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Annual Upgrades to the Genetic Evaluations

The LAMBPLAN and MERINOSELECT analyses are continually being developed to improve the genetic evaluation and supply the best tools possible to producers, aiming to help improve genetic gain across the sheep industry. Major updates to the Sheep Genetics analyses are implemented once a year to minimise any disruption that may result from the changes. This year there are significant updates to both LAMBPLAN and MERINOSELECT. It is important to understand the enhancements made to the analyses and why you may see changes to the ASBVs of your animals. All updates detailed below will be applied to LAMBPLAN on the 15th of April and MERINOSELECT on the 21st of April.

Analysis Upgrades

**2016- SINGLE STEP CARCASE ANALYSIS**

Until 2016 all genomic information was incorporated into ASBVs using a “blending” approach. Blending combined pedigree based estimated breeding values with genomic breeding values from separate analyses to create a blended ASBV.

In May 2016 Sheep Genetics moved to the “Single Step” approach to calculate ASBVs for carcase traits to improve the application of genomics within this sub-analysis. The Single Step analysis combines genomic and pedigree information with performance records in a single model to calculate ASBVs for all traits in the model.

Updating to the Single Step sub-analysis for carcase traits allowed genetic correlations with related traits to be used more effectively. This resulted in a larger number of animals having eating quality breeding values estimated.

To compliment the Single Step carcase analysis, two new indexes were introduced with a focus on joint improvement of eating quality and lean meat yield for terminal sire breeders.

**2017- SINGLE STEP IS HERE**

Since the implementation of the Single Step carcase sub-analysis, we have been working on the implementation of Single Step for the main analyses in the TERMINAL, MATERNAL and MERINO runs.

In 2017 we make the transition to using the single step approach over all main analyses, as well as the WEC analysis for all three breed groups and visual trait analyses for Merinos. The reproduction analysis will remain unchanged at this stage due to the limited records available. However, there is ongoing work to develop genomically enhanced Research Breeding Values (RBVs) for reproduction traits later this year.

The benefits of moving to a full single step analysis include:

- Simultaneous use of all information – no need for blending.
- More accurate genetic relationship between animals identified and utilised, meaning better use of information from similar animals, with the possibility of correcting pedigree errors.
- Genomics used for a wider range of traits and the genetic correlations between all relevant traits are now considered.
- The accuracy of ASBVs better reflects how effectively genomic information contributes due to genotyped animals relationship to the reference population.
- Genomic information contributes to the calculation of relatives ASBVs, i.e. the siblings or progeny of a genotyped animal will benefit.
- Industry data now contributes to the reference population.

While we are confident that the changes to the analyses will give better estimates of animals genetic merit you will see some changes to ASBVs. The correlation between the old and new analyses is very strong, although some animals will change for some traits. Changes you will see in ASBV’s are due to the following:

- Influence of genomic information from a larger number of animals and traits.
- Impact of correlated information from a larger number of traits.
- The carcase traits being moved back into the main analysis, so that all animals have breeding values estimated for carcass and eating quality traits. The addition of the carcass and eating quality data into the main analysis also has a correlated impact on the other production traits.
- Genetic groups will be fitted using a different methodology.
There are still some limitations to be able to use genomic information in the analyses. We can only use genotypes from four major breeds, Border Leicester, Poll Dorset, White Suffolk and Merino. We are continuing to collect genomic data from other breeds, but at this stage we cannot include these in the routine genetic evaluation.

The value of genomic testing to the genetic evaluation is still determined by linkage (genomic relationship) to reference animals and other records available on those animals. Some animals from relatively closed flocks that are not well represented in the reference population may end up with low accuracies for breeding values that may not pass reportable thresholds.

Animals will still need to have some pedigree and performance included in the analysis in addition to a genotype. Having only a genotype on an animal is currently not enough information for ASBVs to be calculated.

Single Step across the main analyses would not be possible without a significant upgrade to the computer software used. Run times with the existing software were too slow to complete the analyses every two weeks. A new program which “solves” the analysis has been developed and we are now able to run these more demanding Single Step models in acceptable run times which will be sustainable for some time to come.

**Single step is a major achievement**

The full implementation of single step is a major achievement and is the result of a long term collaboration between Sheep Genetics, AGBU and the Sheep CRC. We have large multi trait across breed analyses, where there are many genetic groups fitted and significant numbers of animals genotyped. Despite this, Single Step has been implemented without compromising run times. The advancements made to the analysis are world leading and result in more accurate, reliable breeding values on more animals.

**Reproduction**

Through across flock genetic evaluations, the sheep industry has made significant genetic progress in growth and carcase traits in young animals, as well as wool production. The other area needing increased effort is maternal efficiency, including reproduction.

The reproduction analysis is currently run as a separate sub-analysis. While the reproduction analysis is not yet being rolled over to use Single Step with the April changes, improvements will be made to the validation of data in the analysis. The main change is that if a flock has 100% survival in their twins within a year (i.e. all twins born are then raised) that year drop of lamb survival records will be removed from the reproduction analysis. This will improve the information being used to identify lamb survival. For these groups, although records on number of lambs weaned will be removed, records on number of lambs born will be retained.

To assist breeders to understand how much of their data are being used in the reproduction analysis an additional report has been developed. This report summarises how much data was used from each drop in the analysis, also highlighting areas in which the data recording for reproduction might be improved.

Sheep Genetics and AGBU are aiming to release RBVs for component traits of reproduction based on the Single Step model later in 2017. These traits include Fertility (whether or not a ewe became pregnant), Fecundity / Litter size (how many lambs she had) and Survival (how many of those lambs survived to weaning). Information on these three traits and joining details can be entered through the Mating Module. We are encouraging breeders to adopt the Mating Module system to improve the general recording of maternal efficiency traits.

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**Key Points**

- Single Step for Main Analyses.
- Performance records are still needed to calculate ASBVs.
- You will see ASBVs change from upgrades.
- More accurate and reliable ASBVs will be estimated.
- These upgrades are world leading in genetic evaluation.
- Reproduction analysis will not be single step
- More data is needed to develop individual repro ASBVs

For further information, we recommend that you watch Daniel Browns presentation from Leading Breeder “Development and Future Plans from AGBU” which can be found on our website.
2017 Regional Forums

Regional forums are a full day workshop, run by Sheep Genetics staff to provide information on LAMBPLAN and MERINOSELECT and how they can benefit your ram breeding enterprise.

Save the Date
- 16th May 2017 - Northern NSW
- 23rd May 2017 - Cowra NSW
- 30th May 2017 - Ballarat VIC
- 6th June 2017 - Burra SA
- 15th June 2017 - Brookton WA

Topics include
- Update on Sheep Genetics
- Data Quality
- Reproduction
- Analysis Changes
- Ramping Up Genetic Gain

Each workshop includes morning tea and lunch and is at a cost of $33.00 inc GST per ram breeding business.

Further details on how to book your place will be provided closer to the date on our website www.sheepgenetics.org.au.

Carcase Scanner Accreditation 2017

Sheep Genetics held an Ultra-Sound Carcase Scanner Accreditation in Armidale NSW in February 2017. Many thanks to Martin Oppenheimer from “Petali” Merino and White Suffolk stud, for the use of his sheep and facilities. The accreditation ran over two days, with the first day involving an afternoon session with the Sheep Genetics team, delivering some of the fundamentals of a genetic evaluation and illustrating the importance of accurate scanning data. The group of scanners were very interactive and asked plenty of questions in regards to data quality, management groups and the importance of scanning data.

It is important for breeders who are utilising muscle scanning to note that, research has shown as the accuracy of a muscle scanning operator decreases, the heritability of EMD also decreases. It is for this reason that we have these mandatory requirements in place to help in keeping the traits that use carcase scans, as accurate and reliable as possible.

The Sheep Genetics carcase scanners accreditation process requires the scanners to take two sets of measurements on at least 40 animals on the same day. There are minimum Correlation and Residual Standard Deviation thresholds that must be met on Michael O’Neil showing MERINOSELECT Database Manager Ermias Zerazion how it is done!
their duplicate measurement of all 40 animals in order to become accredited.

It is a strict requirement of Sheep Genetics Breeders Quality Assurance Guide that all carcase scanning information be measured by an accredited or provisionally accredited scanner. For this reason, we now require all breeders to submit the accreditation number of their scanner when sending in data. An accredited or provisionally accredited scanner must supply their accreditation number to you at scanning, which can be confirmed by checking they are listed on the Sheep Genetics website.

It is also a timely reminder to ensure when you are muscle scanning your sheep that animal’s fulfil the following requirements:

- Each individual animal weighs a minimum of 30kg.
- There must be on average, greater than 1.5mm of fat depth. (This allows for a variation to be seen between animals measured).
- Animals are to be scanned by an accredited scanner, and that scanners 5 digit accreditation number provided to Sheep Genetics.

If measurements taken at scanning do not meet the above requirements data may not be used in the analysis.

A list of accredited scanners can be found below.

### Current Accredited Scanners List

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<tr>
<th>Name</th>
<th>Location</th>
<th>Telephone</th>
<th>Email</th>
</tr>
</thead>
<tbody>
<tr>
<td>Trevor Pearce</td>
<td>Young NSW</td>
<td>M:0428 993 061</td>
<td><a href="mailto:tpscanning@gmail.com">tpscanning@gmail.com</a></td>
</tr>
<tr>
<td>Tim Lawrence</td>
<td>Armidale NSW</td>
<td>M: 0419 147 419</td>
<td><a href="mailto:timlawrence1974@gmail.com">timlawrence1974@gmail.com</a></td>
</tr>
<tr>
<td>Stefan Spiker</td>
<td>Hamilton VIC</td>
<td>M: 0427 733 201</td>
<td><a href="mailto:stefan.als@bigpond.com">stefan.als@bigpond.com</a></td>
</tr>
<tr>
<td>Steve Milne</td>
<td>Hamilton VIC</td>
<td>M: 0428 786 327</td>
<td><a href="mailto:sjdjmilne@bigpond.com">sjdjmilne@bigpond.com</a></td>
</tr>
<tr>
<td>Ian Bradtke (P)</td>
<td>Peterborough SA</td>
<td>M: 0407 729 341</td>
<td><a href="mailto:ian@lazerline.com.au">ian@lazerline.com.au</a></td>
</tr>
<tr>
<td>John Lehmann</td>
<td>Mt Bryan SA</td>
<td>M: 0428 934 034</td>
<td><a href="mailto:john@pollville.net">john@pollville.net</a></td>
</tr>
<tr>
<td>Rachel Chirgwin</td>
<td>Saddleworth SA</td>
<td>M: 0428 600 265</td>
<td><a href="mailto:rachel@cvsuffolks.com.au">rachel@cvsuffolks.com.au</a></td>
</tr>
<tr>
<td>Tamesha Gardner (P)</td>
<td>Kojonup WA</td>
<td>M: 0408 001 353</td>
<td><a href="mailto:stocksmart@idavale.com">stocksmart@idavale.com</a></td>
</tr>
<tr>
<td>Peter Moore</td>
<td>Williams WA</td>
<td>M: 0427 176 332</td>
<td><a href="mailto:scanwest@bigpond.com">scanwest@bigpond.com</a></td>
</tr>
<tr>
<td>Mike O’Neil (P)</td>
<td>Northam WA</td>
<td>M: 0409 684 332</td>
<td><a href="mailto:micviconeill@bigpond.com">micviconeill@bigpond.com</a></td>
</tr>
<tr>
<td>Chris Parker</td>
<td>Hamilton Vic</td>
<td>M: 0429 992 477</td>
<td><a href="mailto:info@summitpark.com.au">info@summitpark.com.au</a></td>
</tr>
<tr>
<td>Nick Lawrence</td>
<td>Bordertown SA</td>
<td>M: 0447 077 705</td>
<td><a href="mailto:pinnaclesuffolks@bigpond.com">pinnaclesuffolks@bigpond.com</a></td>
</tr>
</tbody>
</table>

**An accredited scanner:** is someone who has met the scanning accuracy criteria to be accredited by Sheep Genetics. It is achieved by submitting several sets of scanning data to demonstrate repeatability.

**(P) Provisional accreditation:** can be achieved by submitting several sets of scanning data to demonstrate repeatability. Carcase data collected by provisionally accredited scanners may be submitted to Sheep Genetics for routine evaluation. Provisionally accredited scanners must attend to the next available Sheep Genetics scanning accreditation workshop to obtain full accreditation.

*All provisionally and fully accredited scanners are required to attend periodic Sheep Genetics scanning accreditation workshops to update their accreditation.*
Sheep Genetics held their biannual Leading Breeder conference in Melbourne on the 1st and 2nd of March. The conference was well attended with over 90 LAMBPLAN and MERINOSELECT clients attending the event themed around Building on the Best – Improving Rates of Genetic Gain. There were four sessions that built on the main theme as well as a dinner on the first night. Dinner speaker Kevin McDermott enlightened the guests about Ireland’s sheep industry and genetic evaluation.

Day one saw the sessions commence with Sheep Genetics’ manager Hamish Chandler welcoming everyone to the two days, as well as summarising the main achievements that have occurred over the last two years, since the last Leading Breeder conference in Adelaide, March 2015. Hamish set the scene for what is possible for breeders to achieve and how speakers over the event plan to help. Following on from Hamish in session one ‘Improving Rates of Genetic Gain Through Sheep Genetics’ Daniel Brown from AGBU presented on the work that has been completed by AGBU. Daniel focused on the changes that we will see in ASBVs due to the genetic evaluation moving to ‘Single Step’ and the confidence that producers should have in these changes being an improvement.

While at Sheep Genetics and in his new role with NSW DPI Luke Stephen has looked at the significant differences between flocks and the amount of progress they make. Luke presented to the Leading Breeders ‘What the Good do Well’ discussing what the main messages and significant differences are in each analysis. Session one finished with Jock Nivison from Yalgoo Partnership who provided a practical outlook on how to achieve your breeding objectives and showcased the relevance of the messages throughout session one.

The second session ‘Improving Rates of Genetic Gain Through Value Chain Initiatives’ did not disappoint and covered the whole value chain from the consumers “Plate” back to the grass roots of the breeder in the “Paddock”. Eating quality is extremely important to our industry, and David Bevis from Coles discussed how important it is to consumers and what is being done to improve the sale of lamb in stores. Producers were then given a
snapshot of the processor’s position from JBS’ Farm Assurance and Supply Chain Manager, Mark Inglis. Mark previewed future possibilities for data feedback to producers and highlighted the importance of eating quality to the processor. This was supported by the General Manager of Research, Development and Innovation for MLA, Sean Starling. Sean presented the new technologies being researched and developed around objective carcase measurement, as well as other innovations that are happening along the value chain. The session finished with Lambpro Stud Manager and Owner Tom Bull sharing his investment and measurement strategy to “Meat” target markets, including the higher end niche eating quality markets.

Following session two, delegates were invited to dinner in the function centre. The dinner gave all delegates a chance to interact and enjoy everyone’s company in a more informal way. Many attendees grabbed the chance to talk with producers from all around Australia and New Zealand. Not to mention Ireland, as the guest speaker Kevin McDermott presented on both the Irish sheep industry and the development of their genetic evaluation. Kevin’s presentation received an overwhelming response as his messages rung true a number of times, while also challenging our industry to not be left behind in the adoption of new technology. Kevin will be in Australia for a year and will be working at MLA for part of this time.

Day two started nice and early with Session three focusing on ‘Improving Rates of Genetic Gain Through Genomics and New Technologies’. Andrew Swan from AGBU started off the session with his presentation ‘Using Genomics to breed for Eating Quality’. Andrew mentioned how increasing the accuracy of information will equal in better responses, showing the benefits of genomic testing and being well linked to the reference population. Tom Granleese from the Sheep CRC followed and discussed the value of different measurements and how to get your genomics measurement strategy right for you. Mark Ferguson presented ‘Four Feet Closer to the Perfect Sheep’ showcasing the New Zealand merino industry and the work being done to develop a genomics test for a footrot breeding value. The practicality of utilising new technology was addressed by Sally Martin, who discussed the tips and tricks she has learnt over the last couple of years as a private consultant. The last speaker in the first session for day two was Daniel Brown who did a quick three minute presentation on weaner survival and the story that is unravelling with more data.

Caris Jones and Clara Collison started off the last session ‘Improving Rates of Genetic Gain Through Business Development’ doing a live demonstration of the Sheep Genetics website. Showcasing the tools that Sheep Genetics have available to help clients when signed in; including the Dashboard, MateSel and Ramping Up Genetic Gain. Tim Byrne from AbacusBio in New Zealand then spoke on a case study on the value of better genetics within a commercial flock in New Zealand. Tim showed how you can quantify the economic impact of better genetics, as well as the analysis of an individual breeding programme. Andrew Swan did a second presentation in Session Four, looking at the impact of climate change on breeding objectives in Merinos. Tom Granleese did a quick three minute presentation* on breeding towards a pure PP flock using genomics. Hamish Chandler then presented on the perception of genetics in the industry, highlighting the results of a market research survey conducted by IPSOS on behalf of MLA. A key finding from the survey was the lack of motivation to improve within our industry. Nathan Scott from Achieve Ag finished off the two days by talking on ‘Getting Motivated and Driving Change’ motivating and inspiring delegates to embrace change and strive to improve their businesses.

Overall Leading Breeder was a great success in 2017 and we thank all of those who attended. If you were unable to attend or would like to revisit the two days you can access the recorded presentations on the Sheep Genetics website. As well as the YouTube channel at http://www.sheepgenetics.org.au/Updates/Leading-Breeder/Leading-Breeder-2017

The Sheep Genetics team are looking forward to Leading Breeder 2019, which will be held in New South Wales at the Dubbo Zoo.

*Tom’s presentation unfortunately didn’t work on the screen and we will be including an article about his presentation in more detail in the next Breeders Bulletin
James grew up on a sheep, cattle and cropping property at Temora NSW. James has a Bachelor of Animal Science and Management for the University of Melbourne. James has held various jobs in the sheep industry, including having worked for Riverina Wool Testers and the NSW Department of Primary Industries where he worked for the Sheep CRC on the information Nucleus project. Presently James is completing his PhD through Deakin University on fibre science, and he has recently started his own sheep business called Preston Livestock Solutions. This business aims to help producers increase returns from their sheep enterprise.

Maximising the most from wool and meat production- a genetic solution. A producer case study  
James Preston – Preston Livestock Solutions

With the ever-increasing costs associated with sheep farming, a sustainable approach requires continual increases in productivity. Improvements in productivity can be achieved through careful selection and the use of appropriate breeding stock. I have been working with my parents, Warren and Margaret Preston at Miroola, Temora NSW to improve their productivity of their self-replacing Merino flock. The following is a summary of the breeding program implemented, and the outcomes to date.

One of the best ways to make improvements in a flock without increasing inputs is to improve the genetics of the flock. This may be as simple as modifying the breeding objective to better respond to current price indicators, or breed to a particular plan. Recent price signals of both meat and wool commodities detail a stronger demand for meat, so changes must be made to the breeding objective to accommodate this. The three changes that were made to the breeding program in order to increase the returns from the flock were:

1. Greater emphasis on growth and reproduction in the breeding objective.
The flock originally consisted of medium to fine wool bloodlines focussing on improving wool quality and culling for visual faults. The breeding direction was changed. To better develop a modern day dual purpose maternal sheep, the progeny must be able to reach slaughter weights before 12 months. They must not be penalised for incorrect carcase specifications or skin value, which is common problem with Merinos lambs. The aim was to produce a dual purpose animal that can generate returns on both meat and wool and at the end of the day support a lamb later on in life. The ewes were also pregnancy scanned, ensuring that the fertility of the flock was maintained.

2. Measuring traits that are important to the breeding program
Selection of ewes at classing was originally based on a visual appraisal. The visual appraisal of subjective wool traits was continued in the evaluation, but a subsequent inclusion of the primary traits incorporated into the breed index were also measured. The traits, which were considered high importance included bodyweight, fibre diameter, fleece weight, fertility (following first joining), and two overall scores based on conformation and visual wool performance. The objectives continually aim to produce a maternal ewe that can reach optimal growth rates within 12 months without compromising the mature ewe size, which has a negative impact on carrying capacity. In addition, the ewe’s wool performance, eating quality or skin value must not be sacrificed in attempting to reach this.

3. The integration of accelerated reproduction technologies to breed rams on-farm to fast track genetic gain
The third and final step was to move away from the tradition of purchasing flock rams from local on-property sales and utilise assisted reproductive techniques such as artificial insemination to make available sires that would normally be out of the price range of many farming enterprises. This gives us the ability to use sires ranked in the top 1% for
the best sires in Australia were based on the MP index generated from sheep genetics website. This data is collected from members who progeny test potential rams at their property or as part of AMSEA Central Test Sire Evaluation program. Sires must excel not only in the production traits included in the breeding objective, but must also satisfy a visual assessment for conformation, wool quality and traits related to overall management of the flock.

Results recently collected from the Sheep CRC genomic flock profiling project confirms that the ASBV index average (MP index) for the first drop of potential ram lambs bred on-farm are in the top 10% of the breed. The Prestons will now weigh up the performance of these rams from a combination of ASBV performance, visual evaluation and conformation scores to pick suitable replacement rams.

**Reproduction Summary Report**

Sheep Genetics have developed an additional report to assist breeders to understand how much of their data is being used in the reproduction analysis. This report summarises how much data was used from each drop in the reproduction analysis, also highlighting areas in which the data recording for reproduction might be improved. Below is a description of the fields in the report as well as an example report. The report will be released at the same time as the Analysis upgrades and will become part of the standard set of analysis result reports.

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<td>Dams</td>
<td>Number of dams of lambs including DAB and DRY</td>
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<tr>
<td>Mate Type</td>
<td>Count of lambs by mating type</td>
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<tr>
<td>Fertility</td>
<td>Percentage of ewes joined resulting in a lamb (Yearling and Adult reported)</td>
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<tr>
<td>Analysis Flags</td>
<td>Yes or No. If ewes are included in analysis for NLB and NLW (Yearling and Adult reported)</td>
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<tr>
<td>Preg Scan Records</td>
<td>Number or preg scans used in analysis to identify fertility and fecundity when a lambing outcome is unavailable.</td>
</tr>
<tr>
<td>Repro Dams</td>
<td>Number of dams used in reproduction analysis</td>
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<td>Ewe Missing</td>
<td>Dams with records in both flanking years but missing in current year</td>
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<tr>
<td>Birth Types</td>
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<tr>
<td>Rear Types</td>
<td>Count of lambs not reared or reared as a single, twin or triplet.</td>
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<td>Count of records for dam excluded due to failed service sire (Yearling and Adult reported)</td>
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**Reproduction Summary**

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**Report field**

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**The LAMBEX Young Guns competition allows the up and coming talent within industry to showcase their experience, research, projects or study. Each Young Gun submits an application outlining their area of interest. A number of the finalist in this years competition presented on areas potentially of interest to breeders, we will showcase some of these in upcoming Breeders Bulletins.**
Making a Measurement Plan

Now that majority of ewes around the country have been joined and AI’ed it is a good time to think about the measurement plan for the 2017 drop lambs and how they will be managed. Genetic improvement will be made by selecting the best animals out of the 2017 drop to stay within the stud. The more accurate the ASBVs are on these animals when making selection decisions, the greater the genetic response will be. Ensuring that measurements are taken at the right time for the individual business, as well as management groups being as effective as possible will improve the accuracy of the ASBVs reported.

When considering future management of the 2017 drop it is firstly important to plan how the ewes will be managed until lambing, then from lambing to weaning, and from weaning to yearling.

Management Groups

Management groups are used to identify differences in management that will impact an animal’s performance. To guarantee that management group information is as accurate and useful as possible breeders should ensure that:

- Management groups are clearly identified for animals that have been run together prior to the measurement of a base trait (e.g. weaning weight).
- All animals in a management group fall within a trait age range when information is recorded.
- Management groups are genetically linked within years and between years. This is done by using a common sire (or sires) across groups and years.
- The number of effective progeny records within each management group is maximised (Keep number of progeny as large as possible with the greatest number of sires represented)
- Animals that have had different treatment after a base trait has been recorded are clearly identified in a management subgroup for the following trait measurement (e.g. show sheep).

To assist in working out how animals will be split it can be useful to “Draw” it out. For example See Figure 1 on page 11.

The bold numbers illustrate the management groups provided by the breeder. The smaller numbers in the bottom of the hexagons represent once split into male and females how the grouping of animals builds over time. The analysis automatically splits animals based on sex, age, breed and previous management groups this ensures that the only differentiations the breeder has to make are management differences.

It is encouraged that splitting animals into multiple subgroups is avoided however it is also crucial that any difference in management that will impact performance is supplied through management groups to Sheep Genetics. Without identifying different management groups the difference in performance cannot be accounted for in the analysis.

In the diagram to the right, we can see that once an animal is split it is then split out for life. Any further subgroups supplied by the breeder further split the animals. Although it may seem in the hogget males we only have one group, due to prior management there are actually four contemporary groups at that age stage (this is not taking into account any other splits that the analysis may automatically make, such as age slicing).

Getting grouping right can be difficult however it is one of the most important parts of the genetic evaluation as it can impact effective use of data. The more effective data is in the analysis the more confident we can be in the ASBVs reported. Effectiveness of data depends on the number of animals being directly compared as well as the number of sire represented in the group. If there is not a good enough representation of sires and large enough numbers of animals we cannot utilise the data effectively.

Measurement Plan

A set measurement plan for the drop helps to ensure that traits that are part of the Breeding Objective are recorded at the correct time. Estimation of breeding values can be made and reported for traits that have not been directly measured; this is due to known correlations between age stages and other traits. The ASBVs that have been calculated through correlations have a lower accuracy than traits that have been directly measured. It is important to plan to measure the traits that are part of the breeding objective at the age stage that is also most important to the breeding objective. Making sure that the most accurate estimation of breeding value is at the age stage where the most change is desired.

The table below illustrates the traits evaluated and reported by LAMBPLAN and MERINOSELECT and the age stage that they can be measured at. The age stage animals will fall into when measured is dependent on the average age of the management group. It is important to consider the breeding objective for the business as well as clients and ensure as many traits as possible are measured at the best age stage and management groups. (See Table 1 on page 12)
Figure 1: Management Group Diagram

**Lambing**
Single and twin bearing ewes managed separately during pregnancy.

Lambs need to be grouped out into two separate base GROUPS.
Males and Females are not directly compared

**Weaning**
All lambs boxed up as soon as marked. Running together when a weaning weight is taken.

Lambs will continue to be split by the base GROUP for life.

**Post-weaning**
Ewes and rams split into two separate groups before being measured on different dates.
Groups are allocated for different management up until the measurement taken.

**Yearling**
A number of young rams selected to be used as young sires. All ewes run together.
Animals that have a difference in management need to be identified.

**Hogget**
All rams still on property for sale and selected to keep are running together. All ewes are still being managed the same.

As animals get older they will only be directly compared to other animals that have had the same pathway as them.
Table 1: Traits evaluated and reported by LAMBPLAN and MERINOSELECT and the age stage that they can be measured at.

<table>
<thead>
<tr>
<th>Trait</th>
<th>Abbreviation</th>
<th>Age stage—Name—Period—Abbreviation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Birth-24hrs</td>
<td>B</td>
<td></td>
</tr>
<tr>
<td>Weaning 42-120 days (6-16 weeks)</td>
<td>W</td>
<td></td>
</tr>
<tr>
<td>Early post weaning 120-210 days (4-7 months)</td>
<td>E</td>
<td></td>
</tr>
<tr>
<td>Post weaning 210-300 days (7-10 months)</td>
<td>P</td>
<td></td>
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<tr>
<td>Yearling 300-400 days (10-13 mths)</td>
<td>Y</td>
<td></td>
</tr>
<tr>
<td>Hogget 400-540 days (13-18 mths)</td>
<td>H</td>
<td></td>
</tr>
<tr>
<td>Adult &gt;540 days (18 mths)</td>
<td>A</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Trait</th>
<th>Abbreviation</th>
<th>Body Weight</th>
<th>Eye muscle depth</th>
<th>Fat depth</th>
<th>Greasy fleece weight</th>
<th>Clean fleece weight</th>
<th>Fat diameter</th>
<th>Coefficient of variation of FD</th>
<th>Staple strength</th>
<th>Scrotal circumference</th>
<th>Worm egg count</th>
</tr>
</thead>
</table>

Legend: Currently available | Currently unavailable
Marketing your ASBVs and the Sheep Genetics Brand

Field day and Sale season is fast approaching. As well as getting your sheep ready to display it is important consider how you are going to display your flocks genetic progress and individual ASBVs to the public. Australian Sheep Breeding Values are a uniform and standard language across the sheep industry and it is important that we have a standard way of reporting them. Sheep Genetics have guidelines for both reporting your ASBVs and branding them with the ASBV logos. Please ensure that these guidelines are met when reporting your flock's genetic progress and individual ASBVs throughout the 2017 season.

Data

Publish Accuracy Values

It is vital that all LAMBPLAN and MERINOSELECT ASBVs are published with their accuracy percentage, as provided in your reports or on the web. An ASBV is the combination of the breeding value and the accuracy percentage. The accuracy percentage reflects the quality and amount of information available on your sheep.

When looking at figures which display no accuracy percentage, the correspondence going to industry is to recognise these figures as within flock breeding values (FBVs) only (which are unlinked, and un-comparable to other flocks).

Publish analysis dates

Australian Sheep Breeding Values are live, as they have the potential to be adjusted and change as more information is used in the analysis. Individual animal’s ASBVs can change not only from data you have submitted but also other flocks you are linked to and genomic information. It is therefore important to publish an analysis date with your ASBVs to avoid confusion and ensure that all are up to date.

Provide a current benchmark

Reporting a relevant benchmark is important to your clients, especially to those looking at ASBVs once a year when purchasing rams. You can create a benchmark from either reporting the average of your flock, breed or analyses for a certain year drop or provide the percentile bands provided by Sheep Genetics. Publishing averages or the percentile bans has two main purposes; a) to provide a benchmark and b) to demonstrate your flock’s position in comparison to industry. This information can easily be accessed from the Sheep Genetics website.

Reporting trait leaders and ‘Elites’

Marketing your sheep is important to your business, being able to identify the animals within your flock that are trait leaders or on an ‘Elites’ list is key. Trait leaders are identified through the Sheep Genetics system as being in the top 10 percentile and are highlighted blue. Sheep Genetics strongly recommend that this colour is used for identifying animals in the top 10% when publishing ASBVs on your animals and not a different percentile band. When reporting that an individual animal is on an ‘Elites’ list please ensure that the index used and other elite requirements are clearly stated.

Branding

The use of the LAMBPLAN or MERINOSELECT ASBV logo in your marketing materials indicates that you are performance recording and allowing buyers to select the best possible animals for their individual breeding programs. The ASBV logo indicates your participation in genetic evaluation and a buyer can be confident of selecting objectively measured animals based on genetic merit.

When an ASBV logo is displayed the following can be certain:

- Animals are reported with ASBVs and can be compared across flock
- Meet minimum standards for across flock linkage
- Meet minimum standards for quality assurance
- Meet minimum standards for trait accuracy
- Have released accuracy information

To use the LAMBPLAN or MERINOSELECT ASBV logos please visit the resources section of the Sheep Genetics website.
History of LAMBPLAN

When did LAMBPLAN start and what was the original model?

LAMBPLAN was officially launched in March 1989. The launch followed a successful 3-year R&D project co-funded by the Meat Research Corporation (one of the organisations that merged to create Meat and Livestock Australia) and NSW Agriculture (now NSW DPI). In that project, weight and fat depth data was collected in terminal sire flocks (mainly Poll Dorset, and mainly in NSW), to estimate the heritability of the 2 traits, enabling EBVs to be calculated.

In the original model, accredited fat scanners visited the stud, weighed and fat measured the animals, and then produced a report either at the time or within a few days. The data processing was done on the scanners’ own computers, and was a within-flock, within-year analysis. Date of birth and birth and rearing status were accounted for.

EBVs were calculated for Yearling Weight (most animals were measured at around 10-12 months old) and Fat Depth at 60 kg, and 3 Indexes were calculated – High Growth, High Lean and Lean Growth.

How have we advanced over the years (within flock, across flock, across breed, single step carcase, single step main analysis)?

The three really big steps in LAMBPLAN (and in parallel in MERINOSELECT) were:

- Moving to across-flock analysis in 1994. Prior to that, only within-flock comparisons were possible. Across-breed analysis was an important development of this, but across-flock was the fundamental shift that opened up opportunity for much faster genetic progress

- Moving to include traits in addition to those recorded by the scanners – weight, fat depth and eye muscle depth. Extending LAMBPLAN to include fertility data, wool data, and later on, traits like worm egg count, lean meat yield, eating quality, lambing ease and so on.

- Moving to use genomic testing opens the door to being able to select for things that cannot be measured easily (or at all) on-farm, and to make it easier to select earlier in an animals life.

From starting with 2 traits, LAMBPLAN (and MERINOSELECT) can now handle more than 60 traits covering growth, carcase value, eating quality, wool weight and value, fertility and survival traits, a range of visual and structural traits, and there are more in the pipeline.

What has the advancement in technology/records allowed breeders to achieve?

The ultimate aim of LAMBPLAN and MERINOSELECT have always been to help breeders identify the animals with the right genes for the job. The jobs that sheep need to perform vary – some are for fast growth and meat value, some for wool production, some for reproduction, and some for various combinations of these.

All the developments that have been made have had this aim in mind. The result is that breeders have a lot more scope to identify the animals with the best genes now – that means being able to select for more traits, to select more accurately, and to balance selection better and better.

That means that selection for profitability – the effect of the animal’s genes on income and cost through the value chain – is getting steadily more effective. It also means that the ram-buyer has more ability to choose the right ram for the job.

How does this stack up to genetic evaluations in other species or countries?

LAMBPLAN and MERINOSELECT are at least as good as any genetic evaluation system in any species in any country – in terms of coverage of important traits, in terms of the availability and relevance of indexes, in terms of covering the whole value chain (ie there are ASBVs for traits relevant to all sectors of the chain), and most importantly, in terms of the level of adoption across industry, and the way breeders use LAMBPLAN and MERINOSELECT to make valuable genetic progress.

The last point links to an extremely powerful aspect of LAMBPLAN and MERINOSELECT – breeders have been absolutely integral to every step in the development, contributing ideas, helping sort out what works and what doesn’t, taking up the challenge of communicating with their clients about the information and opportunities.
This partnership between breeders and scientists is as strong as in any industry in the world, and is enormously valuable.

**The future is exciting!!**

The opportunities are unlimited: if we keep improving the quantity and quality of the data – which is essential to generating reliable ASBVs, if we keep focussed on identifying animals’ genetic merit for things contributing to income, cost and hence profit, and if we keep making sure that smart research and practical focus are working together, we will:

- Keep making progress at very high rates, and probably go faster in the future
- Keep adding value to lambs and to wool sheep, while holding costs or even reducing them
- Keep pace with the cost-price squeeze, or even outpace it – which is what the lamb industry as a whole has been doing now for over 25 years

There’ll be more traits – nutritional content of meat, feed efficiency, and resistance to some major diseases are just some of the possibilities; there’ll be more and more use of genomics backed by rock-solid performance data; and there’ll be more use of advanced tools like MATESEL.

Plenty of challenges and opportunities – working together will continue to ensure valuable outcomes from a brilliant system.

LAMBPLAN has been a major factor in the growth in value of the Australian lamb industry since the early 1990s – it’s more than doubled in value in real terms – in today’s dollars. There is no reason why genetic improvement can’t continue driving that growth across the whole sheep industry.

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### Updated Fee Schedule

1 July 2017 will see the implementation of the new Sheep Genetics Fee Schedule. The current fee schedule has been in operation from 2010 with no increases in pricing since 2015. The new schedule has been discussed and approved by the Sheep Genetics Executive and Advisory committees and is set out below. (Prices listed inc GST where applicable)

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### Software Support

Software Support: If you are using one of the freeware Pedigree Master programs and need assistance in setting up or using please contact one of the data managers listed on our website. These programs are free as they do not have a helpdesk, using a data manager to get going can be beneficial to your business.
Sheep Genetics staff should always be the initial contact point for all communication