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A REVISITING OF THE GENETICS OF LAMB SURVIVAL AND RELATED TRAITS, AS PART OF THE FIT TO LAMB PROJECT

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SUMMARY

Measurable genetic gains in lamb survival have been reported in research and industry flocks, despite low heritability estimates. The study reported herein utilised Sheep CRC Information Nucleus Flock data (2007 to 2011) and MLA Resource Flock data (2012-2023) to complete an updated univariate analysis for lamb survival and its indicator traits. Direct genetic, maternal genetic, maternal permanent environmental, common litter and genetic groups variances were estimated for 18 traits using an animal model. Direct heritability estimates were low for all lamb survival traits (0.01) and generally low for indicator traits except for birth weight (0.12), metacarpal length (0.29), crown-rump length (0.20), thorax circumference (0.12) and birth coat score (0.39). Maternal heritabilities were low and equal to or greater than direct heritabilities for lamb survival traits and were generally low for indicator traits. The proportion of phenotypic variance accounted for by permanent environmental effects or genetic groups effects was often larger than direct genetic effects for lamb survival traits and varied across indicator traits. Common litter effects accounted for the largest proportion of variation across all traits, ranging from 11% to 76%.

In summary, lamb survival traits are lowly heritable with equal proportions of variance explained by direct and maternal effects. Some indicator traits appear more heritable and may be useful in selection programs as potentially correlated traits.

INTRODUCTION

Poor lamb survival is a major contributor to sheep reproductive inefficiency in Australia (Hinch and Brien 2014) and internationally, with only 70-85% of lambs born surviving to weaning (Dwyer *et al.* 2016). The prospects for achieving genetic improvement of lamb survival within a breed have generally been viewed as limited, based on very low estimated heritability (Everett-Hincks *et al.* 2005; Safari *et al.* 2005a; Safari *et al.* 2005b; Everett-Hincks and Cullen 2009). Despite this, measurable genetic gains in lamb survival have been reported in research flocks (Cloete *et al.* 2009) and in New Zealand (SIL 2024) and Irish industry flocks (N. McHugh, *pers. comm.*).

For genetic evaluation purposes and for designing effective breeding strategies, it is essential to have reliable estimates for genetic parameters. In an earlier paper, Brien *et al.* (2010) provided phenotypic and genetic parameters for lamb survival and related traits, based on data collected from 2007 to 2009 in the Sheep CRC's Information Nucleus (IN) flock. In this paper, we update and add to the earlier estimates, in relation to results from univariate analyses only, using IN data collected from 2007 to 2011 and data from the MLA Resource Flock (MLA RF) collected from 2012 to 2023 including data from up to an additional 12,352 lamb records.

MATERIALS AND METHODS

The Sheep CRC's Information Nucleus (IN) flock consisted of genetically linked flocks run at eight sites in Australia, containing Merino and crossbred ewes that were artificially inseminated annually to Merino, maternal and terminal breed rams. The MLA RF began as the IN, but has been run at two research sites only, with management following a similar protocol to the IN, except that pedigrees are verified by DNA analysis.

IN and MLA RF data on 27,603 lambs was utilised to estimate genetic parameters for lamb survival at birth, 3 days of age, 7 days of age and weaning (LS0, LS3,LS7 and LSW respectively), as well as indicator traits; birth weight (BWT), metacarpal length (ML), crown-rump length (CRL), thorax circumference (THO), rectal temperature (RT), observed birth vigour (OBV), birth coat score (BCS), maternal behaviour score (MBS; currently defined as a trait of the lamb however will be analysed as a trait of the dam at a later date) and lambing ease score (LE). Five timed behaviour traits were also analysed; time taken after release for the lamb to bleat (BLT), stand (STD), contact the ewe (CONT), contact the udder (UDD) and follow the ewe (FOLL). Further details on the design, data collection and management of the IN is reported by Brien *et al.* (2010) and Geenty *et al.* (2014). The design and management of the MLA RF is briefly reported by Hebart and Brien (2018).

Table 1. Summary statistics for lamb survival and indicator traits including the number of additional records included (+N) since Brien *et al.* (2010), the number of sires, dams and number of contemporary groups (N_CG). Trait units are presented within parentheses

Trait	N	+N	Mean	Median	s.d.	Sires.	Dams	N_CG.
LS0 (0/1)	25,638	-	0.93	1	0.26	739	11,567	41
LS3 (0/1)	26,313	11,121	0.88	1	0.32	739	11,653	41
LS7 (0/1)	26,677	-	0.86	1	0.34	739	11,685	41
LSW (0/1)	26,709	11,517	0.85	1	0.35	739	11,694	41
BWT (kg)	27,240	12,352	4.8	4.7	1.1	739	11,721	41
ML (cm)	10,213	-243	10.0	10	1.2	269	5,101	18
CRL (cm)	19,442	8,991	45.8	46	5.0	402	7,994	32
THO (cm)	10,210	-244	39.0	39	3.9	269	5,102	18
RT (°C)	18,695	8,881	39.1	39.2	0.9	438	7,927	33
OBV (1-5)	22,997	9,472	2.3	2	1.1	715	9,777	40
BCS (1-7)	23,251	8,699	2.5	2	1.0	478	9,116	39
MBS (1-5)	13,114	827	2.5	2	1.1	281	5,987	23
LE (1-5)	17,468	7,442	1.1	1	0.5	538	7,272	38
BLT (sec)	16,382	7,719	8.5	3	16.6	402	7,394	32
STD (sec)	12,550	3,752	16.1	6	26.2	289	6,091	24
CONT (sec)	12,253	3,682	29.0	17	33.0	289	5,938	24
UDD (sec)	3,613	-109	70.4	60	46.4	204	2,439	16
FOLL (sec)	6,645	-199	57.2	44	41.5	205	3,754	16

Statistical analysis. Variance components were estimated for all traits using the restricted maximum likelihood (REML) method within an animal model in ASREML-R 4.2 (Butler *et al.* 2023). A deep pedigree was utilised; 171,363 individuals comprising 18,326 and 66,212 unique sires and dams respectively. All traits were analysed on the observed scale. All models included fixed effects of contemporary group defined by cohort (year by site; 41 levels), sex (male or female), sire breed type (3 levels), dam breed type (4 levels), age of dam (1-8 years), type of birth (single, twin or multiple) and the interaction between cohort and age (days) as a co-variate. Data was filtered to retain complete records across all fixed effects. Birth time (0, 1 or 2 indicating the trait was observed at birth, within 4hrs of birth or >4hrs of birth respectively) was fitted as an additional covariate for RT, OBV, BCS, MBS, LE and timed behaviour traits. Direct additive, maternal genetic, maternal permanent environmental, litter and genetic group variances were estimated. Litter was defined as the combination of year of birth x dam id. Genetic group variance was fitted via a Q matrix constructed for 147 genetic groups (Swan *et al.* 2014).

RESULTS AND DISCUSSION

Mean lamb survival was highest at day 0 (93%, Table 1) and decreased with age to 85% by weaning. The biggest decrease in mean lamb survival was between 0 and 3 days (5% decrease) indicating that most lamb losses occur up to 3 days of age, with marginal decreases in survival thereafter till weaning.

Table 2. Estimates of additive genetic (V_a), maternal genetic (V_m), maternal permanent environmental (V_{mpe}), litter (V_c), genetic group (V_{gg}) and phenotypic (V_p) variance components as well as direct (h^2) and maternal (m^2) heritability estimates and common litter effects(c^2)

Trait**	V_a	V_m	V_{mpe}	V_c	V_{gg}	V_e	V_p	h^2	m^2	c^2
LS0	0.001	0.001	0.001	0.015	0.002	0.042	0.062	0.01	0.01	0.25
LS3	0.001	0.002	0.004	0.017	0.001	0.068	0.094	0.01	0.02	0.19
LS7	0.001	0.003	0.004	0.016	0.002	0.079	0.105	0.01	0.03	0.16
LSW	0.001	0.003	0.005	0.016	0.002	0.087	0.112	0.01	0.02	0.14
BWT	0.100	0.138	0.025	0.092	0.147	0.322	0.825	0.12	0.17	0.11
ML	0.269	0.004	0.000*	0.381	0.000*	0.289	0.942	0.29	0.00	0.40
CRL	3.639	1.367	0.000*	4.296	1.627	6.935	17.864	0.20	0.08	0.24
THO	1.206	0.905	0.131	1.955	0.730	5.359	10.285	0.12	0.09	0.19
RT	0.042	0.000*	0.017	0.343	0.006	0.799	1.208	0.03	0.00	0.28
OBV	0.082	0.000*	0.011	0.634	0.022	0.272	1.021	0.08	0.00	0.62
BCS	0.354	0.025	0.000*	0.271	0.040	0.209	0.898	0.39	0.03	0.30
MBS	0.044	0.217	0.000*	0.770	0.256	0.020	1.307	0.03	0.17	0.59
LE	0.006	0.002	0.000*	0.110	0.004	0.063	0.185	0.03	0.01	0.59
BLT	5.277	4.706	0.206	103.38	7.616	158.96	280.15	0.02	0.02	0.37
STD	17.810	9.044	5.201	271.01	6.534	353.74	663.34	0.03	0.01	0.41
CONT	20.126	201.44	14.203	544.47	188.30	226.29	1194.8	0.02	0.17	0.46
UDD	102.58	0.000*	168.35	732.63	0.000*	935.56	1939.1	0.05	0.00	0.38
FOLL	49.956	27.074	89.238	1228.8	34.761	197.67	1627.5	0.03	0.02	0.76

*indicates variance components that hit the boundary due to negligible variation. **Trait units can be found in Table 1. ***Standard errors range 0.01-0.05 for h^2, m^2 and c^2 estimates.

Direct (V_a) and maternal genetic (V_m), maternal permanent environmental (V_{mpe}), litter (V_c) and genetic groups (V_{gg}) variances were able to be estimated separately for each trait. Direct heritability (h^2) estimates were low for lamb survival traits (0.01; Table 2) in line with reviewed estimates by Safari *et al.* (2005b). Indicator traits also generally had low h^2, except for BWT (0.12), ML (0.29), CRL (0.20), THO (0.12) and BCS (0.39). Estimates of h^2 were all equal to or smaller than those reported in Brien *et al.* (2010), except for BCS, though total phenotypic variances (V_p) reported were very similar (e.g. for Ls3 and LsW). Given the greater number of variance components estimated herein compared to Brien *et al.* 2010 (especially the separation of maternal components as well as V_c), it is reasonable to assume that V_a may have been over-estimated in the prior study. Estimates of maternal heritabilities (m^2) were low and equal to or greater than h^2 for lamb survival traits (Table 2), similar to estimates by Safari *et al.* (2005b), though not all of the papers reporting m^2 analysed in this review disentangled maternal genetic and permanent environmental variances, including Brien *et al.* 2010. Estimates of m^2 were highest for BWT (0.17), MBS (0.17) and CONT (0.17). Although small, V_{mpe} estimates accounted for 2.3%, 3.8%, 3.9% and 4.1% of V_p for LS0, LS3, LS7 and LSW, respectively. Estimates of V_{gg} were generally small (accounting for up to 9% of V_p the variance) except for BWT, MBS and CONT (accounting for 17.8%, 19.6% and 15.8%, respectively).

Common litter effects (c^2) accounted for the largest amount of variation across each trait. For lamb survival traits, c^2 appeared to decrease with age with 0.25 reported for LS0 compared to 0.14 for LSW (Table 2), consistent with Everett-Hincks *et al.* (2014) who reported c^2 values of 0.13 and

0.09 for LS3 and LSW respectively. Structural traits (ML, CRL and THO) reported c^2 of 0.40, 0.24 and 0.19 respectively while scored traits (VIG, MBS, LE) averaged c^2 of approximately 0.60. Timed traits generally returned c^2 values of approximately 0.40 except for FOLL which had the highest c^2 of the dataset at 0.76. These c^2 values remained equally high or higher for all traits when BWT or BWT quadratic (for lamb survival) co-variates, fit within type of birth, were added to the model (data not shown) indicating that the larger values observed are not capturing an effect of BWT.

CONCLUSION

Estimates of direct genetic and maternal heritabilities were updated for 18 traits including lamb survival and related characters. Direct and maternal heritabilities for lamb survival traits are confirmed as low when derived from a linear mixed model analysis. Common litter effects accounted for the greatest amount of variation across all traits (11% to up to 76%). Several indicator traits have heritability estimates well above those for lamb survival traits and may have potential value for use in selection programs to increase genetic gain, depending on the magnitude of their genetic correlation with lamb survival (yet to be reported from data used in this study) and their ease of recording.

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