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Prepared by: Dr Daniel Brown, Dr Andrew Swan, Dr Kim Bunter, Mr Aaron McMillan and Dr Robert Banks
Animal Genetic and Breeding Unit

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Genetic Evaluation for the Australian Sheep Industry: Better targeted and faster genetic gain

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Abstract

Research and development work at the Animal Genetics and Breeding Unit (AGBU) focused on the development of OVIS, the software program used to estimate the breeding values for Sheep Genetics (SG), and its supporting infrastructure.

Research included the estimation of genetic and phenotypic parameters (heritability's, genetic and phenotypic correlations and adjustment factors) required for the OVIS genetic evaluation, and the investigation of alternative models and traits. Development of OVIS and its surrounding infrastructure occurred continually, including; the addition of new traits, inclusion of genomic information, extra reporting functions, diagnostic tools and accommodating changes in data and clients. This report details the research and development work conducted and outcomes achieved.

Results and outcomes of the project were presented and discussed at the Sheep Genetics Technical Committee meetings, in scientific papers, conference contributions, newsletter articles, and at field-days directly interacting with breeders.

Executive Summary

In this project the Animal Genetics and Breeding Unit (AGBU) conducted research and development for OVIS, the software program used to estimate the breeding values, and its supporting infrastructure, for Sheep Genetics (SG) between July 2010 and June 2016.

- Research and development focused on the definition and delivery of the genetic evaluation for SG.
- The major outcome of this project has been to facilitate more accurate selection of breeding animals for the Australian sheep flock. This has been achieved by producing more accurate breeding values for a greater range of traits in a timelier manner. Additional outputs, including breeding value accuracy, inbreeding coefficients and selection indexes assist to improve selection accuracy.
- As part of the SG development process the genetic evaluation system was scientifically scrutinised by a technical committee consisting of leading sheep geneticists and breeders from across Australia. This process included:
 - Comparison of alternative models for existing and new traits and the testing and implementation of new models.
 - Investigations into genetic group allocation and development and implementation of improved methods.
 - Updating variance components and adjustment factors for all breeds.
 - Development of new reporting software.
 - Implementing new systems for routine evaluation including blending and single step analyses to utilise genomic information.
- Development of OVIS occurred continually including; the addition of new traits, extra reporting functions, diagnostic tools and accommodating changes in data and clients. These enhancements and other processes implemented by industry have enabled annual genetic progress to increase in all breeds.
- Delivery of genomically enhanced breeding values via blending and single step methods were key outcomes of this project.
- New software and web site functionality has been developed to provide SG staff and breeders with a range of diagnostic information and reports.
- Results from research were presented in peer reviewed scientific papers, conference contributions, newsletter articles, information forums and at field-days with breeders.
- The software engine to generate SheepObject indexes from OVIS breeding values is in place. Indexes are being routinely generated from OVIS analyses and now all standard SG indexes come from SheepObject. The ability to develop customised indexes for individual breeders is now in place with an integrated web interface available. Results show that customised indexes are robust and mostly highly correlated with standard indexes given the wide range of production systems and sheep enterprises catered for.

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1 Abbreviations

AGBU Animal Genetics and Breeding Unit

ASBV Australian Sheep Breeding Value

GEBV Genomic Estimated Breeding Value

HD High Density genotype (800k)

LD Low Density genotype (12k)

RBV Research Breeding Value

SG Sheep Genetics

2 Background

The Animal Genetics and Breeding Unit (AGBU), which has developed genetic evaluation systems for Australian livestock industries for more than 35 years has a strong sheep genetics research team with a proven track record. For the last 15 years AGBU has been delivering ASBVs for LAMBPLAN and MERINOSELECT on a routine basis using its OVIS software, underpinned by substantial R&D efforts. The AGBU evaluation systems (OVIS for sheep, and BREEDPLAN for beef cattle) are among the world's leading livestock genetic evaluation systems. Sheep genetics research at AGBU supported by MLA and AWI in the 2010-2016 contract (for which this document is the Final Report) has focused on the integration of genomic information in routine evaluations, estimation of the parameters required for OVIS (adjustment factors, heritability's, genetic correlations), development of new breeding objectives and indexes for the main breeds, improved models of evaluation for wool and meat sheep, inclusion of new traits and on the further development of the software, including extra reporting functions, diagnostic tools, introduction of new clients with complex recording programs, and accommodating changes in data for existing clients. Contributions to Sheep CRC, Sheep Genetics extension efforts and routine analysis were also a key part of the project.

This project recognised the need for Australia's sheep genetic evaluation system to encompass new areas and incorporate new methods to remain at the forefront of sheep genetic improvement. This is important to MLA and AWI in achieving their objectives of increasing the rate of genetic improvement in Australia's sheep flocks.

3 Project Objectives

- Accelerate genetic change in the Australian sheep industry through the provision of a world-class genetic evaluation system.
- Develop Australian Sheep Breeding Values (ASBVs) for new traits which improve the specification of breeding objectives.
- Enhance breeding objectives.
- Analysis of breeding program design.
- Industry engagement to increase adoption and genetic gain

4 Methodology

4.1 PROGRAM 1 – Accelerate genetic change in the Australian sheep industry through the provision of a world-class genetic evaluation system

4.1.1 Strategies

- Genomically enhanced sheep breeding
- Estimation of genetic parameters
- Validation of underlying methods and models
- Multi-breed genetic evaluation
- Maintenance of a commercially viable suite of software

4.2 PROGRAM 2 – Develop ASBVs for new traits which improve the specification of breeding objectives

4.2.1 Strategies

- Novel traits and measures examined for inclusion in genetic evaluation
- Expand OVIS to incorporate new traits, as required

4.3 PROGRAM 3 – Enhance breeding objectives

4.3.1 Strategies

- Improved definition of breeding objectives in conjunction with the Sheep CRC
- Delivery of breeding objectives

4.4 PROGRAM 4 – Analysis of breeding program design

4.4.1 Strategies

- Tools for current breeding program analysis
- Calculate cost benefit parameters for additionally recorded traits or information
- Development of new genetic progress reporting software

4.5 PROGRAM 5 – Industry engagement to increase adoption and genetic gain

4.5.1 Strategies

- Engage key sheep breeders
- Breeding Objectives
- Scientific communication
- Ongoing Training

5 Results

5.1 Genomically-enhanced ASBVs

Genomically-enhanced ASBVs were first produced in April 2011. Research Breeding Values (RBVs) for (new) carcass traits were estimated using the single step approach (a more detailed description has been published in the Applied Genomics for Sustainable Livestock Breeding conference, AAABG, and WCGALP14 papers listed below). A strategy for delivery of blended ASBVs for standard ASBV traits in the Sheep CRC “pilot projects” was also developed and implemented.

During the project extensive research and development was undertaken to produce the pipeline for routine delivery of genomically-enhanced ASBVs and RBVs (for new traits), which has been successfully developed and implemented. This pipeline was also modified to accommodate the changes in analyses over time, such as the across-breed maternal analysis and the estimation of indexes using the RBVs rather than ASBVs.

The pipeline also had to be modified to improve the adjustment of RBVs for breed effects (to correct a bias caused by the inclusion of genetic group/breed effects in GEBVs) and update accuracies of genomic predictions (2014).

During the later years of the project work focussed on the development of the “single step” method of incorporating phenotype, pedigree and genotype data in a single analysis for the routine evaluations. This strategy involved many staff from AGBU’s sheep and beef groups working on different aspects of the single step method for introduction into both the OVIS and BREEDPLAN software systems. The work involved many test runs using Sheep Genetics data and variance component estimation software to evaluate models and feasibility. This work led to the official release of single step multiple trait breeding values for carcass and eating quality traits by Sheep Genetics in April 2016.

The feasibility and utility of using high density (HD) genotypes in the current genomic analysis pipeline was investigated. A computing strategy was developed to compute the inverse genomic relationship matrix required for GBLUP (which uses only genomic and not pedigree data) and single step analyses from HD genotypes. While there is an increase in computing time for this step, it is not significant for the overall process, and it would be straightforward to use HD genotypes for GBLUP analyses. However, preliminary estimates of accuracies show there is no significant benefit for the estimation of ASBVs by using HD over the current approach of using 50K and 12K tests.

5.2 New traits

5.2.1 Scan traits recorded at weaning age and repeated weaning weight records

Terminal sire breeders increasingly wish to record carcass measurements at earlier ages than was previously accepted by Sheep Genetics (post weaning was the youngest stage for accepting carcass records). To fully utilize the data provided by breeders, some weaning stage information was being pushed up from weaning into the early post weaning stage, which is a suboptimal work-around.

Once sufficient data were available, research was conducted to evaluate the potential for using weaning scan traits. Fat and eye muscle depths taken between 100 and 200 days of age appear to be heritable, and also moderately to highly correlated with those taken in the more traditional post-weaning period (200 to 300 days). However, preliminary results also suggested that scan traits measured at ages less than 200 days are genetically different traits to those taken later in life. OVIS was modified to add new traits for fat and eye muscle depth traits recorded at weaning age into the analysis.

5.2.2 Post weaning wool traits

Akin to weaning scan traits, many Merino breeders are recording wool traits at earlier ages than was used by Sheep Genetics. Preliminary analyses were conducted to demonstrate the value of these early age records. More detailed analyses were subsequently conducted to both assist development of the new version of OVIS and help the Advisory and Executive Committees make decisions on reporting post-weaning breeding values. A range of research was also conducted to update the genetic parameters for MERINOSELECT.

The changes required were made to OVIS and associated software to add a series of new post weaning wool traits. This system was fully tested and completely implemented into the routine runs.

5.2.3 Additional visual traits

During the project the analysis was expanded to include additional visual traits. OVIS now produces routine ASBVs for 14 visual traits, including breech traits, dag score, and aspects of fleece quality represented by colour, character, weathering and fleece rot.

5.2.4 Additional adult weight and wool traits

During the project the analysis was expanded to include additional adult weight and wool traits. This is described in more detail below in section 5.16.

5.3 Combined across-breed maternal analysis

Extensive research and development was undertaken to develop a combined across-breed maternal analysis. The outcome of this work was the delivery of an updated analysis for each of the maternal within-breed runs, with the view to implement a combined maternal run in March 2012.

Changes made to the routine analyses included;

- Genetic groups defined by breed and time period
- Reproduction and WEC run as independent analyses
 - Reproduction without genetic groups fitted
 - WEC has genetic groups fitted by flock
- Heterosis adjustment, based on breed proportions, is included in all these analyses
- Allocation of dummy dams to accommodate maternal effects for lambs born via embryo transfer
- Base adjustment ~ Australian animals in 2005 were fixed to their previous analysis solutions

A new across-breed analysis was completed and results provided to industry in March 2012 with significant positive feedback received from industry, and became routinely available thereafter.

5.4 Breeding Objective and Index development

5.4.1 New MERINOSELECT INDEXES

New MERINOSELECT indexes were published during 2012, and extensively updated following industry consultation in 2014. These indexes target three production systems: Dual Purpose (DP), Merino Production (MP), and Fibre Production (FP), and in future updates can be managed within this framework. Detailed predictions of the likely outcomes of using the new indexes were also calculated. As part of this work, a new stochastic simulation program for evaluating breeding programs for the Australian sheep industry was written. This program will be a valuable tool for future research.

5.4.2 Custom indexes

Custom indexes have been developed for seven Maternal and Merino breeders during the project.

5.4.3 SheepObject

There are further opportunities to improve the model used by Sheep Object. A discussion paper outlining these was presented to the Technical Committee.

5.4.4 New Dohne Index

A new index was developed, in consultation with the Dohne Council, to better suit their breeding objectives. This index was presented to the breeders for feedback, with the new index approved for implementation in the July 2015 runs. Following a comparison of the parameter estimates estimated from Dohne data with those available for Merinos, it was also recommended to the Dohne Council to use the more up-to-date and complete MERINOSELECT genetic parameters. They also accepted this recommendation and this change was implemented in July 2015.

5.4.5 DPWEC Merino index

DPWEC is an additional index developed for MERINOSELECT as a supplement to the standard indexes. It is based on the DP breeding objective used for the DP and DP+ indexes, with the addition of a reduction in post-weaning worm egg count (PWEC) targeted to contribute 25% to the economic gain. This strategy was based on an assumed measurement program including clean fleece weight, fibre diameter, staple strength (in males), body weight, eye muscle and fat depths, and PWEC.

5.4.6 New LAMBPLAN indexes with emphasis on eating quality

A major outcome of the project was the introduction of eating quality indexes for the LAMBPLAN analyses, underpinned by single step genomic ASBVs for carcass and eating quality traits.

The foundation for this development was an extensive consumer eating quality trial undertaken by the Sheep CRC, based on samples taken from Information Nucleus (IN) animals. Ten samples were taken from both loin and topside portions of carcasses from IN slaughter animals (n=1400+), prepared using a standard cooking method, and then consumed by the taste panels. The taste panel members scored each sample for five traits on a 0 – 100 scale: odour, flavour, juiciness, tenderness, and overall liking. In addition, they scored “overall satisfaction” on a 1 to 5 scale on each sample, analogous to an MSA grade. At the conclusion of the session they also recorded “willingness to pay” for these 1 to 5 grades.

This data has now been analysed by AGBU to estimate genetic parameters and correlations between these consumer panel traits, as well as shear force and intramuscular fat. An eating quality trait was subsequently defined and using some assumptions about impacts of eating quality on carcass price (through willingness to pay data), an economic value was estimated for eating quality.

Two new terminal sire indexes were developed which included emphasis on eating quality. These were released with the new eating quality ASBVs in April 2016.

5.4.7 Comparing terminal sire eating quality indexes

The development of terminal sire indexes including eating quality in the breeding objectives has been outlined in the previous milestone reports, and has now been published (Swan, Pethick and Pleasants, 2015, "Breeding to improve meat eating quality in terminal sire sheep breeds", AAABG Lorne). Predictions of genetic gains in this study were based on genetic parameters estimated from the IN resource flock data. We have now compared indexes on IN animals recorded for all traits (including carcass and eating quality) using EBVs derived from multi-trait single step analyses. Four indexes were compared:

- CPLUS: current Carcass+ index
- LMY: a new SheepObject index including carcass traits such as lean meat yield (LMY), designed as an update of CPLUS
- LMYEQ: LMY with consumer eating quality added as a breeding objective trait
- LMYEQIMF: LMYEQ with extra emphasis to increase intra-muscular fat (IMF)

Single step analyses including all of these traits were performed using all available LAMBPLAN and resource flock data. The validation animals were 877 IN terminal sire progeny which had been part of the CRC consumer eating quality trial. These animals have been genotyped, and have phenotypes for all traits in the table above. Two single step analyses were performed, the first including all carcass trait records on the 877 validation animals (data), and the second excluding their carcass records and the carcass records of their half-sibs who were not part of the eating quality trial. Genotypes of the validation animals were included in both analyses. The comparison of interest between these two analyses is how effective the eating quality indexes are when animals have genotypes and records on all index traits, versus genotypes only (i.e. the likely scenario for a breeder selecting young rams). A single trait analysis of the eating quality trait (topside MSA score, tmsa) was also performed to provide independent EBVs for eating quality for the test animals.

Antagonistic correlations were evident at the trait level, between lean meat yield and the eating quality traits (intramuscular fat = -0.32, shear force = 0.26, and tmsa = -0.08). The index however was favourably correlated with all traits (lean meat yield = 0.26, intramuscular fat = 0.48, shear force = -0.08, and tmsa = 0.09).

The results demonstrate that it is possible to achieve desirable outcomes in both lean meat yield and eating quality, even with the genotype-only analysis. The additional emphasis on intra-muscular fat in the LMYEQIMF index is desirable.

Critical to realised outcomes from use of these indexes are the genetic correlations among carcass and eating quality traits. While the Sheep CRC trials provided a good start, it is hoped that more data will be added from new trials in order to increase the precision of genetic parameters. This is particularly the case for the consumer taste panel eating quality traits, and for lean meat yield.

5.5 Further work on reproduction traits

Reproduction traits have been the focus of considerable work throughout this project.

5.5.1 Redevelopment of the reproduction analysis

Throughout the project a number of key changes have been made to the reproduction analysis:

- Data for direct reproduction records only included for flock/drops which pass data filtering
- Correlations with weight and scrotal circumference reduced to ensure that actual direct fertility data is critical to obtaining breeding values for the fertility traits
- A new program has been developed by AGBU to extract and filter reproduction data for ewes from the pedigree
 - Management groups are no longer inferred from birth weight groups
 - Only flock-drops with reproductive data are included in analyses
 - The filters are currently applied at the ewe level:
 - Fertility $\leq 99.5\%$
 - Survival $\leq 99.5\%$
 - Ewe level filters are based on the proportion of the lambs with dam pedigree known (not the entire drop)
 - Includes service sire cleaning
 - 1 year old ewes must have $\geq 50\%$ fertility in a flock-drop
 - 2+ year old ewes must be $\geq 70\%$ fertility in a flock-drop
 - Conception method of dry ewes (“DRY” lamb tags) is inferred from service sire information
 - Exclusions are applied
 - Ewes with >4 lambs per year are not used
 - Ewes with lambs born more than 1 day apart are not used
 - Ewes with lambs of different conception methods are not used
 - Ewes with lambs at different Sites are not used
 - Ewes with lambs of different Service Sires are not used
 - A detailed summary report of each drop’s reproduction data is also generated
 - Error and exclusion reports are generated, assisting breeders to improve their data entries for both reproduction and lamb characteristics
 - Resulting data are similar to that previously supplied directly from the LAMBPLAN and MERINOSELECT databases
- A new version of OVIS including updated genetic parameters has been developed, tested and implemented.
 - Two new traits have been added with one observation each (yearling number of lambs born (YNLB) and yearling number of lambs weaned (YNLW). Separating yearling from adult performance is necessitated by the fact that the performance of ewes in these age groups is different, both phenotypically and genetically.
 - The 6 existing observations for nlb/nlw were retained to maximise accuracy
 - These now will be used for observations from 2 – 7 yr old ewes
 - Contemporary group definition = flock, year of joining/lambing, ewe age (1, 2, 3+), previously lambled at 1yr old (0 or 1) (adult ewes only) and conception method
 - Season is not included in the contemporary group definition, as there was no advantage from defining season
 - Reproductive traits are corrected for heterosis, estimated for each ewe from breed proportions (limited by missing pedigree)
 - Only flock/drops with reproductive data will be included in reproductive analyses
 - Weight and scrotal circumference from other flock/drops will not be included in the analysis

- Additional data was added from pregnancy scan records

In tandem with Sheep Genetics there has been progress towards enabling software developers to improve their provision of accurate and complete reproductive data to Sheep Genetics. Version 2 of an “xsd” format should facilitate developers to provide extracts which include the reproductive outcomes for all ewes joined.

The longer term strategy is required to further develop an improved reproduction trait analysis. Strategies to improve the quality of data recording in industry flocks have been introduced, including specification of more stringent requirements for flock recording software development. Improvements in data quality will enhance accuracy of ASBVs for reproductive traits, as well as early in life traits for lambs. The improved reproductive analysis will:

- Increase the stringency of data filters, to better identify valid phenotypes for the component and composite reproductive traits
- utilise mating information supplied from breeders to refine contemporary group information, and allow better data validation and models
- Include 3 component traits (fertility, litter size and lamb survival).
- Continue to use pregnancy scan data as a proxy for fertility, litter size and NLB traits
- Include key correlated traits (weight, fat/emd, fleece weight, wrinkle and scrotal circumference)
- Include genomic information

Construction of indexes will also need review as with this new approach not all animals will have a valid NLW ASBV. An index based on component traits is also more transparent and flexible for breeders.

5.5.2 Pregnancy scan records

Analysis of pregnancy scan data has been performed using data from SARDI (research flock-Merino), Bundilla (Industry-Merino), Cashmore (Industry-maternal) and CSIRO Fine Wool (research flock-Merino) flocks which record scan data independently of mothering up data on lambing outcomes. Genetic parameters from these data sources provided the starting point for parameters used in OVIS for analysing pregnancy scan data.

This work has been presented to the Technical Committee and a manuscript has been published in Animal Production Science as part of the second Sheep CRC Reproduction-focused Special Edition.

The Technical Committee resolved to use pregnancy scan records in Sheep Genetics analyses, when pedigree based outcomes (ie. lambs or dummy lamb tags) are not provided. Only data from scanning which is accurate enough to count foetal numbers will be used. A stumbling block is the reliance on on-farm software packages to collect the data adequately (eg. complete with contemporary groups and joining details). It was also recommended to the TC that a system (accreditation and/or breeder data checks) needs to be put in place to ensure that the pregnancy scan data is relatively accurate.

Work was completed to change OVIS to use pregnancy scan data for the reproduction analysis where it is available. Data are now being used within the routine runs and implementation was completed in April 2016.

5.5.3 Elders Victoria Sire Evaluation Reproduction Trial

In 2012 The Elders Victoria Sire Evaluation conducted a reproduction trial on daughters of sires entered at the site in 2010. The daughters comprised 290 (2yo) maiden ewes from 19 sires, mated naturally to a syndicate of flock rams. The reproduction information collected was pregnancy scan, including number of foetuses, and rearing type based on DNA pedigree collected on lambs at weaning. Four reproduction traits were derived from this information: fertility (*ewes pregnant per ewe joined*), scanning result (*number of foetuses per ewe joined*), scanning litter size (*number of foetuses per pregnant ewe*), and NLW (*number of lambs weaned per ewe joined*). The first three traits are components of NLW, which is the reproduction trait included in selection indexes for Merinos. Breeding values (EBVs) for sires were estimated using only the trial data, under a sire model.

Trait means were 0.79 for fertility, 0.85 for scanning result, 1.08 for scanning litter size, and 0.57 for NLW, while lamb survival from scanning to weaning was 0.67 (0.72 in singles and 0.39 in twins). There was considerable variation between sires for all reproduction traits, with EBVs for fertility ranging from -0.23 to 0.17, scanning result from -0.22 to 0.21, scanning litter size from -0.05 to 0.12, and NLW from -0.09 to 0.13. Importantly, high EBVs for NLW could occur for different reasons, with differences between sires in fertility, litter size, and lamb survival. This highlights the potential value of separating NLW into its component traits in the MERINOSELECT genetic evaluation system.

EBVs for body weight were moderately correlated with reproduction traits (0.29 to 0.61). Higher body weight EBVs were most strongly associated with higher fertility i.e., the ability of maiden ewes to conceive. EBVs for increased fat were also moderately correlated with higher reproduction, but part of this effect was due to a stronger than expected correlation ($r=0.62$) between body weight and fat EBVs.

Indexes used for Merino sire evaluation sites to date have not included reproduction because no EBVs based on direct measurements for reproduction traits have ever been available. Using the NLW EBVs from this trial, indexes with and without reproduction could be compared, and showed significant changes in ranking (correlations between 0.71 and 0.87). The impact was greatest for the Dual Purpose+ index in which reproduction has the highest importance. This highlights the value of recording reproduction when evaluating the overall productivity of Merino sheep.

Perhaps the most important outcome of this trial is that it shows that obtaining highly useful data on reproduction is readily achievable, simply by recording pregnancy scanning data and rearing types at weaning. The most accurate data will include lambing observations as well, but most often collecting these will be impractical or not prioritised, especially in larger flocks. By following the procedures used in this trial, breeders would be able to realise most of the benefits of recording reproduction.

This report on this project has become the most downloaded document in the history of the Merino Superior Sires web site (<http://www.merinosuperiorsires.com/>). This highlights the interest among Merino breeders for improved availability of reproduction ASBVs.

5.5.4 Lamb survival

Lamb mortality treated as a trait of the ewe has historically been defined as the percent of lambs weaned (PLW). However, as litter size varies both within and across flocks, this can create numerical difficulties both for genetic evaluation purposes and in predicting response to selection. For example, somewhat regardless of mean flock litter size both the genetic and phenotypic correlations between the litter size at birth and litter size at weaning are generally moderate and positive, whereas the accompanying genetic correlations between litter size and the percent of lambs weaned can vary across flocks from slightly to strongly negative, even when accompanied by only moderately negative phenotypic correlations. Part of this issue arises from the impact of scale effects resulting from different litter sizes and the typically very different survival rates of singles and multiples. This means that simple rescaling of lamb survival traits, which is the case for the trait definition PLW, is insufficient for obtaining accurate parameter estimates and genetic evaluation across flocks with varying litter sizes. Current work has examined some alternative trait definitions for lamb mortality, all defined as traits of the ewe. This work also demonstrates that treating PLW as separate traits for single and multiple births provides a simple strategy to obtain more biologically meaningful estimates of genetic correlations between litter size and the PLW, because it allows for heterogeneous variances and changes to the mean survival rate with litter size. The genetic correlation between PLW defined for singles versus multiples is <1 in flocks where significant numbers of multiples are born, as would be expected given that the factors influencing survival of lambs are not identical for single vs multiple births.

5.5.5 Single step analyses for reproduction traits

Previous analyses by Daetwyler et al (2014) combined data from Sheep Genomics and CRC reference flocks with derived phenotypes for genotyped industry sires to perform a GBLUP. This type of analysis is unwieldy to implement for routine evaluation and the accuracies were low (averaging 0.11 across traits). Therefore we evaluated prospects for single step analyses which combined reproductive data from Sheep Genetics used in the MERINOSELECT and MATERNAL analyses, Sheep Genomics (Merino only) and the CRC IN followers. Traits analysed were NLB, NLW and the component traits: fertility (FERT), litter size (LSIZE) and rearing ability (RA, or PLW as above) of the ewe. All traits were not available in all data sources, and it was also not possible to fully replicate the current OVIS analysis, which is a multi-trait analysis accounting for heterogeneous variances. Therefore, single step (SS-GBLUP) analyses were compared with results from a pedigree based BLUP (ABLUP) and a genomic only based BLUP (GBLUP) using the combined data, with and without genetic groups.

For Merinos, 60% of the data came from 10 flocks (80% from 20 flocks), including 3 which are no longer operational and 1 from NZ. However, in excess of 300 Industry sires had both genotyped (N~2000) and un-genotyped (~7000) daughters with records and the number of ewes in the reference flocks (SG+IN) was large (~3700). Correlations between single step and OVIS EBVs for NLB and NLW were around 0.9 for comparable models (minus genetic groups), but <0.3 if genetic groups were fitted in the SS-GBLUP analysis. Accuracies for all traits, except RA, were consistently increased within and across genetic groups in the single step analyses. However, the single step results need to be cross-validated further using

independent Industry data. Preliminary results suggest that a single step model applied to NLB or NLW for Merino's using the combined data would generate a useful improvement in the accuracy of current EBVs, driven largely by improvements in accuracy for FERT and LSIZE. These analyses also suggest that there is no value in fitting genetic groups for reproductive traits in the MERINOSELECT analyses.

The same comparisons were made using the combined data for MATERNAL breeds. In contrast to the Merino data, the combined data for maternal breeds represented more flocks (N=248), with 80% of the data from 60 flocks, but the reference flock (IN ewes only) was very small (N=1200), containing few daughters per sire. Less than 800 ewes, representing >350 sires, were genotyped. Correlations between single step and OVIS EBVs were also around 0.9, driven again by the bulk of industry data common to both analyses. However, accuracies were not consistently improved between ABLUP and SS-GBLUP. The comparatively poorer results (ie. less increase in accuracy compared with ABLUP) for maternal breeds were probably due to the small reference population combined with too few daughters per sire. Therefore, it is not currently recommended to implement single step methods for MATERNAL analyses.

5.5.6 The impact of including season in the CG definition for repro traits

The impact of including season in the CG definition for repro traits was investigated. This effect was originally fitted to separate ewes from different lambing events within a calendar year as we did not have management grouping information available for the repro records. The conclusions of this work were:

- The season classifier in the CG definition had a large impact on the number of CGs formed for all breeds
- In some cases this appears a sensible option and in others maybe not.
- Despite the large impact on the number and size of CGs the impact on ASBVs is relatively minor.
- It is likely that a more sensible approach could be found which produces better group formation across all runs
 - Relying of the breeders' management groups alone appears inadequate
 - Including season appears to separate some groups that should not be separated
 - An interval based slicing procedure would seem appropriate but may be difficult to program to produce sensible outcomes across all flocks
- Obtaining reproductive data via a mating module will further reduce the need for season in the CG definition

5.6 Investigation of impact of wrinkle on reproduction rate

An investigation of the literature and Sheep Genetics data was conducted to examine the relationships between wrinkle and net reproduction rate.

The literature clearly demonstrates a negative association between wrinkle and reproduction rate across breeds.

The Sheep Genetics data supports this earlier research. A one unit reduction of early breech wrinkle ASBV translates phenotypically to approximately 10 to 30% more lambs born and weaned. However, it is difficult to accurately separate within- and across-flock effects in the Sheep Genetics data.

5.7 Merino Bloodline Performance reconciliation

A study was conducted to reconcile the differences between the Merino Bloodline Performance results (MBP) and Sheep Genetics mean breeding values for flocks. The work focussed on:

1. Varying pricing: What is the relationship between MBP dollar values and SG indexes under 2 or more (low and high) pricing models, and with varying levels of emphasis on meat and wool income?
2. Analysis of Staple Strength: What is causing the low correlation of the staple strength trait between the 2 systems?
3. Sheep Genetics Indexes in MBP: How can SG indexes be applied to MBP production data?
4. MBP pricing applied to MS database: Can MBP pricing be applied to MS flock results? This could only use traits common to both MBP and MS.

The analyses for each of these investigations has been completed and reported to AWI and the Sheep Genetics Technical Committee.

5.8 Joint analysis of Sheep Genetics and wether trial databases

A study was conducted to investigate the value of including the wether trial data into the MERINOSELECT analysis. A combined data set was constructed for analyses. The main conclusions of this work were:

- SG and MBP provide benchmarking of generally a quite different sample of flocks, with only 58 flocks (9%) well represented in both datasets.
- The OVIS analysis of the MBP data set is moderately to highly correlated with those estimated using ASREML.
- A combined analysis is feasible. However, in the MERINOSELECT analysis genetic groups are fitted as random effects, which will affect the ability to estimate bloodline effects for flocks only represented in MBP. More work is required to fully understand this issue and to examine ways to overcome this potential limitation.

5.9 Clustering of flocks in MERINOSELECT

At present Merino flocks rather arbitrarily choose to be in a Merino type (Super fine, Fine-Medium or Strong). A study was conducted to investigate if Sheep Genetics could allocate flocks to groups using objective measurements. Flock mean ASBVs were extracted from the SG MERINOSELECT database and used for principal component analysis (PCA). These principal components were then used to cluster flocks into logical groups.

The PCA appears to separate most flocks into meaningful groups quite well. However, interpretation of the clusters is somewhat challenging and does not always seem to reflect logical or accepted industry groupings. Some flocks which do not have breeding values for some traits also appear to be incorrectly classified. For example, if a very wrinkly flock does

not have accurate ASBVs for breech wrinkle it is likely to have ASBVs close to average for EBWR and thus be clustered incorrectly.

More work is required to investigate higher levels for the accuracy requirements for ASBVs used in the average and the number of animals available for each flock.

Clustering based on sires breeding values does not appear very useful at this stage.

Further work will be conducted to investigate the value of genomic information to assist with clustering of flocks. A full report of this work was presented to the Dec 2016 Technical Committee meeting.

5.10 Index Drift

There have been ongoing concerns expressed by a small number of breeders and consultants about ASBVs and indexes of high merit animals changing over time. To investigate whether this perception has any basis or not we extracted the index values from the last few years' worth of routine analysis and summarised their change over time. For each animal a regression was calculated of index value over this period of time and this regression was then summarised over all animals, the top 10% of animals based on the first run (18 Nov 2010) and bottom 10% based on the first run (18 Nov 2010).

Despite the changes to the analyses over this time period it appears not to have affected the average index values very much. The impact of the major change to the reproduction analysis in 2012 was not evident because in all 3 groups of animals the average NLW ASBV was close to 0 both before and after the change.

Because the runs cover 2.4 years, we can calculate that 68% of the animals change by ± 3.3 index points or less after 12 months. Furthermore, 95% of the animals change by ± 6.7 index points or less after 12 months. Over the whole period (2.4 years) 95% of the animals are within 16 index points of their starting index value. Changes in index values are both positive and negative and of similar magnitude. Therefore, the perception of a reduction over time only for high merit animals is incorrect.

The conclusions of this work were:

- On average indexes are stable over time.
- The top and bottom 5 or 10% of animals are not changing any more or less significantly than the whole population.
- Index values are equally likely to increase or decrease over time.
- The changes that have been observed are within the expectations from theory

5.11 Dohne analysis

5.11.1 Parameter Estimation

Detailed investigations were performed on the Dohne database and documented for the Technical committee. The most important results were:

- Data
 - There were large amounts of full pedigree data available for 25 traits.
 - These data included Australian and South African flocks.
- Variance components
 - Heritability estimates were similar to but generally slightly lower than those currently being used in the Dohne analysis.
 - Maternal effects were significant for body weight and fleece weight, but the size of the effects tended to be smaller than those estimated in Merino sheep.
 - Sire by flock interactions were significant for all traits but generally explained less than 5% of the phenotypic variance. The effect was highest for WWEC (9%) and lowest for HFD at (0.4%). This level of variation is similar to Merinos.
- Genetic correlations
 - Generally the correlations estimated were similar to the correlations used in the current Dohne and Merino analyses.
 - The correlations between scanned carcass traits and body weight were slightly different (negative) and the Dohne estimates were consistent with recent estimates from CRC Information Nucleus data. The current correlations used in MERINOSELECT should be investigated further.
- Adjustment factors
 - Birth and Rearing type
 - The estimated adjustment factors for birth type were very similar to those being used in the Merino analysis.
 - However, the estimated rearing type adjustments were inconsistent.
 - The results and distribution of rearing types in the data suggests this information is not being recorded properly.
 - Age
 - The estimated age adjustments were consistently greater than those being used by the Merino analysis and could simply be a function of higher growth rates observed in Dohne sheep.
 - Dam age
 - For most traits the estimated adjustment factors were quite different to those from the Merino analysis. This was especially apparent at older ages. Further work is required to validate these adjustments.
 - Body weight fitted to scanned eye muscle and fat depths
 - For most traits the estimated adjustment factors were quite different to those from the Merino analysis. Further work is required to validate these adjustments.

In general the parameters and adjustments estimated from the Dohne database were similar for most traits to those used for the MERINOSELECT analysis. Some small differences do exist and further work should be conducted to validate these differences.

5.11.2 Reproduction Data

Historically the Dohne analysis did not include any reproduction records as breeders had not been recording unsuccessful matings (DRY tags) and dead lambs (DAB tags) in the past. However the Dohne Association has been encouraging breeders to record better reproduction data for the last few joinings. A test analysis was conducted for the Dohne run with reproduction records included to evaluate the possibility of implementing the traits in the routine Dohne analysis.

After the normal SG data filtering there were 20,359 reproduction records available from 15,330 animals. These come from 66 flocks and 113 flock-year subclasses. There were 9 flocks with yearling reproduction data.

Many flocks had more than one year of reproduction data. Many flocks were also not recording rearing information. 45 flocks had both NLB and NLW while 21 flocks only had NLB because they had not supplied valid rearing information.

The conclusions of this study are:

- Adequate data are now available to analyse reproduction records in the Dohne breed.
- This should be considered at the same time as a combined Merino-Dohne analysis.
- Recording of rearing type should be improved/encouraged.
- Ongoing linkage between breeds and flocks should be fostered and encouraged.

A new reproduction analysis was fully implemented for the Dohne run in March 2015.

5.11.3 Combined Merino – Dohne analysis

A combined Merino and Dohne analysis was performed in 2014 to examine the linkage between these two datasets and evaluate changes to breeding values.

Over 95% of all Dohne flocks with data were classed as linked. For WEC, only 3 Dohne flocks had WEC recorded, of which 2 were linked. For the reproduction analysis there were 104 flocks with reproduction data, of which 55 were Merino and 49 were Dohne. However, the 55 Merino flocks have 124,080 (86%) records and the 49 Dohne flocks 20,486 (14%) records. There were 25 sires that had progeny in both Dohne and Merino (including INF) flocks.

It was apparent that the genetic groups had a small impact on ranking of Dohne flocks but a larger impact on the variation between flocks. Reproduction traits were driving most of the changes in the index. While there was enough linkage to meet the required thresholds for reporting as ASBVs, there were a very small number of sires and progeny contributing to linkage. It is likely that outside a few key Merino flocks which have used Dohne sires, comparisons between the two breeds will be of questionable value. More linkage is required to ensure the breeds are adequately benchmarked for all traits.

5.12 Estimation of parameters for Sheep CRC

AGBU was contracted to estimate genetic correlations between traits across all traits groups in the INF database. This work involved:

- Adapting programs to automate ASReml runs for the INF data (traits, models and genetic groups consistently defined).
- Conducting analyses across each breed type.
- Developing a web site to display results.
- Further analyses on GxE effects.

As part of this process additional analyses were conducted to identify the most appropriate methods for fitting genetic groups in these data. A manuscript was prepared from these studies and published in Animal Production Science.

This work has continued with key outcomes including:

- Additional functionality to web site such as downloads and GxE analysis results.
- Detail investigations into GxE for a range of traits.
- Detailed analysis of adult weights and condition scores.
- Investigation of the impact of various ASBVs on reproduction and its interactions across years and flocks.

Two discussion papers based on this work were presented to the Technical committee. Please note that the majority of this work is funded from outside the MLA contract, but that the website and underlying databases have been highly valuable for the on-going development of the Sheep Genetics system.

5.13 Review of fat and EMD correlations with body weight

The current MS analyses assume positive correlations between liveweight and live animal ultrasound carcass traits. However, recent estimates from the Dohne data and CRC information nucleus data sets have both been negative. The same correlations are slightly negative in the parameters used for the Terminal sire analysis. A review and investigation of these estimates was conducted to evaluate the appropriateness of the current parameters.

In both Terminals and Merinos the sampling of sires from industry to be used in INF has influenced the relationships observed between traits in their progeny. The current parameters being used in MERINOSELECT agree with those recently estimated and at this point in time there is insufficient evidence to suggest that they should be changed.

This work also demonstrates that it is better to estimate the correlations between traits without fitting any trait covariates, and to derive conditional parameters post-analysis. This is the approach we are currently using in the INF analyses. The Technical Committee should consider adopting this approach in Sheep Genetics analyses.

A discussion paper outlining this work was presented to the Technical Committee meeting.

5.14 Weaning weight as an adjustment factor for fleece weight

In some pre-Sheep Genetics genetic evaluation systems weaning weight was used as an adjustment for fleece weight to removed early age maternal and systematic environmental effects. OVIS could be modified to incorporate fleece weight adjusted for weaning weight. However, at this point in time AGBUs recommendation is not to make this change due to the following reasons:

- Less than 10% of the fleece weight records would be able to be used for these traits.
- The weaning weight adjustment also removes across-flock variation.
- The adjustment also changes the traits definition by removing genetic variance, covariance with other traits and also reducing maternal effects.

Given the differences in variance components and correlations with other traits the only option to include fleece weight adjusted for weaning weight as a trait is to add 8 additional fleece weight traits. These traits will not need a maternal effect modelled. Breeders using these traits will have a lower accuracy and less spread in their BVs for the normal fleece weight traits. This will also have a similar effect on their index values and accuracies. Breeders would need to have the pros and cons of these new traits clearly explained

A discussion paper outlining this work was presented to the Technical Committee meeting.

5.15 Genetic groups for MERINOSELECT Visual trait analysis

The visual trait analysis for the Merino run has historically had no genetic groups fitted. Test analyses were completed with flock based genetic groups (100 flock groups were formed) to evaluate the impact of these genetic groups. This work was presented to the Technical Committee meeting. The outcome of this work was to include genetic groups in the MERINOSELECT Visual trait analysis.

5.16 Lifetime productivity

5.16.1 Adult weight and condition score

Detailed analysis of adult weight and condition score has been conducted using data in the Sheep Genetics databases. Three main projects have been completed:

- A series of genetic analyses were conducted to estimate genetic parameters for adult weight traits for Maternal, Merino, Terminal and INF databases. Univariate analysis were undertaken to look at fixed effects and determine the most appropriate model to fit. Subsequently bivariate and multivariate analyses were run to obtain correlation estimates between ages. The correlation estimates from bivariate and multivariate analyses were similar. Merino and Maternal genetic correlation estimates using a multi-trait model were high, over 0.9 for adult weight traits with some but not all not being significantly different to 1. Terminal correlations for adult weight traits were also high ranging from (0.77 - 0.93). The genetic estimates for Terminals should be revisited in the future when more records are available to confirm that they are consistent with the other breed groups.
- Additional analysis of adult weight and condition score was carried out in MERINSOLECT database. A preliminary analysis was conducted to aid in the development of OVIS to include repeat records for adult weight. This work was presented at a Technical Committee meeting. A paper was also submitted to and accepted for the World Congress in Vancouver in August 2014.
- Detailed analysis of adult weight and condition score in the Sheep CRC database across all breeds. Further analyses of these data were conducted to quantify the value of these traits and change of weight and condition score throughout the year.

The conclusion of all these studies was that adult weight and condition score is genetically the same trait across time and can be included in OVIS as a repeated record trait. This work has assisted with the development of OVIS V3.0 with additional adult records as described above. OVIS was modified to included 2, 3 and 4 year old records. Breeders are being

encouraged to supply these records as pre-joining weights and submit them via the mating module.

5.16.2 Adult wool traits

A series of genetic analyses were conducted to estimate genetic parameters for Adult wool traits from the Merino databases. This work demonstrated that:

- Early age measurements are good predictors of lifetime performance.
- Very high correlations exist between adult measurements across ages.
- A repeatability model is suitable for the inclusion of additional adult wool measurements.
- Breeders should be encouraged to record at least one adult wool measurement.
- This work has assisted with the development of OVIS V3.0 with additional adult records as described above.

5.16.3 ASBVs of sire groups over time

ASBVs are subject to change over time as more information becomes available. This was investigated using groups of sires selected based on an individual sire and year. For each site and year all the 2 year old sires were selected and tracked over time. ASBVs and their accuracies were summarised from late 2009 to mid-2014. This work was compiled for an AWI funded project, and the results were presented to the Technical Committee.

5.17 Scan trait heritability

As a result of observations from Sheep Genetics staff that carcass scanners were having difficulty with accreditation, it was decided to investigate the heritability of these traits across each database. The implication is that if scanning accuracy has deteriorated, a reduction in heritability might be evident. A series of analyses were undertaken to estimate heritability trends for fat and muscle scan traits within the three major breed groups Terminal, Maternal and Merino. While some breed groups and trait combinations showed some slight changes in heritability, post weaning carcass fat in the maternal database showed a large reduction in heritability over the period (1996-present). This work was presented to the Technical Committee meeting.

The trend in scan heritability was investigated due in part to some issues with scanners performance during accreditation and to assess the appropriateness of the current parameters being used in the analyses.

Analyses were also undertaken to assess the effect of restricting the data as a form of data quality control. Trends in age of measurement, weight, muscle and fat at measurement were also presented along with trends showing the number and percentage of animals recorded for the traits and also the percentage of sites which had measurements taken.

While some breed groups and trait combinations showed some slight changes in heritability most were relatively flat over time. Maternal post weaning C-site fat however showed a

large reduction in heritability over the period (2001-present). Maternal EMD heritability while having dropped substantially is now only slightly above the value used in the routine analyses.

It was recommended that the heritability for PCF in the Maternal analyses be reduced to 0.25 in line with the results of this report. Given the results shown in these age categories it would be prudent to review all age categories for the three analyses for scan traits to ensure that they are still representative for the current data.

5.18 Changes to the routine ASBV analysis

Since 2012 Sheep Genetics have scheduled changes to routine analysis to occur in March / April of each year. The key issues were identified and endorsed by the Technical Committee prior to implementation. Many of these changes were a direct result of the investigations described above. Each year extensive test runs were completed and discussed at Technical and Advisory Committee meetings and then extended to the industry.

5.18.1 2013 Enhancements

1. Reproduction analysis – implement additional management grouping. At the time the grouping strategy was based around flock, year, ewe age class (1, 2 and 3+), conception method, and whether the ewe had previously lambed at 1 year of age (0 or 1). However, some flocks had different management groups for ewes at lambing relative to weaning, and historically we were not able to capture this information. An interim solution was implemented to fit these management groups where they are provided by the breeder.
2. Reproduction analysis – Yearling data. It was identified that the threshold for failed service sires should be reduced to 20% rather than 70% for yearling ewes and the correlations with adult reproduction should be reduced.
3. Reproduction analysis – modified data filtering. Changes were made to only filter failed service sires for natural mating. Filtering was also changed to count ewes rather than lambs.
4. Update years for genetic group allocation in MS analysis. Flocks with sufficient data over time are allocated groups over time to better accommodate genetic trends in the base animals. The last time period group at the time spanned over 10 years for 2001 to 2013. An additional time period group was then created from 2006 onwards. This group was used in approximately 65 flocks at the time of implementation and resulted in improved genetic trends for most flocks.

5.18.2 2014 Enhancements

1. RBVs to ASBVs – Blended RBVs released as ASBVs, ensuring that genotyped animals have only a single ASBV reported for all OVIS traits.
2. Yearling reproductive trait groups – sub groups applied for some flocks joining ewe lambs.
3. Extra adult weights – some additional adult records were added from the visual trait database and ewe joining weights.

4. Index update – The standard indexes in the MERINOSELECT analysis were extensively modified to improve the emphasis of some key traits following industry consultation.
5. Genetic Groups in the visual analysis – Flock based genetic groups were implemented into the visual trait analysis.
6. Carcass traits – Carcass trait phenotypes included in the Maternal breeds analysis.
7. Standard weight for carcass adjustment – NSIP runs changed to use more appropriate standard weights for carcass traits.
8. Reproduction trait analysis – reproduction analysis implemented for Dohne analysis.

5.18.3 2015 Enhancements

A large body of work was devoted to developing a new version of OVIS, its parameter files and run scripts to release new features in March 2015.

The key changes to OVIS included:

1. A single version of OVIS used for all Sheep Genetics analyses
 - There were previously 3 different versions of OVIS being used which had different trait definitions and functionality. There are also 4 different variance component files (LAMBPLAN + MS, Dohne, NSIP and Goats).
2. All 11 sets of genetic parameters merged into one parameter file with the same traits available. Although not all breeds have all traits defined and used.
3. Post weaning wool traits added.
4. Two additional adult trait observations added.
5. Single step carcass and eating quality traits added to OVIS parameters.
6. SheepObject breeding objective traits added to OVIS parameters.
7. Genetic parameters updated using results from CRC INF analyses.
8. The Merino parameter set was updated with recently published correlations between carcass (scanned) traits and other production traits.
9. Gestation length traits added (direct and maternal).

5.18.4 2016 Enhancements

A large body of work was devoted to developing a new version of OVIS, its parameter files and run scripts to release new features in March 2016.

The key changes to OVIS included:

1. Additional post weaning wool traits were added:
 - Post weaning staple length (psl) and staple strength (pss).
2. Two additional adult trait observations added:
 - Age based 5 and 6 years of age (A5 and A6).
3. Full multi-trait single step carcass and meat quality traits added to OVIS.
4. Additional visual traits added into the parameter databases.
5. Genetic parameters component traits of reproduction added into the parameter databases.
6. Using pregnancy scanning records for reproduction traits.

7. Improved storage of genetic parameters.

5.19 Other activities

- NSIP
 - Updated parameters for NSIP analyses.
 - Within breed linkage analyses developed for the across breed NSIP analyses.
- Dohne
 - Estimation of genetic parameters and adjustment factors for Dohne Merino.
 - Updated parameters for Dohne analyses.
 - Estimation of variance components for Dohne grade scores.
- Effect of ewe lamb joining on later production traits.
- Investigating the effects of heterosis adjustment and correlated traits on genetic group effects.
- Merino Bloodline Performance reconciliation.
- Investigation of the relationship between wrinkle and fertility in MERINOSELECT data.
- Investigation of linkage for reproduction traits in the Border Leicester data.
- Investigation of key industry sires to genotype.
- Investigation of genetic relationships between INF sires and industry animals.
- Principal component / cluster analysis of MERINOSELECT data.
- Technical committee survey for 2012 work plan.
- Conduct staple strength and adult-only analysis for genomic prediction.
- New parameters for Boer goat analysis.
- Investigation of relationship between WEC and production traits in Coopworths.
- Created program to pre-populate mating modules.
- Extensive editing and review of the Breeders Guide.
- Analysis of show-ring sires in CTSE data.
- Extraction of data for CRC staff and other MLA projects.
- Extraction of ABVS for INF sires from each routine analysis.
- Estimation of EX_INF ASBVs for Merino, Maternal and Terminal databases.
- PICSE students
 - Talks during camp.
 - Hosting students for 1 week industry placement at AGBU (every year of the project).
- Collaboration with Forbes Brien
 - AWI breech strike prediction work.
 - Lamb survival papers and analyses.

5.20 Communication and Extension

5.20.1 Presentations

- R&D insights – Melbourne March 2011
- Applied Genomics for Sustainable Livestock Breeding (2 presentations) – May 2011
- AAABG presentations (3 presentations) - Perth July 2011

- SuperBorders conference - Bendigo June 2011
- Merino 2020 Conference – Wagga Wagga (Aug 2011)
- Service Provider workshop - Armidale (Nov 2011)
- Leading Breeder workshop - Armidale (Nov 2011)
- PICSE Teacher Development – Armidale (Dec 2011)
- PICSE student camp – Armidale (Dec 2011)
- White Suffolk conference and SuperWhites meeting (Feb 2012)
- Meat Elite meetings (Feb 2012)
- Donhe symposium – Adelaide (March 2012)
- Cleanskins symposium – Adelaide (March 2012)
- Sheep Genetics Advisory meeting – Sydney (Jan 2013)
- Reproduction workshop and follow up webinars
- Dohne Webinar (July 2013)
- Attend and present at AAABG – NZ (Oct 2013)
- Attend and present at 2 Sheep Breeders day – NZ (Oct 2013)

5.20.2 Meetings and Workshops

- CRC pilot project / IMG meetings (approximately 12)
- Breeding objectives workshop – Armidale January 2011
- Breeding objectives workshop – Coffs March 2011
- CRC reproduction workshop – Perth July 2011
- ZPLAN workshop – CSIRO June 2011
- Advisory Committee – Melbourne May 2011
- CRC meeting with Jen Smith – AGBU July 2011
- ThinkTank for Breeding for flystrike resistance – Sydney (Nov 2011)
- Sheep CRC genomic analysis meeting – Armidale (Nov 2011)
- CRC reproduction workshop – Adelaide Feb 2012
- MLA strategic meeting – Armidale Feb 2012
- AWI Lifetime productivity project meetings (on going)
- MLA round table meeting – Sydney (Sep 2012)
- CRC extension meeting – Sydney (Oct 2012)
- INF data analysis meeting – Sydney (Oct 2012)
- Meeting with Hazeldene – Armidale (Nov 2012)
- Bloodline Reconciliation meeting – Sydney (Dec 2012)
- CRC Meat traits meeting – Sydney (Feb 2013)
- AMSEA meetings (usually 2 p.a.)
- Bloodline Reconciliation meeting – Sydney (Dec 2012)
- Leading Breeder Workshop – Bendigo (Feb 2013)
- AWI Lifetime productivity project meeting in Armidale (May 2013)
- Corriedale Breeders (Mar 2013)
- CRC planning meeting – Coffs (Mar 2013)
- CRC data analysis workshop – Perth (Mar 2013)
- CRC large scale genotyping meeting – Sydney (May 2013)
- Service provider training workshop – Melbourne (May 2013)
- CRC data analysis meeting – Armidale (July 2013)

- Attend and present at Sheep CRC genomics workshop – Sydney (Aug 2013)
- CRC Post grad conference – Coffs (Nov 2013)
- NSW DPI planning meeting – Armidale (Nov 2013)
- Impact of Large-Scale Genomic Data on Statistical and Quantitative Genetics Conference (Seattle, November 24-26, 2013). Attended by A. Swan
- Leading Breeder meeting – Wagga (March 2014)
- Sheep CRC meat traits meeting – Armidale (March 2014)
- Sheep CRC data analysis meeting – Armidale (March 2014)
- Sheep Genomic training – Armidale (March 2014)
- Sheep Genetics Advisory meeting – Sydney (April 2014)
- AMSEA and MCG meetings in Sydney (April 2014)
- Software provider meeting – Sydney (May 2014)
- Service provider training – Melbourne (May 2014)
- Meeting with DPI about possible collaborations – Armidale (July 2014)
- CSIRO Phonemics workshop – Armidale (Sep 2014)
- AGBU Breeding Focus Workshop: Building Resilience workshop (Oct 2014)
- Resource Flock 2015 Joining Planning Meeting (Oct 2014)
- CRC/SG/AGBU - Grassgro modelling, Genetics Tool Development, Addressing Barriers to adoption (Nov 2014)
- Sheep CRC genomics meeting – Armidale (Nov 2014)
- Sheep CRC data analysis meeting – Armidale (Dec 2014)
- R&D priorities and opportunities for lamb survival – CSIRO Armidale (January 2015)
- Leading Breeder 2015 - Adelaide (March 2015)
- Sheep Genetics Advisory meeting - Sydney (March 2015)
- CRC GxE meeting - Sydney (March 2015)
- Service Provider Training – Melbourne (May 2015)
- Trans-Tasman meeting – Sydney (May 2015)
- NSW DPI Genetics Symposium – Armidale (May 2015)
- AMSEA meeting – Sydney (April 2015)
- RD4P lamb survival meeting - Sydney (June 2015)

5.20.3 Student Supervision

During the life of the project multiple postgraduate students have been supervised by staff working in the project. The table below shows a summary of these students.

Name	Course	Duration	Topic
Jo Newton	PhD	Feb 2012 to Feb 2015	Sexual maturity and yearling reproductive performance in ewes: Genetic analysis and implications for breeding programs
Tom Granleese	PhD	Jan 2012 to Feb 2016	Optimised Livestock Breeding Programs Using Female Reproductive Technologies and Genomic

			Selection
Tracie Bird-Gardiner	MResc	July 2012 to June 2016	Genetic Analysis of Flystrike in sheep
Michael Aldridge	PhD (School of Animal and Veterinary Science, The University of Adelaide)	Mar 2014 to Expected Mar 2017	Genetic improvement of Australian Meat Goats
Steve Milne	Master of Animal Science (Animal Breeding Management (Sydney Uni)	Jan 2011 to Dec 2012	The effect of previous parity in Poll Dorset and White Suffolk sheep on genetic and phenotypic predictions of birth weight in subsequent parities.
Robert Jones	MResc	July 2011 to July 2013	Genetic parameters for Lamb Autopsy Traits
Michele Porto Pires	PhD, Sao Paulo State University	June 2015 to September 2015	Short visit: G*E GWAS for worm egg count in sheep
Rafael Keith Ono	PhD, Sao Paulo State University	June 2015 to September 2015	Short visit: breeding objectives for Santa Ines sheep
Jerome Raoul	PhD, INRA Toulouse, France	July 2016 to June 2017	One year visit: management of major genes for reproduction

Whilst not being a formal supervisors we have also had key supervisory roles with at least four additional students from other institutions including Michael Wheelan (PhD, Southern Cross University), Nick Linden (PhD, Victorian Dept. Primary Industry), Lina Maximini (PhD, University of Natural Resources and Life Sciences, Vienna) and Paul Blackburn (PhD, South Australian Research and Development Institute). All these supervisory roles have led to published articles or papers that are still in preparation. these students have spent time at AGBU working with us.

5.20.4 Scientific Publications

5.20.4.1 Conference Papers

Bell, A M; Henshall, J M; Gill, J S; Gore, K and Kijas, J W (2013). "Success rates of commercial SNP based parentage assignment in sheep." Proc. Assoc. Advmt. Anim. Breed. Genet. Napier, New Zealand, July 20-23. 20: 278-281.

Bird-Gardiner, T L; Brown, D J; Smith, J L and Mortimer, S I (2013). "Inheritance of flystrike recorded in a non-seasonal rainfall environment." Proc. Assoc. Advmt. Anim. Breed. Genet. Napier, New Zealand, July 20-23. 20:183-186.

Boerner, V and Johnston, D J (2013). "Accuracy of Igenity direct genomic values in Australian Angus." Proc. Assoc. Advmt. Anim. Breed. Genet. Napier, New Zealand, July 20-23. 20:211-214.

Brown, D J; Swan, A A; Gill, J S and Banks, R B (2013). "Strategies to objectively group merino flocks in sheep genetics." Proc. Assoc. Advmt. Anim. Breed. Genet. Napier, New Zealand, July 20-23. 20:66-69.

Brown, D J; Swan, A A and Gill, J S (2013). "Genetic correlations across ages for greasy fleece weight and fibre diameter in Merino sheep." Proc. Assoc. Advmt. Anim. Breed. Genet. Napier, New Zealand, July 20-23. 20:110-113.

Bunter, K L and Brown, D J (2013). "Yearling and adult expressions of reproduction in maternal sheep breeds are genetically different traits." Proc. Assoc. Advmt. Anim. Breed. Genet. Napier, New Zealand, July 20-23. 20:82-85.

Daetwyler, H D; Bolormaa, S; Brown, D J; van der Werf, J H J and Hayes, B J (2013). "A genomic prediction cross-validation approach combining ewe repeated phenotypes and ram daughter trait deviations." Proc. Assoc. Advmt. Anim. Breed. Genet. Napier, New Zealand, July 20-23. 20:360-363.

Li, L; Brown, D J and Gill, J S (2013). "Genetic parameters for body weight, carcass and wool traits in Dohne Merino." Proc. Assoc. Advmt. Anim. Breed. Genet. Napier, New Zealand, July 20-23. 20:241-244.

Moghaddar, N; Swan, A A and van der Werf, J H J (2013). "Accuracy of genomic prediction from multi-breed sheep reference population." Proc. Assoc. Advmt. Anim. Breed. Genet. Napier, New Zealand, July 20-23. 20:220-223.

Newton, J E; Brown, D J; Dominik, S and van der Werf, J H J (2013). "Age at first oestrus. A useful trait for early reproductive performance?" Proc. Assoc. Advmt. Anim. Breed. Genet. Napier, New Zealand, July 20-23. 20:86-89.

Piper, L R; Swan, A A and Brewer, H G (2013). "Current flock effects on lifetime reproductive performance of simulated selection at hogget age in Merino sheep, for fleece weight, fibre diameter, body weight and relevant selection indexes. III. High rainfall region results." Proc. Assoc. Advmt. Anim. Breed. Genet. Napier, New Zealand, July 20-23. 20:102-105.

- Rowe, J B; Gill, J S; Banks, R G and van der Werf, J H J (2013). "Genomics for the Australian sheep industry: from design to delivery." Proc. Assoc. Advmt. Anim. Breed. Genet. Napier, New Zealand, July 20-23. 20:14-17.
- Swan, A A and Brown, D J (2013). "The impact of measuring adult fleece traits with genomic selection on economic gain in merino selection indexes." Proc. Assoc. Advmt. Anim. Breed. Genet. Napier, New Zealand, July 20-23. 20:233-236.
- van der Werf, J H J; Brown, D J and Swan A A (2013). "Prediction of genomic breeding values across genetic groups." Proc. Assoc. Advmt. Anim. Breed. Genet. Napier, New Zealand, July 20-23. 20:340-343.
- Aldridge, M; Brown, D J; Hooke, T and Pitchford, W S (2014). "Situation analysis for the performance recording of Australian meat goats." In Proceedings of the 10th World Congress on Genetics Applied to Livestock Production, Vancouver, Canada, 17-22 August. Paper 911.
- Banks, R G (2014). "Who benefits from genetic improvement?" In Proceedings of the 10th World Congress on Genetics Applied to Livestock Production, Vancouver, Canada, 17-22 August. Paper 009.
- Bird-Gardiner, T L; Brown, D J; Smith, J L; Mortimer, S I and Refshauge, G (2014). "Breech strike indicator traits for Merino sheep in non-seasonal rainfall environments." In Proceedings of the 10th World Congress on Genetics Applied to Livestock Production, Vancouver, Canada, 17-22 August. Paper 891.
- Brown, D J and Swan, A A (2014). "Genetic analysis of adult body weight and condition scores in Merino sheep." In Proceedings of the 10th World Congress on Genetics Applied to Livestock Production, Vancouver, Canada, 17-22 August. Paper 907.
- Clark, S A; Brown, D J and van der Werf, J H J (2014). "The effect of using genomic breeding values to manage the loss in response to selection caused by genotype by environment interactions." In Proceedings of the 10th World Congress on Genetics Applied to Livestock Production, Vancouver, Canada, 17-22 August. Paper 409.
- Daetwyler, HD; Bolormaa, S; Kemper, K E; Brown, D J; Swan, A A; van der Werf, J H J and Hayes, B J (2014). "Using genomics to improve reproduction traits in sheep." In Proceedings of the 10th World Congress on Genetics Applied to Livestock Production, Vancouver, Canada, 17-22 August. Paper 156.
- Mortimer, S I; Swan, A A; Brown, D J and van der Werf, J H J (2014). "Genetic parameters revisited for ultrasound scanning traits in Australian sheep." In Proceedings of the 10th World Congress on Genetics Applied to Livestock Production, Vancouver, Canada, 17-22 August. Paper 345.
- Newton, J E; Brown, D J; Swan, A A; Dominik, S and van der Werf, J H J (2014). "Effects of selection accuracy, risk and young ewe fertility on breeding program design." In Proceedings of the 10th World Congress on Genetics Applied to Livestock Production, Vancouver, Canada, 17-22 August. Paper 912.

Swan, A A; Brown, D J; Daetwyler, H D; Hayes, B J; Kelly, M; Moghaddar, N and van der Werf, J H J (2014). "Genomic evaluations in the Australian sheep industry." In Proceedings of the 10th World Congress on Genetics Applied to Livestock Production, Vancouver, Canada, 17-22 August. Paper 334.

van der Werf, J H J; Banks, R G; Clark, S A; Lee, S J; Daetwyler, H D; Hayes, B J and Swan, A A (2014). "Genomic selection in sheep breeding programs." In Proceedings of the 10th World Congress on Genetics Applied to Livestock Production, Vancouver, Canada, 17-22 August. Paper 351.

Aldridge, M; Brown, D J and Pitchford, W (2015). "Genetic and phenotypic relationships between kid survival and birth weight in Australian meat goats." Proceedings of the 21st Conference of the Association for the Advancement of Animal Breeding and Genetics. Lorne, Victoria. September 28 - 30, pp 350-353.

Banks, R G (2015). "Realising genetic improvement for the Extensive Livestock Industries as a whole." Proceedings of the 21st Conference of the Association for the Advancement of Animal Breeding and Genetics. Lorne, Victoria. September 28 - 30, pp 233-236.

Banks, R G and Tier, B (2015). "Considerations in the use of commercial data for genetic evaluation in beef and sheep in Australia." Proceedings of the 21st Conference of the Association for the Advancement of Animal Breeding and Genetics. Lorne, Victoria. September 28 - 30, pp 169-172.

Brown, D J and van der Werf, J H J (2015). "Genetic correlations between purebred and crossbred performance of Poll Dorset sheep." Proceedings of the 21st Conference of the Association for the Advancement of Animal Breeding and Genetics. Lorne, Victoria. September 28 - 30, pp 177-180.

Bunter, K L and Brown, D J (2015). "Revisiting total weaning weight as a selection criterion." Proceedings of the 21st Conference of the Association for the Advancement of Animal Breeding and Genetics. Lorne, Victoria. September 28 - 30, pp 201-204.

Graham, P; Swan, A A and Banks, R G (2015). "Merino breeding objectives under climate change." Proceedings of the 21st Conference of the Association for the Advancement of Animal Breeding and Genetics. Lorne, Victoria. September 28 - 30, pp 245-248.

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Hatcher, S and Brown, D J (2015). "Is fibre comfort factor required in Merino breeding programs?" Proceedings of the 21st Conference of the Association for the Advancement of Animal Breeding and Genetics. Lorne, Victoria. September 28 - 30, pp. 205-208.

Hatcher, S; Brown, D J; Brien, F D and Hebart, M L (2015). "Genetic relationships between breech cover, wrinkle and lamb survival in Merino sheep." Proceedings of the 21st Conference of the Association for the Advancement of Animal Breeding and Genetics. Lorne, Victoria. September 28 - 30, pp 354-357.

Li, L; Swan, A A; Brown, D J and van der Werf, J H J (2015). "Australian sheep breeding values for worm egg count retain predictive power across flocks in the presence of GxE." Proceedings of the 21st Conference of the Association for the Advancement of Animal Breeding and Genetics. Lorne, Victoria. September 28 - 30, pp 386-389.

McMillan, A J and Brown, D J (2015). "Effect of different data exclusion policies on the heritability of fat depth in maternal, Merino and terminal sheep." Proceedings of the 21st Conference of the Association for the Advancement of Animal Breeding and Genetics. Lorne, Victoria. September 28 - 30, pp 417-420.

Meyer, K; Swan, A A and Tier, B (2015). "Computing for multi-trait single-step genomic evaluation of Australian sheep." Proceedings of the 21st Conference of the Association for the Advancement of Animal Breeding and Genetics. Lorne, Victoria. September 28 - 30, pp 429-432.

Moghaddar, N; Swan, A A and van der Werf, J H J (2015). "Accuracy of genomic prediction for Merino wool traits using high-density marker genotypes." Proceedings of the 21st Conference of the Association for the Advancement of Animal Breeding and Genetics. Lorne, Victoria. September 28 - 30, pp 165-168.

Mortimer, S I; Swan, A A; Pannier, L; Ball, A J; Jacob, R H; van der Werf, J H J and Pethick, D W (2015). "Genetic parameters for eating quality traits of Australian lamb." Proceedings of the 21st Conference of the Association for the Advancement of Animal Breeding and Genetics. Lorne, Victoria. September 28 - 30, pp 209-212.

Piper, L R; Bindon, B M; Swan, A A and Brewer, H G (2015). "Genetic selection for litter size in cattle." Proceedings of the 21st Conference of the Association for the Advancement of Animal Breeding and Genetics. Lorne, Victoria. September 28 - 30, pp 101-105.

Swan, A A (2015). "Fibre diameter measured in the post-weaning age window is genetically the same trait as yearling fibre diameter." Proceedings of the 21st Conference of the Association for the Advancement of Animal Breeding and Genetics. Lorne, Victoria. September 28 - 30, pp 338-341.

Swan, A A; Pleasants, A and Pethick, D (2015). "Breeding to improve meat eating quality in terminal sire sheep breeds." Proceedings of the 21st Conference of the Association for the Advancement of Animal Breeding and Genetics. Lorne, Victoria. September 28 - 30, pp 29-32.

Swan, A A (2012). "Genomic selection in the Australian sheep industry." In: Pig Genetics Workshop Notes 2012, Hermes, S and Dobos, K J (eds). Armidale, Australia, pp. 13-18.

Brown, D (2015). "Genetic improvement for internal parasite resistance." Joint annual meeting ADSA – ASAS, Orlando, Florida, July 12-16.

5.20.4.2 Journal Papers

Asadi Fozi, M; van der Werf, J H J and Swan, A A (2012). "Modelling genetic covariance structure across ages of mean fibre diameter in sheep using multivariate and random regression analysis." *Animal Production Science* 51(11): 1019-1026 doi: 10.1071/AN12139.

Maximini L; Brown D J; Baumung, R and Fuerst-Waltl, B (2012). "Genetic parameters of ultrasound and computer tomography scan traits in Austrian meat sheep." *Livestock Science* 146 (2-3):168-174 doi: 10.1016/j.livsci.2012.03.007.

Swan, A A; Johnston, D J; Brown, D J; Tier, B and Graser, H-U (2012). "Integration of genomic information into beef cattle and sheep genetic evaluations in Australia." *Animal Production Science* 52 (3):126-132 doi: 10.1071/AN11117.

Hans D Daetwyler, Andrew A Swan, Julius HJ van der Werf and Ben J Hayes (2012) Accuracy of pedigree and genomic predictions of carcass and novel meat quality traits in multi-breed sheep data assessed by cross-validation. *Genetics Selection Evolution* 44, 33. doi:10.1186/1297-9686-44-33

Barwick, S A; Tier, B; Swan, A A and Henzell, A L (2013). "Estimation of accuracies and expected genetic change from selection for selection indexes that use multiple-trait predictions of breeding values." *Journal of Animal Breeding and Genetics* 130 (5):341-348 doi: 10.1111/jbg.12011.

Moghaddar, N; Swan, A A; and van der Werf, J H J (2013). "Genomic prediction of weight and wool traits in a multi-breed sheep population." *Animal Production Science* doi: org/10.1071/AN13129.

Misztal, I., Vitezica, Z.G., Legarra, A., Aguilar, I. and Swan, A.A. (2013), Unknown-parent groups in single-step genomic evaluation. *Journal of Animal Breeding and Genetics*, 130: 252–258. doi: 10.1111/jbg.12025

Brown, D J; Jones, R M and Hinch, G N (2014). "Genetic parameters for lamb autopsy traits." *Animal Production Science* 54 (6):736-744 doi: org/10.1071/AN13227.

Huisman, A E; Brown, D J and Fogarty, N M (2014). "Ability of sire breeding values to predict progeny bodyweight, fat and muscle using various transformations across environments in terminal sire sheep breeds." *Animal Production Science* doi: org/10.1071/AN14666.

Moghaddar, N; Swan, A A and van der Werf, J H J (2014). "Comparing genomic prediction accuracy from purebred, crossbred and combined purebred and crossbred reference populations in sheep." *Genetics Selection Evolution* 46:58 doi: 10.1186/s12711-014-0058-4.

Newton, J E; Brown, D J; Dominik, S and van der Werf, J H J (2014). "Genetic and phenotypic parameters between yearling, hogget and adult reproductive performance and age of first oestrus in sheep." *Animal Production Science* 54 (6):753-761 doi: org/10.1071/AN13245.

Pethick, D W; Ball, A J; Banks, R G; Gardner, G E; Rowe, J B and Jacob, R H (2014) "Translating science into the next generation meat quality program for Australian lamb." *Meat Science* 96 (2):1013-1015 doi: 10.1016/j.meatsci.2013.09.011.

Brown, D J, Swan, A A, Gill, J S, Ball, A J and Banks, R G (2015). "Genetic parameters for liveweight, wool and worm resistance traits in multi-breed Australian meat sheep. 1.

Description of traits, fixed effects, variance components and their ratios.” *Animal Production Science* doi: org/10.1071/AN14787.

Brown, D J and Swan, A A (2015). “Genetic parameters for liveweight, wool and worm resistance traits in multi-breed Australian meat sheep. 2. Genetic relationships between traits.” *Animal Production Science* doi: org/10.1071/AN14788.

Meyer, K; Swan, A A and Tier, B (2015). “Technical note: Genetic principal component models for multitrait single-step genomic evaluation.” *Journal of Animal Science* 93 (10): 4624-4628 doi: 10.2527/jas.2015-9333.

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Rowe, J and Banks, R G (2015). Sheep industry productivity – the role of genomics and digital data.” *Farm Policy Journal* 12 (1): 21-31.

Swan, A A; Brown, D J and van der Werf, J H J (2015). “Genetic variation within and between subpopulations of the Australian Merino breed.” *Animal Production Science* doi: org/10.1071/AN14560.

Brown, D J and Fogarty, N M (2016). “Genetic relationships between internal parasite resistance and production traits in Merino sheep.” *Animal Production Science* doi.org/10.1071/AN15469.

Brown, D J and Swan, A A (2016). “Genetic importance of fat and eye muscle depth in Merino breeding programs.” *Animal Production Science* 56 (4): 690-697 doi.org/10.1071/AN14645.

Brown, D J; Fogarty, N M; Iker, C L, Ferguson, D M; Blache, D and Gaunt, G M (2016). “Genetic evaluation of maternal behaviour and temperament in Australian sheep.” *Animal Production Science* 56 (4): 767-774 doi.org/10.1071/AN14945.

Bunter K L; Swan, A A; Purvis, I W and Brown, D J (2016). “Pregnancy scanning can be used as a source of data for genetic evaluation of reproductive traits of ewes.” *Animal Production Science* 56 (4): 679-689 doi.org/10.1071/AN14630.

Li, L and Brown, D J (2016). “Estimation of genetic parameters for lambing ease, birthweight and gestation length in Australian sheep.” *Animal Production Science* 56 (5): 934-940 doi.org/10.1071/AN14129.

Walkom, S F and Brown, D J (2016). “Genetic evaluation of adult ewe bodyweight and condition: relationship with lamb growth, reproduction, carcass and wool production.” *Animal Production Science* doi.org/10.1071/AN15091.

5.20.4.3 Book chapters

Dominik, S and Swan, A A (2014). “Resilience, tolerance, robustness and genotype x environment interaction in Merino sheep breeding.” In S Hermes and S Dominik (Eds.),

Breeding Focus 2014 – Improving Resilience, pp 115-127, Armidale, NSW: University of New England.

Kinghorn, B P; Banks, R G and Simm, G (2014). Genetic Improvement of Beef Cattle. In D Garrick and A Ruvinsky (Eds.), The Genetics of Cattle 2nd edition, pp 451-473, Wallingford, Oxfordshire: CAB International.

Walkom, S F and Brown, D J (2014). “Breeding for resilience and resistance in Merino sheep.” In S Hermes and S Dominik (Eds.), Breeding Focus 2014 – Improving Resilience, pp 141-156, Armidale, NSW: University of New England.

6 Conclusions

The objectives for this project have been achieved. The system developed for routine genetic evaluations continues to work well. This is also strengthened due to the excellent cooperation between AGBU, SG and MLA staff. More recently, facilitated by SG and Sheep CRC, there has been an increase in the collaborative work conducted with leading geneticists from other research organisations. Research has been conducted on a range of issues related to the genetic evaluation system and the results have been implemented into OVIS to improve the accuracy of the EBVs. All databases have been increasing in size and the release of ASBVs through SG has highlighted the benefits of this research and development. Additional EBVs, reports, and diagnostic tools have been developed to enhance the service provided to sheep breeders.