Welcome to the Spring edition of the Breeder’s Bulletin

Welcome to the Spring Breeders Bulletin, the last few months have continued in the same fashion as the beginning of the year with lots of events and very busy for all staff.

We have had some internal changes in this period, with Hamish Chandler accepting the Genetics Program Manger role with MLA, this means that we are currently recruiting for a Sheep Genetics Manager.

David Rubie has also moved on from the MERINOSELECT Database Officers position, Ermias Zerazion has accepted the position, a brief introduction is included with this newsletter.

The staff changes have meant that other staff are currently assisting to cover the workload and we ask that people are patient as we endeavour to continue with business as usual.

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.

Breeder events 2017

Dates have been set for the major Sheep Genetics breeder events of 2017, further information can be found below and over the page about the Leading Breeder and Regional Forums.

Service Provider events

Scanner accreditation will be held in Armidale on the 15th and 16th of February, this ensures that Scanners meet the requirements for Muscle and Fat depth scanning.

Service Provider workshop will be held in Melbourne on the 3rd and 4th of May, this event allows providers to gain valuable information to assist their clients businesses.

Christmas Holiday period

The Sheep Genetics office will be closed from Friday 23rd December and will reopen on Tuesday 3rd January 2017. Please be aware that there will be some changes to analysis dates over this period due to the public holidays. Please refer to the website for information.

A 2017 Calendar of run dates is included with this newsletter, if you have not received one please let us know.

Leading Breeder
1st Mar 2017 - Save the Date

The 2017 Leading Breeder conference will be held in Melbourne on the 1st and 2nd of March. The 2 day conference will be held at the Best Western Airport Motel and Convention Centre.

The Leading Breeders conference is a great way to stay up to date with the latest information from Sheep Genetics and associated industry partners. The two days will also include a dinner on the evening of the 1st March. More information will be available closer to the date.
Regional Forum Wrap Up

Sheep Genetics ran seven regional forums in 2016 at Armidale NSW, Young NSW, Wodonga VIC, Hamilton VIC, Launceston TAS, Hahndorf SA, and Williams WA. Across all of the forums we had a total of 180 attendees including LAMBPLAN, MERINOSELECT and DOHNE clients, commercial producers, agents and consultants. The forums discussed the analysis upgrades, indexes, basics of ASBVs and plans for 2017.

The afternoon sessions of the forums went through the new Ramping up genetic gain project. The project, a collaboration between Sheep Genetics, Sheep CRC and NSW DPI aims to deliver key genetic information on an individual flock basis to all sheep genetics clients. During these sessions the fundamental areas to making genetic gain were discussed including selection accuracy, selection intensity and generation interval. The attendees were presented with a number of graphs breaking down how different flocks are making different rates of progress. An interactive session at the end of the forums was a highlight for many. The participants were given a new flock report outlining details of their flock’s genetic progress over the past five years. These reports included information on pedigree, percentage of flock with certain traits recorded, number of contemporary groups for those traits, selection efficiency for males and females, index accuracy, sire summaries and reproduction summaries.

The new ramping up genetic gain reports have been well received and many participants enjoyed the interactive session of the forum. Some of the comments included “the report on your own flock performance is very useful, it really brings it together in a useful format and demonstrates the relevance of the information we collect” and “I got a lot more out of it than expected”.

Overall the regional forums were well received with plenty of discussion throughout the day on key aspects of the genetic evaluation and how to make the most genetic progress within your flocks.

Sheep Genetics would like to thank all the participants for attending, and for the feedback provided. we hope to see you all in 2017, please note the dates below and further information will be provided closer to the date.

2017 Regional Forums - 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

Ramping Up Genetic Gain Project Update

The ramping up genetic gain project, released at the regional forums are continuing to be developed. A number of service providers will be road testing the reports with breeders, to ensure the reports are delivering information that is understandable and effective in describing genetic progress on an individual flock basis. The feedback from the regional forums and the road testing will be used to finalise the reports, and allow the reports to be accessed by all Sheep Genetics members. When released, the reports will be accessible from the Sheep Genetics Dashboard. Feedback is welcomed to assist in the continual improvement of the reports.
The Importance of Pedigree

Pedigree is a fundamental part of any genetic evaluation, without being able to identify animals with common genes we are unable to evaluate genetic performance and estimate an accurate breeding value. The amount of pedigree on an animal submitted to Sheep Genetics can vary from no pedigree, sire only, dam only or full pedigree where both the sire and dam are identified. Although the genetic evaluation can handle a small amount of animals with less pedigree, it makes it harder to establish the animal’s genetic merit. When a parent is not known the ASBVs will be of lower accuracy as well as have less non-genetic factors accounted for. Although it would be wonderful to see 100% of animals in the Sheep Genetics database with full pedigree, we understand that this is not always practical. To ensure that the ASBVs reported are as stable as possible, Sheep Genetics have pedigree proportion guidelines in place. These guidelines are set so all producers can have confidence in the ASBVs used when making selection decisions.

An ASBV can be calculated with different amounts of information, this is reflected in the accuracy figure reported with each ASBV. The more information that is used to calculate an ASBV the more confident we can be that it is close to the True Breeding Value of that animal. Pedigree is used to identify extra information that can be used along with that animal’s performance measurement. When the sire is known, not only the sire’s performance is used but performance from all other progeny recorded from that sire is also utilised, as it is recognized that they share genes in common. The accuracy of the ASBV reported increases significantly when a sire is known, this is generally due to the larger number of progeny that a sire has recorded compared to a dam each year. Due to the sire being so important in a genetic evaluation, the Sheep Genetics pedigree guideline is that at least 70% of the year’s drop has an individual sire known. Although identifying the dam does not increase the amount of information used to calculate an ASBV as much as a sire, the analysis can identify fixed effects and be more correct in its calculations when a dam ID is supplied.

It is widely known that an animal’s performance can be influenced by non-genetic factors including age, birth type, rear type and age of the dam. Sheep Genetics aim to account for these factors and estimate solely the genetic performance of an animal. For example a Merino born and raised as a twin can produce over 7% less wool than a single born at Yearling age stage. This is not due to the genes that it will pass on but fixed effects and can only be accounted for in the analysis if the Birth Type and Rear Type of the animal is known. For majority of the non-genetic fixed effects the animal’s Dam needs to be identified for the impact on performance to be accounted for. An animal may be identified as born as a twin from pregnancy scanning and lambing paddocks, however whether they were reared as a twin can only be identified if the dam is known.

The performance of progeny out of younger and older ewes is lower than that of progeny from dams that are 4 or 5 years of age. The analysis can only eliminate the difference in performance due to the age of the sheep’s dam when the dam is identified. When these non-genetic effects are not identified, it is assumed that the animal is a single born and reared lamb out of a ewe in peak production. Any impact on performance is not accounted for and the ASBV calculated is not as precise.
LAMBEX Young Guns

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.

Charlie Shadwell

Charlie has always been interested in and participated in the lamb industry. He is currently at Farrer Memorial Agricultural High School in Tamworth, NSW. Charlie is involved in various activities relating to agriculture through his involvement at school and extracurricular activities. After the completion of Year 12 Charlie is planning on heading to University to undertake an Agricultural degree majoring in Animal Genetics, which he wants to use in his future specialising in Embryo Transfer, Artificial Insemination and as a Genetic Scientist. Please read Charlie’s LAMBEX article over the page.

Sheep Genetics strongly recommend that dam pedigree is recorded when possible, especially when early age stage traits are important to the breeding program. Up until recently the only way to record dam pedigree has been through manually mothering up lambs either at birth or not long after in the yards. Advancements in technology now allow for the Dam to be recorded in a number of ways, including manually mothering up, Pedigree Matchmaker and DNA parentage tests. Different methods of identifying dam have different pros and cons which need to be considered in regards to both the breeding and management programs of the flock. Manually mothering up allows you to collect added traits at birth as well as an accurate date of birth. Pedigree Matchmaker will give you the most likely match between Dam and Lamb through reading their Electronic tags as they walk to and from a feed or water source at a fairly low price. The DNA parentage test is available for around $17+GST per animal and has the added benefit of a Poll/Horn test for Merinos when tested through the Sheep CRC. Sheep Genetics accepts pedigree identified by all methods, trusting that the individuals submitting data have confidence in their methods before supplying to Sheep Genetics.

The amount of genetic progress that a flock can make each year is dependent on how accurate their selection decisions are. By identifying both sire and dam the flock can have greater confidence in the ASBVs being reported back from Sheep Genetics. Selection decisions will be more accurate which will result in greater improvements being made each year towards the flocks breeding objective.

Key Points
- Identifying pedigree is vital to the genetic evaluation
- Sheep Genetics strongly recommend >70% of animals have a single sire identified
- Identifying Sire and dam can increase the accuracy of the ASBV by 15% in comparison to no pedigree
- Many non-genetic factors can only be accounted for when the Dam is identified.

Impact of Amount of Information Recorded on Breeding Value Accuracy

![Impact Graph](image)

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Why Should Commercial Producers Improve Lean Meat Yield?

*Charlie Shadwell Farrer Memorial Agricultural High School, Year 10, Wool Science Student*

Lambs are normally sold on farm or in saleyards on a per head basis and/or direct to processors on carcase pricing grids, using weight and fat tissue depth. These measures are poor predictors of final carcase Lean Meat Yield Percentage (LMY %) and value to the customer is not distributed accurately along the value chain. This results in unclear market signals to producers, because the price grids have no capacity to reflect value to the end consumer.

For producers at present, LMY % is not commonly measured or paid for, however there are good reasons why producers should aim to improve the LMY % of their flock. Across a number of breeds, research has shown that fast growth and high muscle sires produce progeny with better feed conversion efficiency. These lambs will reach target weights quicker, requiring less feed thus reducing production costs. In addition, these lambs can be finished to heavier weights without becoming overly fat and accruing penalties. This results in larger margins and higher profits to the grower.

Improvements in LMY % will become increasingly more important for producers if processors and retailers can easily measure and therefore provide clear market signals discriminating for fat. With the advancements in new agricultural technologies LMY % testing equipment for example Hyperspectral imaging (HSI) will become cheaper and easier for processors to use. With the introduction of technologies like this, rapid changes will be implemented with price signals quickly passed onto producers.

The new Lamb Eating Quality (LEQ) index developed in May 2016 will lead to improved eating quality while increasing LMY %, provided stud producers are carrying out genomic testing on young rams. Genomic testing provides increased selection accuracy on key carcase and eating quality traits such as intramuscular fat and shear force, which enables breeders to partly overcome the antagonism between LMY % and eating quality. LMY % will boost commercial producer’s profits, allowing them to grow and turn off prime lambs quicker and cheaper.

Producers should be aware that processors will soon reward by paying premiums for lambs with higher saleable meat yield.

As an example, the figure shows two (2) carcases from the Sheep Co-operative Research Centre (CRC) flock that had similar carcase weight (23.0 and 23.6kg) but different fat scores (2 and 4 respectively) and considerable differences in GR fat (110mm from the mid-line over 12th rib on the sheep) and saleable meat yield. The fat score 2 lamb had 10mm fat at the GR site and 56% saleable meat, whereas the fat score 4 animal had 20mm fat and 48% saleable meat; the leaner animal produced 2kg more lean meat than the fat animal.

Resource Flock

The resource flock plays a crucial role in the successful use of genomics to predict breeding values. In the past the genomic information from DNA tests has been used to develop research breeding values (RBVs). In 2016 Sheep Genetics moved to a single step analysis for carcase traits and are working towards a full single step analysis. This means that performance, pedigree and genomic information can be analysed in one single step and produce more accurate breeding values. Eating quality traits are now calculated using 16 years of correlated trait information and the data coming from the resource flock.

The resource flock uses semen from sires nominated by breeders. The resource flock does not work like a progeny test as it aims to have progeny born from the most diverse range of sires. There are only a small number of progeny born from each sire, as it aims to sample genes rather than sire lines. The progeny have all performance traits measured and are genomic tested with a 50k test. While sires are tested with a 600k test.

The diversity of genetics in the resource flock is utilised to identify DNA sequence variations that relate to performance for traits of interest. When an animal is DNA tested the patterns of the SNP’s are compared to the patterns of individual animals in the resource flock. Once we identify the animals that are most closely related by the SNP’s, the performance that is measured on the resource flock animals can then be used to predict the performance of the DNA tested animals. It is important to note that in order to make genomic predictions the resource population is a necessity.

The key benefit of submitting sires to be used in the resource flock is a stronger relationship can be achieved between your animals and resource flock progeny. The more closely related the animals are to the resource flock, the more similar the genes they carry meaning a more accurate prediction can be made for the traits of interest. This means higher accuracies for breeding values where genomics are contributing. Linkage can also be improved when submitting sires to the resource flock as these animals are compared to a diverse range of genetics in the same contemporary group.

Quick Facts

2016
- 2374 ewes inseminated across 4 sites
- Resource flock combined data collected on research stations and commercial farms

2015
- All rams used were genotyped with a 600k SNP test
- Phenotypic measurements were taken on 2138 animals

2014
- Slaughter data was recorded for 1829 lambs
Understanding Carcase and Eating Quality Traits

Sheep Genetics report ASBVs for a number of carcase traits, including eating quality traits that can be estimated through using genomic information (DNA samples). As eating quality becomes increasingly important to consumers, it is important that we balance both carcase traits and eating quality traits in our breeding programs.

<table>
<thead>
<tr>
<th>Trait</th>
<th>DRESS %</th>
<th>LMY %</th>
<th>IMF %</th>
<th>SF5 kg</th>
<th>EMD mm</th>
<th>FAT mm</th>
<th>CCFAT mm</th>
</tr>
</thead>
<tbody>
<tr>
<td>ASBV</td>
<td>2.0</td>
<td>2.4</td>
<td>-0.1</td>
<td>-0.5</td>
<td>2.2</td>
<td>-1.0</td>
<td>-1.2</td>
</tr>
<tr>
<td>Acc</td>
<td>52</td>
<td>62</td>
<td>50</td>
<td>45</td>
<td>70</td>
<td>68</td>
<td>51</td>
</tr>
</tbody>
</table>

- **Dressing Percentage**: Rams with more positive dressing percentage (DRESS) ASBVs produce lambs that have a higher dressing percentage at slaughter. A ram with an ASBV of 2.0 will produce progeny 1.0 percent higher than progeny of a ram with an ASBV of 0.

- **Intramuscular Fat**: Intramuscular fat (IMF) is a measure of the chemical fat percentage in the loin muscle of a lamb and is often referred to as marbling. IMF has been shown to have a significant impact on the flavour, juiciness, tenderness and overall likeability of lamb. Rams with more positive Intramuscular Fat (IMF) ASBVs produce progeny with higher levels of intramuscular fat.

- **Eye Muscle Depth**: Eye Muscle Depth (EMD) ASBVs estimate the genetic difference between animals in eye muscle depth at the C site. Rams with more positive ASBVs for EMD will produce progeny that have more muscle, independent of weight, and a higher lean meat yield. EMD is reported as Weaning (WEMD), Post Weaning (PEMD), Yearling (YEMD) and Hogget (HEMD) ages.

- **Fat Depth - C Site**: Carcase C site fat (CCFAT) ASBVs estimate the genetic difference between animals in fat depth at the C site, as measured on the carcase. ASBVs for CCFAT are calculated through genomic information. A ram with an ASBV of -1.2 will produce progeny 0.6 mm leaner than progeny of a ram with an ASBV of 0.

- **Lean Meat Yield**: Rams with more positive Lean Meat Yield (LMY) ASBVs produce lambs that have a higher Lean Meat Yield percentage at slaughter. Lean meat yield is expressed as a percentage of the initial Hot Standard Carcase Weight. All bone and salvage fat is removed. A ram with an ASBV of 2.4 will produce progeny that are 1.2 percent higher than progeny of a ram with an ASBV of 0.

- **Shear Force (5 days)**: Shear force is a measure of the force or energy required to cut through the loin muscle of lamb after 5 days of ageing, the ASBV is reported in deviations of kilograms of force. Rams with more negative SF5 ASBVs produce lambs with more tender meat.

- **Fat Depth - GR Site**: Rams with more negative FAT ASBVs produce progeny that are leaner. FAT ASBVs estimate the genetic difference between animals in GR fat depth. FAT is reported as Post Weaning (PFAT), Yearling (YFAT), Hogget (HFAT) ages and Carcase (CFAT) ages.

- **Note**: A useful rule of thumb for converting ram ASBVs into production differences is to simply halve the ASBV (as rams contribute half the genetics of the lamb)

- **Accuracy** – published as a percentage, is a reflection of the amount of effective information that is available to calculate the ASBV. All ASBVs are now published with accuracies. The higher the percentage, the closer the ASBV is to the true breeding value of the animal. Breeding values without accuracies are Flock Breeding Values (FBVs) and can only be compared within the flock.
Recording the full distribution of the flock

Being impressed by your best sheep is always a good feeling, and often many will only want to tell us about their favourite or best performing. However are you doing your best sheep any favours?

When recording a year drop of lambs it is important that we know about the full distribution of animals. When all animals in the year drop are recorded we can analyse the full distribution of the genetics in the flock, understand which genetics are really the best, what the average is and which animals are the lowest performing. Because breeding values are based on how much an animal varies from the average of the group, only recording a selected cohort of the animals causes biased and misleading data to contribute to the breeding values. If all animals are not recorded, or only the best performers are recorded, we have a biased cohort of data. This misrepresents the genetic potential of animals and makes the better performers not look as good.

In the example below we have a year drop of animals and the average weight is 45 kg. This represents a normal distribution of all animals recorded. The difference between the average of the drop and the best performing animal is 6kg. Therefore the best animal is said to be 6 kg better than the average of the year drop. If we were only told about the better animals the average of this cohort would become 49kg and the best animal would only be 2kg better than the average

As we know, not all animals can be kept for all their life and be recorded, especially in the male proportion of your flock. This way we have the most diverse range of genetics to make comparisons against at any age stage measurement.

An alternative approach includes:

1. Before classing animals out take as many measurements as possible.
2. Record as per normal with remaining males
3. Utilise the Cull and Commercial ID’s to submit data of ‘culls’ to Sheep Genetics to help the ‘keepers’ ASBVs (Cull and Commercial animals are not charged, if correct procedure from the QA Manual is followed)
4. Record the full distribution of the sisters (ewe drop)
Adult weight and Condition Scoring

Adult ewe size has become an important subject for producers as costs of feed and labour are higher with larger ewes. Feedback from breeders during the Maternal Index review was unanimous that the breeding objective is to maintain or even decrease adult ewe weight. The relationship between liveweight at different age stages is very strong, so as long as we select animals for greater early growth we will increase adult liveweight. Unless we measure adult weight and select the animals that we can identify as ‘Curve Benders’.

The amount of gain that can be made through selection decisions towards your breeding objective depends on your selection accuracy, intensity and generation interval. It is because of this that Sheep Genetics recommend all traits within your breeding objective are measured, increasing the accuracy of the ASBVs and consequently your selection accuracy and gain. This is fundamental when considering traits that different responses are desired at different age stages, such as liveweight.

Figure One: The demonstrated relationship between liveweight and age, with and without measuring at later age stages. (Graph not to scale)

Adult weight is treated as a repeat measurement, meaning any measurements taken between 2 to 6.5 years of age can be used in the analysis. A common question Sheep Genetics gets is ‘when should adult weight be measured?’ Although adult weight can be measured at any time of the year, the information can be useful for not just the estimation of an AWT ASBV. If taken pre-joining the live weight can be utilised for reproduction information as well as aiding management decisions that are recommended by Lifetime Ewe Management.

Lifetime Ewe Management has demonstrated that a ewe’s liveweight and condition can have a huge impact on lambing percentage. Liveweight and condition scoring during joining can be recorded and submitted to Sheep Genetics through the Mating Module in your software. It is important to note that Condition Scoring is different to Fat Scoring. Condition scoring is done by feeling from the spine over the short ribs. If you are condition scoring and submitting this information to Sheep Genetics, please make sure that your scoring lines up with the scoring system described over the page.
The National Livestock Genetics Consortium has been developed to increase collaboration and to accelerate genetic gains within the livestock industry. As genetics has cumulative effects across the entire supply chain it is critical that the NLGC achieve the vision of improving the impact of genetics investments with the focus on delivering transformational technologies to the Australian livestock industry. The NLGC has a skills based task force consisting of researchers, producers (beef and sheep), breed societies and production sector representatives, heading the project to deliver effective RD&A outcomes for industry. The skills base task force is responsible for analysing projects, delegating funds and presenting projects to the right organisations for collaboration. This will ensure the right people are working on projects, funds are effectively divided across genetics projects and species and research projects are not duplicating resources. The collaborative coordination of these projects aims to double the rate of improvement in industry genetic value by 2022.

What does this mean for Sheep Genetics
Sheep Genetics is not directly involved in the NLGC. The NLGC provides a platform for genetics research to be supported and facilitated through funds. Research that takes place will feed through into Sheep Genetics in terms of implementation of new technology and the adoption of these technologies. Anyone who has genetics research projects in mind or proposals developed are encouraged to present these to the NLGC. These projects will ultimately assist in the exploration of disruptive technologies to accelerate productivity gains and data delivery in the livestock industry.
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
Hamish Chandler
Fiona McLoughlin
Nicole Williams

LAMBPLAN
Clara Collison
Stephen Field

MERINOSELECT
Caris Jones
Ermias Zerazion

Technical Committee
Dr Rob Woolaston (Chair)
Dr Rob Banks - AGBU
Dr Daniel Brown - AGBU
Dr Andrew Swan - AGBU
Dr Kim Bunter - AGBU
Mr Neil Judd - AWI
Mr Richard Apps - MLA
Dr Julius Van Der Werf - UNE
Dr Sam Clark - UNE
Mr Sam Gill - MLA
Dr Ben Hayes - UQ
Dr Sue Mortimer - NSW DPI
Mr Mark Mortimer - Industry
Mr Hamish Chandler - Sheep Genetics

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

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