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BREED COMPARISONS IN COMBINED LAMBPLAN: GENETIC GROUP AND LINKAGE ASSESSMENT

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SUMMARY

In response to changing industry selection practices and a desire for a simpler genetics landscape, Sheep Genetics is developing a Combined LAMBPLAN evaluation that merges the Maternal and Terminal sire analyses. A key challenge, especially when combining multi-breeds for genetic evaluation, is ensuring fair comparisons across diverse genetic backgrounds. To address this, genetic groups have been redefined and assessed for prediction accuracy, and across-flock linkage has been evaluated to determine the degree of connectedness and robustness of prediction across the combined population. Results show that the new genetic groups effectively capture population structure and that strong linkage supports robust across-flock comparisons. These findings provide key evidence for implementing the Combined LAMBPLAN evaluation to improve the accuracy and relevance of Australian Sheep Breeding Values (ASBVs).

INTRODUCTION

Genetic evaluations play a critical role in improving the productivity and efficiency of livestock industries. In Australia, Sheep Genetics (SG) has traditionally conducted separate evaluations for Maternal and Terminal sheep breeds (Brown *et al.* 2007). However, as breeding objectives shift, and producers adopt flexible breeding strategies and regularly incorporate genetics from diverse sources they have a need to assess animals across these two analyses. A growing number of animals from the separate analyses are common between the two evaluations. An increase in the number of composite animals, and the use of outside breed sires reflect a reduced reliance on strict breed classifications and an emphasis on performance-based selection (McMillan *et al.* 2023).

To better capture genetic relationships across these populations and improve evaluation accuracy, a combined analysis is being developed, integrating the LAMBPLAN Maternal and Terminal analyses into a Combined LAMBPLAN genetic evaluation (Walkom *et al.* 2025). A key challenge in this transition is ensuring that animals from a diversity of breeds and environments are fairly treated.

In both current LAMBPLAN analyses, genetic groups account for breed differences and genetic trends in the base populations (Brown *et al.* 2007). Genetic group formation is based on breed and time periods. The current LAMBPLAN analysis utilises a multi-trait estimate of sire linkage across flocks (Brown *et al.* 2007). This linkage value measures the flocks' connectedness and gives breeders the confidence to compare animals across flocks and breeds. This linkage is created by using sires across multiple flocks and time periods. In addition, the Information Nucleus Flock (van der Werf *et al.* 2010), other resource flocks, and breeder groups provide strong comparisons through direct head-to-head comparisons.

This study aims to (1) calculate genetic group accuracies in the new combined analysis and (2) evaluate across flock linkage in the new Combined LAMBPLAN genetic evaluation. By quantifying these factors, we provide insights into the effectiveness of the combined evaluation to deliver accurate Australian Sheep Breeding Values (ASBVs) across a broader population.

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MATERIALS AND METHODS

The data for these analyses was taken from a combined dataset of the Maternal and Terminal analyses built by Sheep Genetics in November 2024, as per Walkom *et al.* (2025). The analyses will focus on two well-recorded trait groups, weight (WT) and ultrasound measured eye muscle depth (EMD), at three age stages: weaning, post-weaning and yearling (wwt, pwt, ywt, wemd, pemd, yemd) and the less recorded carcase trait of abattoir measured intramuscular fat (imf)

Genetic Group Definition. With the initiative to combine the analyses, particularly regarding data reduction described by Walkom *et al.* (2025), a new set of 92 genetic groups were defined to reflect this new dataset, using the same classifiers: breed and time periods. Efforts were made to collapse groups where appropriate to ensure computational efficiency this reduced the number of genetic groups from 111 and 94 respectively in the current Maternal and Terminal analysis.

Genetic Group Accuracy Estimation. To evaluate the accuracy of genetic group estimates, a reduced version of the full mixed model was considered, incorporating only contemporary groups and genetic groups. The model is expressed $as\ y = X\mathrm{B} + ZQg + \cdots + e$ where: y is the vector of observations, X is the design matrix for fixed effects (B), Z is the incidence matrix linking records to genetic group effects, Q is the incidence matrix relating individuals to genetic groups, g is the vector of genetic group effects, and e is the residual error term. To obtain the prediction error variance (PEV) matrix for genetic groups, the equations corresponding to contemporary groups were absorbed into the genetic groups' equations, resulting in the following expression:

$$PEV = \left[Q'Z'ZQ + I\frac{\sigma_e^2}{\sigma_{gg}^2} - Q'Z'X(X'X)^{-1}XZQ\right]^{-1}\sigma_e^2$$

where σ_e^2 is the residual variance and σ_{gg}^2 represents the genetic group variance. The accuracy of genetic group estimates was computed using the diagonal elements of the PEV matrix, with the accuracy for each genetic group calculated as: $\sqrt{}(1 - \frac{PEV_{ii}}{\sigma_{gg}^2})$, where PEV_{ii} represents the prediction error variance of the genetic group.

Linkage Analyses. The routine linkage analyses were conducted on the new combined data following procedures found in Huisman *et al.* (2005). This is a sire-based analysis conducted at a flock level for the phenotypic data recorded from 2019- 2024. The linkage for the weight and eye muscle depth traits were assessed within the trait but across stages, with linkage for intramuscular assessed as a single trait.

RESULTS AND DISCUSSION

Genetic Group Accuracy Estimation. Figure 1 presents the genetic group accuracy for the newly defined groups, demonstrating the effectiveness of estimating genetic group effects within the combined LAMBPLAN dataset where adequate data is available. The weight traits show very high accuracy, benefiting from extensive records across most genetic groups. Only 5% of the weight genetic groups have an accuracy of prediction under 85%. In contrast, for eye muscle depth traits approximately 40% of genetic groups have an accuracy of prediction under 85 %. This is due to generally fewer performance records for eye muscle depth across stages, resulting in a poorer ability to predict the genetic groups. However, post-weaning muscle depth, which is very well recorded, follows a similar pattern to that observed for weight traits. Intramuscular fat, the trait with the least amount of recording, has 48% of the genetic groups above 85% prediction accuracy. The major breeds tend to have more recording and, thus higher accuracy. The minor breeds tend to have less data, and their genetic group solutions with low prediction accuracy will be regressed to the mean.

These findings confirm that the new genetic group definitions provide robust estimates particularly for the breeds with more representation in the analyses. The high accuracy for key traits and breeds underscores the effectiveness of the updated framework in supporting reliable genetic evaluations across the diverse combined LAMBPLAN dataset.

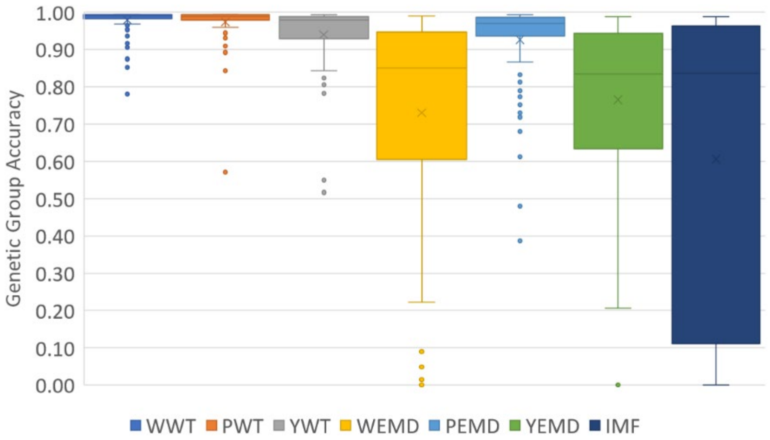

Figure 1. Accuracy of genetic group effects for a range of traits in the Combined LAMBPLAN dataset

Linkage Analyses. Table 1 summarises the linkage analyses for the WT, EMD, and IMF trait groups for the Combined LAMBPLAN dataset.

Table 1. Summary of linkage for three trait groups in the Combined LAMBPLAN dataset

	WT	EMD	IMF
Total flocks	758	708	36
Average number of linked flocks (NOLF)	19.4%	19.6%	33.5%
Average linkage to linked flocks	69%	68%	56%
Linked flocks	728	690	35

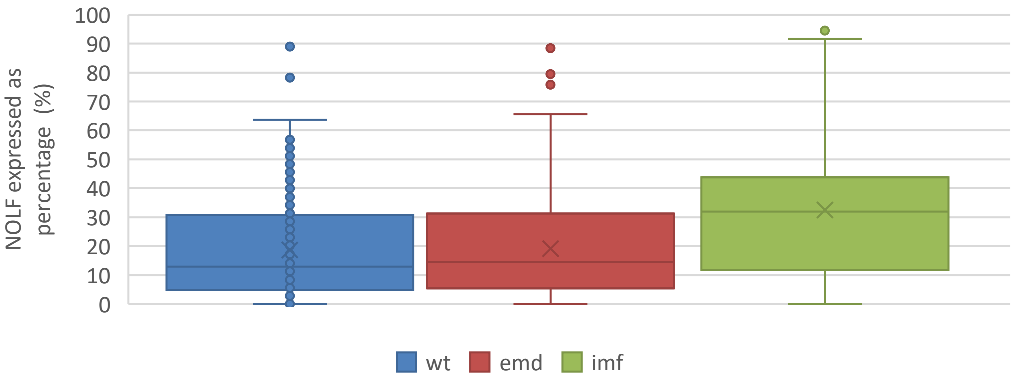

Figure 2. Distribution of individual flocks' number of linked flocks (NOLF) in combined LAMBPLAN dataset

Figure 2 presents the distribution of number of linked flocks (NOLF) for individuals flocks. The data reveal a broad range, indicating that most flocks maintain connections with a substantial portion of the population. Flocks, on average, are linked to approximately 20% of the total flocks for the weight and eye muscle depth groups and 30% for those flocks recording IMF, which are fewer. The Information Nucleus Flock and MLA Resource Flocks are key by linking over 80% of the flocks. This is a positive outcome regarding the utility of the combined analysis and value of the structured resource flocks.

The heatmaps of flock linkage not shown here reveal that although historical patterns reflecting the distinction between maternal and terminal animals are traceable, the resource flocks intersect these divisions. This connectivity results in high linkage for the resource flocks, with proportions ranging from 78% to 88% for weight, 75% to 88% for eye muscle depth, and 83% to 94% for intramuscular fat. Similar patterns exist for organised breeder groups, which have high linkage within these groups but also links to the wider industry.

The presence of these highly connected flocks facilitates strong genetic links between what might otherwise be more isolated groups. This suggests that while some historical divisions exist, a clear genetic divide between maternal and terminal animals is not obvious, reinforcing the validity of comparisons across these groups. Overall, results confirm the connectedness within the population, supporting the integrity of genetic evaluations and ensuring broad connectivity among flocks.

While this paper focussed on weight and carcase traits. Further work is being conducted for the other trait groups in particular reproduction which is essential for breeders with a maternally focused breeding objective.

CONCLUSION

This study demonstrated the ability of the Combined LAMBPLAN analysis to accurately estimate genetic group effects from a diverse breed background and the ability to compare ASBVs between the vast majority of flocks. Given these results, the Combined LAMBPLAN analysis will have the ability to provide well-estimated ASBVs that are comparable across previous analysis divides, providing breeders with the ability to accurately select animals from a broader gene pool.

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