

25 years of multibreed: How a genetic evaluation has shaped the Australian sheep industry

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Introduction

Throughout the lifetime of the national genetic evaluation, the Australian sheep industry has transitioned from a wool centred industry to one focused on dual purpose lamb production systems. This has coincided with both an evolution to the breeding objectives but also the composition of the national flock. As the industry shifted, the genetic evaluation has evolved with it. The evaluation framework and its multibreed design have evolved to remain aligned with industry priorities. A history of continuous improvement in-step with the evolution of the breeding directions of industry has brought with it many challenges and will, in the future, bring forth many more. This paper examines how a new generation of multibreed genetic evaluations has been integrated into commercial delivery systems to meet current industry demands and position the evaluation framework for future needs.

Evolution of the Evaluation

Sheep Genetics was established in 2005 to deliver a national across-flock genetic evaluation system to the Australian sheep industry (Brown *et al.* 2007). Sheep Genetics has been providing a single national multibreed genetic evaluation “language” for Australian sheep breeders since the release of the Terminal LAMBPLAN evaluation in 2000 (Brown *et al.* 2000), via what would later become Australian Sheep Breeding Values (ASBVs, Collison *et al.* 2018). Even in the infancy of development the merits of providing across and within breed comparisons was noted (Banks 1990). This led to the implementation of three evaluations based around breed types, Terminal, Maternal and Merino sheep. An industry desire for greater across type comparisons triggered the release of the Combined LAMBPLAN genetic evaluation in 2025 bringing together the Terminal and Maternal breeds in a single meat sheep evaluation (Walkom *et al.* 2025).

Servicing the multibreed nature of the analysis has brought with it many complexities. Breed differences have been addressed within the genetic groups model since the inception, with grouping done at a breed/flock level (Brown *et al.* 2007). The Sheep Genetics evaluations transitioned to a genomic analysis in 2017 (Brown *et al.* 2018), creating the intricacy of balancing breed influence within the genomic relationships. Initially the Single-Step G-BLUP only used genomic information from the breeds with a reference data set sufficiently large to provide reliable genomic prediction. The breeds represented was later expanded with the growth in the reference data set, via the resource flock (van der Werf *et al.* 2010) and breeder genotyping programs, and the implementation of techniques that better align the genomic and pedigree information (Gurman *et al.* 2019). More recently, Alexandri *et al.* (2025), develop methods to identify genetic structure within the Australian sheep industry, improving both DNA imputation accuracy and genomic prediction into the minor breeds and composite breeds. With the development of the Combined LAMBPLAN genetic evaluation, the ability to adjust for breed within the evaluation was improved with the implementation of the metafounder techniques of Legarra *et al.* (2024), as per. Gurman *et al.* (2025). Upon the completion of the Combined LAMBPLAN Evaluation, Sheep Genetics will provide two core

analyses, MERINOSELECT, for Merino type sheep, encompassing over 5.2 million animals and 10 breeds and Combined LAMBPLAN with over 4.6 million animals and 51 breeds.

An Industry Structure Supporting Multibreed Evaluations

The Australian sheep industry has been built around a ewe base that has been predominately of Merino origin, focused on wool and lamb production, historically either self-replacing or part of a maternal or terminal breed cross. To service the seed stock sector, three core evaluations were developed to service the wool focussed Merino (MERINOSELECT), self-replacing maternal breeds and terminal breeds (LAMBPLAN), effectively grouping breeds by type and underlying breeding objective (Banks 1990).

Within each of these evaluations the ability to fairly compare animals across flocks and breeds is dependent on the establishment of and existence of genetic linkage (Huisman *et al.* 2005). Linkage in the Sheep Genetics analysis environment is based on the representation of sires across sites. Thus, to achieve across breed comparison there must be a willingness to run progeny from sires of multiple breeds head-to-head. This is being achieved because of several factors. Firstly, a significant number of breeders who are effectively running multiple flocks (breeds) head-to-head on the same site, 8.5% of flocks share a site. Secondly, the Australian Sheep Cooperative Research Centre (CRC) Information Nucleus Flock (INF, van der Werf *et al.* 2010) and its later reincarnations have been providing across breed, and breed type, comparisons since 2007 and encompassing sires from 22.5% of all flocks represented in Sheep Genetics across Merino, maternal and terminal breed types. The INF 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 now methane. At the time of this paper approximately 2,430 sires from 612 flocks have had progeny recorded and managed head-to-head. Finally, genetic linkage has also been achieved through the sharing and use of outside sires within flocks, 45% of the 2024 LAMBPLAN drop were born to a sire from an outside flock, 6% were from another breed.

Seedstock sheep breeders in Australia have had a relatively open view to cross breeding with many key breeds represented in LAMBPLAN now composites, resulting in approximately 87% of the 2024 born animals exhibiting some level of heterosis. The multibreed nature of the evaluation has allowed and highlighted to breeders the virtue of selecting animals on genetic merit (ASBV) not breed and this has led to the rise of ‘composite’ breeds most noticeably in the Maternal breed types (McMillan *et al.* 2023). In the LAMBPLAN maternal evaluation 34% of animals born over the last 5 years are composite animals, bred for favourable reproductive characteristics, referred to as ‘commercial maternal’. However, at the same time, breeds such as the Poll Dorset and Border Leicester with strong societal standing and defined roles within the industry have remained relatively pure (McMillan *et al.* 2023). Choosing to select within or across breed has not limited genetic gains with the Poll Dorset breed delivering a 1% annual improvement on the Terminal Carcase Production Index over the last year, in line with a 1.6% annual improvement on the Maternal Carcase Production Plus Index being achieved by the maternal composite breeders.

Minor Compromises for Greater Good

To produce breeding values that reflect the genetic variation of the population, and provide an accurate prediction of the selection advantage, the genetic parameters and adjustment factors should reflect the population in question. As part of the development of the Combined LAMBPLAN analysis de las Heras-Saldana *et al.* (2025) showed that whilst within breeds the heritability estimates for a variety of traits differed slightly, the range was minimal and similar to the pooled estimates across breeds. Whilst, some breeds will experience either an over or underestimated spread of genetic variation, cross validation results demonstrated high

levels of stability and prediction accuracy in the breeding values estimated from the multibreed analysis within breeds with a single set of parameters and adjustment factors (Gurman *et al.* 2025).

The combination of breed types within Combined LAMBPLAN (Walkom *et al.* 2025) has exacerbated the phenotypic variation within the analysis population in growth and maturity pathways. It was originally hypothesised that this diversity would mean the necessity to fit interactions at a breed level in a more complex way to deliver accurate ASBVs. However, the correlation between breeding values with and without breed interactions ranged from 0.90 to 0.99 (de las Heras-Saldana *et al.* 2025). These results suggest that the use of more complex models yielded minimal to no advantage over the simpler more parsimonious models where fixed effects are based on the pooled population. Consequently, within and across breed selection and access to the evaluation is not limited by the breed of the animal, but simply by the genetic linkage of the flock.

Enabling Growth not Limiting Opportunity

The multibreed nature of the Sheep Genetics evaluations has evolved around the industry structure and continues to enable high quality within and across breed genetic estimates of the national flock. However, the value of a multibreed evaluation also comes from the ability to innovate across the whole population irrespective of breed.

Unfavourable genetic correlations between eating quality and growth, meant that the industry index of the early 2000s with a high growth focussed breeding objective was causing a decline in eating quality (Swan *et al.* 2015). A multibreed focus to the problem meant that carcase and eating quality phenotypes, their corresponding ASBVs and industry indexes to improve Eating Quality are provided across all breeds and types. Since 2020, the IMF ASBVs across terminal breeds has improved at a rate of 8.4% per year.

The shift in industry away from wool has also seen a rise in ‘shedding’ breeds with industry extracting value in these breeds in self-replacing maternal flocks, instead of their previous terminal focus. With an overall objective to produce a self-replacing shedding maternal, the breeders of maternal flocks have been selecting and incorporating shedding sires from the terminal types (Dorper, Australian White, etc.), much like when they targeted terminal sires to improve carcase traits. This has seen a significant increase in across breed type selection, with 35% of LAMBPLAN flocks sharing animals between the terminal and maternal analyses. 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. In conjunction, many of the terminal shedding breeds do not have access to nor the ability to compare against the maternal breeds within the component reproduction analysis (Walkom *et al.* 2025). Consequently, the Combined LAMBPLAN analysis will provide a single evaluation and common language from which all non-Merino-type sheep could be compared. Meaning once again the evaluation will not limit the breeder’s ability to follow their breeding objective.

Future Frontiers

The multibreed evaluations place Sheep Genetics in the ideal position to service the needs of industry. However, with it will come many future research and development challenges. In the near future many of these will be based on overcoming the scale of the evaluations. The MERINOSELECT evaluation for example contains over 4.6 million animals and 724 thousand genotypes, with an annual growth of 37% more genotypes per year over the last 10 years. This brings forth the question of the role of information within the evaluation and if computational gains can be made through better utility of the industry submitted data.

Genomic-only breeding values informed from the Sheep Genetics MERINOSELECT analysis have been used to predict mean flock merit since 2018 (Swan *et al.* 2018). The longer-term challenge for developing a commercial Flock Profile test for industry flocks is accommodating their crossbred structure (Brown *et al.* 2025). Lamb production flocks generally incorporate breed components across all the major breed types, Merino, Maternal and Terminal, which are spread across the MERINOSELECT and LAMBPLAN evaluations. Therefore, the results required for a commercial flock profile of genotype only product would need to be aligned relative to the tested individual's association with the different ASBV analyses. This would in turn enable accurate genetic benchmarking and selection within the Australian commercial population of over 70 million sheep.

Conclusions

A history of continuous improvement in-step with the evolution of the breeding directions of industry has brought with it many challenges and will, in the future, bring forth many more. However, the ability to collaboratively overcome these challenges and the genetic progress within the Australian sheep industry can be in part associated with the success of the National multibreed evaluations.

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