



The Breeder's Bulletin

Edition 1, 2019



Genetic Evaluation enhancements to be implemented May 2019



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2019 Regional Forums

Why Attend a Regional Forum?

Every year Sheep Genetics offers a series of Regional Forums nationwide. These forums are a fantastic opportunity for breeders to talk directly with Sheep Genetics staff, plus hear about the latest updates to the analysis and ways to get the most out of their breeding program.

All Sheep Genetics members are encouraged to attend these forums and feedback every year from participants has shown that the forums have provided highly useful information for their breeding programs.

In a recent analysis of data, the average genetic gain of flocks that attended a regional forum was investigated. On average across the Terminal, Maternal and Merino analyses after a flock had attended a regional forum their index trend (or the number of index points they gain per year) increased at a greater rate than those who did not.

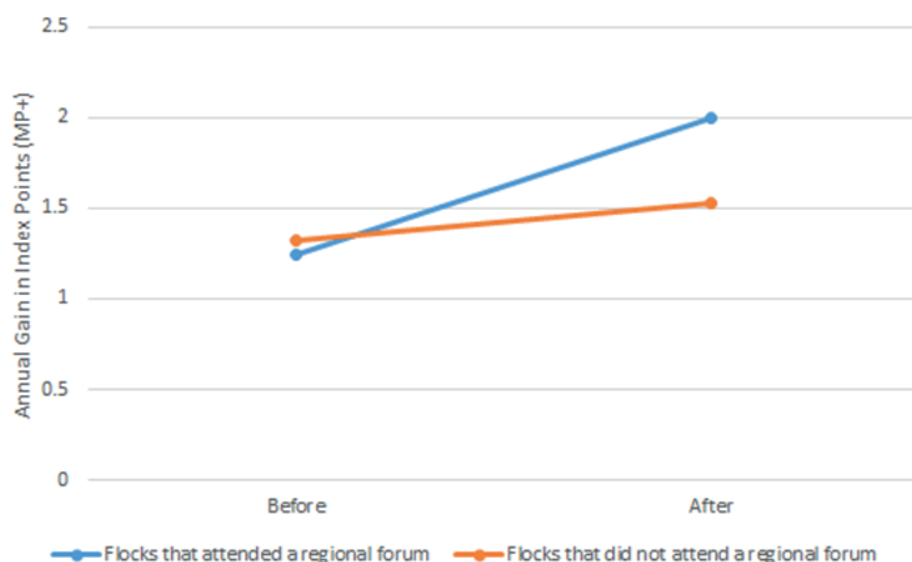
Below illustrates the rate of gain on the MP+ index before and after Merino breeders attended a regional forum in comparison to those that did not.

This year Sheep Genetics will be hosting 5 regional forums. These forums will be held at the following locations:

- 16th May – Glen Innes, NSW
- 23rd May – Bendigo, VIC
- 30th May – Wagga Wagga, NSW
- 6th June – Adelaide, SA
- 11th July – Perth, WA

Please see enclosed flyer for more information.

Change in the rate of progress flocks make depending on if they attend a regional forum



Sheep Genetics is calling for expressions of interest from Service Providers regarding hosting workshops between the Sheep Genetics team and their clients. These workshops aim to provide a half-day session tailored to the key themes of interest for the group of breeders.

The workshops would:

- Be held around a Regional Forum, in the same area and in the days prior to or following the event.
- Have pre-determined content areas that you would like the team to address.

If you would like to take advantage of this opportunity to facilitate interaction between Sheep Genetics and your clients, please contact Emma McCrabb (emccrabb@mla.com.au or 02 8055 1829). Expressions of interest are required at least 3 weeks prior to the Regional Forum being held in the location of interest.

Gestation Length Variation and Sire Parentage

Are you determining sire parentage by leaving a gap between single-sire matings? Is this gap long enough to accurately assign sire?

Having incorrect pedigree has significant impacts on the animal's breeding values as not only are we incorrectly assigning a parent but also relatives i.e. half-sibs.

A form of allocating sire parentage is to leave a gap between single-sire mating and the back-up sire, meaning there is a window where there are no rams with the ewes. The corresponding lambings, based on gestation length, allow progeny to be assigned to sires.

The Sheep Genetics recommendation for how long this gap should be is a minimum of 10 days between sires, although where possible a gap of 14 days is more desirable. This recommendation stems from analysis of the gestation length which breeders are submitting to Sheep Genetics. This gestation length can be collected when mate date (for example in an AI program) and date of birth are known.

Analysis of the terminal sire database for lambing ease and gestation length has found the average gestation length to be 147.4 days, however, most notably; the accompanying standard deviation is 2.3 days. The standard deviation reported in the paper refers to one standard deviation. What this translates to in practical terms is that although the average gestation length is

147.4 days, we should expect over 30% of lambs to be born outside a 145 to 150 day window (the average \pm 2.3 day).

Therefore, in order for us to expect to assign 95% of progeny with correct sire (two standard deviations either side of the mean), we need a gap of 10 days. The "ideal" situation of a 14-day gap allows for three standard deviations from the mean, which is 7 days, therefore expecting to capture 99.7% of progeny with correct sire.

Although these figures are based upon analysis of the terminal database, it is important to note that similar results in the standard deviation of gestation length have been seen in all breeds, including both maternal and merino. Therefore, the gap between initial single-sire mating and back up mating needs to allow for this variation in gestation length.

Strategies to help allocate accurate sire parentage:

- As recommended, leave a gap of at least 10 days, ideally 2 weeks, between single-sire mating and back up sire mating to ensure that almost all lambs are being assigned the correct sire parentage.
- Alternatively, leave a gap less than 10 days, however DNA parentage test the lambs born \pm 7 days from the change of sires in the overlap.

2019 Enhancements to the Genetic Evaluation

The LAMBPLAN and MERINOSELECT analyses are continually being developed to improve the genetic evaluation and supply the best tools possible to producers to help improve genetic gain across the sheep industry. Major enhancements to the evaluations are implemented once a year to minimise any disruption that may result from the changes. A summary of the analysis enhancements can be found below, more detailed documentation of the changes can be found on the Sheep Genetics website: <http://www.sheepgenetics.org.au/Updates/Analysis-changes>.

It is important to understand the enhancements that have been made to the analysis and why you may see some changes in the breeding values of some animals as well as how these breeding values and indexes are being reported. All updates detailed below will be added to LAMBPLAN on the 1st May run and MERINOSELECT on the 7th of May.

These enhancements are so that Sheep Genetics can deliver better breeding values on more animals back to you!

This year the key developments are:

1. Reproduction Research Breeding Values (RBVs) for maternal breeds.
2. Genomic information being included for additional breeds.
3. Reporting of inconsistencies between pedigree and genomic information back to breeders.
4. The new Terminal Carcase Production index and the phasing out of Carcase Plus and LAMB2020.
5. The new Maternal Wool Production Plus (MWP+) index.
6. New index documentation for all indexes and analyses

1. Reproduction Research Breeding Values (RBVs)

Breeds/Analysis Affected: Maternal analysis only – Coopworth, Border Leicester, and Composite Maternal

Type of Change: New breeding values

Key Points:

- Number of Lambs Weaned is the primary trait used in selection of reproductive performance, however this trait is a compound trait that combines many stages of the reproductive cycle
- There are now 3 new component traits available that will be released as RBVs. These are conception (con), litter size (ls) and ewe rearing ability (era)
- This gives breeders the opportunity to target the component traits of reproduction that they are interested in
- There will also be additional traits released for Maternal Behaviour Score (MBS) and Condition Score (CS)

Detail:

The 3 new component traits for reproduction will be available for both yearling and adult stages where yearling traits are reported with a “Y” in front of the trait abbreviation (e.g. YCON). These traits will be available in a unique set of reports that are sent out with the analysis results and will be reported on the website in purple, as they are RBVs not ASBVs. RBVs, like ASBVs can be used to compare all animals that have a value displayed on the website. In addition to these component traits maternal behaviour score and condition score will also be reported as RBVs on the website. Please note that these are RBVs and in due course when developed into ASBVs might be subject to some change. Furthermore, the genetic linkage between flocks for some traits is lower than ideal and more confidence should be placed on comparisons within flocks rather than across flocks.

The definitions of the new traits are outlined in the table below:

Trait	Abbreviations	Unit of Breeding Value	Trait Description	Example
Conception	YCON/CON	%	The ability of ewes to get in lamb in comparison to all the ewes in the same joining event.	Sires that have a higher conception breeding value will produce daughters that have a higher conception rate.
Litter Size	YLS/LS	%	The number of the foetuses a ewe has in comparison to all the ewes that got in lamb.	Sires that have a higher litter size breeding value will produce daughters that give birth to more lambs.
Ewe Rearing Ability	YERA/ERA	%	The ability of the ewe to rear the lambs that she gives birth to.	Sires that have a higher ewe rearing ability breeding value will produce daughters that rear more of their litter.
Maternal Behavior Score	MBS	Score	The raw trait for maternal behavior score is measured on a 1 to 5 scale. Where a ewe with a 1 score does not move from the birth site of the lamb during tagging, therefore a lower breeding value is desirable.	Sires with more negative breeding values will produce daughters that do not move as far from the birth site.
Condition Score	CS	Score	The condition score of the ewe at joining.	Sires with a more positive breeding value will produce daughters that have a higher condition score at joining.

2. Genomic Information for Additional Breeds

Breeds/Analysis Affected: Composite Maternal, Coopworth, Corriedale, Dorper, White Dorper, Hampshire Down, Southdown, Suffolk and Texel.

Type of Change: Additional information being used in the analysis.

Key Points:

- Until now the only breeds that have had genomic information included in the analysis are Border Leicester, White Suffolk, Poll Dorset and Merinos.
- Technical advancements in the analysis have now meant that genotypes from some other breeds can be included in the analysis.
- For many of these breeds the additional benefit from genotyping their animals will be very minimal at this stage.

Detail:

The breeds listed are now able to submit genomic data that will be used in the evaluation where previously genotypes from these breeds have been excluded. However, for most of these they will receive little to no benefit from genomic information now being used in the evaluations. This is because there are not enough animals in the reference population (animals with a genotype and a phenotype) that underpins the genomic evaluation.

These breeds will also be required to test on a higher density platform greater than the 15K platform that White Suffolks, Poll Dorsets, Merinos and Border Leicesters use. If you are one of these breeds that are interested in genotyping to develop a reference population, please contact Sheep Genetics for more information and advice about the density of platform to use.

3. Reporting of inconsistencies between pedigree and genomic information

Breeds/Analysis Affected: All breeds with genomic information being used in the evaluation.

Type of Change: New report.

Key Points:

- The genetic evaluation now uses information on animals' relationships from both pedigree information supplied by breeders through their software and if available, genomics (note: genomics does not refer to DNA parentage).
- Sometimes there are discrepancies where the sire or dam listed in the pedigree of the animal does not match with the relationships inferred from the genomic information.
- There is now a new report where these inconsistencies between pedigree and genomic information will be reported to breeders.

- Breeders can use this report to check their information and work with Sheep Genetics to rectify the inconsistency.

Detail:

Attached to the analysis results email there will be an additional PDF that outlines any inconsistencies between pedigree and genomic information. Where possible the correct parent will also be recommended (if the potential parent also has a genotype). It is advised that breeders carefully look through this document to determine the cause of the errors and if the suggested parent is possibly the correct one. It is important that the breeder confirms the mistake and it is their responsibility to correct it. There is documentation on the analysis updates page that describes how to interpret these reports.

4. The new Maternal Wool Production Plus (MWP+) Index

Breed/Analysis Affected: Maternal – in particular Corriedales and SAMMs.

Type of Change: New index.

Key Points:

- The Dual Purpose Dollar (DP\$) index was out-of-date and was therefore reviewed.
- The Maternal Wool Production Plus (MWP+) is the new index that will replace DP\$.
- MWP+ has a focus on improving wool quality and quantity whilst simultaneously improving reproduction and carcase traits.

Detail:

Maternal Wool Production Plus (MWP+) is the new replacement index for the Dual Purpose \$. It has a focus on improving wool quantity and quality, whilst also focusing on growth and reproduction as key traits in the index. This will be the primary selection index for Corriedale and SAMM breeders as well as for maternal breeders that have a strong focus on wool quality. The index will be reported on the maternal search site as well as on the specialised search pages for Corriedales and SAMMs. Further information can be found in the updated index documentation on the Sheep Genetics website.

5. The new Terminal Carcase Production (TCP) Index and the phasing out of Carcase Plus and LAMB2020

Breed/Analysis Affected: Terminal.

Key Points:

- Carcase Plus and Lamb2020 indexes were designed to select solely for lean meat yield and as a result are reducing eating quality. Carcase Plus, when used with genomics results in eating quality declining at a faster rate.
- Carcase Plus and Lamb2020 are over 15 years old and now out of date indexes.
- Terminal Carcase Production is the new index designed to replace Carcase Plus that focuses on improving the key production traits of growth and muscle whilst simultaneously maintaining eating quality.
- LAMB2020 no longer exists, whilst Carcase Plus will be available for this year only to assist in the transition period.
- Resources will be available to assist breeders and their clients adapt to the changes.

Detail:

The TCP index continues to deliver genetic gain that reflects the current supply chain price signals. The predicted response for muscling and growth will continue to increase, however overall consumer liking will cease to decline. The emphasis on each trait is balanced by its relative economic value to a terminal lamb production system, making Terminal Carcase Production an economic index.

It is worth noting that TCP is in different units to Carcase Plus. This means that the average index values and the variation between animals will be different. Therefore, it is important that both ram breeders and commercial ram clients re-benchmark themselves to the new index values.

Sheep Genetics recognises that phasing out Carcase Plus will be a significant change for the industry. Therefore, for the period between April 2019 and April 2020 Carcase Plus will still be available. TCP will replace Carcase Plus as the primary index on reports but it will still be available this year for ram sale catalogues and to assist in the transition to TCP. It is strongly encouraged that ram breeders begin working with their ram clients this year whilst both indexes are available to transition to the new index, as Carcase Plus will not be available for the 2020 ram selling season. Furthermore, we will be providing resources for industry to use. These include:

- Flyer for stud breeders – outlining the changes in greater detail.
- Flyer for commercial ram buyers where changes are outlined that breeders can use in their communication.
- Updated commercial ram buyer index documentation so that the indexes available are more clearly outlined (please see point 6 for more detail).
- Webinar – this video will be available online as a resource that clients can be referred to.

6. New Index Documentation

Breed/Analysis Affected: All.

Type of Change: New documentation.

Key Points:

- The previous index documentation on the Sheep Genetics website was not consistent across analyses.
- In addition, the previous documentation did not meet the needs of both the commercial ram buyer and the seed stock breeder.
- This documentation has now been redeveloped so that:
 1. The messaging is consistent across all documents
 2. There is a commercial ram buyer version and a seed stock breeder version.

Detail:

The updated index documentation will be housed on the Sheep Genetics website under the “Getting Started” tab.

The commercial version of the document is aimed at allowing commercial breeders to identify what index best suits their production system so that they can use it in their ram purchasing decisions. There will also be a section on how to best use an index in ram buying decisions. This documentation will be a useful resource for seed stock breeders to use in their communication with clients.

Furthermore, there will be new documentation that outlines more detail about the trait contribution for the indexes as well as the recording assumptions for each of the indexes that is targeted at Sheep Genetics clients. This will allow them to best identify a selection index that matches their breeding objective and program.

2019 Scanner Accreditation Workshop

The 2019 Scanner Accreditation was recently held in Armidale and Guyra. The sheep and facilities were kindly provided by a local commercial producer.

The accreditation ran over three days, with the first day involving set up, and a Sheep Genetics discussion about the importance of carcase scanning in genetic evaluation. Scanners were examined on the second day with 40 sheep scanned twice randomly and their fat depths and eye muscle depths recorded. Those sheep were then taken the following day to the University of New England to be computed tomography (CT) scanned between the twelfth and thirteenth ribs.

There are minimum correlation and residual standard deviation thresholds that must be met on their repeated measurements of all 40 animals in order for scanners to become accredited.

The correlation between the CT scanning and each individual scanner was also analysed with good results on the day. This indicates that ultrasound scanning is still a reliable predictor of muscle and fat depth in relation to CT scanning - the gold standard.

The topic of scanning in the drought was brought up for discussion with the scanners. While sheep may not be as heavy, it is the variation which is important for genetic evaluation. Scanners were urged to ensure that sheep meet the minimum requirements for scanning

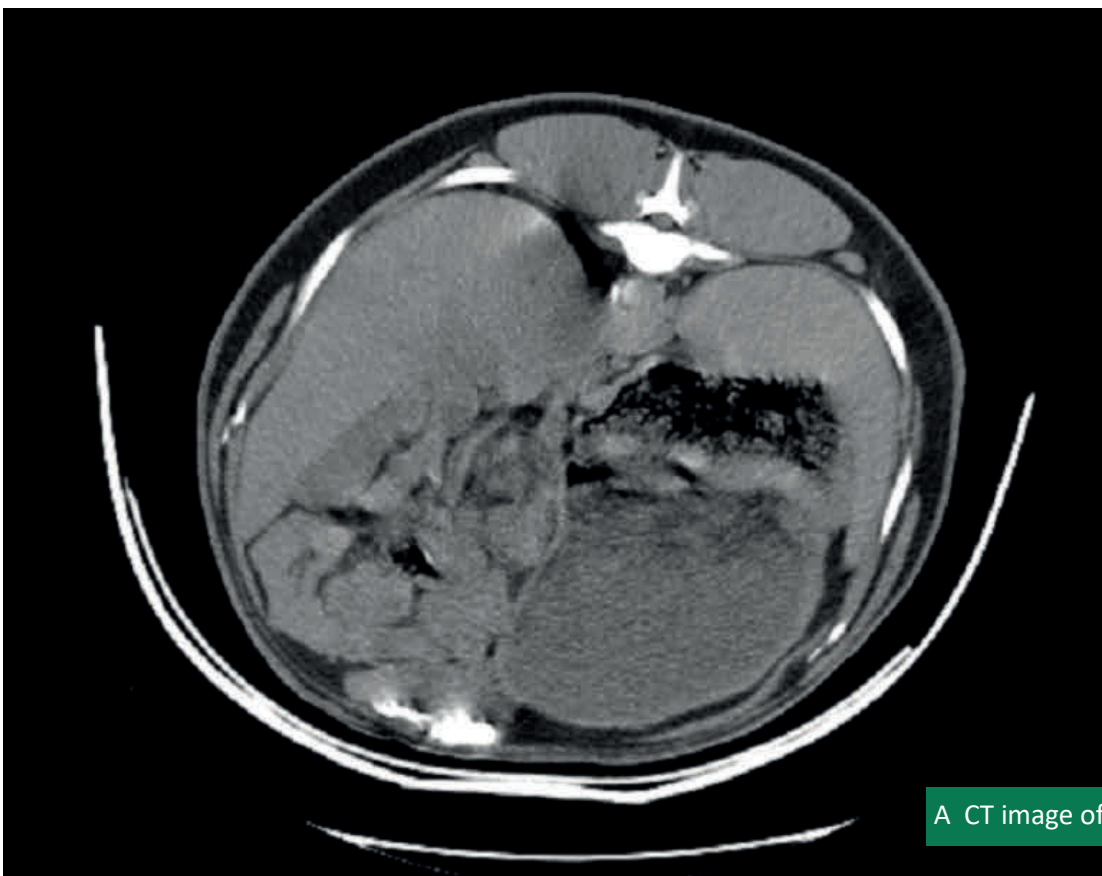
which are:

- Each individual animal weighs a minimum of 30kg.
- There must be on average, greater than 1.5mm of fat depth.

The heritability of fat and muscle has been found to be higher in groups of sheep that meet these requirements and have good variation.

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

It is a strict requirement of the Sheep Genetics Breeders Quality Assurance Guide that all Australian carcase scan information be recorded 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. You can confirm your scanner is accredited by checking the Sheep Genetics website. A current list is included on the following page.



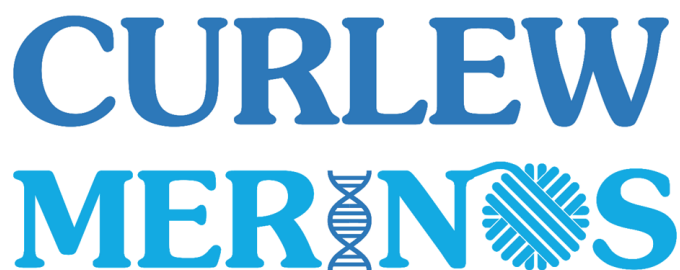
A CT image of the C site on a sheep

Accredited Scanner List

Name	Status	Location	Telephone	Email
Trevor Pearce	Accredited	Young NSW	Mob: 0428 993 061	tpscanning@gmail.com
Tim Lawrence	Accredited	Armidale NSW	Mob: 0419 147 419	timlawrence1974@gmail.com
Jake Burey	Accredited	Holbrook NSW	Mob: 0427 507 409	jburey01@gmail.com
Ric Power	Accredited	Goulburn NSW	Mob: 0437 131 925	richard.power@landmark.com.au
Steve Milne	Accredited	Hamilton VIC	Mob: 0428 786 327	sjdjmilne@bigpond.com
Chris Parker	Accredited	Hamilton VIC	Mob: 0429 992 477	info@summitpark.com.au
Ian Bradtke	Accredited	Peterborough SA	Mob: 0407 729 341	ian@lazerline.com.au
Rachel Chirgwin	Accredited	Saddleworth SA	Mob: 0428 600 265	rachel@cvsuffolks.com.au
Nick Lawrence	Accredited	Bordertown SA	Mob: 0447 077 705	pinnaclesuffolks@bigpond.com
Peter Moore	Accredited	Williams WA	Mob: 0427 176 332	scanwest@bigpond.com
Mike O'Neill	Accredited	Noggerup WA	Mob: 0409 684 332	micviconeill@bigpond.com
Tamesha Gardner	Accredited	Kojonup WA	Mob: 0408 001 353	stocksmart@idavale.com
Liz Barby	Accredited	Kojonup WA	Mob: 0419 194 798	liz.barby@gmail.com

Scanner listing can be found on the Service Provider menu on our website.

Breeder Snapshot: Kealys, Curlew



Property name: Curlew

Breed: Merino

Enterprise: 600 merino stud sheep, 12000 self-replacing merino flock, Merino and White Suffolk cross lambs

Location: Edenhope, VIC

Rainfall: 500mm

"We are extremely grateful to these stud breeders for sharing their knowledge so openly and honestly with us."

The Kealy's attribute the success of implementing ASBVs on their merino stud Curlew, to those MERINOSELECT veterans who have helped them along the way. We sit down with Elise Kealy to hear more about how her family are utilising MERINOSELECT in their business.



How long have you been using MERINOSELECT and what was your pathway to getting involved in MERINOSELECT?

We began subscribing to MERINOSELECT in 2012, after participating in a pilot genetics workshop that year.

What are your breeding objectives, and how does it relate to your business direction?

Our business direction is to run a profitable self-replacing merino flock. We aim to breed the most

profitable sheep we can for our western Victorian environment, and our stud provides our commercial flock with the genetics to achieve this goal. Our breeding objective is constantly evolving to incorporate new research and based on feedback from end users, including ram clients, wool processors and meat processors.

What index are you using?

We feel that the MP+ index aligns most closely with

our breeding objective. However, we take the time to individually assess the merits of each animal based on their ASBV's for individual traits, in conjunction with visual classing.

What software do you use?

We use Pedigree Master.

Do you employ a service provider?

No, we handle all our data ourselves, which we think helps us better understand the calculation of ASBV's. We are extremely grateful for the help the MERINOSELECT staff give us when we have queries relating to data submission.

How do you collect pedigree?

Ewes are run as one mob all year round, except at joining and lambing. Ewes are single sire mated, then boxed back together. One week before lambing they are divided back into their sire groups. Ewes are pregnancy scanned to assist in the recording of birth type. Ewes are monitored during lambing, with their individual lambing date recorded. One week post lambing, we manually mother up and tag lambs, boxing all groups back in together. It is not a perfect system, but it currently suits our operation.

Any road blocks you have faced, and how you overcame these challenges?

We have not had any major road blocks, but we have done a lot of liaising with other stud breeders who have been using MERINOSELECT for much longer than us. They have been able to assist us with any questions we have and forestall any problems before they occur. We are extremely grateful to these stud breeders for sharing their knowledge so openly and honestly with us.

We feel that MERINOSELECT has enabled us to make amazing gains in the last few years. The downside of this is that we are now in a situation where it is much harder to continue to improve our flock in all areas at our current rate of gain. We can continue make incremental gains in individual traits, and across multiple traits at a time, but we think it will be a real challenge to make the same leaps and bounds that we have since we first joined MERINOSELECT.

Do you use any other programs or technology in your breeding program?

We have used MateSel this year for the third time and find it to be a great tool. It takes an enormous amount of work out of preventing inbreeding and coancestry and allows you to see the potential results of your matings before they

occur. We have also used genomics the last couple of years to increase accuracy of our stud rams and ensure we are making decisions based on the best information we can get. For data collection and recording we find a Datamars and an XR 5000 to be excellent tools.

How are your commercial clients using the genetic information that you provide them? Do you have any examples of success stories?

For our clients who select on ASBV's, it removes the environmental impact that influences the phenotype of the rams, allowing them to select genetically superior rams. There are also many traits that we are selecting for, such as worm resistance, that cannot be assessed visually, and ASBV's allow people to make genetic gain in these areas.

For our clients who don't select on ASBV's, they too have noticed the change. Prior to implementing ASBV's our genetic gain was quite small. Since we fully adopted ASBV's in 2012 our genetic gain has increased enormously. Clients who don't use ASBV's have commented on how much better their lambs grow out now. We have a long term client who has marked 135% merino to merino. Our shearers have commented on how the sheep are becoming plainer, and we have been able to do this while increasing fleece weight.

What excites you about the future of sheep production?

We have only had ASBV's in our stud flock for the last 6 years and we can see a huge improvement in our stud sheep in this time. We are really looking forward to when the benefits of this are extrapolated out over our commercial flock of 12,000.



L to R: Bernie, Elise and Tony Kealy in the Curlew shed

Custom Index Development

Considering a custom index for your flock? The process of custom index development requires extensive consultation between the breeder, Sheep Genetics and AGBU, and has a timeline of between 8 and 12 months from start to finish. The first step in this process, after approaching Sheep Genetics, is to complete the Custom Index Survey, and provide written confirmation that you would like to proceed.

Due to the outlay of time and resources by staff, Sheep Genetics is introducing two levels of custom index development.

The first is the creation of a new custom index, which upon completion will cost the breeder a total of \$2500. However if during this process the breeder chooses to not move forward with the index, there will still be a cost associated, dependent on time and resources

engaged so far in the process.

The second is a review of an existing index (custom or standard). As the work required in reviewing the index is comparable with the development of a new index therefore the cost associated is the same.

A recurring theme with custom index development is that through the process it can be realised that the index under development is very similar to a standard index. This occurs as the standard indexes are based on current economic figures, and aim to suit a range of production systems. Therefore, Sheep Genetics recommends that unless there is a significant difference between your breeding objective and the standard indexes, that breeders continue to use the current indexes, possibly with additional trait emphasis in selection.

Leading Breeder 2019 Wrap Up

Sheep Genetics held their biannual Leading Breeder conference in Dubbo on the 20th and 21st of March. The conference saw a record number of delegates with over 170 registrations for the conference (the largest ever for a Leading Breeder). Delegates included Leading Breeders as well as service providers operating in the genetics space and hailed from 6 Australian States and New Zealand. The event was themed around *Breeding Sheep for a Future Environment*. There were four sessions that built on the main theme of the conference. Furthermore, the conference was a celebration of the 30 years of genetic evaluation since the birth of LAMBPLAN in 1989. Former Sheep Genetics Manager, Richard Apps who is now the Manager for Co-innovation and Objective Measurement for MLA, chaired the event.

Sheep Genetics' Manager Daniel Brown commenced the first session on Day one by welcoming everyone to the conference and describing the MLA Sheep Genetics Landscape, as well as summarising the main achievements of the 30 years of evaluation. Daniel also covered the space that Sheep Genetics operates in and what is on the horizon in regards to the project scene for genetics and the upcoming analysis changes for 2019. Following on from Daniel was Jamie Heinrich from Ella Matta White Suffolk and Poll Merino Stud. Jamie presented on *The challenges and opportunities with sheep breeding* and drew upon his global experiences and trends that he had seen emerging for

lamb in other countries. He then went onto expand seed stock breeders can be incorporating these decisions into their breeding programs and what were some of the on-farm considerations. The first session concluded with a series of short presentations that were chaired by the MERINOSELECT and LAMBPLAN Development Officers, Emma McCrabb and James Taylor. These short presentations followed by a Q and A panel aimed to provide a key snapshot of where a number of genetics projects are up to. It included presentations from Troy Fischer on the Superwhite Producer Innovation Fast Track Project, Peter Blackwood on the Corriedale Eating Quality Genomics Project, Mark Mortimer on the Merinolink DNA Stimulation Project and Julius van der Werf on the MLA Resource Flock.

The second session *Breeding within an integrated supply chain* did not disappoint and covered the whole value chain from consumer and market trends through to the breeder. Natalie Isaac the Global Manager from the Industry Insights and Strategy team within MLA spoke about how breeders can Target the Global Consumer. Her presentation enlightened the audience about the growing global demand for sheepmeat, where there are opportunities to expand and what's important to consumers that breeders have the ability to select for. Sarita Guy from the Animal Genetics and Breeding Unit followed from Natalie and presented on the data capture and feedback as part of the ALMtech

(Advanced Livestock Measurement Technologies) Project. The audience were enthralled by Sarita's presentation that described the technologies that are being investigated to measure fat depth, eating equality, Lean Meat Yield and capture health traits on carcasses in plants. She also covered how this data may be captured and fed back through the supply chain to provide data on genetically informed animals to allow for better breeding decisions. The session concluded with breeder Phil Clothier from Woolumbool Sheep Studs presenting on how he has been able to breed for consumer outcomes within their flocks whilst focusing on the profit drivers that currently exist in the market.

Following session two, conference delegates attended the dinner. In recognition of the 30 years of genetic evaluation, the dinner celebrated the involvement of all people that contributed pre and post the launch in 1989 as well as those that were part of the formation of Sheep Genetics in 2005. The MC for the evening was Caris Jones, who relished the opportunity to host the event. It was broken into 3 decades 1989-1999, 2000-2009 and 2010-present. After entertaining the audience with the highlights of the decade, milestones in genetic evaluation and an overview of genetic gain, Caris then invited three key people that were involved in genetic evaluation at each stage for a Q and A panel. It was great to have many of the people involved in the early inception attend the dinner and share their insights. The dinner was a great success and was a real celebration of the achievements of the past and a testament to all those involved throughout the lifetime of genetic evaluation in sheep.

Day two started with a session focusing on *Breeding for welfare and reproduction* after the re-cap from the conference MC Richard, Peta Bradley from Sheep Genetics started the session with a snapshot of "Reproduction and Welfare in the Sheep Industry". Peta discussed the current recording levels for these traits in the analyses, how breeders have been able to overcome some of the antagonistic relationships between welfare and reproduction traits and what some of the traits that are going to be become important in the future will be and how will these measured. David Johnston from AGBU provided some outside perspective in his presentation on "Enabling

genetic improvement of reproduction in tropical beef cattle" whilst simultaneously highlighting some of the challenges in recording reproduction in both species but showed what is possible by recording and selecting animals on this information. Following on from David, his fellow colleague Kim Bunter introduced the new reproduction RBVs that will be rolled out in the maternal analysis as part of the 2019 analysis changes. Lynton Arney from Inverbrackie Border Leicester Stud finished off the third session and tied all the concepts discussed into a presentation on breeding, recording and selecting for reproduction traits and how he has achieved this in his stud.

The final session of the conference was *Creating opportunities through genetics* and Sarah Blumer from Murdoch University presented on "Maternal efficiency in future breeding programs" and gave the audience the opportunity to consider the impact of single trait selection on the profitability per hectare as opposed to selecting for traits in a balanced manner. Following on from Sarah, Andrew Swan from AGBU spoke about "Selecting sheep for the future environment" and the

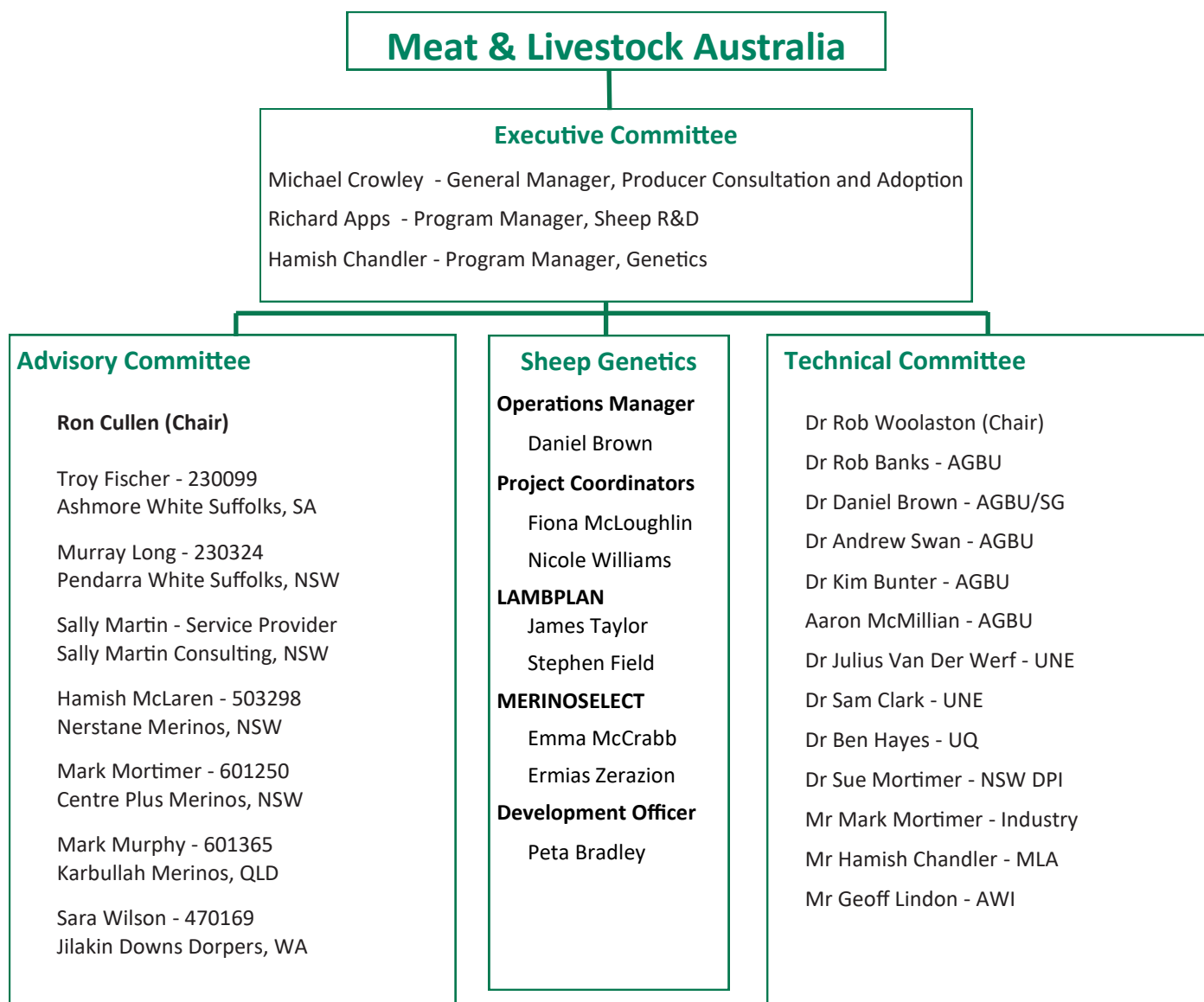
benefits of selection indexes in helping achieve this. One of the highlights of Andrew's talk which was reinforced throughout the conference was that if you want to improve a trait the best way is to measure the trait directly and select for it. Hamish Chandler, Program Manager – Genetics MLA

provoked thoughts in his session "A Resource Flock of the future" getting the audience to consider how the reference population has evolved in the analysis and where phenotype recording will occur in the future. To conclude the conference Clara Bradford National Adoption Manager – Genetics, MLA, got the audience to adopt a selfie and asked them to post it on social media using the hashtag of the forum #leadingbreeder19. Now with a room full of adopters Clara introduced the Genetics adoption campaign including a preview of the advertisement video. She also discussed the breeder's role as part of the National Adoption Plan.

Leading Breeder 2019 was a huge success and Sheep Genetics would like to thank everyone that attended. If you were unable to attend or would like to revisit any presentation from the two days you can access the recorded presentations on the Sheep Genetics website shortly.



Sheep Genetics Organisational Structure



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

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