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

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ABSTRACT: Previous research identified that a review of the current industry New Zealand lamb survival trait was necessary as its recording accuracy was reliant on farmers notifying their Sheep Improvement Limited bureau of lamb deaths. This paper reports the decision rules and genetic parameters for a new lamb survival trait for the New Zealand sheep industry. These rules define the new lamb survival trait (NEWSUR) using lamb birth fate (BFATE) codes and the presence/absence of lamb weight measurements. Six univariate animal models were tested and used to estimate variance or covariance components and the resulting direct and maternal heritabilities for NEWSUR. The models differed in the way they adjust for the effect of day of birth, the exclusion or inclusion of a litter (dam/year of birth) random effect, and the application or not of a logit transformation of the phenotypes. For both the linear and logistic methods, models including the random effect of litter provided the best fit for NEWSUR according to log-likelihood values. Log-likelihoods for the linear and logistic models cannot be compared; therefore, a cross-validation method was used to assess whether the logit transformation was appropriate by analyzing the predictive ability of the models. The mean square errors were slightly lower for the linear compared with the logistic model, and therefore, the linear model was recommended for industry use. The heritability attributed to direct effects ranged from 2 to 5.5%. A direct heritability of 5.5% resulted from a linear model without litter effect and omitting the effect of day of birth on survival, whereas a direct heritability of 2% resulted from the logistic model fitting a random litter effect. The heritability attributed to maternal genetic effects ranged from 1.9 to 7.7%. A maternal genetic heritability of 7.7% resulted from the logistic model omitting the litter effect, whereas a maternal genetic heritability of 1.9% resulted from the linear model fitting a random litter effect. The addition of the litter random effect substantially decreased the maternal heritabilities in all cases and was recommended for industry use to avoid overestimation of the maternal genetic variance. Sheep Improvement Limited has implemented NEWSUR and the associated genetic evaluation model based on information described in this paper. Industry-wide implementation will enable sheep breeders to produce more accurate genetic evaluations to their commercial clients.

Key words: heritability, lamb survival, litter effect, maternal genetics

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INTRODUCTION

Lambing percentage is one of the most significant traits affecting profitability on New Zealand sheep farms (Hawkins and Wu, 2011). Since the early 1990s, lambing percentage has increased at about 1%/yr from a relatively stable level of approximately 100% (McDermott et al., 2008). As lambing percentage increases, the proportion of ewes having twin and
triplet litters increases. Lamb mortality rate in multiples is higher than in singles, with triplets being particularly susceptible (Everett-Hincks and Dodds, 2008). Improving lamb survival (LS) has become increasingly important to the New Zealand sheep industry.

Lamb survival is a complex trait influenced by direct genetic, maternal genetic, and environmental effects (Brien et al., 2014). Low heritability estimates have been reported across a number of studies meaning that LS is predominantly controlled by environmental factors, limiting its genetic improvement (Amer and Jopson, 2003; Safari et al., 2005).

Sheep Improvement Limited (SIL; http://www.sil.co.nz) is New Zealand’s national sheep genetic evaluation system and records LS to weaning but genetic progress has been limited due to the low heritability of the trait and also due to the current method of farmer recording.

The objectives of this paper are 3-fold: first, to review the current SIL lamb survival trait (SILSUR) and develop a more accurate and consistently recorded LS trait (new lamb survival trait [NEWSUR]) for industry implementation; second, to define new decision rules for data inclusion and exclusion in SIL genetic evaluation system; and lastly, to revise the genetic evaluation model, estimate variance components, and investigate maternal genetic effects and correlations to produce EBV for NEWSUR.

This research will allow SIL to adopt an improved genetic evaluation for LS, which will in turn increase the rate of genetic gain through the design of appropriate animal breeding programs to reduce lamb mortality rates.

MATERIALS AND METHODS

Data

Animal performance records were extracted from the SIL national sheep recording database in October 2011 and consisted of 3,427,496 lamb records of lambs born between 1990 and 2010 from 596 performance recorded flocks. These flocks cover a range of breeds and crosses (2 breed combinations) but are predominantly Romney, Coopworth, Perendale, Texel, and some composites (defined as a combination of 3 or more breeds; Price, 2000).

Lamb Survival Trait Definitions

Lamb survival is recorded as a binary trait in SIL. Lambs that survive to weaning are given a “1” and those that die are given a “0.” However, the SIL system relies on notification from the sheep breeder that a lamb has died by assigning a lamb birth fate (BFATE) code (Table 1); otherwise, they are assumed alive at weaning.

Rules to define SILSUR are described in Fig. 1; lambs without BFATE record are considered alive and lambs with a BFATE record are considered dead except for lambs with BFATE “E” (embryo transfer progeny), “L” (AI progeny), “M” (died of misadventure), or “4” (culled at birth). Lambs with BFATE “E” or BFATE “L” are treated similarly to lambs without BFATE, because those birth fates have no effect on genetic merit. Survival of lambs with BFATE “M” are set to missing so they are removed from the analysis and lambs with BFATE “4” are lambs alive but not tagged. Besides, SILSUR data rules exclude records where the mean LS for a flock and year of birth is <55 or ≥93% as it is assumed that farmer recording errors have largely led to survival rates below and above these limits. (These will be referred to as “survival limits” throughout the remainder of this document). Moreover, some flocks have had their data permanently excluded for particular years with known issues. Proportions of survival reported in Fig. 1 were observed after application of the survival limits.

The definition of NEWSUR is based on using a combination of BFATE codes and the presence/absence of weight measurements to assess whether a lamb has survived until weaning age (i.e., 100 d). The weight measurements used are weaning weight, live weight at 6 mo of age, live weight at 8 mo of age, live weight at 10 mo of age, live weight at 12 mo of age, live weight at 18 mo of age, and greasy fleece weight at 12 mo of age. The rules used to assign NEWSUR are described in Fig. 2. Lambs with BFATE “E” (embryo transfer progeny) or “L” (AI progeny) are treated similarly to lambs without BFATE. Then, if these lambs have at least 2 recorded weights, they will be considered alive; otherwise their survival will be set to missing. Lambs with BFATE “H” are counted as dead because lambs would have died without breeder’s intervention. Lambs with BFATE “F” are considered

<table>
<thead>
<tr>
<th>Table 1. Sheep Improvement Limited lamb birth fate (BFATE) codes</th>
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<tbody>
<tr>
<td>BFATE code</td>
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<tr>
<td>-----------</td>
</tr>
<tr>
<td>E</td>
</tr>
<tr>
<td>F</td>
</tr>
<tr>
<td>H</td>
</tr>
<tr>
<td>J</td>
</tr>
<tr>
<td>J3</td>
</tr>
<tr>
<td>K</td>
</tr>
<tr>
<td>L</td>
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<tr>
<td>M</td>
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<tr>
<td>P</td>
</tr>
<tr>
<td>R</td>
</tr>
<tr>
<td>1</td>
</tr>
<tr>
<td>4</td>
</tr>
</tbody>
</table>
Figure 1. The current Sheep Improvement Limited lamb survival trait. BFATE = lamb birth fate; M = died of misadventure; H = hand reared; F = fostered; J = born dead; J3 = died within 3 d of birth (autopsy); K = died between birth and rearing; 1 = died between rearing and weaning; 4 = culled at birth (alive but not tagged); NA = not available.

Figure 2. Rules used to define the new lamb survival trait. BFATE = lamb birth fate; H = hand reared; F = fostered; M = died of misadventure; 4 = culled at birth (alive but not tagged); NA = not available.
Estimation of EBV for the New Lamb Survival Trait

Data Preparation. The NEWSUR data were edited to remove missing records and effect levels with low number of observations after applying SIL survival limits, resulting in data sets of differing sizes for NEWSUR and SILSUR. For age of dam classes (AOD), hogget dams (1-yr-old ewes) or dams with missing age or age <1 yr old were removed. Dams older than 7 yr of age were grouped into age group 7. Lambs from litter sizes greater than 3 (birth rank > 3) were removed from the data set. Lambs with a missing birth date were also removed. Sex is known to affect LS but the industry standard is to not record the sex of lambs found dead at tagging. Including 3 classes of sex (male, female, and unknown) in the analysis was not appropriate as unknown sex animals had zero survival. Accordingly, for the purpose of estimating variance components, the sex of dead lambs was assigned at random with equal probability for each sex as done by Lopez-Villalobos and Garrick (1999). To estimate maternal genetic effects accurately, at least 3 generations of animals were required and, therefore, 6 yr of records were included in the analysis. A subset of 6 yr of lambing data (2005 to 2010) was created for NEWSUR and then used to estimate the variance components of NEWSUR. In this subset, the 944,211 lambs (from 212 flocks) were the progeny of 16,084 sires and 353,783 dams with 5,418 paternal grand-sires, 10,798 paternal grand-mothers, 13,590 maternal grand-sires, and 179,359 maternal grand-mothers. There were 144,636 single-born lambs, 647,008 twin-born lambs, and 152,567 triplet-born lambs of various breeds and breed composition (predominantly Romney, Perendale, Coopworth, and Texel).

Genetic Parameter Estimation. All analyses were performed using ASReml 3.0 (Gilmour et al., 2009). Six univariate animal models were tested to estimate variance or covariance components and genetic parameters for NEWSUR were derived. All models included the fixed effects of flock (212 flocks), year of birth of the lamb (6 levels: 2005 to 2010), litter size at birth or birth rank (3 levels: single, twin, and triplet), AOD in years (6 levels: 2–7 yr), and sex of lamb (2 levels: ram and ewe) and their interactions. The random direct and maternal genetic effects and the covariance between direct and maternal genetic effects were also fitted in all models. The different models investigated are summarized in Table 2. Models A1, A2, A3, and B analyzed NEWSUR as a normally distributed trait and models LogA and LogB analyzed NEWSUR as a logit transformed trait using model A3 and model B, respectively. Models A1, A2, and A3 differ in the way they deal with the explanatory variable “lamb day of birth.” Model A1 ignores lamb day of birth, model A2 fits day of birth (Day 1 to Day 355) within flock and birth year as a covariate, and model A3 fits day of birth classified in periods of 2 wk (25 classes) within flock and birth year as random effects. Model B is the same as model A3 but has an extra random nongenetic effect that is specific to a litter (interaction between dam and year of birth) fitted. This litter effect reflects common environmental effects unique to the litter as well as nongenetic effects expressed in full sibs and genotype × year interaction effects expressed in the dam.

Heritabilities and genetic correlations were calculated from the variance estimates produced by
ASReml 3.0 (Gilmour et al., 2009). The total heritability was obtained by summing genetic variances attributed to direct and maternal effects and the covariance (doubled). Genetic correlations between direct and maternal genetic effects were calculated by dividing the covariance between direct and maternal effects by the SD of direct and maternal genetic effects.

Comparison of Models Based on their Predictive Ability. First, the best linear model was chosen as the one with the highest restricted likelihood. The same method was used for comparing logistic models. Second, because log-likelihoods for the linear and logistic models cannot be compared, the following procedure was performed to assess whether a logit transformation was appropriate for NEWSUR by analyzing the ability of the 2 models to predict the LS phenotype. A 3-fold cross-validation method was used, where survival records from lambs born in 2010 were randomly allocated to 1 of 3 groups, and EBV were estimated 3 times using both models, sequentially setting all observations in 1 of the 3 groups to missing. The phenotypes were then predicted from the 2 fitted models for the subset where the phenotypes had been set to missing. The variances of the difference between observed and predicted values, that is, mean square error (MSE), obtained with both models were then calculated and compared with an intercept model (using the average LS as a predictor).

RESULTS AND DISCUSSION

Comparison between Existing and New Survival Phenotypes

The incidences of NEWSUR and SILSUR, before application of the survival limits, were compared in Table 3. With NEWSUR, 11.3% of lambs recorded alive with SILSUR are now considered missing. Most of these lambs are lambs without a BFATE code and are assigned alive by default by SIL. With NEWSUR, these lambs without a BFATE code and without at least 2 weights are considered missing. Another significant difference between NEWSUR and SILSUR is that 42% of lambs considered missing with SILSUR are now considered alive with NEWSUR. Most of these lambs are lambs with an “M” (died by misadventure) BFATE code (or BFATE code combination, as lambs may have more than one code to describe their fate) and are considered missing by SIL, despite having at least 2 recorded weights.

### Table 3. Cross-frequencies of the new lamb survival trait (NEWSUR) and the current Sheep Improvement Limited lamb survival trait (SILSUR; and conditional percentages, per row/column if appropriate)

<table>
<thead>
<tr>
<th>NEWSUR status</th>
<th>SILSUR status</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dead</td>
<td>Alive</td>
</tr>
<tr>
<td>388,993</td>
<td>10,901</td>
</tr>
<tr>
<td>(99.6%/96.3%)</td>
<td>(0.4%/2.7%)</td>
</tr>
<tr>
<td>Alive</td>
<td>701</td>
</tr>
<tr>
<td>(0.2%/0.0%)</td>
<td>(88.4%/99.3%)</td>
</tr>
<tr>
<td>Missing</td>
<td>840</td>
</tr>
<tr>
<td>(0.2%/0.2%)</td>
<td>(11.3%/93.7%)</td>
</tr>
<tr>
<td>Total</td>
<td>390,534</td>
</tr>
<tr>
<td>(11.4%)</td>
<td>(87.3%)</td>
</tr>
</tbody>
</table>

Genetic Parameters Estimation

All fixed effects fitted in the 6 models investigated for NEWSUR were significant at $P < 0.001$. Estimates of variance or covariance components and derived genetic parameters for NEWSUR are reported in Table 4 for the linear models tested and in Table 5 for the logistic models. Variance components of both logistic models cannot be compared with those obtained for the linear models. However, heritabilities and correlations can be compared as they are ratios of variances.

Estimates of residual variances, direct genetic variances, and total phenotypic variances were relatively constant for the linear models (i.e., models A1, A2, A3, and B).

Estimates of maternal genetic variances were relatively constant but decreased with the addition of the random effect of litter fitted in model B. This decrease was also observed for the logistic models, indicating that a part of the litter variance has been attributed to maternal genetic variance when the litter random effect was not fitted. Consequently, the maternal genetic variance would be overestimated in models without the litter random effect fitted. This finding is similar to that made by other authors investigating genetic parameters for the LS trait (Van Wyk et al., 2004; Everett-Hincks et al., 2005, 2014) and for analyses involving other traits where the maternal genetic variance is estimated (Hagger, 1998; Al-Shorepy and Notter, 1998; Van Wyk et al., 2004).

The ratio of litter variance to total phenotypic variance was greater than the direct and maternal genetic ratios in models B and LogB, indicating a common environmental or nongenetic resemblance among littermates. This is similar to what was reported in previous studies on LS (Amer and Jopson, 2003; Van Wyk et al., 2004; Everett-Hincks et al., 2014).

The heritability attributed to direct effects ranged from 2 to 5.5% for all models. Model A1 generated the greatest direct heritability whereas the LogB model
Table 4. Estimates of variance components and genetic parameters (with their SE in parentheses), proportion, and restricted log-likelihood for the new lamb survival trait (NEWSUR) using different linear models

<table>
<thead>
<tr>
<th>Item</th>
<th>A1</th>
<th>A2</th>
<th>A3</th>
<th>B</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\hat{\sigma}^2$ (BDAYc)</td>
<td>0.007 (0.002)</td>
<td>0.007 (0.003)</td>
<td>0.007 (0.003)</td>
<td>0.014 (0.002)</td>
</tr>
<tr>
<td>$\hat{\sigma}^2$ (litter)</td>
<td>0.109 (0.002)</td>
<td>0.108 (0.002)</td>
<td>0.108 (0.002)</td>
<td>0.098 (0.002)</td>
</tr>
<tr>
<td>$\hat{\sigma}^2$ (e)</td>
<td>0.007 (0.003)</td>
<td>0.006 (0.002)</td>
<td>0.005 (0.002)</td>
<td>0.005 (0.003)</td>
</tr>
<tr>
<td>$\hat{\sigma}^2$ (a, m)</td>
<td>0.001 (0.003)</td>
<td>-0.001 (0.002)</td>
<td>-0.001 (0.002)</td>
<td>-0.002 (0.002)</td>
</tr>
<tr>
<td>$\hat{\sigma}^2$ (a)</td>
<td>0.121 (0.003)</td>
<td>0.119 (0.003)</td>
<td>0.126 (0.004)</td>
<td>0.123 (0.004)</td>
</tr>
<tr>
<td>$\hat{\rho}$ (a, m)</td>
<td>0.055 (0.000)</td>
<td>0.052 (0.000)</td>
<td>0.043 (0.000)</td>
<td>0.040 (0.002)</td>
</tr>
<tr>
<td>$\hat{\rho}$ (a)</td>
<td>0.064 (0.000)</td>
<td>0.064 (0.000)</td>
<td>0.055 (0.000)</td>
<td>0.019 (0.001)</td>
</tr>
<tr>
<td>$\hat{\rho}$ (m, a)</td>
<td>-0.186 (0.003)</td>
<td>-0.212 (0.003)</td>
<td>-0.136 (0.003)</td>
<td>-0.438 (0.003)</td>
</tr>
<tr>
<td>$\hat{\rho}$ (g)</td>
<td>0.012 (0.003)</td>
<td>0.011 (0.003)</td>
<td>0.011 (0.003)</td>
<td>0.004 (0.002)</td>
</tr>
<tr>
<td>$\hat{\sigma}^2$ (g)</td>
<td>0.097 (0.000)</td>
<td>0.092 (0.000)</td>
<td>0.085 (0.000)</td>
<td>0.035 (0.000)</td>
</tr>
<tr>
<td>LnL</td>
<td>$-1,564,964.02$</td>
<td>$-1,562,810.38$</td>
<td>$-1,558,802.22$</td>
<td>$-1,555,568.89$</td>
</tr>
</tbody>
</table>

1 $\hat{\sigma}^2$ (BDAYc) = estimated variance of the day of birth (classified in periods of 2 wk) × flock × year of birth effect; $\hat{\sigma}^2$ (litter) = estimated variance of the litter effect; $\hat{\sigma}^2$ (e) = estimated residual variance; $\hat{\sigma}^2$ (a) = estimated direct additive genetic variance; $\hat{\sigma}^2$ (a, m) = estimated covariance between direct and maternal effects; $\hat{\sigma}^2$ (m) = estimated genetic maternal additive genetic variance; $\hat{\sigma}^2$ (g) = estimated phenotypic variance; $\hat{k}^2$ (a) = estimated direct heritability; $\hat{k}^2$ (m) = estimated maternal heritability; $\hat{\rho}$ (a, m) = estimated genetic correlation between direct and maternal effects; $\hat{\rho}$ (g) = estimated total genetic (direct + maternal) variance; $\hat{h}^2$ (g) = estimated total heritability; LnL = restricted log-likelihood.

2 $\hat{A}$ = model with no day of birth fitted; $\hat{A}$ = model where the interaction between effects day of birth, flock, and year of birth is fitted as fixed covariates; $\hat{A}$ = model where the interaction between day of birth classes, flock, and year of birth is fitted as random effects; $\hat{B}$ = same as $\hat{A}$ but with an extra random litter effect fitted.

generated the lowest heritability when the same data set was used. The heritability attributed to maternal effects ranged from 1.9 to 7.7% for all models. The greatest maternal heritability was reported with model LogA and was lowest for model B. These values were low but in agreement with literature. A study involving 7 commercial New Zealand sheep flocks provided heritability estimates for LS ranging from 0.8 to 7% for direct effects and from 0.2 to 7.5% for maternal effects (Amer and Jopson, 2003). Safari et al. (2005) reviewed heritability estimates for LS trait from 16 studies and reported an averaged heritability of 3 and 5% for direct and maternal effects, respectively. Hatcher et al. (2010) found heritabilities ranged from 2 to 5% for direct effects and from 3 to 7% for maternal effects in Australian Merino sheep.

The maternal and direct genetic effects appeared to be negatively and slightly to moderately correlated (from −0.14 to −0.44) for models without phenotype transformation. This negative genetic correlation suggests that some genes that support survival in the individual may also contribute to poor survival in their progeny and vice versa. However, Robinson (1996) showed, using simulated data, that negative estimates of correlation between the direct and the maternal genetic effects may be obtained in the absence of a true antagonism between them. For both logistic models, the genetic correlation between direct and maternal effects was positive but low (from 0.02 to 0.03). The sign of the correlation differed between the logistic models and the linear models but the estimates of correlation had a large SE in logistic models. Therefore, the correlation between direct and maternal genetic effects for NEWSUR was significant for linear models and not significant for logistic models. Some previous studies on LS (Morris et al., 2000; Everett-Hincks et al., 2005, 2014; Cloete et al., 2009) also reported negative correlations between direct and maternal genetic effects using linear or logistic models. In a study of LS in Rambouillet and Finn sheep with linear and threshold models, Matos et al. (2000) obtained positive correlations, albeit with large SE too.

Table 5. Estimates of variance components and genetic parameters (with their SE in parentheses), and restricted log-likelihood for the new survival trait (NEWSUR) using 2 different logistic models (LogA and LogB)

<table>
<thead>
<tr>
<th>Item</th>
<th>LogA</th>
<th>LogB</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\hat{\sigma}^2$ (BDAYc)</td>
<td>0.358 (0.015)</td>
<td>0.347 (0.015)</td>
</tr>
<tr>
<td>$\hat{\sigma}^2$ (litter)</td>
<td>0.355 (0.010)</td>
<td>0.355 (0.010)</td>
</tr>
<tr>
<td>$\hat{\sigma}^2$ (e)</td>
<td>3.290 (0.000)</td>
<td>3.290 (0.000)</td>
</tr>
<tr>
<td>$\hat{\sigma}^2$ (a)</td>
<td>0.128 (0.007)</td>
<td>0.083 (0.006)</td>
</tr>
<tr>
<td>$\hat{\sigma}^2$ (a, m)</td>
<td>0.006 (0.010)</td>
<td>0.002 (0.007)</td>
</tr>
<tr>
<td>$\hat{\sigma}^2$ (m)</td>
<td>0.315 (0.012)</td>
<td>0.141 (0.010)</td>
</tr>
<tr>
<td>$\hat{\sigma}^2$ (g)</td>
<td>4.102 (0.019)</td>
<td>4.220 (0.019)</td>
</tr>
<tr>
<td>$\hat{k}^2$ (a)</td>
<td>0.031 (0.002)</td>
<td>0.020 (0.002)</td>
</tr>
<tr>
<td>$\hat{k}^2$ (m)</td>
<td>0.077 (0.003)</td>
<td>0.033 (0.002)</td>
</tr>
<tr>
<td>$\hat{k}^2$ (g)</td>
<td>0.454 (0.013)</td>
<td>0.229 (0.011)</td>
</tr>
<tr>
<td>LnL</td>
<td>$-1,454,703.73$</td>
<td>$-1,402,085.36$</td>
</tr>
</tbody>
</table>

1 $\hat{A}$ = model where the interaction between day of birth classes, flock, and year of birth is fitted as random effects and where phenotypes are transformed using a logit transformation; $\hat{B}$ = same as model LogA but with an extra random litter effect fitted.
**Comparison of Models Based on their Predictive Ability**

Model selection of random effects was assessed for inclusion based on log-likelihood values. Log-likelihood values obtained for NEWSUR with no transformation of phenotypes are reported in Table 4, and those for logistic models are reported in Table 5. With or without a logit transformation of NEWSUR, the models that included litter effect (i.e., models B and LogB) were superior to the models without this effect. Inclusion of the random effect of litter (dam/year) in survival analyses in populations where multiple births are prevalent is relatively common (Van Arendonk et al., 1996; Knol et al., 2002). Therefore, the inclusion of litter effects in the genetic evaluation model for NEWSUR is required to avoid inappropriate weighting of the contribution of LS from multiple births when calculating NEWSUR EBV.

Log-likelihood values cannot be used to compare the linear and logistic models; therefore, MSE were calculated, as described in the methodology, to assess whether model LogB was a better fit for LS trait when compared with the model B. The MSE were slightly lower with the linear model B (from 0.1275 to 0.1284) than the logistic model LogB (from 0.1283 to 0.1293) and much lower than the intercept model (ranged from 0.1624 to 0.1672). Accordingly, the linear model B seems to be a better fit for NEWSUR than the model with a logit transformation (model LogB).

**Conclusions**

According to the results of this large study, the new decision rules to assign NEWSUR could reclaim and include more records in the genetic analysis of LS. Variance or covariance components and derived genetic parameters for NEWSUR were estimated with linear and logistic models. The correlation between direct and maternal genetic effects was negative for the linear models and positive but not significantly different from zero for the logistic models. The heritability estimates were low but consistent with those found in other studies on LS in sheep. This study also showed that the maternal heritabilities may be overestimated when the litter random effect was not fitted. Among the tested models, models fitting the random effect of litter effect displayed the best fit for NEWSUR according to their log-likelihoods values (i.e., models B and LogB). In terms of predictive ability, model B performed slightly better than model LogB. Therefore, model B, which is the linear model fitting the random litter effect, would be the model of choice to implement the genetic evaluation of NEWSUR for the New Zealand sheep to improve the genetic progress for LS to weaning.

**LITERATURE CITED**


