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FIXED EFFECTS AND GENETIC PARAMETERS FOR THE COMBINED LAMPLAN EVALUATION OF AUSTRALIAN SHEEP

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SUMMARY

The Australian sheep industry consistently improves performance through genetic evaluation provided by Sheep Genetics. Sheep Genetics is developing an enhanced evaluation system combining Terminal and Maternal breeds into a single LAMPLAN analysis. This improvement includes a review of fixed effects to ensure their suitability and an evaluation of alternative methods for their inclusion. This study outlines the steps taken to model fixed effects directly within the model, rather than through pre-adjustment, and to estimate genetic parameters. In the updated multi-trait analysis, two main changes were incorporated in the fixed effect model, 1) birth type and rearing type were combined into a single effect to account for their interaction, and 2) the age of the dam was fitted as class effect (rather than a quadratic polynomial). Including the effects directly in the model resulted in an improvement in the fit compared to using the current pre-adjustment methods. These enhancements should lead to more accurate breeding values for industry, and this will be the subject of further studies.

INTRODUCTION

In Australia, Sheep Genetics uses the OVIS (Brown *et al.* 2006) software to undertake the national genetic evaluation of sheep. Estimated breeding values (EBVs) are currently calculated by fitting a model with a single fixed effect of contemporary group using pre-adjusted phenotypes that account for systematic effects such as age (separated by sex), age of dam (linear and quadratic), birth and rearing type and liveweight (Brown *et al*. 2006). Although this approach is both accurate and computationally less demanding than fitting effects in the model, it requires estimating adjustment factors for each systematic effect on an ongoing basis (Brown and Reverter 2002). In most cases, adjustment factors remain unchanged over long periods of time and are often based on subsets of data such as well-recorded reference populations. However, this can be problematic because of high levels of genetic variability included in the design of reference flocks. Routinely revisiting fixed effects is necessary due to partial confounding (e.g. birth and rearing type) and the need to better account for any interactions. Importantly, given the decision to combine the terminal and maternal LAMBPLAN evaluations (Walkom *et al.* 2025), a meticulous assessment of the assumptions used for the national evaluation was required. This study describes the main steps followed to assess the modelling of fixed effects and estimation of genetic parameters for main traits in the Combined LAMBPLAN analysis.

FIXED EFFECTS MODELLING

All records from the Combined LAMBPLAN (Walkom *et al*. 2025) were used in the evaluation of fixed effects. To maximise the use of full dataset and to overcome the large number of records

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available for weight traits such as birth weight (>2M), weaning weight (>4M) and post-weaning weight (>2M) required subsetting the data for analysis. A 'split-apply-combined' approach was applied in which the data for each trait was grouped by flock, year of birth, sex and breed type, with results combined for further analyses. This strategy maximised the use of all records to determine which effects were important across traits and identify where it would be necessary to fit interactions between the standard effects and factors such as breed and/or site.

The approach to evaluate the fixed effects of interest for each trait included fitting a linear model with fixed effects for the contemporary group (CG), birth (BT) and rear type (RT), or combined birth and rearing types (BRT), age of dam (AOD) and weight (WT; only for scan traits) [Model 1]. The adjustment factors were calculated as the ratio of the base level divided by the predicted mean. Further, multiple linear models were fitted to both the estimated adjustment factors (BT, RT, AOD) or the solutions (WT or age) to examine variation in effects of flock, sex, yob, breed [Model 2], site and their interactions. From each model, the variance explained (R^2) by the effect fitted in the model were compared. In general, for all the traits evaluated, the flock explained larger variance (R^2 from 0.06 to 0.71) compared to yob (R^2 from 0 to 0.05), sex (R^2 from 0 to 0.07) and breed (R^2 from 0.001 to 0.07). As expected more complex models that fitted all the effects or interactions resulted in larger variance explained (R^2 from 0.2 to 0.78).

Developing an approach that deals with the necessary interactions in a more parsimonious way while delivering accurate EBVs is important. Therefore, EBVs generated by the current model used in OVIS analysis were compared to those from models that fitted the fixed effects or their interactions. The correlations of EBVs generated from these models ranged from 0.9 to 0.999. These results suggest that the use of more complex models yield breeding values highly correlated with the current model used in OVIS. Therefore, the use of complex models would not be required.

A linear mixed animal model was fitted in ASReml v4.2 (Gilmour *et al.* 2015) to examine the importance of heterosis. In addition to the fixed effects mentioned above, heterozygosity coefficients were included in the models. Heterozygosity was calculated based on the pedigree and estimated both direct (DHB) and maternal (MHB) heterosis applying the classic "dominance" model described by Dickerson *et al.* (1973). A conditional Wald F statistic was applied to estimate the significance of fixed effects (p-value < 0.05).

In the final model, birth type (BT) was fitted only for birth weight (BWT) as class effect for single (1), twin (2), and triplet (3) levels. For traits where birth and rearing type were significant, a combined birth-rearing type (BRT) effect was fitted (six levels: 1-1, 2-2, 2-1, 3-3, 3-2, 3-1). The age at measurement was included as a linear covariate for females (ageF) and males (ageM) separately. Age of dams (AOD) was fitted as class effect with levels for two-years-old to 10 years-old-dams, dividing one-year-old dams into yearling and hogget at 420 days of age and an additional class of unknown age of dams. Heterozygosity, as DHB and MHB, were included only if significant in previous models. Weight (WT) was fitted as a covariate effect for the ultrasound scan, with both linear and quadratic terms. New contemporary groups were fitted, as defined by Walkom *et al.* (2025). The random effects consisted of genetic groups defined in McMillan *et al.* (2025), animal genetic, maternal genetic and permanent environmental.

A multi-trait analysis was performed using OVIS to compare results from the current model compared with fitting the effects directly in the model. A more complex model was tested in which the age solutions from Model 1 were split into categories based on six quantiles. Figure 1 shows the root mean square errors (RMSE) calculated on the solutions from three models: 1) using the preadjusted data in OVIS (preadjust model); 2) using age by sex interaction (age_MF model); and 3) fitting the age quantiles (age_Q6 model). In general, RMSE values were larger for solutions from the preadjusted model. Moreover, similar errors (RMSE) obtained in the other two models indicated that more complex models are not required to improve the efficiency of the analysis. The multi-trait analysis indicated that a change in approach from pre-adjusting data for systematic effects to directly fit the effects in the solver would be advantageous, given a better fit to the data with no impact on computing performance. Additionally, the effects are always current and relevant to the entire dataset. In contrast, pre-adjustments typically remain unchanged over long periods of time and are often based on subsets of data such as well-recorded reference populations where estimating effects can sometimes be problematic because of high levels of genetic variability included in the design. Moreover, avoiding the re-estimation of adjustment factors represents an efficiency gain for research projects in long term.

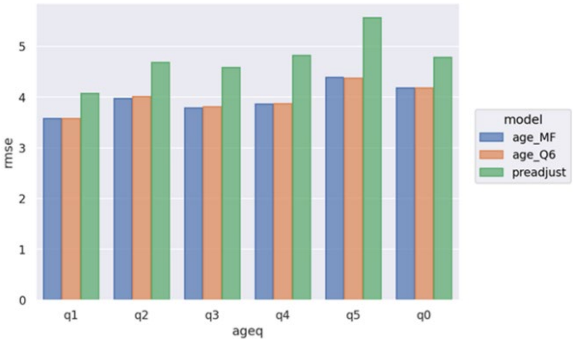

Figure 1. Root mean square error (rmse) for post-weaning weight fitting preadjusted data (green), age*sex interaction (blue) interaction or six age effects based on solution distributions (orange) in the models. The age solutions from the split-combine-apply were categorised into six quantiles (age_Q6)

GENETIC PARAMETERS

Initially, the genetic parameters for six terminal (Poll Dorset, Texel, Suffolk, White Suffolk, Dorper and White Dorper) and four maternal (Border Leicester, Corriedale, Coopworth, Composite Maternal) breeds were estimated and compared with the estimates obtained using all the breeds in the Combined LAMBPLAN. The records used in each dataset were from the most representative flocks selected, as indicated in de las Heras-Saldana *et al*. (2023). The final models were fitted in univariate model using the Combined LAMBPLAN dataset for birth weight (bwt), weaning weight (wwt), post-weaning weight (pwt), yearling weight (ywt), and adult weight (awt). In general, differences in genetic variances between the terminal and maternal breeds were not bigger than those already existing within breed type (Figure 2). Larger dispersion in ywt and awt reflects the lower number of records assigned to those traits for each breed, compared to a larger number of records in bwt, wwt and pwt (Walkom *et al*. 2025). Outliers corresponded to breeds with lower records, such as Texel, Suffolk, Dorper and White Dorper.

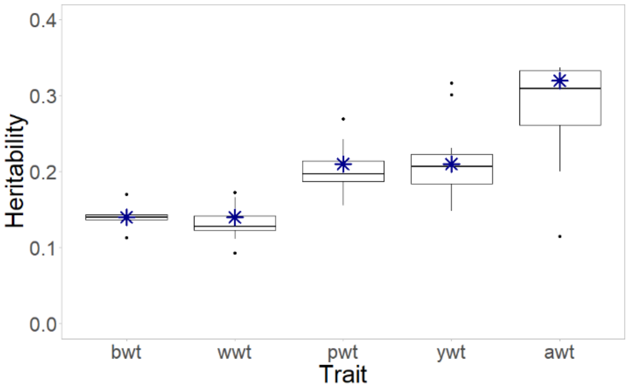

Figure 2. Distribution of heritabilities (h^2) estimates for the breeds in Terminals and Maternals (boxplots) and the current h^2 calculated in the combined LAMBPLAN dataset (indicated as '*')

CONCLUSIONS

Fitting fixed effects directly in the solver represents an efficiency gain for the national genetic evaluation of sheep since this approach is data-driven, always current and, avoids the maintenance of adjustment factors. It was also concluded that even with the combining of the two analyses, fitting global effects for BRT and age of dam remained the most worthwhile solution. These enhancements should lead to more accurate breeding values for the industry. In future analyses will consider a strategy to adjust weight for carcass traits and fitting a breed interaction.

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