017
l^2	0.050 ± 0.016	0.000 ± 0.000	0.000	0.000
H^2	0.006 ± 0.003	0.009 ± 0.005	-	-

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INDUSTRY IMPLICATION

The evidence from this analysis suggests that improvement of lamb survival by selection will have limited impact within Merinos. Identification of dams with higher progeny survival will lead to some current generation improvement, as shown by the moderate maternal environmental variance, but only modest future generation improvement.

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