

DERIVING BREEDING VALUES FOR NET REPRODUCTION RATE FROM COMPONENT TRAITS IN SHEEP

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SUMMARY

Genetic analyses for sheep reproduction traits in LAMBPLAN and MERINOSELECT have recently been upgraded to separate number of lambs weaned per ewe joined (NLW) into the component traits of conception (CON), litter size (LS) and ewe rearing ability (ERA). Methodology was developed to combine breeding values for component traits post-analysis into the net reproduction traits: reproduction rate (RR, lambs born per ewe joined) and weaning rate (WR, lambs weaned per ewe joined). Comparisons from the LAMBPLAN maternal analysis show that RR and WR breeding values were closely aligned to single trait number of lambs born per ewe joined (NLB) and number of lambs weaned per ewe joined breeding values, ≈ 0.93 for RR with NLB, and ≈ 0.85 for WR with NLW. The derived net reproduction breeding values are useful as a tool for transition from old to new upgraded analyses.

INTRODUCTION

New genetic analyses for component traits of sheep reproduction have been developed for LAMBPLAN maternal breeds in 2019 (Bunter *et al.* 2019), and MERINOSELECT in 2020 (Bunter *et al.* 2020), and have been available to breeders as research breeding values (RBVs). These are scheduled for transition to Australian Sheep Breeding Value (ASBV) status in 2021. The component traits are conception (CON, ewes pregnant per ewe joined), litter size (LS, lambs born per ewe lambing), and ewe rearing ability (ERA, lambs weaned relative to lambs born). Together, these traits describe the reproductive cycle from mating to lambing and then weaning. This development allows breeders to select on components separately, as determined by their relative importance in different production systems. In this paper we show how breeding values for component traits can be combined post-analysis into a breeding value for net reproduction rate which can be used to support legacy indexes, and as a transitional mechanism to assist breeders who are currently familiar with an equivalent net reproduction breeding value, number of lambs weaned (NLW).

MATERIALS AND METHODS

Two derived net reproduction traits are defined, reproduction rate (RR) which combines conception and litter size, and weaning rate (WR) combining all three components (CON, LS, ERA). Units for RR are number of lambs born per ewe joined, and for WR are number of lambs weaned per ewe joined. Therefore, RR is a replacement for the current NLB breeding value, and WR for NLW. Further, WR can be used as a replacement for NLW in existing selection indexes.

To derive net reproduction breeding values, component traits are expressed relative to phenotypic performance. Firstly, baseline phenotypic means are calculated for each component trait with an adjustment for genetic trend. For example, the baseline mean for CON is:

$$\mu_{con} = \sum_i (y_{con_i} - \hat{u}_{con_i}) n_{con}^{-1}$$

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Where y_{con_i} is the phenotype for the i^{th} animal, \hat{u}_{con_i} the estimated breeding value, and n_{con} the number of CON phenotypes in the analysis. Baseline means for LS and ERA are calculated accordingly (μ_{ls} and μ_{era}).

Predicted daughter performance is then calculated for the i^{th} animal, for CON as:

$$con_i = \mu_{con} + 0.5 \times \hat{u}_{con_i}$$

And for LS as:

$$ls_i = \mu_{ls} + 0.5 \times \hat{u}_{ls_i}$$

The expected frequencies of the j^{th} litter size category given ls_i ($p_{ij}, j = 1,2,3,4$) are then derived using the mathematical model of Amer *et al.* (1999), graphically represented in Figure 1. We note that this model is very accurate and repeatable across populations and breeds, including across countries.

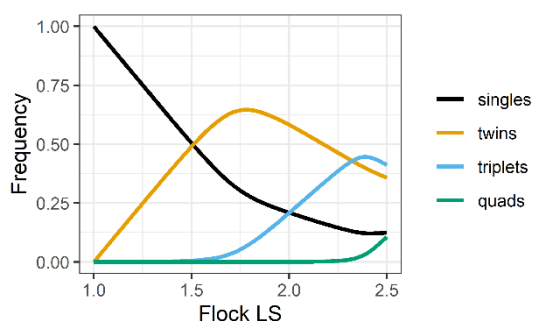


Figure 1. Frequency of litter size categories given mean flock litter size (Amer *et al.* 1999)

Predicted daughter performance for RR can then be calculated as:

$$rr_i = con_i \times \sum_j p_{ij} \cdot j$$

Where \overline{rr} is the mean predicted daughter performance for all animals in the pedigree.

Derivation of WR requires calculation of survival rates for each litter size category ($s_{ij}, j = 1,2,3$) given predicted daughter performance for LS (ls_i) and ERA (era_i), the latter calculated as:

$$era_i = \mu_{era} + 0.5 \times \hat{u}_{era_i}$$

Individual survival rates are not straightforward because survival is a much more random biological process than litter size, so we use numerical optimisation of the following equations:

$$s_{i1} - (era_i - (p_{i2} \times s_{i2} + p_{i3} \times s_{i3})/p_{i1}) = 0$$

$$s_{i2} - (era_i - (p_{i1} \times s_{i1} + p_{i3} \times s_{i3})/p_{i2}) = 0$$

$$s_{i3} - (era_i - (p_{i1} \times s_{i1} + p_{i2} \times s_{i2})/p_{i3}) = 0$$

Subject to the constraints:

$$0.8 \leq s_{i1} < 1$$

$$s_{i1} - s_{i2} \leq 0.2$$

$$s_{i2} - s_{i3} \leq 0.2$$

With litter size frequencies (p_{ij}) determined by predicted daughter performance for LS (ls_i) as above. Also note that survival rates are only calculated for singles, twins and triplets: frequencies for quadruplets are too low for reliable calculation.

Optimised survival rates calculated using this method on the LAMBPLAN maternal reproduction analysis (8 December 2020) are shown in Figure 2.

Predicted daughter performance for WR is then calculated as:

$$wr_i = con_i \times \sum_j s_{ij} \cdot p_{ij} \cdot j$$

The derived breeding value for WR is:

$$\hat{u}_{wr_i} = 2 \times (wr_i - \overline{wr})$$

The methods were validated using the LAMBPLAN maternal reproduction analysis of 8 December 2020. Firstly, single trait REML analyses were run for the directly observed traits NLB and NLW derived from CON, LS, and ERA phenotypes, with the resulting breeding values compared to RR and WR breeding values calculated from component trait breeding values from the full multi-trait LAMPLAN analysis.

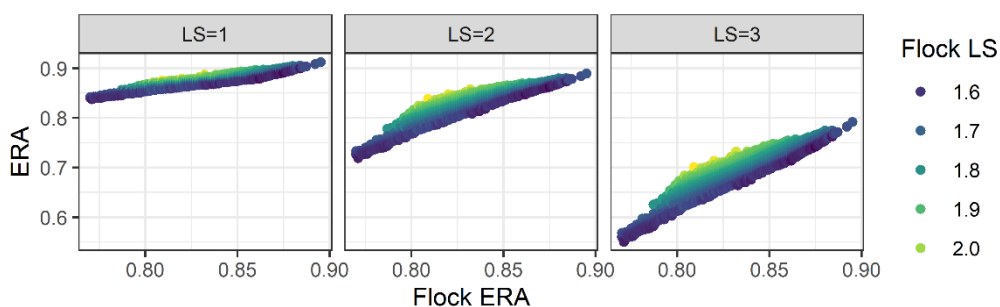


Figure 2. Survival rates (y-axis) for litter size categories (LS=1,2,3) calculated by optimisation given predicted daughter performance for Flock ERA (era_i , x-axis) and Flock LS (ls_i)

RESULTS AND DISCUSSION

Results in Table 1 show high correlations between direct breeding values for NLB or NLW and corresponding derived net breeding values within-flock, higher for NLB with RR (≈ 0.93) than for NLW with WR (≈ 0.85). In within flock analyses with complete reproduction records these correlations can exceed 0.95 (analyses not presented). The correlations in Table 1 are expected to be lower than within flock results because derived net breeding values originate from the full multi-trait analysis (15 traits described by Bunter *et al.* 2019) with different data, and because of incomplete observations of the complete reproductive cycle for many females. That is, in the across flock analysis it is common for females to have records for LS but not CON or ERA, due to quality control filtering at the flock and contemporary group levels. There were also genetic group effects apparent, with lower correlations (not shown) observed in composite breeds compared to straight-bred animals.

An alternative to deriving net reproduction traits post-analysis would be to explicitly include NLB and NLW phenotypes as additional traits in the new analysis, but with yearling and adult expressions this would mean adding four traits to multi-trait models which currently have up to 19 traits. This would involve substantial effort in developing covariance matrixes, made difficult by dependencies between component and net traits, and would increase analysis run-times.

A second reason not to include NLW explicitly relates to the modelling of contemporary groups at different points of the reproductive cycle. For CON and LS groups are defined at joining because the outcomes are determined at this time (apart from low level impacts of foetal loss on LS). By contrast, for ERA, groups are defined from lambing. Because NLW covers the whole cycle both groupings are relevant. However, breeders routinely group animals for lambing based on pregnancy scanning for management purposes i.e., single bearing and multiple bearing ewes are grouped separately for differential feeding. This means that lambing groups can often be highly confounded with NLW trait values. We have previously observed that when such groups are modelled for NLW the resulting breeding values are poor predictors of phenotypic performance.

Table 1. Comparison of NLB with RR and NLW with WR breeding values for sires and dams used from 2015 in the LAMBPLAN maternal across flock analysis (data from 8-Dec-2020). Comparisons include correlations, standard deviations ([trait]_sd), and intercept and slope from regression of “direct” trait on “derived” (e.g. NLB ~ RR)

Group		NLB with RR				
	number	corr	NLB_sd	RR_sd	intercept	slope
Sires	1542	0.928	0.138	0.156	0.01	0.82
Dams	82990	0.933	0.124	0.137	0.01	0.84
		NLW with WR				
	number	corr	NLW_sd	WR_sd	intercept	slope
Sires	1472	0.855	0.091	0.110	0.01	0.71
Dams	72403	0.853	0.079	0.095	0.02	0.71

CONCLUSIONS

New reproduction analyses for LAMBPLAN maternal sheep and MERINOSELECT represent a major advance on the current analysis of NLB and NLW, due to a greatly improved data processing pipeline, use of genomic information, and because they provide breeders with the ability to focus on components of reproduction separately. Net reproduction rate breeding values (RR and WR) derived from component trait breeding values post-analysis are useful as a tool to transition from the old to the new analyses and are shown in this study to be highly correlated with comparable breeding values for NLB and NLW.

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REFERENCES

- Amer, P.R., McEwan, J.C., Dodds, K.G., and Davis, G.H. (1999) *Livest Prod Sci* **58**: 75.
 Bunter, K.L., Swan, A.A., Gurman, P.M., and Brown, D.J. (2020) *Anim Prod Sci* **61**: 333.
 Bunter, K.L., Swan, A.A., Gurman, P.M., Boerner, V., McMillan, A.J. and Brown, D.J. (2019) *Proc. Assoc. Anim. Breed. Genet.* **23**:560.