Sheep GENETICS

mla
MEAT & LIVESTOCK AUSTRALIA

Combined LAMBPLAN

A summary for Sheep Genetics members

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A message from Sheep Genetics

Dear Valued Breeders,

We are excited to welcome you to this year's Sheep Genetics Analysis Enhancements booklet.

2025 marks a significant milestone for Sheep Genetics with the launch of the first module of the world-leading **Combined LAMBPLAN analysis**. This new analysis not only future-proofs our genetic evaluations but also lays the foundation for an expanded product offering—introducing new traits and genetic selection tools that will deliver even greater value to the commercial sector.

This release aligns with Meat & Livestock Australia's new strategy, which places a strong emphasis on delivering **multibreed genetic evaluations** to underpin the integrity and credentials of Australian livestock. It's a pivotal step forward in ensuring our evaluations remain globally competitive, scientifically robust, and commercially relevant.

As always, these enhancements are made possible through our close collaboration with the **Animal Genetics and Breeding Unit (AGBU)**. I would like to sincerely thank the AGBU team for their years of dedicated research and development that have culminated in this year's advancements.

The first module of the Combined LAMBPLAN analysis will be released with the results of the 15th of August 2025 Analysis. Whilst this year's enhancements relate to our LAMBPLAN breeds I would encourage our MERINOSELECT clients to engage with the updates being made. The work done as part of the Combined LAMBPLAN evaluation enables similar enhancements to be made to the MERINOSELECT evaluation in the future.

This booklet provides detailed information about the 2025 Analysis Enhancements. You can also find short explainer videos on our website. If you have any questions, please don't hesitate to reach out to the Sheep Genetics team.

Warm regards,

Peta Bradley

Manager – Sheep Genetics

A message from the Animal Genetics and Breeding Unit

Dear Valued Breeders,

We are excited to be a part of another significant milestone in the national genetic evaluation for Australian sheep. It has been 25 years since the release of the multibreed LAMBPLAN Terminal evaluation and 13 years since LAMBPLAN Maternal, however, the release of Combined LAMBPLAN is probably the largest and most significant change to the evaluation.

Combined LAMBPLAN should not be seen as just bringing two analyses together but also as a significant body of work to future proof the evaluation and address legacy issues that were restricting the utility of the analysis.

The team at AGBU, in collaboration with Sheep Genetics, have not only combined the data from the two LAMBPLAN evaluations but have also reviewed all aspects about how the evaluation is constructed. These developments have resulted in a new evaluation that;

1. Allows greater across breed comparisons to meet the needs of industry
2. Made improvements to how data is managed within the analysis, improving the effectiveness of phenotypes
3. Made changes to improve analysis efficiency and longevity
4. Improved our ability to predict the genetic merit of all individuals

The team at AGBU is immensely proud of the research behind Combined LAMBPLAN and look forward to continuing the collaboration with Sheep Genetics to deliver the later phases of Combined LAMBPLAN.

Warm regards,

Dr Sam Walkom (Senior Research Fellow) and **Dr Daniel Brown** (Principal Scientist) at the Animal Genetics and Breeding Unit (AGBU)

Introduction to Combined LAMBPLAN

Sheep Genetics and the Animal Genetics and Breeding Unit (AGBU) are proud to release Combined LAMBPLAN. This will be a world leading evaluation for all Maternal and Terminal breeds, enabling the direct comparison of their genetic merit.

Combined LAMBPLAN has come about due to a desire to meet the demands of an evolving industry and will enable:

- The ability to directly compare the genetic merit of all Terminal and Maternal breeds (excluding Merinos and Dohnes)
- The future ability to develop and provide better commercial genetic selection tools and outcomes under a single analysis e.g., Flock Profile and other commercial genomic products
- New commercial indexes to be created using recently developed and refined index software
- Simplicity. Each animal receives one set of ASBVs that are fully comparable to all other animals in Combined LAMBPLAN, allowing better decisions for a wider variety of unique production systems
- Updates to the genetic parameters and computation which underpins the genetic evaluation
- Computational updates to the evaluation allowing for long-term sustainability of the evaluation

Combined LAMBPLAN will be implemented as a research analysis in a staged approach over the course of 2025, and through to 2027, with the current Maternal and Terminal analyses continuing to be run in parallel and used until Autumn 2027.

The Combined LAMBPLAN analysis will be a research analysis run in conjunction with the current Maternal and Terminal analyses. For this reason, Sheep Genetics suggests that ram breeders use the current analyses (Maternal and Terminal runs) to report ASBVs for the upcoming sale season. As more phases are released, the number of traits available will increase, with selection indexes being the final phase release in 2027. Throughout the releases, Sheep Genetics will target resources towards ram buyers to ensure they are also informed of the updates and changes.

Table 1 shows the staged releases for Combined LAMBPLAN analysis, with the first stage implemented with the analysis run results of the 15th of August 2025. It is important to note that the current Terminal and Maternal analysis runs (as well as the MERINOSELECT analysis) will take priority over the Combined LAMBPLAN analysis. While Sheep Genetics aims to run the Combined LAMBPLAN analysis every 2 weeks alongside the current Terminal and Maternal analysis runs, if there is limited time the individual runs will take priority. Therefore, it is important to ensure you're checking the analysis date when you're looking at Combined LAMBPLAN results.

Table1. Summary of the staged releases and associated updates for the Combined LAMBPLAN analysis.

Phase	What	When
1	Growth, carcase, eating quality	Mid 2025
2	Lambing ease and WEC	Late 2025
3	Component reproduction	Early 2026
4	Wool and visuals	Mid 2026
5	Combined LAMBPLAN research indexes	Mid 2026
6	Turn off Maternal and Terminal analyses	April 2027

Sheep Genetics will provide periodic updates on implementation dates to provide breeders with the most up-to-date timeline possible. This booklet will also be updated online to provide a summary of the changes and the impact of the changes occurring at each phase. Sheep Genetics will also run webinars with each phase release; these will be recorded and published online so you can watch at any time.

QR code to the online version of booklet

Contents

This booklet outlines the changes made in the process of developing the Combined LAMBPLAN evaluation. It aims to equip Sheep Genetics ram breeders with the relevant knowledge to understand why ASBVs look different, as well as why flock and animal re-ranking has occurred.

Preparing for Combined LAMBPLAN

Below is a check list of tips to help you understand and prepare for the updates occurring as part of Combined LAMBPLAN

- ✓ Review the enhancements detailed in this booklet and assess which updates will have the most impact on your flock
- ✓ Attend the webinars (or watch online later) associated with each release phase
- ✓ Check the percentile bands to re-benchmark the ASBVs
- ✓ Take time to review all sections in your flock's results dashboard on the website including reviewing your Data Quality Score (DQS) Report, linkage, Genomic Pedigree Inconsistencies Report, data summary, genetic trends, etc.
- ✓ Utilise the Sheep Genetics comparison tool to assess the re-ranking of animals in your flock
- ✓ Look out for emails from Sheep Genetics regarding data quality considerations
- ✓ Sign up to the Sheep Genetics Monthly Updates email to get updates on Combined LAMBPLAN
- ✓ Contact Sheep Genetics for a copy of your flock's Combined LAMBPLAN report, which details the level of change occurring in your flock. *Please note, this document will only be provided with a 1:1 meeting, or via a service provider*

Sheep Genetics comparison tool

Sign up to Sheep Genetics monthly eNewsletter

The Sheep Genetics and AGBU teams recognise that this will be a significant change in ASBVs due to these enhancements, along with some re-ranking of animals between and within flocks. The extent of this re-ranking significantly varies across breeds and flocks. The Sheep Genetics team are dedicated to helping breeders understand these changes and communicate them with their ram buying clients, but our ability to identify and diagnose reasons for changes within your flock will be limited due to the sheer volume of changes occurring. Please be patient during this time and treat staff with respect.

Don’t be afraid of change!

“To improve is to change…” – Winston Churchill

“Change is the catalyst for innovation. Without it, we stagnate”

Accessing Combined LAMBPLAN

- Combined LAMBPLAN RBVs will be available on the Sheep Genetics search site. Select Combined LAMBPLAN from the drop-down list of analyses. These results will be exportable when logged in and will be sent to your email in an excel format
- Percentile Bands for Combined LAMBPLAN will also be available on the Sheep Genetics search site
- Please note, Combined LAMBPLAN results will not be available in an XML for download into your data management software. This is to limit confusion and ensure the ASBVs within your software remain as the current Terminal and Maternal ASBVs

Changes to the data analysis pipeline

Changes have been made to the data pipeline between Sheep Genetics and the Analysis software (OVIS) that analyses data. This includes some data processing now occurring within the Sheep Genetics database, which is beneficial for two key reasons as it:

1. Allows Sheep Genetics the ability to provide more feedback to breeders at the point of data submission
2. Reduces the computation requirements in the analysis, meaning the analysis time may be reduced. This is essential for the longevity of evaluation as it continues to increase in size and computational complexity

This change will have no impact on ASBVs or on the data submission process for breeders, however it is an important step to ensure the resilience of the evaluations going forward. It also enables more direct reporting of data quality aspects to breeders to ensure the most accurate data is being used in the analysis.

Who will this impact?

This enhancement will have no impact on ASBVs

Moving some data processing to the Sheep Genetics database enables more direct feedback to breeders and ensures longevity of the Sheep Genetics evaluation via reduced computational load

Combining datasets and streamlining data used

The largest change to ASBVs in Combined LAMBPLAN will come as a result of combining the Terminal and Maternal datasets. Currently, just over 30% of LAMBPLAN flocks have animals represented across both analyses. However, there is a large portion of animals that are unique to either the Terminal or Maternal analyses and combining the data will result in a significant change to the sheep population represented in the evaluation. Table 2 displays a summary of data in each of the current Terminal and Maternal analyses as well as the Combined LAMBPLAN analysis based on research datasets in July 2025.

Table 2. Summary of the number of animals, pedigree, flocks, breeds, and genotypes for both current Terminal and Maternal analyses and Combined LAMBPLAN (as of July 2025)

Terminal		Maternal		Combined LAMBPLAN	
4.1m	Animals	2.9m	Animals	4.4m	Animals
60k	Sires	38k	Sires	63k	Sires
4.9k	Flocks	3.8k	Flocks	4.5k	Flocks
73	Breeds	65	Breeds	79	Breeds
222k	Genotypes	107k	Genotypes	300k	Genotypes

Combining the Terminal and Maternal datasets resulted in 3 key differences to the dataset being evaluated, which are explored further below:

1. **Improved comparisons and linkage between breeds/animals some of which were not previously compared. This has also brought about an increase in the size of the reference population (animals with a phenotype and genotype) for each trait**
2. **The removal of non-informative records to reduce computational demands**
3. **A change in the 'base' year to reflect the new dataset**

1. Comparisons and linkage between new breeds and animals, and increase reference size

Until now, the genetic merit of Maternal and Terminal animals/breeds have not been compared directly within a single genetic evaluation. In Combined LAMBPLAN these comparisons of genetic merit can be made directly. However, by combining the data distribution in ASBVs for each trait will change and is different to that observed in the current Terminal and Maternal analyses. A key enabler making Combined LAMBPLAN possible is that there is sufficient linkage, via head-to-head comparisons between Terminal and Maternal breeds. A significant source of these comparisons is the Resource Flock, where progeny from influential Maternal and Terminal sires have been managed together and their performance has been compared in the same environment for a large variety of traits. Breeders running a terminal and a maternal flock within a single site are also providing linkage that has helped enable Combined LAMBPLAN.

The reference population within the Combined LAMBPLAN evaluation is ever growing with all animals with a phenotype and genotype contributing to the reference, for the traits they are recorded for. The Resource Flock provides a large proportion of this reference, especially for the hard to measure but objectively important carcase traits including carcase composition, eating quality, and carcase yield. Merging the Terminal and Maternal datasets in Combined LAMBPLAN will result in an increase in the size of the reference population, which in turn will generally increase accuracy of ASBVs. The impact of the increased reference population will be most noticeable in the composite breeds due to links to both analyses.

2. Removal of non-informative records

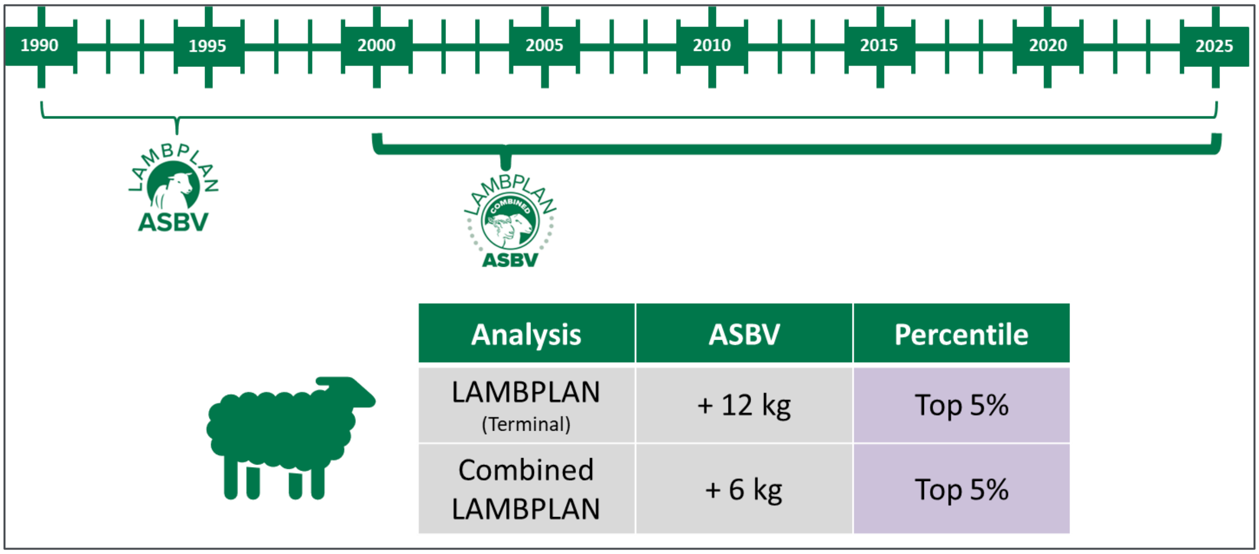
Currently, the Terminal and Maternal analyses use all phenotypes and pedigree in the Sheep Genetics database, some of which spans back more than 40 years. The continual growth in the scale of the analyses, especially due to the incorporation of genomics, is associated with an exponential growth in computational demand. Decisions to remove data were made to reduce analysis demands, where minimal impact on the breeding values of the current selection candidates would occur. The changes being made include:

1. **Removing phenotypes from prior to year 2000.** The relative importance value of older performance data to the estimation of current animal's ASBVs declines over time. Validation was carried out to assess the impact of removing pre-2000 phenotypes showing this decision had minimal impact on the ASBVs of current selection candidates. The year 2000 provided a nice place to draw a line as it coincides with the start of the reference population. It is important to note that all historical pedigree will remain in place to help describe the relationships between individuals.
2. **Removing Sheep Improvement Limited (SIL) (New Zealand genetic evaluation) phenotypic data from the dataset.** Traditionally Sheep Genetics has had a data sharing agreement with the New Zealand Sheep Improvement Limited (SIL), where Maternal and Terminal data provided to SIL has been included in the analysis. As a result of the one-way flow of genetics between the two countries the influence of the NZ data on the current selection candidates in Australia was limited. This significantly reduces the size of the analysis and computational requirements.
3. **Removing syndicate sire groups as sire pedigree.** Given the relatively small use of syndicate sire groups in the LAMBPLAN evaluations, syndicate sire groups will no longer be used as direct sire pedigree in the Combined LAMBPLAN analysis. Instead, animals with an unknown sire will be allocated back to an appropriate genetic group. While syndicate matings can still occur, sire pedigree will need to be identified through other methods, such as genotyping. Sheep Genetics will contact any flocks affected by this change.
4. **Removing hogget age stage EMD and FAT phenotypes.** Due to limited data for fat and muscle traits measured at hogget age in Terminal and Maternal sheep, phenotypes collected from animals over 500 days old will no longer be used in the analysis. Sheep Genetics will contact any flocks affected by this change.

3. Updating the ‘base’ year for ASBVs

The implementation of Combined LAMBPLAN is also going to see the ‘base’ year for ASBVs change. The base for most traits is currently set at 1990, meaning that the value of zero for each trait is the average ASBV of the 1990 drop. Given the removal of the pre-2000 phenotypes, the base is being updated to the year 2000 drop. Therefore, the value of an ASBV will be relative to the average performance of the Combined LAMBPLAN animals born in 2000. Figure1 shows an example of an animals ASBV and what Percentile Band it sits in for each given analysis, with the ranking of that animal remaining the same across both the current Terminal and Combined LAMBPLAN analysis (i.e., in the top 5% percentile). It’s important to note that scale of change will vary across traits and which analyses the animal was originally published in.

As a result of the changes to the data being analysed the ‘base’ year has been updated to 2000, the start of the phenotypic data. In this example the animal is in the top 5% percentile for PWT, whilst their rank within the population remains the same, the value of the ASBV is different.



Analysis	ASBV	Percentile
LAMBPLAN (Terminal)	+ 12 kg	Top 5%
Combined LAMBPLAN	+ 6 kg	Top 5%

Figure 1: Re-benchmarking against Percentile Bands following the change in base year of ASBVs to 2000

This change will have a large impact on how the ASBVs for each trait appear. This change is not associated with re-ranking, rather with the number associated with each Percentile Band. Consequently, it is important to review the Percentile Bands for Combined LAMBPLAN and re-benchmark your flock.

For more information on percentile bands please scan the QR code.

Who will this impact?

Combining of data sets: all flocks, particularly composite flocks that have pedigree coming from both the Maternal and Terminal evaluations.

Removal of old data and updating the base: this will impact all flocks.

When more tiers of Combined LAMBPLAN are released and commercial producers are using Combined LAMBPLAN ASBVs to purchase rams, re-benchmarking will be important for them to understand how their flock and ram purchases compare relative to industry.

Contemporary group formation enhancements

Contemporary groups are used in the analysis to compare the performance of animals that have been managed under similar production conditions (i.e., have had the same non-genetic impacts on performance). In the analysis, an animal's own performance for a particular trait is compared against the average performance of all other animals run together at that point in life. In the current Terminal and Maternal analyses, contemporary group formation occurs in-part at Sheep Genetics upon file submission, and in-part in the analysis during the evaluation. As part of the updates being made for Combined LAMBPLAN, the formation of contemporary groups will solely occur at Sheep Genetics, allowing Sheep Genetics to provide better feedback to ram breeders on data submission.

Along with this update, there are two other key changes for contemporary groups:

1. **Lifetime contemporary group formation has been adjusted to better reflect on farm management, resulting in both larger number of animals within a contemporary group and less contemporary groups in the Combined LAMBPLAN analysis.**
2. **Single animal contemporary groups removed**

1. Single animal contemporary groups will no longer be analysed as this data is not effective. Lifetime contemporary group formation changes

Lifetime contemporary groups are formed for each animal, so that the analysis knows which animals have had the same non-genetic impacts on performance and therefore can be compared directly and which cannot be. These contemporary groups build over an animal's life from birth with each phenotypic measurement taken. Contemporary groups are formed based on the supplied lambing group, along with flock, year of birth, conception method (only split if embryo transfer), and sex. Then for each phenotypic measurement taken, the day of measurement and on farm management group are also used to form contemporary groups for animal comparisons of phenotypic performance. In the analysis, the logic behind contemporary group formation was that animals measured together are managed together, with animals grouped together when they shared measurement points (date of measurement) across their life. However, over time the frequency and diversity of traits being recorded within industry has changed. This was causing some undesirable splitting of lifetime contemporary groups, for example, a sub-group of animals were recorded for a trait (often visual traits) even though they were still being managed with the unrecorded contemporaries.

In Combined LAMBPLAN, the only three traits will contribute to an animal's lifetime contemporary group: weight, fleece weight, and worm egg count. This removes contemporary group splitting based on visual traits and other traits where entire drops are not frequently measured. This will result in larger number of animals compared within contemporary groups on average, with higher numbers of effective progeny in each group and ultimately leads to more accurate head-to-head comparison. This is especially relevant for traits measured later in life like carcase and eating quality traits, and yearling/adult fleece traits. The change in contemporary group formation will mean that number of progeny and sires represented within a contemporary group may change, and therefore an animal's performance relative to its contemporaries may change, which will in turn have a moderate impact on ASBVs for the associated animals and relatives.

2. Single animal contemporary groups removed

Genetic evaluations rely on effective comparisons between animals and sires within contemporary groups to differentiate an individual animal's performance against other animals that have been run under the same non-genetic/environmental conditions. Where there is only one animal no effective comparisons of performance can be made. Therefore, in Combined LAMBPLAN, performance data will not be used where there is a single animal within a contemporary group. This data is not effective, and removal will not impact the associated animals breeding values.

Who will this impact?

Flocks recording a large number of traits, particularly visual traits.

Genetic model updates

The Sheep Genetics evaluations are based on a Best Linear Unbiased Prediction (BLUP) analysis. As part of this analysis there are several inputs used to help describe the underlying genetics of the traits being analysed and the non-genetic impacts on performance. Such inputs include genetic parameter estimates like trait heritability and genetic correlations between traits. These genetic parameters are used within the evaluation to model our understanding of the underlying genetic factors influencing how an animal performs. The Sheep Genetics analyses also include fixed effects which are known, non-genetic factors that impact performance and are accounted for within the analysis that describe variation in performance of traits that cannot be inherited.

As part of the development of Combined LAMBPLAN updates to the analysis included:

1. **Review of the genetic parameters to best reflect the population within the analysis. This included updating the assumptions for trait heritability and genetic correlations between traits**
2. **Review of heterosis (also known as hybrid vigour)**
3. **Review of fixed effects (the impact of age, dam age, birth- and rear-type) to best reflect the population within the Combined LAMBPLAN dataset**

1. Genetic Parameters

Genetic parameters are used within the evaluation to account our understanding of the underlying genetic factors influencing how an animal performs. Genetic variation within traits is described primarily via two main parameters, heritability and genetic correlations.

- The phenotypic (trait measurement) performance of an animal for a trait is determined by both non-genetic/environmental and genetic factors. The proportion of variation in phenotypic performance that can be explained by genetic impacts known as heritability. With traits that have a higher genetic impact on phenotypic performance having higher heritability, and lower heritable traits have less genetic impact on phenotypic performance

- Genetic correlations between traits refers to the relationships between traits, where selection for one trait can have a correlated response in the second trait. The strength and favourability (positive or negative) of the genetic correlations will differ between combinations of traits and range from 1 to –1
- Traits means were updated and are a reflection of the average value for each trait based on the phenotypic data in the Combined LAMBPLAN analysis dataset

Genetics parameters are calculated to reflect the data submitted to the evaluation and are updated periodically to ensure they are still relevant to the animals being submitted and analysed in the evaluation. The current Maternal and Terminal evaluations use a set of genetic parameters that reflect the population specific to each analysis, therefore these genetic parameters needed updating for the Combined LAMBPLAN analysis. Given the multibreed nature of the Combined LAMBPLAN dataset, implementing breed specific parameters was reviewed, but a universal (one single value) approach was found to be more appropriate. There were no significant differences in genetic parameter estimates within breeds in the Combined LAMBLAN analysis, so a universal set of genetic parameters is used for the Combined LAMBPLAN analysis

2. Heterosis

Heterosis (also known as hybrid vigour) adjustments are made within the current Maternal and Terminal evaluations to account for a boost in performance from unrelated animals. This boost in performance (heterosis gain) for an individual only influences the animal itself and is not heritable, therefor not passed onto its progeny. The analysis accounts for the gain in performance associated with heterosis, so the breeding values of individuals are not inflated. Due the perceived greater breed differences between Terminals and Maternals, AGBU explored fitting breed specific heterosis adjustments, where specific breed crosses would have a different level of heterosis accounted for. This was found to provide no significant advantage over a universal heterosis approach and was also computationally more demanding. Therefore, a universal heterosis adjustments will be applied in Combined LAMBPLAN.

3. Fixed effects

Fixed effects are known, non-genetic factors that impact performance, therefore, in the genetic analyses an animal’s performance is adjusted for fixed effects such as their age in days, the age of their dam, and their birth- and rear-types. Currently Sheep Genetics pre-adjusts the data using adjustment factors unique to each trait and age stage. These would be recalculated periodically (approximately every 5 years) to reflect the data being used in the evaluation. This will change in Combined LAMBPLAN, ultimately resulting in more accurate adjustments for non-genetic impacts on performance and removes the need to re-calculate them periodically. In Combined LAMBPLAN, fixed effects will be fit directly into the analysis, meaning that for each run the impact of each fixed effect will be re-estimated using all the data available in the analysis, and the calculated impact of such fixed effects on performance will be adjusted in that run. The impact of changes to the fixed effects will be noticed between the current Terminal and Maternal analyses and Combined LAMBPLAN, due to the refresh required with combining the data. However, adjustments made for fixed effects will not significantly differ between Combined LAMBPLAN analysis runs due to the relative size of the dataset. Fitting fixed effects directly into the analysis removes the need to re-estimate and update these every few years in the future, and ensure the adjustments best reflect the analysis population and improving the serviceability of the analysis.

All enhancements made to the genetic analysis that underpin breeding values will result in the more accurate calculation of ASBVs. Breeding values will change as a result of these updates, but the change will result in ASBVs that provide more accurate estimates of genetic merit.

Who will this impact?

All animals, particularly ASBVs for carcase and eating quality traits due to updates to genetic parameters. Larger changes were made to carcase trait genetic parameters as the population recorded for these traits has increased significantly since these were last updated.

Better utilising genomic information

The use of genomic information in the Terminal and Maternal LAMBPLAN analyses has increased significantly since the introduction of single step (genomically enhanced) evaluations in 2017. The Combined LAMBPLAN evaluation will incorporate over 300,000 genotypes. With the growing uptake of genomic technology, and the genetic diversity of breeds within Combined LAMBPLAN, updates have been made to how genomic information is utilised, resulting in more accurate ASBVs.

The key changes taking place include:

1. **Increased weighting placed on genomic relationships (lambda) compared to breeder supplied relationships**
2. **The analysis has also been updated to better identify more accurate relationships between animals through updates to the genomic model and breed structure**

1. Increase in the weighting of genomic relationships (lambda)

Relationships between animals and relatives' performance are key factors that underpin ASBVs. In the genetic analysis, relationships between animals may be identified through two key sources of information; the pedigree supplied by the breeder (i.e., collected via lambing rounds) and, where an animal has a genotype, the genomic relationships identified by DNA. The weighting of the use of the genomic relationships is referred to as lambda and is currently set at 50% in the current Maternal and Terminal evaluations. In Combined LAMBPLAN, lambda will increase to 95% which means that95% of the information used to identify relationships between genotyped animals will be informed by the genomic relationship, and 5% of the relationship between animals coming from breeder supplied pedigree. This weighting factor of the genomic relationship is only relevant to animals which have a genotype. Genomics allows for a much more accurate relationships between animals to be identified and more accurate understanding of the genes in common, resulting in more accurate ASBVs. Where an animal does not have a genotype, 100% of its relationships to other animals will be informed via the pedigree supplied by breeders. Updating lambda will have a significant impact on ASBVs as the relationships between animals which underpin ASBVs are changing.

Please note, an increase in lambda changes the relationship between animals in the evaluations but does not change the relevance and necessity of phenotypic information.

2. Updating genomic model and breed structure

Since the introduction of a single step (genomically enhanced) evaluation in 2017, the number of genotypes submitted to LAMBPLAN has increased year on year, with over 300,000 genotypes in the Combined LAMBPLAN evaluation. With this increase in the number of genotypes used in the evaluations, updates to the analysis are necessary in Combined LAMBPLAN to allow for better computation of relationships between animals in a diverse multibreed population. Combined LAMBPLAN will see the introduction of an enhanced genomic analysis approach, which will lead to more accurate ASBVs through identifying more accurate relationships.

Genetic groups are used in the Sheep Genetics evaluations to help describe breed and population structure. Genetic groups help to inform the ASBVs of animals with little to no information on their genetic merit (i.e., missing pedigree), using the performance animals of a similar breed to underpin ASBVs for animals with missing pedigree information, not just the average of all the animals in the analysis. Building on from the previous year's enhancements into the genomic structure of the LAMBPLAN datasets, the genetic group structure has been refined to reflect the 36 main breed specific genetic groups. Some of these larger genetic groups are separated into 10-year windows to reflect genetic changes within breeds over time. The 2024 enhancements into the genomic reference update highlighted common genes across breeds/populations, meaning the analysis now doesn't consider these breeds to be independent and allows us to account for similarities between breeds, for example, composite breeds and their foundation breeds. This has significantly improved our ability to estimate the genetic group effects and account for the genomic structure within the multi-breed population. These improvements will lead to some changes in breeding values as they are linked to how the analysis describes the relationship between animals and across breeds

Technical Review of Combined LAMBPLAN

Combined LAMBPLAN represents a major research effort led by AGBU in collaboration with Sheep Genetics. Given the scale of the changes, the Combined LAMBPLAN breeding values have undergone thorough validation. This testing ensures confidence in the technical updates and confirms that the new analysis delivers more accurate breeding value. Our aim was not to simply combine the data but also to improve the analysis, allowing greater and more accurate comparisons of genetic merit. The analysis enhancements were validated via several methods, which focused on comparing how well ASBVs predict future performance. Analysis enhancements were also reviewed and endorsed by the Sheep Genetics Technical Committee of independent geneticists.

Validation results showed that the Combined LAMBPLAN analysis provides:

- More accurate predictions of future progeny performance. Significant improvements were seen across the board, but particularly in the carcase traits where combining the dataset has led to an increase in the genomic reference underpinning the ASBVs
- Improvements in how well the analysis describes the variation in breeding values. Across traits, Combined LAMBPLAN does a better job of aligning what a unit change in the ASBV means compared to the prediction of future progeny performance

Ultimately, there have been significant enhancements implemented for the Combined LAMBPLAN analysis, in particular, the expansion of the genomic reference, inclusion of more informative data, changes to the influence of the genomic relationship, and the refinement of the genetic model. Such enhancements will result in not only will the ASBVs change but there will also be changes to the accuracy of ASBVs. On average, there has been improved accuracy of Combined LAMBPLAN ASBVs, with composite breeds benefitting most from the combination of the two data sets, as well as the carcase traits where the reference population has greatly increased. However, as a result of reducing the heritability of the growth traits (i.e., weights) there is a slight decrease in the observed accuracy of these traits.

Phase 1 release – 15th August 2025

Phase 1 release will see 24 traits published with Combined LAMBPLAN ASBVs. Please remember that the Combined LAMBPLAN analysis is a research analysis that will be run in parallel with the current Terminal and Maternal analyses until the final phase in 2027. Over the course of the Combined LAMBPLAN analysis tier releases, enhancements may be made to the analysis before final release in 2027.

COMBINED LAMBPLAN PHASE 1 RELEASE TRAIT TABLE			
BWT	**WEMD**	**SHEARF5**	**CEMD**
WWT	**PEMD**	**DRESS**	**CCFAT**
PWT	**YEMD**	**LMY**	**MWWT**
YWT	**WFAT**	**IMF**	**MBWT**
HWT	**PFAT**	**CWT**	**PSC**
AWT	**YFAT**	**CFAT**	**YSC**

As a breeder, what should I do with this information?

Combined LAMBPLAN will produce ASBVs that look different to the current Maternal and Terminal LAMBPLAN evaluations. We highly recommend you re-benchmark your flock using the Percentile Bands produced for Combined LAMBPLAN and assess changes in ranking at a flock and animal level. Whilst there will be some re-ranking, the validation work competed in the development of Combined LAMBPLAN shows that the ASBVs are a more accurate estimation of genetic merit. The current Terminal and Maternal analysis have served industry well, but the Combined LAMBPLAN analysis is even more accurate, more resilient, and enables more future genetic selection tools to be developed.

Sheep Genetics has developed a comparison tool to assist breeders in quantifying the changes occurring in their flock. This tool enables a comparison of animal's ASBVs and relative percentile in their current LAMBPLAN analysis (either current Terminal or Maternal) to their ASBVs and percentiles in Combined LAMBPLAN. The tool is simple and straightforward to use; all you have to do is:

- ✓ Search for your animals in the Combined LAMBPLAN Sheep Genetics website and download ASBVs
- ✓ Do the same in the current Terminal or Maternal LAMBPLAN search function
- ✓ Import both files into the file compare tool
- ✓ Assess flock averages, relative to the Percentile Bands
- ✓ Assess individual animal re-ranking and movement relative to the Percentile Bands

Please note, Sheep Genetics have limited ability to identify specific reasons for re-ranking between animals and flocks due to the sheer volume of changes occurring. Before contacting Sheep Genetics, please ensure you:

- ✓ Use the information contained in this document to identify the reason for changes in ASBVs and re-ranking where possible
- ✓ Only contact Sheep Genetics for more information when animals and/or flocks have moved significantly and you are not able to understand the reason for the change
- ✓ Are specific in your query when contacting Sheep Genetics. Provide an animal ID, or a small list of IDs, along with the trait/s of concern
- ✓ Query response times may be delayed, due to the expected volume of queries.

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