Welcome

Welcome to the latest Breeders Bulletin.

Sheep Genetics has recently implemented a landmark enhancement for the genetic Improvement of sheep in Australia with the full implementation of a single step analysis to more optimally use genomic information across all our analyses (except reproduction). This is a world leading achievement and only a result of some excellent collaboration between many parties and most importantly a large number of Sheep Genetics members, so thank you for your contribution to this achievement. There are a number of key benefits from single step which improve the value of genomic information but there is no doubt that good pedigree and phenotypic data recording are still vital.

At present one of the key focuses is on the delivery of genomically assisted breeding values for reproduction traits. We are working with breeders and software providers to make sure we are collecting the reproduction data as completely as possible. The Sheep CRC and MLA are working collaborative with breeders to genotype and phenotype more ewes for reproduction traits to bolster the reference population. We are now working on a new analysis and plan to deliver RBVs for a range of new traits as soon as possible.

At Sheep Genetics we have also recently completed a large number of industry consultation events ranging from our flagship Leading breeder conference, Regional forums, Service and software provider workshops and some key field day events. All these events have been well attended and we have had some positive feedback from the participants, so well done team and thanks to those all those who attended!

October saw us welcome Peta Bradley as the MERINOSELECT Development Officer. We have been lucky to appoint Peta (pictured below) into this role she has a great balance of practical, academic and personal skills across a number of industries which will be great for the Sheep Genetics team and MERINOSELECT clients. Caris continued to support MERINOSELECT throughout the transition period and we wish her well for her new role as Project Manager - Genetics.

Two other key activities was the delivery of several MateSel training workshop to catch up on the backlog and also the fine tuning and further release of the Ramping Up Genetic Gain report. Many breeders would have now seen these reports over the last few years and they are proving to be a useful flock diagnostic tool.

I hope you find this Breeders Bulletin interesting and useful, and if you have any suggestions for improvements or ideas for future topics please feel free to ring the office or email them to us at info@sheepgenetics.org.au

Daniel Brown Sheep Genetics Manager
Regional Forum Wrap Up 2017

Sheep Genetics has concluded running five regional forums at Inverell NSW, Cowra NSW, Ballarat VIC, Burra SA and Brookton WA. Across all the forums we had a total of 134 attendees including LAMBPLAN, MERINOSELECT and DOHNE clients, commercial producers, agents and consultants. The forum focused on analysis upgrades, your flocks breeding objective, managing rates of progress and reproduction.

To target actions the participants had the opportunity to write down what their breeding objective was, evaluate what traits they are currently measuring and what proportion of the flock is being measured for those traits. We then discussed what impacts rate of progress, and how balancing the breeder’s equation is fundamental to making genetic progress towards the breeding objective.

Improving reproductive performance and survival of lambs is a key target for industry, hence a full session on recording reproduction was delivered.

Many of the take home messages in the feedback indicated that reproduction is a key area where breeders are focusing on better recording and improving.

The day concluded with an interactive session based on the Ramping up genetic gain reports that were released at regional forums in 2016. Breeders had the opportunity to discuss and identify areas within their flock where improvements could be made to ultimately boost genetic gain. Once again the reports were well received and we hope to have these reports available to all breeders via our website by the end of the year.

Overall the regional forums were well received with plenty of discussion throughout the day on key aspects of the genetic evaluation, reproduction and how to make the most genetic progress within breeder’s flocks. Sheep Genetics would like to thank all the participants for attending leading breeder and the regional forums, especially those breeders who made an extra special effort to travel long distances. Also we appreciate the feedback provided and we hope to see you all in 2018.
Data Quality Tip - Effective Progeny

Measuring and collecting records on your stud flock can be laborious, time consuming and costly, so it is important to ensure every bit of effort and dollars put into recording, the most effective results are achieved out the other end. The flow on effect from this is selection decisions become more accurate and genetic gain improves.

In the analysis some records are more useful or effective then other records. This means that some records are weighted heavily in the calculation of the breeding value and other records are hardly being used. For every record collected we want to make sure the record effectiveness is as close to one (100%) as possible (See Figure 1 below). The usefulness of records in the analysis contributes to the accuracy and stability of breeding values.

The main reasons that some records are not as useful as others are due to:

- Group size
- Number of sires in a group

Group Size
If there are only small numbers of animals in a contemporary group, we have a lot less certainty about the animals performance compared to having a much larger contemporary group. In the graph (Figure 1) we can see that if there are only two animals in a group the data is only 20% effective. In comparison if there are 20 progeny in a contemporary group we get closer to 100% effective records. Because we are referring to contemporary group, if the management group size is 40 animals, when it is split in half for male and female – the group size already is back to 20.

Number of Sires in a Group
Just having lots of progeny is not always going to ensure effective records. It is important to consider the number of sires that are represented in a contemporary group and how evenly represented. Ultimately we are trying to maximise the amount of genetic comparisons. If there is only one progeny in a group by one sire, the data is 0% effective. Equally, if there were 20 progeny in a group but only by one sire the data is still 0% effective. This is because all of the animals are half siblings and we do not have diversity of genes in the group to determine relative performance. If there were 20 progeny and 19 were from the same sire and one animal was from a different sire, the effectiveness of these records is still quite low, because we can only compare the performance of those 19 animals with the performance of one animal. If there were 20 progeny from two sires each with 10 progeny each, we get closer to 50% effective records.

To achieve as close to 100% effective records it is best practice to ensure group sizes are as big as possible and as many sires are represented in the contemporary groups.

If you have any queries relating to effective progeny numbers please contact Peta Bradley (MERINOSELECT) or Clara Collison (LAMBPLAN) to discuss.
Recording Reproduction

What is Reproduction?
The reproductive rate of breeding ewes is recorded across a ewe’s lifetime, with each lambing opportunity adding further information to the ASBVs for reproductive rate. Currently there are four reproduction breeding values. Number of lambs born (NLB) and number of lambs weaned (NLW) and Yearling Number of Lambs born (YNLB) and Yearling number of lambs weaned (YNLW). NLB relates to the fertility and litter size of the ewe and NLW relates to lamb survival.

How is it measured?
Each time a ewe is put to the ram it is classed as a lambing opportunity. Therefore more than one lambing can contribute to reproduction breeding values. The purpose of collecting reproduction data is to account for the non-genetic factors impacting a ewe’s performance, hence identify the better performing ewes. Capturing reproduction data occurs throughout the lambing period.

Joining
When putting the rams out all that is required to be recorded, is the date. Identifying the date when the ram went in and came out gives information regarding the length of opportunity the ewe had to get pregnant, and assists in identifying sires if a backup ram is used. The dates can also assist with further management i.e. when to pregnancy scan. Also at joining ewe weight and condition score can be measured. This information can contribute to AWT ASBV’s and also research into the development of a condition of the ewe ASBV. It is the easiest time to weigh and fits in to a measurement plan without extra labour.

Group Codes of Ewes
During the lambing period it is also important to know how the ewes have been managed. This is how ewes are run up until the next measurement. At joining, the group code is how the ewes were run up until joining. When the ewes are pregnancy scanned, their group will be how they were run between joining and scanning. At lambing, the group code is how the ewes were run between scanning and lambing i.e. single group and twin group. The group codes allow the identification of any non-genetic factors that may influence the performance of the ewe and her lambs.

Pregnancy scanning
Pregnancy scanning ewes allows the identification of dry ewes, and wets or multiples. Entering the dry ewes is an indication of fertility – Comparing fertile ewes to infertile ewes for that lambing opportunity. Scanning for multiples is an indication of litter size. If litter size is identified using a pregnancy scan, the information will contribute to NLB ASBV’s prior to any lambs being born. Meaning we can have a much clearer idea of NLB earlier. Scanning for multiples can also influence management of ewes between scanning and lambing.

Lambing
At lambing it is important to record birth type, especially if the ewes are scanned. Birth type will always be used as preference over a pregnancy scan. However if there is not a lambing outcome, for example bad weather prevented recording and multiple lambs were lost before being able to identify the mothers the pregnancy scans are used.
Therefore pregnancy scans are used for NLB records if dam pedigree is not identified. Dead at Birth Lambs need to be recorded as a DAB lamb with sire and dam data for lamb mortality data.

Lamb Survival is an issue for the sheep industry. The rear type is something that is often forgotten about or missed. Recording what lambs were born and then go on to be raised is crucial data for the NLW record. This is recorded at weaning, if a lamb was born as a twin the BT would be 2 however was raised as a single its rear type is a 1. The twin that died would have a BT of 2 and a RT of 0. All of the information is recorded every year on the ewe.

As NLW is a trait of the ewe, an important piece of information required is dam pedigree. We must be able to identify the outcome of the joining and how many lambs were raised by matching the lamb or lambs to the dams.

Maternal Behaviour Score
When in the paddock recording which ewe had what lamb, tagging and weighing lambs and Maternal Behaviour Score (MBS) can also be measured. The maternal behaviour of a ewe is an important factor in lamb survival, especially in the early stages of the lamb’s life. To produce a MBS ASBV and utilise correlations with other traits in the analyses, more data is required.

The behaviour of the ewe can be measured through a scoring system that is constructed around the distance the ewe moves from the lamb during the tagging process. MBS is correlated to both reproduction and growth. Indicating that improving maternal behaviour will not only improve lamb survival but also growth in the lamb and reproduction in your ewes.

The scoring system for MBS is a single score of 1,2,3,4 or 5. As a rule of thumb, a ewe with Score 1 shows excellent maternal behaviour and stays close to the lamb. A ewe with Score 6 show poor maternal behaviour and show little interest in the lamb.

Component trait RBV’s
Recording all of the detail above will allow NLB and NLW ASBV’s to be calculated. However it will also contribute to the development of the component trait RBV’s for reproduction. The component traits are Fertility (pregnant or not), fecundity (litter size) and Lamb survival (rears lamb until weaning). By having the component traits breeders will be able to specifically select for the component of reproduction in which they need to improve the most. For example a breeder may have many ewes in lamb but only as singles. So they would select for fecundity to improve the number of lambs. Also many breeders many have large litters but the ewes cannot support the lambs so they directly select for lamb survival.

These traits require no extra work or data then what is currently required to get into the reproduction analysis, however provide much more accurate means of selecting for the components that impact reproduction.
Strategies for optimal use of parentage and low density 15k genomic tests

Tom Granleese UNE

Key messages
- Parentage test $21 (plus GST) – more reliable, faster turn around
- Low density 15k $35 (plus GST)
- Genomic testing an entire drop can increase genetic gain of the breeding objective by up to 20% when first mating age is 18 months
- Genomic testing an entire drop can increase genetic gain of the breeding objective by up to 33% when using ram lambs only as sires
- Genomic testing all males provides 75-80% of maximum overall benefit depending on breeding objective
- Not all males need to be tested to provide that maximum overall benefit

Parentage test update
The Sheep CRC have recently released an improved Parentage Test. Unfortunately the test has increased in cost to $21 + GST. The increase in price has been caused by updating to a more stable platform that will decrease turn-around time and deliver more reliable results (less “too close to call” results).

Other improvements include increasing from the 180 SNP panel to 800 SNPs which will enable research to deliver more accurate horn/poll results and also identify genetic carriers for conditions such as Myostatin, Scrapie resistance, Callipyge, Hairy lamb, Inverdale, Microphthalmia, Spider lamb, Texel Chondro and Yellow Fat.

The parentage test is compatible with both the old parentage test and low density 12k/15k tests. The better news is that the 15 low density (LD) test has reduced from $50 to $35 + GST.

Genotyping benefits

Parentage testing
The costs (above) and benefits need to be weighed up when using parentage testing. It is an expensive method to record pedigree. The benefits however are:
- no more mothering up (although birthweight, birth date, birth type, lambing ease, maternal birth score, litter size are lost which is very important in maternal and terminal breeding objectives)
- provides reproductive data on ewes
- simplifies mating and lambing structures (enables syndicate mating with accurate pedigree)
- more accurate pedigree which enables more accurate ASBVs
- test for horn/poll status (Merino)
- test for other recessive genes
- compatible with 15k LD test and 50k HD test

Low density 15k testing
Genomic testing has the potential to increase rates of genetic gain by up to 20% for Merino “Plus” indexes and terminal eating quality breeding objectives annually if all male and female 18 month old selection candidates (first possible matings) are chosen on ASBVs and breeding objectives remain constant over years. This can raise to up to 33% if all ram lambs are genotyped and available to mate. However genotyping entire drops may not appear realistic which we will touch on later.

Genomic testing on the 15k LD tests provides extra accuracy and variation in traits particularly where traits are measured late in life or not measured at all. Figure 1 shows two flocks that breed terminal sheep. The blue flock does not genotype and the maroon flock does. The traits (shearforce and lean meat yield) are not measured. The blue flock demonstrates little variation in ASBVs and rely on genetic correlations to contribute the most information. The maroon flock genomic tests a significant portion of their flock and we can observe much more variation in their flock as the ASBVs uses genomic information in the calculation of ASBVs. Variation in ASBVs can also be increased by measuring any key trait in an entire drop. The greater variation allows “correlation breakers” to be identified and enables accelerated rates of genetic gain where a multi-trait breeding objective or selection index is used.

The principle of increasing variation in ASBVs applies to all breeds of sheep that can utilise genomics. Increasing rates of gain by selecting on genomic enhanced breeding values has been validated across a range of industries and species.
With the latest change of ASBV estimation moving to Single-Step analysis, this means any sheep with a recorded trait and/or progeny with recorded traits and genotypes become part of the reference population. This means genomic prediction becomes more accurate for new sheep that are tested and are related to the genomic population. Because of this, we would strongly encourage ram breeders to genomic test all their sires that have measured progeny. This allows breeders or buyers of rams to increase the genomic prediction accuracy of the sheep they want to test.

The benefits of LD 15k genomic testing are:
- Same benefits of parentage testing
- Increase variation and accuracy of ASBVs in younger sheep in hard to measure and/or unmeasured traits
- Becoming part of the reference population if measurements made on tested animal and/or progeny increases accuracy of genomic prediction for closely related animals
- Differentiate ASBVs between full siblings at young age
- Help maximise genetic gain and minimise inbreeding using mating programs such as “Matesel”
- Compatible with parentage and 50k tests

**Best value for money – case studies**

There are many scenarios in which producers can use genomic technologies and there is no one-size-fits-all approach. There are many factors to consider with budget being the biggest one. Recently with the price reduction of LD testing to $35 and parentage rising to $21 the Sheep CRC have had some enquiries about how best to use LD testing. The best value for money (as ram breeders) and biggest genetic benefit is to test ram selection candidates.

Selection intensity of rams are much higher than ewes resulting in rams contributing 75-80% of the benefit of genomic selection. Ewes then contribute the remaining 15-20% benefit. Therefore if the total maximum benefit of genomic testing is 20% extra gain, testing rams only can increase the rate of genetic gain by 15%. Furthermore producers do not

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**Figure 1:** Plot of ASBVs for shearforce (SF5) and lean meat yield (LMY) for a flock that does not genotype (blue) and a flock that does genotype (maroon)

![Plot of ASBVs for shearforce (SF5) and lean meat yield (LMY) for a flock that does not genotype (blue) and a flock that does genotype (maroon)](image-url)

- Identify “Correlation breakers”
  - Non-genotyping flock - little variation
  - Genotyping flock - large variation

- Lower the better
- Higher the better

Courtesy Daniel Brown - AGBU 2017
need to test all their ram selection candidates to achieve the maximum benefit assuming pedigree on the entire drop is known with some preliminary phenotypes included in ASBVs. Because the selection intensity is very high in rams, testing the top 30% of 18 month old ram selection candidates (ranked on ASBV index) will maximise the benefit. Testing 50% of ram lambs is required if mating at a younger age. To extract the final 25% potential gain (equating to 5% extra genetic gain) from ewes, close to 100% of ewe selection candidates would need to be tested annually. This demonstrates the inefficiencies of testing females due to a much lower selection intensity and significantly lower genetic contributions to a flock’s genetic progress.

We do recommend that you genomic test potential donors for MOET and/or JIVET programs. This is a relatively small cost compared to the reproductive technologies and helps maximise your genetic investment. We recommend if you MOET 10 ewes, to genomic test 35 ewe candidates and to JIVET 10 ewe lamb donors, to test 45 potential candidates (Granleese et al. 2017).

Next we will look at some pros and cons of different situations:

**Mothering up vs Parentage testing**
- Both methods return pedigree and reproduction data (if we know dry ewes)
- Mothering up is cheaper but more labour intensive over a period of time
- Mothering up runs risk of mis-mothering and inaccurate pedigree
- Mothering up means the use of single-sire matings
- Parentage testing is less time consuming but birth weights, birth types and dates of birth are potentially forfeited which is extremely important to generate accurate ASBVs for early-in-life traits
- Parentage testing allows for syndicate mating
- Parentage screens for recessive diseases and for poll gene status
- Mothering up gives better data for accounting for fixed effects that account for age, weight, birth type, lambing ease, gestation length and maternal behaviour score

**Parentage testing all vs LD all**
Some flocks are already parentage testing (PT) their entire drop. With the cost of PT increasing 30% and genomic testing (GT) reducing by 30%, there is an interest in how to maximise the use of both technologies whether “double-testing” is cost-effective. Double-testing is where breeder parentage test to assign pedigree and then identify a proportion of the best ranked animals have to then have LD tested. There is no extra labour required in recollecting TSUs or blood when double-testing as the samples are stored in the lab in the USA. You simply have to submit a file to the Sheep Genomics Office on the animals who you would like to have LD tested.

Table 1 shows some scenarios comparing the costs and benefits of different genomic testing scenarios assuming all selection candidates are available for selection at 18 months of age. Here we can see that double-testing is the most cost-effective way increasing rates of genetic gain using genomic testing.

In Table 2, where we assume ram selection candidates are available for selection at 7 months of age, and selection is made on ASBVs, we can observe that simply LD testing all rams is the most cost-effective method of increasing rates of genetic gain.

**Table 1:** Assumes 1000 head born per year in nucleus and all sheep are first eligible to be mated at 18 months of age. Table shows total cost of genotyping, cost as a percentage compared to parentage testing all animals born only, extra genetic gain possible and dollars spent per extra % of genetic gain.

<table>
<thead>
<tr>
<th>*Assuming 1000 head born per year in breeding nucleus</th>
<th>Parentage Only</th>
<th>LD Rams Only &amp; PT(^\wedge) all ewes</th>
<th>PT(^\wedge) all &amp; then Double-Test top 20% Rams</th>
<th>PT(^\wedge) all &amp; then Double-Test top 30% Rams</th>
<th>LD all Rams and Ewes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total genomic costs ($)</td>
<td>21000</td>
<td>28000</td>
<td>24500</td>
<td>26250</td>
<td>35000</td>
</tr>
<tr>
<td>Cost as % to PT(^\wedge) only</td>
<td>100%</td>
<td>133%</td>
<td>117%</td>
<td>125%</td>
<td>167%</td>
</tr>
<tr>
<td>Extra genetic gain possible</td>
<td>0%</td>
<td>15%</td>
<td>13%</td>
<td>14%</td>
<td>20%</td>
</tr>
<tr>
<td>$ spent/extra % genetic gain ($)</td>
<td>0</td>
<td>467</td>
<td>269</td>
<td>375</td>
<td>700</td>
</tr>
</tbody>
</table>

*The extra gain assumptions are made for Merino indexes, Terminal Indexes that include EQ traits and Maternal indexes that include reproduction traits; ^Parentage test*
There is a risk that young genomic tested animals may not receive reportable ASBVs. This is usually because individuals do not meet accuracy thresholds. To increase chances of meeting accuracy thresholds for particular traits, increasing the mid-parent breeding value accuracy is key. To achieve this you can:

- Make sure pedigree is as complete and deep as possible
- Performance recording in ancestors is submitted to Sheep Genetics
- Using highly accurate artificial insemination sires
- Genomic testing sire teams
- Performance and/or progeny recording of genotyped animals
- Recording traits on genomic tested individuals (if possible or old enough)

What is in the pipeline?

- RBVs for reproduction data for Border Leicesters and Maternal Composites are being developed
- Better prediction of Horn/Poll (we are looking for phenotypes on any sheep that is parentage tested or LD tested) – contact tgranle2@une.edu.au for more information

Flock Profile – Merino commercial

LD 15k genomic tests are now available to commercial Merino producers for $800+GST. Commercial Merino producers receive a flock average for Merino traits so they can make better ram purchasing decisions. Clients who buy your rams and do a Flock Profile will get more accurate results if you are genotyping your ram teams (at the very least) with measurements on those genotyped sire progeny such as ywt, ycfw, ydcv, yfd, ysl, pemd, pfat.

Table 2: Assumes 1000 head born per year in nucleus. Ram lambs are first available for mating at 7 months of age and ewes first mated at 18 months of age. Table shows total cost of genotyping, cost as a percentage compared to parentage testing all animals born only, extra genetic gain possible and dollars spent per extra % of genetic gain

<table>
<thead>
<tr>
<th></th>
<th>Parentage Only</th>
<th>LD Rams Only &amp; PT all ewes</th>
<th>PT^ all &amp; then Double-Test top 30% Rams</th>
<th>PT^ all &amp; then Double-Test top 50% Rams</th>
<th>LD all Rams and Ewes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cost ($)</td>
<td>21000</td>
<td>28000</td>
<td>26250</td>
<td>29750</td>
<td>35000</td>
</tr>
<tr>
<td>Cost as % to PT only</td>
<td>100%</td>
<td>133%</td>
<td>125%</td>
<td>142%</td>
<td>167%</td>
</tr>
<tr>
<td>Extra genetic gain possible</td>
<td>0%</td>
<td>25%</td>
<td>17%</td>
<td>22%</td>
<td>33%</td>
</tr>
<tr>
<td>$ spent/extra % genetic gain</td>
<td>($0</td>
<td>283</td>
<td>303</td>
<td>393</td>
<td>424</td>
</tr>
</tbody>
</table>

*The extra gain assumptions are made for Merino indexes, Terminal Indexes that include EQ traits and Maternal indexes that include reproduction traits. ^Parentage test
Maternal ASBV’s - MWWT

The weight of lambs at weaning is influenced by many factors. Research shows that approx. 60% of the variation between the weight of the lamb at weaning can be attributed by non-genetic effects, 20% of the difference between the lambs genetics for growth and the remaining 20% due to differences in the maternal contribution made by the mother (half of which is genetic contribution, 10%).

The maternal contribution provided by the mother is an important consideration for sheep enterprises. The difference in contribution of the dam to weaning weight is driven by such things as the amount of milk the lamb receives, the quality of the milk and the mothering ability of the dam.

Interpreting maternal ASBV’s

Maternal ASBV’s provide an estimate of the maternal contribution of a dam to the weaning weight of her lamb/s. For sires maternal ASBV’s are an estimate of the maternal contribution that his daughters will provide to the weaning weight of their progeny.

Maternal weaning weight ASBV’s are expressed in kilograms and is an indication of the expected difference in the weight of the lamb/s due to the maternal contribution of the ewe.

More positive maternal weaning weight breeding values are generally more favourable, depending on the environment.

Finding an optimum maternal weaning weight ASBV is dependent on the production system and the environment in which the ewes are run. Selection for the Maternal Weaning weight ASBV may be warranted when ewes are run under a good plane of nutrition and lambs are sold as weaners. However some environments may not support ewes with a more positive maternal environment. It may take these ewes longer to go back in lamb the following year.

How is maternal weaning weight calculated

Maternal ASBV’s are calculated by partitioning the difference in weaning weight into direct growth and maternal components. The following is a simplistic demonstration of how the analysis uses the weaning weight of the lamb to calculate its maternal weaning weight ASBV.

Initial calculation of an ASBV

Before the maternal contribution can be considered, it is necessary to outline the calculation of an ASBV. Simplistically, the calculation of an ASBV is a straight forward process. The information required is the animals own performance, the performance of its peers and the heritability of the trait. This can be defined as follows:

\[
\text{ASBV} = (\text{Animals performance} - \text{Average Performance of Peers}) \times \text{Heritability}
\]

For example:

If a lamb weighed 5kg heavier than average of its peers at weaning its ASBV would be:

\[
\text{Weaning weight ASBV} = 5\text{kg} \times 0.20 = +1.00\text{ kg}
\]

Of Course, in the statistical analysis (OVIS) the calculations become far more complicated. In the genetic evaluation, the calculation of an ASBV of an animal includes:

- The animals own performance
- The performance of all know relatives in all flocks
- The relationship between traits
- The performance of all flocks over years of recording
- Genomic information (if available and utilised)

Calculation of Maternal ASBVs

Knowing the simple calculation of an ASBV, let’s consider the calculation of maternal ASBV’s. In this scenario the lamb has an adjusted weaning weight of 40kg, compared to the group average of 35kg. That is the lamb is 5kg heavier than the average weight of his peers.

As illustrated above research has shown 60% of the variation between the weaning weights in lambs can be attributed by non genetic factors, 20% due to genetics and 20% due to the maternal contribution of the ewe. The contribution of the ewe is separated in half, into the environmental component provided by the ewe and the genetic
component passed onto her daughters. In technical terms this means the heritability of the maternal weaning weight breeding value is 10% and the heritability of weaning weight is 20%.

With all of this information, the analysis can partition the 5kg superiority of the above lamb into growth and maternal components.

**Maternal ASBV:**

\[
\text{Maternal ASBV} = (\text{Animals Performance} - \text{Average Performance of Peers}) \times \text{Heritability}
\]

\[
= 5\text{kg} \times 0.10
\]

\[
= + 0.5\text{kg}
\]

**Weaning weight ASBV:**

\[
\text{Weaning weight ASBV} = (\text{Animals performance} - \text{Average Performance of Peers}) \times \text{Heritability}
\]

\[
= 5\text{kg} \times 0.2
\]

\[
= +1\text{kg}
\]

In contrast to the weaning weight ASBV, the extra weight of the lamb due to the maternal effects, reflects the ewe’s genetic potential, so only half of the ASBV is inherited by the lamb. Therefore the ewes Maternal ASBV will be 0.5kg and the lambs MWWT ASBV will be 0.25kg. The lambs weaning weight ASBV will remain at 1kg.

As previously stated the calculations used in the analysis are far more complicated. In the analysis the calculation of maternal breeding values can also be influenced by:

- The later weight performance of the animal
- Other lambs from the ewe of the lamb
- The performance of all known relatives.

That is there are thousands of calculations that go into producing an ASBV for every animal in a large performance recorded population.

**Recording information for maternal ASBVs**

As the maternal ASBV’s are calculated based on partitioning weaning weight into direct growth and maternal components, a weaning weight needs to be recorded for the calculation of MWWT ASBV and also full pedigree.

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**Genetic Disorders in Sheep**

A range of genetic disorders can occur in sheep. For example a genetic disorder, like hypotrichosis (a hairless condition) shown below, generally has a low frequency and often is only observed in some sheep populations.

Even though these disorders only occur at low frequencies, it is important to collect samples to get more information and to develop efficient tests to breed against them. With samples of affected animals, we can help try and eliminate them from the Australian sheep population.

Therefore we are requesting that you contact us when you have a sheep with a known or suspected genetic disorder, so we can work with you to collect information from the affected animal and possibly unaffected relatives. Information provided will be kept confidential and your help is greatly appreciated.
Sheep Genetics Organisational Setup

Meat & Livestock Australia

Executive Committee
- Michael Crowley - General Manager, Producer Consultation and Adoption
- Richard Apps - Program Manager, Sheep R&D
- Hamish Chandler - Program Manager, Genetics

Advisory Committee
- Ron Cullen (Chair)
  - Murray Long - 230324
  - Pendarra White Suffolks, NSW
- Mark Mortimer - 601250
  - Centre Plus Merinos, NSW
- Mark Murphy - 601365
  - Karbullah Merinos, QLD
- Dale Price - 161886
  - Majardah Poll Dorsets, SA
- Warren Russell - 501704
  - Melrose Merinos, VIC
- Sara Wilson - 470169
  - Jilakin Downs Dorpers WA

Sheep Genetics
- Manager: Daniel Brown
- Project Coordinators: Fiona McLoughlin, Nicole Williams
- LAMBPLAN: Clara Collison, Stephen Field
- MERINOSELECT: Peta Bradley, Ermias Zerazion

Technical Committee
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Sheep Genetics staff should always be the initial contact point for all communication

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