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COMBINED LAMBPLAN: EXPANDING THE MULTI-BREED NATURE OF THE LAMBPLAN EVALUATION

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SUMMARY

The Australian sheep industry continues to mix breeds across all sectors, including ram breeding. Genetic evaluation needs to change with industry and provide relevant comparisons across breeds. This has prompted a development to combine the LAMBPLAN Terminal and Maternal evaluations. Combining analyses will provide a single breeding value ‘language’ across non-Merino breeds and continue to allow breeders to access selection tools to meet their breeding objectives irrespective of breed. This study summarises the key technical enhancements to deliver the Combined LAMBPLAN analysis, including: business decisions around data usage, formation of lifetime contemporary groups, genetic group structure and the use of a meta-founder model, fixed effects models, heterosis adjustments and parameter re-estimation. The combined evaluation will provide an improved utility of ASBVs for the Australian prime lamb industry.

INTRODUCTION

Sheep Genetics (SG) was established in 2005 to deliver a national across-flock genetic evaluation system to the Australian sheep industry for terminal, maternal and Merino sheep (Brown *et al.* 2007). Sheep Genetics provides a single national genetic evaluation “language” for Australian sheep breeders. The SG evaluations have focussed on industry-recorded data from three major breed types: 1) LAMBPLAN - terminal sire breeds, 2) LAMBPLAN - maternal/dual purpose breeds and 3) MERINOSELECT - Merino breeds. The two LAMBLAN evaluations represent across-flock multi-breed evaluations. Having a uniform language, Australian Sheep Breeding Values (ASBVs), to describe genetic evaluation for Australian sheep has proven extremely successful (Collison *et al.* 2018). This has, in part, enabled Australian sheep breeders to select for a diversity of breeding objectives irrespective of breed. Subsequently, a decline in the purity of the animals in the LAMBPLAN evaluations and the rise of composite animals has been observed (McMillan *et al.* 2023). This has also corresponded to an increase in common animals across LAMBPLAN analyses, with 35% of flocks represented in both, as breeders look to different genetic sources to achieve their desired genetic gains. An unintended consequence of sharing terminal and maternal genetics is that the common animals are provided with two ASBVs, which cannot be compared, exhibit a significant base difference and are not underpinned by the same information, ultimately creating confusion about how to interpret ASBVs across the analyses.

Some flocks, primarily the ‘shedding’ breeds (i.e. Dorpers, Australian White and Ultra Whites) who are breeding a self-replacing ewe wanted to shift to the Maternal analysis. This change would produce a substantial increase in the size of the LAMBPLAN – maternal analysis. Consequently, the decision was made to combine the LAMBPLAN evaluations and provide a single evaluation and common language from which all non-Merino-type sheep could be compared. This paper covers the historical technical advancements to the Sheep Genetic evaluation that enable the combined analysis

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and how the evaluation is being changed to overcome the technical constraints associated with using genomics from diverse breed and composite populations.

TECHNICAL ADVANCEMENTS

Genomic reference flock. A significant feature of the Australian Sheep Cooperative Research Centre (CRC) program was the information nucleus flock (INF) (van der Werf *et al.* 2010). Via the INF and its later incarnations, the reference flock population has provided head-to-head comparisons of Merino, maternal and terminal sire types primarily for live animal and carcase traits. The reference flock was the initial industry investment into genomics and remains the cornerstone for the genomic reference flock for hard-to-measure traits such as intra-muscular fat, shear force, worm egg count and any future methane records. At the time of this paper approximately 1,700 sires of maternal and terminal origin have had progeny recorded.

Single-step genetic evaluation. The LAMBPLAN evaluations changed to a genomic single-step model in 2017 (Brown *et al.* 2018). The development of this model was associated with improvements in the accuracy and bias of the estimated breeding values in forward and cross-validation studies of the LAMBPLAN Terminal data, compared to the pedigree model (Gurman *et al.* 2018). The single-step GBLUP model further grew to a breed-adjusted GRM, which reduced the breed structure that was implicitly forming in the unadjusted GRM, resulting in an improvement in cross-validation accuracies and bias estimates (Gurman *et al.* 2019).

Sheep Genetics database re-development. Combining analyses was made possible due to the re-development and implementation of a single Sheep Genetics database, completed in 2022. This encapsulates the pedigree, phenotypic and genomic information for the MERINOSELECT and the two LAMBPLAN evaluations in one repository. The combined co-managed central database significantly reduces the associated risks for Sheep Genetics of maintaining consistency across multiple databases. This new platform provided the flexibility to allow the new analysis models and methods required for the development of the Combined LAMBPLAN analysis.

THE PROPOSED EVALUATION

A combined dataset. At the time of writing (January 2025) the LAMBPLAN terminal and maternal analysis were publishing ASBVs for 4.1m and 2.8m animals. Given the scale of these evaluations, the significant overlap of animals and to expedite timely delivery of analyses, several business decisions were made to develop the future Combined LAMBPLAN database. These decisions were focussed on data reduction including removal of fictional dams (remnant of old decommissioned software), New Zealand data (phenotypes and unlinked pedigree), multi-sire groups and historic Australian data from animals born before 2000 (phenotypes). Data reduction decisions were found to have negligible impact on the rank or spread of the breeding values of current selection candidates during initial testing. The Combined LAMBPLAN development discussed in this paper and the work presented by Alexandri *et al.* (2025), de las Heras-Saldana *et al.* (2025), Gurman *et al.* (2025) and McMillian *et al.* (2025) have been performed on a dataset of growth and development traits built by Sheep Genetics in November 2024 (Table 1). The pedigree included 4.8m animals, with 3.7m recorded for at least one trait presented in Table 1. The analysis also incorporates 246k genotypes imputed to 61.5k SNP density.

Contemporary group structure. The lifetime grouping of animals as part of contemporary group formation has been improved so that the contemporary group better reflects a group of animals that have been managed together. Contemporary group (CG) construction and age slicing of groups were moved out of the analysis software and applied within the SG database, providing greater flexibility and improved transparency for breeders. This reduced the number of small CGs in the later age stages and was made alongside the decision to remove data for single animal CGs.

Table 1: Summary of Combined LAMBPLAN research dataset, November 2024

Trait Description	Trait Code	Animals	Records	Mean (SD)	#cg	cg size
Birth Weight	BWT	2,262,969	2,262,969	4.82 (1.08)	55,629	40.7
Weaning Weight	WWT	2,932,332	3,327,446	36.53 (9.94)	105,564	31.5
Post-wean Weight	PWT	2,050,519	2,322,479	50.25 (12.24)	78,704	29.5
Yearling Weight	YWT	667,005	667,005	59.36 (15.42)	30,063	22.2
Hogget Weight	HWT	277,096	277,096	69.19 (17.40)	14,505	19.1
Adult Weight	AWT	120,529	185,917	70.88 (12.97)	16,052	11.6
Carcase weight	CWT	30,370	30,370	24.29 (4.15)	2,027	15.0
Weaning fat depth	WCF	268,023	268,023	3.27 (1.21)	12,324	21.7
Post-wean fat depth	PCF	1,586,894	1,586,894	3.52 (1.34)	54,394	29.2
Yearling fat depth	YCF	429,450	429,450	3.87 (1.63)	17,132	25.1
Carcase GR fat depth	CFAT	22,745	22,745	15.22 (6.09)	1,703	13.4
Carcase C-site fat depth	CCFAT	25,886	25,886	4.61 (2.47)	1,823	14.2
Intramuscular fat	IMF	27,297	27,297	4.25 (1.11)	1,947	14.0
Shear Force	SF5	24,910	24,910	32.46 (11.03)	1,757	14.2
Weaning eye muscle depth	WEMD	267,913	267,913	28.77 (4.72)	12,322	21.7
Post-wean eye muscle depth	PEMD	1,589,755	1,589,755	30.33 (5.10)	54,440	29.2
Yearling eye muscle depth	YEMD	429,341	429,341	31.57 (5.47)	17,123	25.1
Carcase eye muscle depth	CEMD	26,746	26,746	33.06 (4.92)	1,845	14.5
Dressing percentage	DRESS	18,570	18,570	46.23 (3.78)	1,388	13.4
Lean meat yield	LMY	8,707	8,707	55.84 (4.63)	567	15.4
Post-wean scrotal circumference	PSC	98,958	98,958	29.95 (3.98)	3,272	30.2
Yearling scrotal circumference	YSC	65,107	65,107	30.06 (3.39)	2,574	25.3

Multi-breed population. The Combined LAMBPLAN evaluation contains data from 76 breeds including but not limited to the major terminal (Poll Dorset, Texel, Suffolk, White Suffolk, Dorper and White Dorper), maternal (Border Leicester, Corriedale, Coopworth, Composite Maternal) and some small representation from Merino breeds. Leveraging the genomic data available, an unsupervised clustering method was utilised to improve the accuracy of breed composition assessment, which led to the development of a more inclusive multi-breed genetic evaluation (Alexandri *et al.* 2025), focussed on genomic population structure, not arbitrary breed allocation. The findings support a shift from relying solely on straight-bred reference populations, allowing for better representation of composite and smaller breeds in genetic evaluations.

Development of a new genetic grouping strategy was performed, taking the breeds and further dividing them into either 5 or 10-year time windows, producing a final count of 95 genetic groups. This has improved the accuracy of breeds across a range of traits (McMillian *et al.* 2025). Analysis of the genetic linkages between breeds confirmed that the Combined LAMBPLAN dataset enables effective comparisons across all the key breeds included in the evaluation.

OVIS solver modification. As a result of research on fixed modelling, an important change in the analysis methodology will be the transition from pre-adjusting the data for systematic fixed effects to directly fitting these effects in the solver (de las Heras-Saldana *et al.* 2025). This produces a better fit of the model to the data with little impact on computing performance. It also means that the effects are always current and relevant to the entire data set, in contrast to pre-adjustments which can remain unchanged over long periods. Data filtering restrictions around age have been adjusted to avoid extreme values and ensure more trustworthy estimates. Pre-adjustments are often based on subsets of data such as reference populations, where estimating effects can be problematic because of high levels of genetic variability included in the design. Not having to re-estimate adjustment factors represents an efficiency gain for research projects.

The decision to bring about significant change to the LAMBPLAN evaluation presents the opportunity to re-evaluate the most appropriate method for aligning the pedigree and genomic information in single-step genomic BLUP. Changing from a breed-adjusted GRM to a metafounder model produces better predictive ability (Gurman *et al.* 2025), indicating a further change to how breeds are modelled within the Combined LAMBPLAN analysis.

CONCLUSION

The Combined LAMBPLAN analysis represents a revolutionary step forward for the Australian sheep industry and is the result of several years of technical development. The new analysis will deliver more robust breeding values and allow breeders to further increase their rates of genetic progress. The Combined LAMBPLAN evaluation will be released in 2025 upon the completion of the research phase, the required implementation work for commercialisation and the relevant validation work to quantify the value of the new models. The evaluation will also be expanded to incorporate reproduction, health and wool traits throughout 2025. Combining LAMBPLAN provides a single breeding value 'language' across the non-Merino breeds and continues to allow breeders to access selection tools to meet their breeding objectives.

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