A decade of Sheep Genetics: what have we achieved?

C.E. Collison¹, D.J. Brown², J.S. Gill¹, H.R. Chandler¹, R. Apps¹, A.A. Swan² & R.G. Banks²

¹Meat and Livestock Australia, University of New England, Armidale 2351, Australia
ccollison@mla.com.au (Corresponding Author)
²Animal Genetics and Breeding Unit¹*, University of New England, Armidale 2351, Australia

Summary

Sheep Genetics (SG) was established to deliver a national across flock genetic evaluation to the Australian sheep industry, including the LAMBPLAN system for terminal sire and maternal breeds, and a newly integrated single across-flock analysis for Merinos. Since its inception SG has continually made significant developments and updates to the evaluations and services it provides. These include the development of new traits, across breed analysis for maternal breeds, utilisation of genomic information, and implementation of single-step genomic methods in routine analyses. SG has also been involved in many extension activities to increase the quality of genetic evaluation data and in the use of Australian Sheep Breeding Values (ASBVs) to increase genetic gain. This paper aims to describe the development of the genetic evaluation, adoption and extension achieved and some of the challenges for SG over the past decade (2007 to 2017).

Keywords: Collison, Sheep Genetics, Genetic Gain

Introduction

Sheep Genetics (SG) has made significant advancements to the Australian national sheep genetic evaluation since its inception in 2005. Combining multiple database (in particular for Merinos) and developing a uniform "language" to describe genetic evaluation for Australian sheep has proven extremely successful and allowed a more streamlined pipeline for delivery of genetic tools and extension activities. SG currently has a total of 1,342 members of which 996 are national and 346 are international, including services provided to breeder organisations in New Zealand, North America, and South America.

Much research has focused on the technical advancements to the genetic evaluation, with the main development work, first outlined by Brown *et al.* (2007), being completed and implemented into the current genetic evaluation. Advances in genomic technologies and development of resource populations (Brown *et al.*, 2018) have seen significant changes to the analyses and these are now incorporated as a key component in the evaluation and in many breeding programs. There have also been some challenges particularly with the implementation of genetic group effects and maintaining data quality and effectiveness.

With the fast moving pace of genetic technologies it is a key priority to support the users. Many extension activities are presented to increase awareness, develop understanding and

continually support both commercial and seed stock producers. This paper describes the development of the genetic evaluation, extension, the level of adoption achieved as well as the challenges for SG over the past decade.

Technical advancements

Estimated breeding values

Since 2005 Australian Sheep Breeding Values (ASBVs) for a range of new traits have been developed including; breech wrinkle, dag scores, adult weight and wool traits, post-weaning age wool traits, ultrasound fat and muscle measurements on animals at 4-7 months of age, improved definition of reproduction traits including for ewe lambs, lambing ease and gestation length. In addition to these, ASBVs derived from genomic reference populations have been delivered for key carcase and eating quality traits such as lean meat yield, intramuscular fat, shear force and dressing percentage. These new breeding values have provided a unique opportunity for ram breeders to select, and make genetic progress for these additional key profit drivers. There has been a clear response from industry with both increased recording of many of these traits and use of new ASBVs at sale time.

Model enhancements

SG has made annual updates to the routine evaluation with the aim of continual improvement to the quality of the ASBVs produced. Over the past 10 years several key model enhancements have taken place which include: combined across-breed maternal runs, adjustment for heterosis, sire by flock interactions, improved reproduction analyses and the implementation of single-step methodology in very large multi-trait analyses (Brown *et al.*, 2018). The implementation of single-step procedures has been a world leading advance, achieving success through collaboration between many organisations, including the Sheep CRC and its partner organisations, MLA and AWI, and international researchers.

Indexes

A range of standard selection indexes have been developed and updated to suit common markets for each breed type. These include:
- Merino: Fibre Production (FP, FP+) with the focus on reducing fibre diameter, Merino Production (MP, MP+) focusing on a balanced emphasis on reduced fibre diameter and increased fleece weight, and Dual Purpose (DP, DP+) with balanced emphasis on meat and wool production.
- For maternal breeds dollar indexes have been updated, producing three standard maternal indexes. These indexes have an important feature in the restriction of adult weight to prevent an increase in mature ewe size, and also have a strong focus on reproduction.
- Terminal sire breeds have four standard indexes, including two eating quality indexes, EQ (Swan *et al.*, 2015) which includes carcase and eating quality traits (consumer eating quality, intramuscular fat, shear force, and lean meat yield) and LEQ which adds birth weight and parasite resistance to the base EQ index. The eating quality

indexes have been well-received across industry with many breeders re-focusing their breeding programs despite the absence (to date) of a value-based payment system for lamb eating quality.

Index development has strengthened the producer consultation process whereby breeder groups are systematically surveyed in regards to their seed stock operations and their commercial client operations. This data is then collated and used to build a breeding objective to model the index. More detail about industry indexes is available at www.sheepgenetics.org.au. Custom indexes are also becoming more widely utilised to assist breeders in achieving specific breeding objectives which vary from those described above.

Genetic Linkage

Genetic linkage between breeds, flocks and years is essential to be able to reliably compare ASBVs across flocks. New tools and reports have been developed to assist breeders quantify their linkage to other flocks. Central test sire evaluations and resource flocks have also contributed significantly to improved linkage. As a result, linkage between flocks is now generally high, with greater than 80% of flocks linked for fleece and weight traits and 65-85% for carcase traits. Reproduction is lower (40-70%) and is an area of future improvement.

Genomics

In a very successful collaborative effort between ram breeders, SG, the Animal Genetics and Breeding Unit (AGBU) and the Sheep CRC, genomic information has been fully incorporated via single-step procedures into the routine SG evaluations (Brown *et al.*, 2018). Breeders now have the ability to obtain moderate to highly accurate ASBV predictions for a range of traits via a SNP genotype (currently 12K imputed to 50K). Genomic evaluations were initially conducted by blending GBLUP genomic EBVs with pedigree based ASBVs (Swan *et al.*, 2012), but that analysis has recently transitioned to a full single-step analysis whereby all information is used simultaneously (Brown *et al.*, 2018). This allows genomics to contribute significantly to the calculation of ASBVs for all traits within the main analyses. Genomics has allowed significant advancements in the selection for eating quality traits as these phenotypes cannot be directly measured on live animals. Limitations still apply, mainly due to insufficient reference populations for small breeds such that reliable predictions are only currently available for the four major Australian breeds (Border Leicester, Merino, Poll Dorset and White Suffolk). In addition, some key traits including reproduction have insufficient reference populations.

Sheep breeders also have access to relatively cheap parentage tests, and there has been an increase in the amount of pedigree information being supplied to the analysis, improving the quality of the ASBVs produced for many breeders.

Adoption

SG has made considerable effort in the last decade to increase adoption and use of genetic tools across the Australian sheep industry. This is demonstrated by an increase in the rate of genetic gain in standard indexes for all of the major analyses (Swan *et al.*, 2017). Not only has the industry made continual genetic progress, there has been an increase in the quantity of participants and the quality of data recorded (Table 1). The animal numbers have increased by 51%, 53% and 85% for Terminals, Merinos and Maternals respectively since 2007. The range of traits available has also increased with 39 Merino and 15 Terminal traits added. The number of records for all of the major trait groups has increased and this is supported by an increase in flocks with data particularly for Merinos.

Table 1. Summary of the SG Database at September 2017.

	LAMBPLAN Terminal Sire	LAMBPLAN Maternal Sire	MERINOSELECT Merino
Animals	2,770,026	2,072,345	2,379,842
Traits Analysed	45	46	76
Flocks in Pedigree	3,893	1,986	1,599
Flocks with Data	1,549	501	476
Linked Flocks (any Trait)	547	171	270
Years of pedigree records	58	53	57
Sires	39,832	25,320	23,184
Dams	725,858	475,826	378,947
Av Generation Interval	2.85	2.78	3.19
Body weight records	5,078,744	3,296,342	3,223,607
Ultrasound scan records	1,650,704	450,182	577,223
Worm egg count records	86,402	105,189	318,980
Wool trait records	9,511	626,559	2,073,321
Reproduction records	120,469	289,125	219,761

Challenges along the way and into the future

Genetic groups in MERINOSELECT

The ability to allow different base genetic merit between flocks and across periods of time is a very import feature of the MERINOSELECT analysis especially in flocks with significant amounts of missing pedigree. However ensuring accurate genetic group estimates has been an ongoing challenge in some large flocks with incomplete pedigree in different tiers of their breeding program. A large research effort has ensued leading to a number of strategies now being in place including; 1) working with ram breeders to ensure their breeding programs are managed to enable reliable ASBVs to be estimated, 2) filtering to remove poorly structured and uninformative data, and 3) careful scrutiny of data quality and linkage during the group allocation process.

Data quality and effectiveness

The effectiveness of the data collected by breeders can be highly variable. This is mainly in relation to the size of the management groups, the amount of pedigree known, and number of sires represented in each group. SG has worked closely with breeders to encourage them to appreciate the importance of data effectiveness. As a result there have been clear improvements across all breeds, especially for traits which are difficult to record such as reproduction.

The amount of pedigree recorded is another key determinate of ASBV accuracy and as with data effectiveness there have been continued improvements on the amount of pedigree information recorded. In the 2015 drop 91%, 75% and 44% of animals in the Terminal, Maternal and Merino analyses respectively had complete pedigree records.

Management grouping is a key challenge for some breeders including understanding the importance of maximising the ability to fairly compare animals head to head, accurately assigning management groups to reflect on farm practices, and invoking practice change to achieve larger group sizes with more sires represented and ensuring adequate linkage across groups.

Recording of reproduction traits has been a barrier in the ability to enhance the reproduction analysis. Although slow, there has been an increase in adoption for reproduction over recent years particularly for maternal breeds. Working with breeders, data managers, and software developers to improve quality and quantity of reproduction traits is a key priority.

Breeder communication and extension

SG conduct a number of extension activities directly and are involved in programs run by other groups. In the past five years 25 regional forums have been run in various locations across Australia and New Zealand. Between 2016 and 2017, 315 breeders/consultants attended one of 12 regional forums, averaging 26 attendees per workshop. These workshops focus on updates to the genetic evaluation, data quality and use of breeding values in breeding programs.

Leading Breeder is a biannual conference held by SG aiming to highlight new developments in genetic evaluation, research, and industry trends across a range of breed groups and wool and meat production systems. The conference is well attended and highly regarded as a calendar event for many breeders.

SG holds an annual service provider workshop to update and expand the knowledge of private consultants working with SG members. Private consultants play a pivotal role in supporting SG members with data management and breeding program design.

Bred Well Fed Well and RamSelect workshops have been run by Sheep CRC and MLA across Australia focusing on the use of ASBVs for ram selection by commercial producers. These workshops have driven the adoption of commercial clients selecting rams with ASBVs.

SG is governed by an Advisory Committee (AC) comprising of the SG Executive, six industry representatives and an independent chair. The AC has been instrumental in shaping the direction of SG and maintaining industry focus.

As part of an ongoing research project to determine the factors which influence the rate of gain of different flocks and how this can be improved, SG in collaboration with AGBU, the Sheep CRC and NSW DPI have released a new report called Ramping up Genetic Gain (Stephen *et al.*, 2018). This report aims to collate the variables that impact genetic gain from the breeders own data, and deliver these in a format allowing benchmarking of flock

performance against industry over a five-year period. The reports are delivered to breeders as a part of SG regional forum workshops. Service providers also have access to the online web version for their SG clients.

Current opportunities to increase genetic gain

SG analyses now have the capacity to utilise ultrasound pregnancy scanning data as a phenotype for number of lambs born (NLB). This increases the opportunity for breeders to obtain NLB records if they cannot identify dam pedigree by traditional methods at lambing time.

Mature ewe size is becoming an industry issue and has recently been added to indexes for maternal breeds. More adult weight data being submitted will enable more precise genetic control of mature ewe size.

Post-weaning wool trait ASBVs are now being calculated, but there is also a general lack of recording of adult wool traits. However, on current evidence genetic correlations between wool traits at different ages are high (Brown *et al.*, 2013).

Lean meat yield and eating quality traits are now calculated as ASBVs due to the implementation of single-step methodology. Selecting for these traits gives breeders the opportunity to find animals that break the antagonistic relationship between eating quality and lean meat yield, and improve the traits simultaneously.

Genomics is widely being adopted across industry with an increase in the numbers of animals genotyped. Genotyping animals allows more accurate selection decisions at a younger age and improves accuracy of hard to measure traits including eating quality and reproduction.

What does the future hold?

SG is currently focusing on improving its operations in a number of areas, including inclusion of abattoir feedback data for carcase traits, a major database re-development, enhanced modelling of reproduction traits, development of decision support tools for design of breeding programs, and improved support for industry consultants to deliver high quality advice for their breeder clients.

Conclusion

Since its inception in 2005, SG has maintained a comprehensive multi-trait genetic evaluation system used by the majority of breeders in the main sheep breeds/types in Australia, along with important overseas users. The service has been steadily upgraded technically, including advances in trait coverage, models for reproductive traits, and in transition to incorporating genomic information (since 2016 through single step). Breeder and producer engagement, through both extension and in-depth consultation, have been a vital part of the evolution of SG. The technical development and industry engagement are reflected in genetic trends in all major breeds which continue to deliver valuable productivity and profitability improvements to sheep producers and value chain partners. The coming years are likely to see further innovation in both analyses and service, with particular emphasis on breeding program design to exploit opportunities opening up via genomics;

continually adapting genetic improvement to the needs of industry. More information can be found at www.sheepgenetics.org.au.

List of References

Brown, D.J., A.A. Swan, V. Boerner, L. Li, P.M. Gurman, A.J. McMillan, J.H.J. Van der Werf, H. Chandler, B. Tier, & R.G. Banks 2018. Single step genetic evaluations in the Australian sheep industry. Proc 11th World Congr Genet Appl Livest Prod.

Brown, D.J., A.A. Swan, & J.S. Gill 2013. Genetic correlations across ages for greasy fleece weight and fibre diameter in Merino sheep. Proc Assoc Adv Anim Breed Genet. 20: 110–113.

Brown, D.J., A.E. Huisman, A.A. Swan, H.-U. Graser, R.R. Woolaston, A.J. Ball, K.D. Atkins, & R.G. Banks 2007. Genetic evaluation for the Australian sheep industry. Proc Conf Assoc Anim Breed Genet. 17: 187–194.

Stephen, L.M., D.J. Brown, C.E. Jones, & C.E. Collison 2018. What the good do well. A look into high performing sheep flocks. Proc 11th World Congr Genet Appl Livest Prod.

Swan, A.A., R.G. Banks, D.J. Brown, & H.R. Chandler 2017. An update on genetic progress in the Australian sheep industry. Proc Assoc Adv Anim Breed Genet. 22.

Swan, A.A., T. Pleasants, & D. Pethick 2015. Breeding to improve meat eating quality in terminal sire sheep breeds. Proc Assoc Advmt Breed Genet. 21: 29–32.

Swan, A.A., D.J. Johnston, D.J. Brown, B. Tier, & H.-U. Graser 2012. Integration of genomic information into beef cattle and sheep genetic evaluations in Australia. Anim. Prod. Sci. 52(3): 126–132.