

Derivation of a new lamb survival trait for implementation in the New Zealand sheep industry

Sylvie Vanderick¹
Benoit Anvray²
Sheryl-Anne Newman²
Ken Dodds²
Julie Everett-Hincks²

¹Gembloux Agro-Bio Tech, University of Liège, Gembloux, Belgium

²AgResearch Ltd, Invermay Agricultural Centre, Mosgiel, New Zealand
jeh@agresearch.co.nz



Background

Lambing percentage is one of the most significant factors affecting profitability on New Zealand sheep farms. Since the early 1990s, lambing percentage has increased at about 1% per year from a relatively stable level of approximately 100%. Top performing sheep farms are now consistently achieving 150% or more.

As lambing percentage increases, the proportion of ewes having twin and triplet litters increases accordingly. Lamb mortality rate in multiples is higher than in singles, with triplets being particularly susceptible.

Sheep Improvement Ltd (SIL, New Zealand's national sheep genetic evaluation system) records lamb survival to weaning but genetic improvement has been limited due to the low heritability of the trait and the current method of farmer recording.

Objectives

Review the existing SIL lamb survival to weaning trait (SIL SUR) and develop a more accurate and consistently recorded lamb survival trait (NEWSUR) for industry implementation.

Define new decision rules for data inclusion/exclusion.

Revise the genetic evaluation model, estimate variance components and investigate maternal genetic effects and correlations to produce breeding values (EBVs) for NEWSUR.

Compare SIL SUR and NEWSUR in terms of genetic parameters and EBVs, and identify flocks by year combinations with unusual relationships between the two traits or where significant re-ranking occurred.

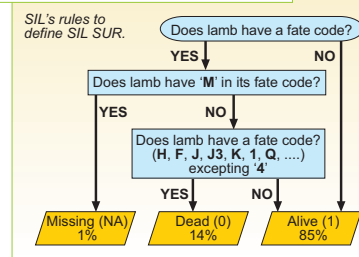
Data source

The original dataset used was exported from the SIL database in October 2011 and consisted of 3,427,496 lamb records, born between 1990 and 2010 from 596 performance recorded flocks.

Current SIL survival trait

SIL lamb survival to weaning is a binary DEAD (0) / ALIVE (1) trait and assumes lambs are alive at weaning unless told otherwise by the breeder or a lamb birth fate code (BFATE) describing the time and cause of lamb death.

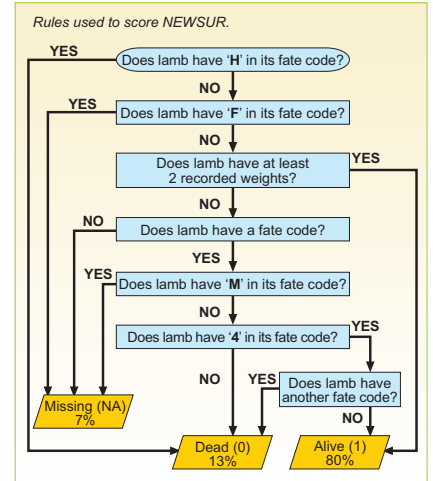
BFATE	Description
F	Fostered
H	Hand-reared
J	Born dead
J3	Died within 3 days of birth (autopsy)
K	Died between birth and rearing
M	Died of misadventure
P	Born dead - Premature
R	Born dead - Rotten
1	Died between rearing and weaning
4	Culled at birth (alive but not tagged)



According to current SIL rules, if survival for a flock and a birth year is less than 55% or greater than or equal 93% then data for this flock by birth year combination are excluded as it is assumed that farmer recording practices have largely led to survival rates below and above these limits. Moreover, there are also some flocks that have permanently excluded data for particular years. The same flock by birth year survival limits have been applied to NEWSUR.

New survival trait

The definition of NEWSUR is based on using a combination of lamb BFATE codes and presence/absence of live weight measurements to assess whether a lamb has survived until weaning. The weight measurements used are weaning weight, live weight at 6, 8, 10, 12 and 18 months, and fleece weight at 12 months of age.



Comparing SIL SUR and NEWSUR phenotypes

Cross-frequencies of NEWSUR and SIL SUR (and conditional %ages per column / row).

11.3% of lambs considered as alive with SIL SUR are considered as missing with NEWSUR. Most of these are lambs without a BFATE code, so considered as alive by default by SIL. With NEWSUR, these lambs without a BFATE code and without at least 2 weights are considered as missing.

		SIL SUR			total
		dead	alive	missing	
NEWSUR	dead	388,993 (99.6%/96.3%)	10,901 (0.4%/2.7%)	4,187 (9.4%/1.0%)	404,081 (11.8%)
	alive	701 (0.2%/0.0%)	2,644,398 (88.4%/99.3%)	18,784 (42.0%/0.7%)	2,663,883 (77.7%)
	missing	840 (0.2%/0.2%)	336,980 (11.3%/93.7%)	21,712 (48.6%/6.0%)	359,532 (10.5%)
total		390,534 (11.4%)	2,992,279 (87.3%)	44,683 (1.3%)	3,427,496

42% of lambs considered as missing with SIL SUR are considered as alive with NEWSUR. Most of these are lambs with an M (died of misadventure) in their BFATE code (or BFATE code combination), as the lamb may have more than one code to describe their fate), and are considered as missing by SIL, but these lambs have also at least 2 recorded weights.

Genetic parameters for NEWSUR

Six genetic models were tested to estimate (co)variance components and the resulting direct and maternal heritabilities for NEWSUR.

All models included the fixed effects of flock, birth year of the lamb (6 levels), litter size at birth (3 levels), age of dam (6 levels) and sex of lamb (2 levels) and their interactions. Fixed effects were all significant at $p < 0.001$.

Differences between the models tested consisted in:

- Different ways to deal with the explanatory variable "lamb date of birth": either ignoring it, fitting it as a fixed covariate within flock and birth year, or fitting it as 25 classes within flock and birth year, but as a random effect.
- Fitting a "litter effect", an extra random effect of dam by lamb birth year.
- Applying a logit transformation to the trait prior to fitting the linear model.

All analyses were performed using ASREML.

The best linear model (which included the two random effects of "litter" and birth year classes) was chosen as the one with the highest likelihood among the linear models. The same was done for the logit models. Secondly, cross validation was used to decide if a logit transformation was appropriate, by looking at the ability of the 2 models to predict the survival phenotype. The linear model was found to fit NEWSUR better. In the linear case, the addition of a random litter effect was found to dramatically reduce (by 71%) the variance associated with the maternal effect, reduce the residual variance by 7% and increase the negative correlation between direct and maternal effects, while leaving the direct genetic variance untouched.

The genetic parameters estimated using the 'best' model for NEWSUR are reported along with the genetic parameters used by SIL.

component	SIL SUR	NEWSUR
σ^2 bdayclass	-	0.007 ± 0.003
σ^2 litter	-	0.014 ± 0.002
σ^2 genetic direct	0.0016	0.005 ± 0.003
Cov (Gd, Gm)	0	-0.002 ± 0.002
σ^2 genetic maternal	0.0012	0.002 ± 0.002
σ^2 total genetic	0.0028	0.004 ± 0.002
σ_e^2	0.1572	0.098 ± 0.002
σ^2 total phenotypic	0.1684	0.123 ± 0.004
h ² direct	0.010	0.040 ± 0.000
Corr (Gd, Gm)	0	-0.438 ± 0.003
h ² maternal	0.0075	0.019 ± 0.000
h ² total	0.0175	0.035 ± 0.000

Comparing SIL SUR and NEWSUR EBVs

3,066,221 animals had SIL SUR and NEWSUR EBVs. The correlation between the two sets of EBVs was computed for animals with EBV reliabilities equal to or greater than the 97.5-percentiles of reliabilities for the traits.

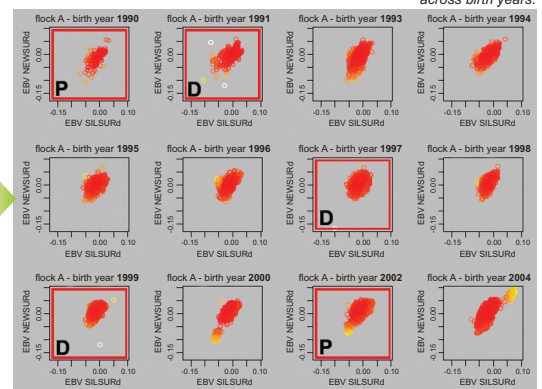
SIL SUR and NEWSUR EBVs were moderately correlated with a correlation between direct EBVs (0.77) slightly lower than the correlation between maternal EBVs (0.80).

Further comparisons between SIL SUR and NEWSUR EBVs were carried out by birth year within flock to detect abnormal relationships between SIL SUR and NEWSUR, based on the following criteria:

- Correlation between SIL SUR and NEWSUR EBVs (C)
- Slope of the linear regression of SIL SUR on NEWSUR (S)
- Maximum Mahalanobis distance between SIL SUR and NEWSUR EBVs (D)
- Proportion of pairs of EBVs with a p-value ≤ 0.05 for an outlier detection chi-square test of the Mahalanobis distances (P).

Abnormal relationships between direct EBVs were detected for 180 flock by birth year combinations (74 flocks from 21 birth years) and between maternal EBVs for 186 flock by birth year combinations (79 flocks from 21 birth years).

An example of an abnormal relationship is presented. Abnormal birth year combinations have been highlighted by a red box, and the reasons why they are considered abnormal are indicated in the left bottom corner (C, S, D or P).



Further analyses are required before implementation.

Recommendations

Recording can be improved using the NEWSUR trait.

The use of the random litter effect in the model is recommended as it was found to fit the data better than a model without litter effect and can potentially avoid the overestimation of the maternal genetic variance.

NEWSUR is more accurate and more heritable than SIL SUR, therefore it will lead to a better genetic evaluation of lamb survival to weaning. However, further analyses are required to explain the unusual relationship between SIL SUR and NEWSUR for specific flock by year combinations.