final report

Sheep Genetics

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Genetic Evaluation for Australian Sheep ~ Expanding the Foundation

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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).

Research included the estimation of genetic and phenotypic parameters (heritabilities, 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, 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 Technical Committee meetings, in scientific papers, conference contributions, newsletter articles and at field-days working 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 for Sheep Genetics (SG) between July 2006 and June 2010.

- 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 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 alternative methods.
    - Updating variance components and adjustment factors for all breeds.
    - Development of new reporting software.
    - Implementing new systems for routine evaluation.

- 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 process implemented by industry have enabled annual genetic progress to increase in all breeds.

- 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, but there are currently no SheepObject indexes among the standards. The ability to develop customised indexes for individual procedures 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.

Contents

1 Background

The Animal Genetics and Breeding Unit (AGBU) routinely runs OVIS to provide Sheep Genetics ASBVs for their LAMBPLAN and MERINOSELECT clients. AGBU also provides full support of OVIS and its EBVs and conducts research and development activities for OVIS, LAMBPLAN and MERINOSELECT. This report comes at the end of a four year period (July 2006 to June 2010). This document details the progress and results that have been achieved for each milestone as set out in the work plan and the research contract.

2 Purpose and description

The purpose of this project was to further improve the capacity of the OVIS system to provide accurate Estimated Breeding Values (EBVs) for the range of traits that contribute to sheep enterprises across a range of production systems and target markets.

For the last 10 years the Animal Genetics and Breeding Unit (AGBU) has been producing EBVs for LAMBPLAN and MERINIOSELECT on a regular basis using its OVIS software developed to estimate the breeding values for sheep. MLA supported research at AGBU has mostly focused on the estimation of the parameters required for OVIS (adjustment factors, heritabilities, genetic correlations), on alternative models and traits and on the further development of the software eg. extra reporting functions, diagnostic tools and accommodating changes in data and new clients.

As LAMBPLAN and MERINOSEELCT increase in adoption across a wider range of sheep enterprises, production systems and target markets, data is becoming available on a larger number of traits. This increase in amount and quality of data makes it possible to improve the statistical models and hence the accuracy of EBVs (which allows more rapid genetic progress).

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

3 Objectives

The objectives of the project were:

1. Through the provision of a world-class genetic evaluation system, support MLA and AWI’s objective for faster genetic change in the Australian sheep industry.
2. Incorporate the SheepObject programs as an integrated part of the whole Sheep Genetics genetic evaluation package.
3. Develop evaluation models for novel traits not yet included in the Sheep Genetics evaluation and incorporate them through the OVIS system to the Sheep Genetics evaluation system.
4. Participate in the SG technical committee and ensure that there is a high level of rigor applied to technical development within SG.
5. Undertake breeding program design analysis using the Z-PLAN program to provide cost benefit analysis on additional traits to be recorded and on improved breeding program designs.

3.1 Additional Details ~ Project Management

Detailed project work plans were developed by Research Organisation staff, MLA and AWI staff and the Sheep Genetics Technical Committee on a regular basis.

At the request of the SG Technical Committee a significant amount of time has been spent working on research and development activities not originally specified in the work plan. This meant that some research topics which were outlined in the original work plan were not completed as these alternate research projects were given a higher priority.

In addition a significant amount of time has also been spent working on activities related to SG. As all staff members working on this project were members of the Technical Committee some time was spent preparing for and attending these meetings.

4 Regular updates of existing variance components meat and wool sheep.

4.1 Analysis of reproduction traits

Evaluation of alternative models for reproduction traits (number of lambs born and weaned) in all breeds was conducted. Additional research was conducted by AGBU and NSW I & I staff. This clearly demonstrated that more reliable breeding values would be produced if a repeatability model was applied to data with a more complete level of recording. Two main recommendations arose from this work;

1. A repeated records model would enable SG to analyse the data more appropriately.
2. To adopt an improved model for analysis additional information is required from breeders.

The Technical Committee recommended the adoption of this approach and in August 2007 changes were introduced as follows;

- MERINOSELECT ~ A repeatability model was implemented in OVIS and the data screened so that only the flocks and years where an adequate level of recording for reproduction rate has been achieved were included in the analysis. The criteria include the number of dry ewes, number of dead lambs and the frequencies of each birth and rearing type.
- LAMBPLAN ~ The data were screened as described above and used with the old model of one average record per ewe.

Implementation of these changes required significant changes to the database, database export routines, OVIS source codes and parameter files. The new model also required breeders to collect additional data. A document detailing the new database requirements was compiled and distributed to breeders.

4.2 Routine analysis of reproduction traits ~ Service sire screening

A number of breeders expressed concern over possible service sire effects on female reproduction traits. Preliminary analyses observed significant service sire effects in industry data. Further investigations were conducted to examine the impact of service sire effects on Sheep Genetics reproduction data and compare models with service sire effects. The results can be summarised as follows:

- Including service sire effects in the model removes both additive and residual variance and results in a decline in the heritability of the traits
- Including service sire effects changes the trait definition from “nlb/w per ewe joined” to “nlb/w per ewe serviced”
- The current model is producing reliable prediction of progeny performance
    - The alternate models did not significantly improve these predictions

- Service sire effects are generally a problem from ram breeding flocks using single sire mating and thus is not an important effect commercially where multiple sire joining is used.
- The data should be screened to remove reproduction records from the analysis were the service sire has been deemed as failed (achieved <70% of the ewes lambing).

Diagnostic testing also revealed that in some breeds (Merino's in particular) the majority of DRY lambs were submitted with missing service sire. Thus the service sire screening was removing a large number of the DRY records. However, it was also observed that the service sire screening was removing a large number of ewe lamb (ewe lambing at approximately 1 year of age) records which is desirable. Thus the service sire screening was edited so that;

- Lambing records with missing sire are not removed from the analysis
- Lambing records from ewe lambs are only excluded if less than 50% of ewes lambed

These strategies have now been implemented in the routine MERINOSELECT and LAMBPLAN runs. A more detailed description of this work is included in the December 2008 Technical Committee papers.

4.3 Routine analysis of reproduction traits ~ Influence of body weight

There have been ongoing concerns that animals with a weight record but no actual reproductive data on themselves (or female relatives) may be getting spurious NLW EBVs and hence indexes. To investigate this issue the variances of breeding values were examined between and within flocks. Genetic parameters were also re-estimated for these traits using current data. The impact of reproduction on MERINOSELECT selection indexes was also studied extensively.

Within flocks, the variation in EBV's and correlations between them are close to expectation given our genetic parameters. Across flocks, the variation was substantial, ranging from 1.3 to 1.8 times the expectation from our within flock genetic parameters. Two of the traits with the highest variation were ycfw and ywt.

This is not a deficiency of the genetic evaluation model; rather it is a reflection of the fact that the Merino is a very diverse breed. The MERINOSELECT analysis is analogous to a multibreed BREEDPLAN including all Bos Taurus breeds.

The following table shows current, old (July 2007) and estimated genetic correlations between NLW and weight/scrotal circumference traits:

	July 2007	Estimated	Current
YWT	0.30	0.24 ± 0.08	0.15
HWT	0.35	0.34 ± 0.06	0.15
AWT	0.35	0.19 ± 0.10	0.15
YSC	0.30	0.35 ± 0.14	0.30
HSC	0.30	0.16 ± 0.11	0.30

The estimated parameters are similar to those defined in July 2007.

A review of the literature on the body weight – reproduction correlation was also conducted and in summary, the average genetic correlation between body weight and NLW from these sources is around 0.3, in line with our current MERINOSELECT parameters.

However, there was evidence from a body weight selection experiment conducted by NSW DPI to support a non-linear relationship at the genetic and phenotypic levels, such that the correlation is more strongly positive at lower body weights but is closer to zero at higher body weights. Given that indexes typically aim to increase or maintain body weight, it is most realistic to assume a lower genetic correlation. However, it will be important to provide a warning that any selection leading to lower body weights may also result in poorer reproductive performance. As a consequence of this likely relationship, the genetic correlations used in MERINOSELECT were reduced, as shown in the “Current” column in the table above.

4.4 Weaning Weight

Sampling distributions for the regression of progeny performance on sires estimated breeding values (EBV) were estimated for weaning weight in the MERINOSELECT database. Mean regression coefficients from these distributions were used to compare the effects of data quality and the model used for evaluation. Results showed that better quality data with dam pedigree and date of birth recorded, and an evaluation model which included sire by flock-year interaction improved the prediction of progeny performance from estimated breeding values (Swan and Brown, 2007).

4.5 Sire by Flock Year effects

4.5.1 MERINOSELECT

Sire by flock interactions were estimated using MERINOSELECT data. A summary of the results of these analysis was included in the Nov 2006 and June 2007 Technical Committee reports. Significant effects were estimated for all traits and as a result of this work changes were implemented into the routine evaluations. Sire by flock year interactions were included in the MERINOSELECT analyses from August 2007. Implementation for the other breeds was planned to follow in January 2008 however due to complications discussed below the Terminal sire analysis was delayed until July 2010.

4.5.2 LAMBPLAN

AGBU completed the bivariate analyses of all traits with data recorded form the Terminal sire, Border Leicester, Coopworth and Corriedale database. These analyses were run with and without the sire by flock effect. This included developing new tools to estimate the correlations between reproduction (as a repeated record model) and all the other production traits. The results observed show that our current parameters were generally very close to these new estimates. However there were large reductions in the direct heritability for body weight and fleece weight traits with the inclusion of the sire by flock effects. This was particularly a problem in the Terminal sire breeds. The reduction was in the range of 0.05 to 0.20 in direct heritably where as for traits without maternal effects the reduction was generally < 0.05.

4.5.3 LAMBPLAN ~ Terminal sire breeds

Sire by flock interactions were estimated using terminal sire data. Recent research efforts have been devoted to understanding the ongoing problem of large reductions in the direct heritabilities which are observed when sire by flock-year effects are fitted for traits with maternal effects also included in the model. The reductions were in the range of 0.05 to 0.20 in direct heritably whereas for traits without maternal effects the reduction was generally less than 0.05. Significant effects were estimated for all traits.

Each traits was analysed with 5 models

1. Current SG model
2. Current SG model + sire*year

3. Current SG model + sire*flock
4. Current SG model + sire*year + sire*flock
5. Current SG model + sire*flock*year

The results showed a very large reduction in heritability with the inclusion of sire*flock*year. The very large drop in direct heritability was concerning. A sire model was then compared with the following random effects;

sire + sfy + ide(dam) + residual

This model produced very similar results to the animal model. To investigate whether this reduction in heritability was due to genotype by environment effects, multivariate models were constructed with each trait broken up into different traits based on mean performance of the contemporary group. Records were assigned to one of 5 traits depending on the quintile of their contemporary group.

The conclusions of this work are;

- In all traits a better fit was obtained with the addition of a sire by environment effect when compared to the basic model.
- When S × Y and S × F were fitted separately it appeared that the two components could not be easily separated leading to slightly inflated estimates of both effects.
- Estimates of S × Y and S × F were of similar size to their contribution of phenotypic variance. However, in all weight traits and scrotal circumference S × Y appeared to be the most important effect, providing a better fit, with higher log likelihood values than S x F. By contrast, for carcass traits and worm egg count S × F appeared to be the most important of the two effects.
- Model 5 did not always give a better fit than Model 4 but the combined effect of S × FY meant that by containing one less random effect it was generally the most appropriate model to choose.
- Estimates of S × FY ranged from 3 to 7 % of the phenotypic variance for weight traits and from 1 to 2 % of the phenotypic variance for carcass traits, scrotal circumference and worm egg count.
- The large reductions in the direct heritability for the weight traits are of some concern. As yet there is no satisfactory explanation for this effect.
- The genetic correlations between quintiles of production were significantly less than 1.0

Further investigations were conducted using weaning weight from the terminal sire database.

Initially different strategies of data selection were investigated;

1. Selecting complete PD flocks with > 10 years of recording
    a. Animal and sire models were compared for a number of data sets
2. Poll Dorset flocks with NSW post code
3. Poll Dorset flocks with 23** post code
4. Flocks with variation in age in their CGs
5. Only selecting sires used across many flock-years since 1995 (>=30 flock years)
6. Flocks with the most daughter-dam combinations of weaning weight records.
7. Only using the Meat Elite flocks

In all these scenarios inclusion of sire by flock year fitted with the maternal genetic effect resulted in a large reduction in the direct heritability. Inclusion of the direct maternal covariance resulted in slightly higher direct and maternal heritabilities. A more detailed description of this work is included in the December 2008 Technical Committee papers.

The data were also analysed within breeds to eliminate any possible effects of crossbreeding within this terminal sire data set. Within breed estimates of variance components for weaning weight were estimated for Poll Dorset, White Suffolk, Suffolk and Texel breeds. There are some significant differences in heritability across the breeds and all breeds have a lower heritability than the current OVIS value of 0.20. The next step in this work is to screen data to only use data with better levels of recording.

A AAABG 2009 conference paper (Brown et al. 2009) was prepared on this topic which included some additional research. The paper is included in the July 2009 Technical Committee report.

The conclusions of this work are;

- When sire by flock year effects are fitted to the entire data set too much genetic variance is removed.
- Fitting sire by flock year effects only to progeny from sires used across multiple flock–years avoids the reductions in heritability. These analyses resulted in parameters similar to the models without sire by flock year included but with a small and significant sire by flock variance
- For the non-weight traits the variance components estimated with the inclusion of the sire by flock-year effects are relatively similar to those currently being used.

A set of new variance components was agreed upon at the July 2009 Technical Committee meeting and test runs have been completed and compared to current ASBVs. These comparisons were reported to the December 2009 Technical Committee meeting. Sire by flock year effects were implement in the Terminal sire run in July 2010.

4.6 Estimates of Heterosis in maternal breeds

Maternal breeders have been requesting an across breed analysis for some time. One of the main reasons this has not been implemented is due to the heterosis that is likely to occur for some traits, especially reproduction. If heterosis is not accommodated the across breed analysis is likely to produce biased ASBVs.

Sheep Genetics data from the Maternal database on 15 sheep breeds and their crosses were analysed to examine breed differences and to estimate crossbreeding effects for eight traits.

The main findings were:

- Significant direct and maternal heterosis estimates were obtained for all traits except Pfat and Pemd
- Preliminary analyses showed negative heterosis for reproduction traits, but the data now needs to be re-analysed using a repeatability model.
- Body weight and fleece weight estimates agree with mean literature estimates.
- There was significant variation in heterosis between the different breed combinations
- An attempt was made to group breeds into types (Merino, Meat, Dual Purpose) and compare mean levels of heterosis between these groups. Trends in the results of these analyses were inconsistent.

Further work is needed before we can be confident about levels of heterosis. This work is required before a reliable across breed maternal analysis can be produced. The analyses are currently being updated incorporating additional data from the maternal central progeny test.

5 SheepObject

5.1 Development of SheepObject

Development of a web interface system for SheepObject was first outlined in milestone 5 of this project. This system has three components:

1. A database to manage breeding objectives, selection indexes and genetic parameters.
2. The SheepObject programs developed during MLA project SHGEN.009, together with software to connect these programs with the database in 1.
3. A web interface allowing users to operate 1 and 2.

The web interface provides the ability for users to manage breeding objectives, selection indexes and genetic parameters.

Breeding objectives: all breeding systems developed under SHGEN.009 can be handled, including Merino, terminal sire by Merino ewes, terminal sire by first cross ewes, and maternal sire by Merino ewes. Two new breeding systems were added, for self-replacing dual purpose breeds and self-replacing meat breeds. Breeding objectives created by other software systems or with user defined economic values can also be included. Once created, objectives can be modified and compared with other objectives.

Selection indexes: are managed in the SheepObject database as “selection index sets”, which define a group of breeding objectives to calculate indexes for, a group of animals within a genetic evaluation on which these indexes will be calculated, the traits measured (selection criteria) for each index, and results including comparative statistics. The idea is that each selection index set allows comparison of indexes and breeding objectives based on both theoretical expectations and application to groups of animals.

Genetic parameters: management of genetic parameters presents a significant challenge for the SheepObject system. There are in excess of 50 traits with estimated breeding values for a number of different breeds in the genetic evaluation system. In addition there are genetic traits which are specific to SheepObject breeding objectives. The web interface includes a system which will simplify the task of managing these parameters. This system has the following features:

- Genetic parameters for each breed stored in the SheepObject database.
- Access to these genetic parameters via the web interface.
- Ability to modify parameters from the web interface, including the capacity to annotate modifications.
- Ability to archive versions of parameter sets.
- Ability to compare archived versions.
- Ability to check whether matrices are positive-definite, and if they are not, to alter them by “bending”. Corrections are then updated in the database.
- Ability to download matrices to csv files.

User management: the web interface includes a user management facility. Objectives and indexes cannot be accessed unless a user has been authenticated. Objectives and indexes are owned by individual users who can make them either private (other users cannot view) or public (other users can view but not alter). Users can alter or delete objectives and indexes which they own. Genetic parameters can only be accessed by nominated users.

A workshop on SheepObject was held on 31 March 2009, with participants including: Andrew Swan, Hans Graser, Allan Casey, Jess Richards, Steve Semple, Geoff Lindon, Jen Smith, Richard Apps, Alex Ball, Sam Gill, Daniel Brown, Julius van der Werf. The purpose was to review SheepObject and the work done on the web interface to the software since 2007, and to plan further development of the system.

The outcomes of the workshop were:

1. A process to validate objectives for terminal and maternal sire breeds was outlined.
2. No further development of the web interface was considered necessary at the moment.
3. The importance of documenting SheepObject was identified.

The full workshop report is attached as an appendix.

The validation process has been applied to one objective, for terminal sires mated to Merino ewes in a dry winter environment (such as the Northern Tablelands of NSW). The objective was shown to be highly robust, and indexes calculated on sires of the 2008 drop progeny in the LAMPLAN Terminal evaluation were highly correlated with the indexes currently used by breeders (0.99 with Carcass Plus and 0.96 with LP2020). Our recommendation based on these results was that SheepObject indexes can be used reliably by terminal sire breeders, and that the software can be used to develop customised indexes. The full report on the development and validation of terminal sire breeding objectives is attached as an appendix to this report.

5.2 OVIS and SheepObject systems operating effectively together to generate a number of standard indices

The software engine to generate SheepObject indexes from OVIS breeding values is in place. Indexes are being routinely generated from OVIS analyses, but there are currently no SheepObject indexes among the standards.

5.3 Customizable indexes available for producers.

The ability to develop customised indexes for individual procedures is now in place with the development of the web interface described above. So far only internal testing has taken place. 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.

6 Novel traits and measures examined for inclusion in genetic evaluation.

6.1 Maternal temperament traits

Data from several MLA funded research projects and SG flocks were merged to study temperament traits. The data sets were;

- MLA funded flight time and agitation box project
- Industry flocks with maternal temperament traits
- Maternal Central Progeny Test

The three temperament traits studied were flight time, agitation score from an isolation box, and maternal temperament scored at tagging. AGBU merged these observations with the SG database to conduct genetic analysis of the temperament traits.

Flight time, agitation score and maternal birth score traits were moderately heritable and there were small but favourable correlations between them. Correlations with other production traits were limited with some trait combinations still lacking data to estimate accurate genetic correlations.

6.2 CRC novel wool traits

A project was conducted in conjunction with Sheep CRC Project 1.2.6, in which wool samples representing some 29 Sheep Genetics flocks were tested for a range of novel traits including resistance to compression, crimp frequency and measured and assessed style traits.

The conclusions from this work include;

- The novel traits of crimp frequency, crimp definition, wool colour and resistance to compression were moderately to highly heritable and therefore could be improved through selection.
- Curvature is significantly genetically and phenotypically related to crimp frequency such that there is little need for direct measurement of crimp frequency.
- The results also indicate that there is significant variation between Merino flocks in their diameter and crimp relationships. That is, some flocks have a measured fibre diameter consistently different to that predicted from their crimp frequency.
- A trueness to type score was able to be derived for each sheep which indicates its fibre diameter relative to that expected based on crimp frequency.
- As curvature and crimp frequency were significantly correlated a TTT score was also generated using fibre curvature rather than measured crimp frequency.
- This scoring system requires further consultation and validation by industry but could be implemented using existing information from Sheep Genetics.
- Phenotypically, resistance to compression could be predicted with moderate accuracy from the other wool measurements made in this study.
- Genetically, resistance to compression was significantly related to many traits, therefore resistance to compression could be included in the breeding objective without the need for direct measurements.

6.3 Lambing ease and gestation length

Lambing ease (LE) and gestation length (GL) are two important traits which influence Australian lamb production. Records for both these traits were available from the Sheep Genetic database. Lambing ease was scored from 0 to 5, with 0 being not observed and 5 being special assistance such as veterinary intervention. Lambing ease records of 0 were not included in these analyses. Genetic analysis was conducted on the traits with the aim of assessing the feasibility of developing a routine genetic evaluation for Sheep Genetics.

Variance components were estimated with all traits treated as traits of the lamb with maternal genetic and permanent environment due to the dam effects included. Lambing ease had low estimates of direct and maternal heritability of 0.06 and 0.04 respectively. There was however a large permanent environment effect due to dam of 0.24. Gestation length was highly heritable (0.53) with high maternal genetic and permanent environment effects (0.16 and 0.25 respectively). Lambing ease and gestation length were positively genetically correlated with birth, weaning and post weaning weight and negatively correlated with number of lambs weaned. LE was not significantly correlated with GL. Various models and ways of expressing traits were also investigated. Details were presented in the May 2008, March 2009 and July 2009 Technical Committee reports.

Modification of the CATCON software (calving ease software used in BREEDPLAN) was completed and new software to extract and prepare the Sheep Genetics data for CATCON was developed. An additional analysis has now been implemented so that ASBVs and accuracies for gestation length and lambing ease are estimated routinely for each breed where these traits are recorded. Currently all the main breeds have LE and GL ASBVs and accuracies produced.

6.4 Days to lambing

The Centre Plus Merino flock submitted data on their reproduction records to test whether days to lambing is a heritable trait in Merino sheep.

Variables of dam, joining contemporary group, whether the ewe reared or lost her lamb, year of joining, service sire, ram in date and ram out date were extracted from the Centre Plus dataset. These data were then merged with additional progeny information: sex and birth date of the current progeny as well as birth type and rear type of the previous progeny which all exist in the Sheep Genetics database. In addition, dam age at lambing was calculated and days to lambing was calculated as the difference between lamb date of birth and ram in date. Any ewes that did not lamb were given a penalty days to lambing record of 205 days. This was calculated by examining the distribution of the days to lambing trait and assigning a penalty that was sufficiently (but not excessively) higher than the longest days to lambing record in the dataset.

The conclusions from this work include;

- There are large phenotypic deviations for days to lambing between ewes but there was not enough data to be able to determine how much of this difference (if any) was genetic.
- This data required extensive editing and manipulation before it was able to be analysed. Appropriate methods of collecting and storing such data need to be developed before further analyses can be conducted.
- Significant fixed effects in this analysis included birth type of previous lamb and a contemporary group * service sire * year interaction.
- There were insufficient data records and insufficient repeat records per ewe to be able to accurately estimate heritabilities or genetic correlations.

6.5 LoinMax data analysis

Breeders have supplied genotype results from the LoinMAX test from Catapult Genetics (now Pfizer). The analysis aimed to quantify the effects of each genotype in these flocks. The data were analysed to estimate the size of effect and examine gene frequencies.

The conclusions of this work were:

- There is a significant effect on muscle in 2 of the 3 flocks examined
- The effect is not consistent across the 3 flocks
- The size of the effect is approximately 1 to 2% of the phenotypic mean
- There was a significant effect on birth weight across the whole data set
- There was a significant effect on fat in one of the flocks
- There was no effect on post weaning weight
- Much of the effects are being captured in the ASBVs
- The genotypes had additional effects above that of the BVs

Some further analyses were performed restricting the dataset to pure Poll Dorset animals. A detailed description of this work is included in the May 2008 Technical Committee papers.

6.6 Myostatin data analysis

Genotype results for the Myostatin locus were provided by Dr Rob Banks on approximately 30 industry sires. The gene, known as Myostatin GDF8, has been shown to produce sheep that have up to 10 per cent more leg and rump muscling and 14 per cent less carcass fat. 19 of the 35 sires listed with Myostatin genotypes were able to be identified in the Sheep Genetics Terminal sire database. The conclusions of this work were;

- There is a significant effect of the gene on muscle and fat
- There is a large (but non-significant) effect on weight when data is analysed across breeds
- Part of the effect is captured in the ASBVs
    - Some of the effects are associated with weight differences between breeds
    - When examined within Texel only data there is no effect on any of the traits investigated
- Much more data is required to verify these results.

A more detailed description of this work can be found in the May 2008 Technical Committee papers.

Additional data was also obtained from the Sheep Genomics project and analyses completed. This work was documented in the September 2008 Technical Committee papers.

6.7 Number of lambs scanned

Reproductive performance of ewes is important to all sheep enterprises and determines the number of lambs available in each generation. Number of lamb born (NLB) and number of lamb weaned (NLW) are the most commonly recorded traits. Many breeders now routinely pregnancy scan using ultrasound scanning and record the number of lambs scanned (NLS). This study aimed to estimate the genetic parameters of NLS, NLB and NLW and the genetic correlations among them in three independent data sets. The three data sets were; 1) CW ~ a Sheep Genetics Coopworth breeder, 2) CP ~ a Sheep Genetics Merino breeder and 3) the Sheep CRC information nucleus flock.

The direct heritability of NLS across the three populations was similar, ranging from 0.06 to 0.07. Animal permanent environment effects were not found in CW, however accounted for 3% and 7% of total variation in CP and INF, respectively. Repeatability was 0.06, 0.10 and 0.13 for CW, CP and INF, respectively. High genetic correlations with NLB and NLS were found in all populations, from 0.89 to 0.99.

Genetic parameters for number of lamb scanned (NLS) from this study are the first reported of its kind. The estimated direct heritabilities were 0.06-0.07 and high genetic correlations were found among NLS, NLB and NLW. These genetic parameters could be used for the genetic improvement of reproductive rate in Australian sheep breeds. With more data available (especially NLB and NLW recorded in 2009), more accurate estimates can be calculated.

This work is continuing with the aim of defining a model and variance components so that number as lambs scanned can be included as additional section criteria to aid in the improvement of reproductive rate. A full report was included in the December 2009 Technical Committee report.

6.8 Estimated Breeding Values for Visual Traits in Sheep Genetics

Visual traits have always been important to sheep breeders, and it is likely that the availability of EBV's for visual traits could help with the adoption of Sheep Genetics ASBV's.

With a standard recording system now available for use in the sheep industry (the AWI-MLA Visual Sheep Scores Guide), development of EBV's for visual traits is now possible. The document attached in the May 2008 Technical Committee papers examines the possibilities of developing a genetic evaluation system for these traits, and covers the definition of traits, priorities for EBV's, analysis models, availability of data, and delivery of EBV's.

ASREML was used to estimate variance components and fixed effects for the wrinkle traits. Using these results and information from research flocks a new OVIS analysis has been developed including four traits: early and late breech wrinkle and early and late body wrinkle. This new OVIS analysis has now been implemented so that ASBVs, accuracies and linkage statistics for visual breach traits are estimated routinely with each MERINOSELECT analysis.

A prototype analysis has been developed with additional traits, including early and late expressions of breech cover, dag score, fleece colour, fleece rot, fleece character, and staple weathering. This is currently undergoing testing.

7 Improved genetic grouping strategies

Genetic groups are a very important part of the SG analysis which allow OVIS to separate the genetic differences within and between different populations/strains/breeds/flocks of sheep. If OVIS did not use genetic grouping all animals with unknown pedigree would start from a base of zero for each trait.

7.1 MERINOSELECT

Improved genetic grouping strategies for the MERINOSELECT analysis has been a major focus over the last 4 years. Investigations by members of the Technical Committee reveal several flocks for which genetic group solutions appeared to be producing strange genetic trends. A significant amount of work was conducted to understand the issues for each of these flocks and communicate with the breeders. A number of meetings were conducted to discuss these issues on a one on one basis.

Research has demonstrated that flocks with long performance recording histories and partial pedigree are having unreliable genetic group solutions estimated and as a consequence, poor estimates of genetic trend. The Technical Committee agreed to remove old data from these flocks to avoid the problems with estimation of the genetic group solutions over time. Removing the old data from the analysis resulted in some re-ranking of sires and flocks. However, the correlations are generally high (>0.9). Dropping data from certain problematic flock produces more favourable changes in the analysis than removing all the older non pedigreed animals.

7.2 LAMBPLAN ~ Terminal sire breeds

Historically the Terminal Sire Analysis allocates base animals to genetic groups based on breed and year of birth. However this only applied to the four main breeds of Poll Dorset, White Suffolk, Suffolk and Texel which represent 87% of the animals in the analysis. All remaining base animal are allocated to one common genetic group. Over the last five years the data has continued to improve in quality and the linkage between breeds has increased sufficiently for SG to make some important enhancements to the terminal sire analysis. OVIS will now use the following genetic grouping strategy;

- There are four groups for the largest breeds (which have previously been used)
    - Poll Dorset, White Suffolk, Suffolk and Texel
    - The New Zealand animals from these breeds also join their Australian counterparts

  - There are approximately another 12 year groups from 1991 to 2002 for each of these breeds
- A further 27 groups have now been added for numerically smaller breeds. These include each of the breeds routinely included in the terminal sire breeds analysis.
- All remaining base animals form a final common group.

This modified grouping strategy produces more reliable ASBVs for the smaller breeds. The impact of these genetic group changes is that all the flocks from the smaller breeds will see some significant changes to their ASBVs. This affect will be more apparent in flocks with large amounts of missing pedigree.

7.3 The effect of selection lines in QPLU$ and SDF on the Sheep CRC Information Nucleus Flock (INF) genetic evaluation

While examining INF data SG staff discovered non-random allocation of dams from QPLU$ and SDF selection lines. The difference in merit of these dams is accounted for in the MERINOSELECT runs as all the source data and genetic groups are included. However as these data are not included in the Terminal sire run these genetic group effects are not accounted for. This issue was investigated in more detail in the Terminal sire data.

To examine these issues numerous runs were completed;

1. A within flock run using INF data only
2. A modified across flock terminal sire run
3. A comparison of 5 techniques for accounting for these dam effects
    a. Normal across flock terminal sire analysis
    b. Additional genetic groups defined for QPLU$ and SDF dams
    c. Additional pedigree added for QPLU$ and SDF animals
    d. Additional pedigree plus source performance data added for QPLU$ and SDF flocks
    e. Combination of source performance data added for QPLU$ and SDF flocks and the extra genetic groups defined for QPLU$ and SDF dams (2 + 4)

In each of these runs the genetic group allocation software was modified to create genetic groups for each selection line at both QLPU$ and SDF.

The results showed that there were differences between selection lines for Carcase+ index traits in QPLU$ and the SDF flocks. At the index level the effects appear to be larger for the QPLU$ flocks in comparison to the SDF flocks. In total there are 26 index points between the highest and lowest ranked QPLU$ genetic group, whereas there are only 7 index points between the SDF groups.

The graphs presented in the March 2009 Technical Committee report show that when using INF data only there are only small differences between the breeding values of sires in either of the analyses. Post-weaning weight appeared to be the trait that showed the most sensitivity to changing the genetic group modelling, however the correlation in sire breeding values was still relatively high between the two analyses. When the genetic groups are applied to the whole industry data set the differences are not as large as the INF data only accounts for a small proportion of the data for sires.

For the five methods for accounting for the QPLU$ and SDF dam merit, with the exception of 2 sires it appears that including the addition genetic groups for QPLU$ and SDF dams corrects for most of these effects. Software is now available to apply the genetic groups in the routine analyses for LAMBPLAN. Given the effects observed above on the sire ASBVs we concluded that including the dam genetic group effects is sufficient. The extra genetic groups were included in the routine Terminal sire runs in March 2009.

A similar investigation was conducted in the Border Leicester analysis. The results showed that there is no significant benefit from fitting these extra genetic groups in the Border Leicester analysis.

A more detailed description of this work was prepared for the March 2009 Technical Committee meeting.

8 Additional Research and Development.

8.1 Linkage analyses

The linkage analysis software was modified to re-order the design matrix which resulted in significant improvements in the time required to invert the matrix. As a result of the improvements in processing time an additional year of data has been included in the linkage analysis.

8.2 Trans-Tasman analyses

Data were made available from the New Zealand Corriedale society which has genetic links to the Australia database. The data were imported into the SG database and analyses were run using OVIS. The breeding values were compared from three analyses; Australian data only, New Zealand data only and a combined Trans-Tasman analysis. While the EBVs compared well it was apparent numerous links were missing in the data. As a result the databases were updated and the analyses re-run. A report was prepared and presented to both the Australian and New Zealand breed societies. The NZ data is now included in the routine analyses for Australian Corriedale.

A Trans-Tasman analysis has also been completed for the Coopworth breed. However the NZ data is not yet included in the routine runs.

8.3 Effects of recording strategies on reproduction ASBVs

Members of the TC expressed concern that flocks that were submitting Dry and Dead lamb records were being penalized. The aim of this work was to quantify the effects of recording body weight, scrotal circumference and reproduction traits on the mean reproduction performance.

The number of animals in each flock with body weight, scrotal circumference or reproduction traits were counted and combined with the mean NLW ASBV, standard deviation of NLW ASBVs and mean accuracy for NLW. This data set was then analysed in the following ways;

1. regression of average merit or accuracy on the number of animals recorded for each trait type
2. a factor of 1 or 0 was created for each trait type. 0 was for flocks with <50 animals recorded and 1 for all flocks with >= 50 records. The effect of this factor on average flock merit and accuracy was then estimated.

These analyses were also repeated for the Border Leicester and Merino analyses.

Conclusions

- Border Leicester
    - Little effect of recording any trait group on the flock mean EBV for NLW

    - The exception was a significant positive (3.4%) for those flocks with body weight and NLW recorded
    - Recording all trait groups gave a significant increase in average accuracy for NLW and in the variation of breeding values within flocks
- Merino
    - Little effect of recording any trait group on the flock mean EBV for NLW except a significant but small negative (-0.6%) for body weight (as a 0 or 1 factor)
    - Recording all trait groups gave a significant increase in average accuracy for NLW and in the variation of breeding values within flocks
- In both data sets the flocks that are recording these trait groups are not above average for NLW.
- The results suggest that the analysis is behaving as expected.

8.4 Toland ~ Selective Recording proposal

An alternative Merino ram selection method has been proposed to the Technical Committee by a Merinoselect breeder. This proposal involves measuring all progeny for post-weaning weight (PWT) and then culling 50% of the male progeny based on both visual culling and PWT EBV's. Results from this analysis were presented at the Feb 2008 Technical Committee meeting where it was proposed that a simulation should be run to determine the effect of varying culling percentages on the selection accuracy of sires and young male animals.

The conclusions of this work were;

- Increasing the total culling percentage results in reductions in both the regression coefficients and correlations for sires and progeny regardless of number of sires.
- Wool traits were affected more than yearling weight.
- The impact of varying the percentage of animals selected on visual scores was minimal.
- It was assumed that visual traits are uncorrelated to production traits in the simulation, which may not be true.
- Comparisons of progeny regressions and correlations could also be split by sex and selection status in males to be more informative.

A more detailed description of this work is included in the September 2008 Technical Committee papers attached to this report. As a result of this work the QA manual is being modified and newsletter articles published to extend the outcomes to industry.

8.5 AMSEA report

A special effort was made comparing EBV's from MERINOSELECT with those from an analysis including only data from the Merino Superior Sires (MSS) database. This was in response to a request from AMSEA who were considering the use of MSS-only EBV's rather than ASBV's. An lengthy report was prepared (see Appendix) and presented at the AMSEA Executive meeting on 25 June 2008. AMSEA decided to continue using ASBV's for future editions of MSS. This has also been noted in the report for Milestone #8 in SGA.005

8.6 Serial Scrotal Measurements

At the request of Richard Apps, the Border Leicester database was used to examine the genetic correlation between and repeatability of scrotal circumference measurements. This database is not constrained to only Border Leicester's however, approximately 90% had the BL breed code in their ID. The conclusions of this study were;

- Large reductions in phenotypic variance as animals age

- Heritabilities basically constant across age
- Genetic correlations are significantly < 1.0 between ages
- Season has not been taken into account at all as most of the measurements are taken during the middle of the year
- The genetic correlations with reproduction rate have been recently estimated and will be documented in the September Technical Committee papers

A more detailed description of this work included in the May 2008 Technical Committee papers.

8.7 Scrotal Circumference and reproduction

In Milestone 9 a report was presented examining scrotal circumference measure across ages. This investigation was extended to examine the genetic correlation between scrotal circumference and reproduction traits.

The results indicated that both post weaning and yearling scrotal circumference are positively correlated with NLB. Given these results both PSC and YSC traits are effective indirect selection criteria for NLB. There is insufficient data to accurately estimate the correlation between HSC and NLB.

A more detailed description of this work is included in the September 2008 Technical Committee papers. The outcomes of this work have been extended to industry via Sheep Genetic staff and newsletter articles. The outcomes were also used for the recent updates to the genetic parameters used for the maternal breeds.

8.8 Analysis of Keiller Evaluation Study and Faulkner 2007 drop data

Additional dataset were provided by Dr Hutton Oddy for investigation of the Carwell and Myostatin genes. Both these data set were analysed for the effects of both genes on post weaning weight, fat and eye muscle depth. The results suggest that the effects of these genes are not consistent across data sets.

A more detailed description of this work is included in the September 2008 Technical Committee papers.

8.9 Alternative trait adjustments by breed and sex for the LAMPLAN analysis

A review of the current adjustments of post weaning fat depth (PCF) and eye muscle depth (PEMD) for the 4 major terminal sire breeds was performed. Currently in OVIS all of these breeds are adjusted using the same adjustment factors. The aim of this review was to determine if there are any breed or sex differences that we may need to adjust for in OVIS.

Data were extracted from the Sheep Genetics database for the Poll Dorset, Texel, Suffolk and White Suffolk breeds. Preliminary analyses were performed by breed using SAS, with simplified models with respect to contemporary groups (eg birth year/month and sex). Sex effects were significant for all traits, but these analyses did not accommodate the more detailed contemporary group information (eg flock and age slice) used by SG. Final analyses to obtain regression coefficients were performed using ASREML, which allowed fitting of the contemporary group structure used in the Sheep Genetics genetic evaluation.

The results indicate that adjusting differentially by breed did not achieve a significant improvement in the ASBVs produced. More detailed reports were included in the September 2008 and December 2009 Technical Committee papers.

8.10 Early age fat and eye muscle depth measurements

A number of Terminal sire breeders wish to record carcase measurements at earlier ages than currently accepted by Sheep Genetics (post weaning is currently the youngest stage which accepts carcase records). To fully utilize the data available some weaning information is currently pushed up from weaning into early post weaning stage.

This study aimed to quantify how much data are available at younger ages and attempt to estimate the correlations with older age carcase assessments.

Data from the July 2009 Terminal sire analysis and Troy Fisher's PhD study were used to estimate variance components and correlations between ages.

Fat and eye muscle depths taking between 100 and 200 days appear to be highly heritable and also moderately to highly correlated with those taken in the more traditional post weaning period (200 to 300 days). These preliminary results suggest that scan traits measured at ages less than 200 days are genetically different traits to those taken later in life. The short term solution of shuffling data from weaning to post-weaning appears not be creating too many problems. A longer term solution would be the addition of weaning age fat and eye muscle depth trait into the analysis. However due to the lack of animals with repeat observations more data would be useful to gain more accurate parameters which can be used to identify the most appropriate models to use for these repeated expressions across ages.

A detailed description of this work was attached in the December 2009 Technical Committee report. Inclusion of weaning fat and eye muscle depth observations into OVIS is currently under investigation.

8.11 Post weaning wool information in MERINOSELECT

There were 2 main reasons for examining the value of post weaning wool information;

- Numerous breeders who measure wool traits at less than 10 months of age would like these data included in the analysis. Currently groups with an average age of less than 232 days (8 months) are excluded.
- There is a belief held by many that the early age measurements of wool traits are unreliable and that Sheep Genetics should not be using measurements until hogget.

Data was obtained from the March 2009 MERINOSELECT data set. The age of recording of fleece weight and fibre diameter was summarised. Adequate data appears to be available to conduct multiple trait analyses of the 4 age based traits. There is also a large amount of data in the system that has been taken at post-weaning ages but the dates adjusted by the breeders and submitted as yearling so that it is accepted by Sheep Genetics.

At the July 2009 Technical committee meeting a data summary was presented and further analyses suggested. Numerous attempts were made to estimate the correlations between post weaning and yearling wool measurements without success. At present in the MERINOSELECT database there is insufficient repeat measurement of animal across ages to estimate these correlations. A detailed description of this work was prepared for the July 2009 Technical Committee meeting.

8.12 Characterisation of breed structures for combined maternal breed genetic evaluation

As part of the process to develop a combined across breed genetic evaluation for maternal sheep breeds, work is underway to characterise the data structure with respect to breeds and flocks in the Sheep Genetics database.

Data were extracted from the combined maternal dataset. These animals represented 8,863 different breed combinations generated from 51 original breed codes. However about 95% of animals with data were represented in the largest 80 breed combinations, which includes both purebreds and crossbreds. It could be established that the most likely contrasts of importance are purebred Border Leicester, Corriedale or Coopworth sheep compared to their high content crossbreds. Adapting genetic evaluation procedures to accommodate different levels of heterosis in these breed crosses is required for a combined maternal breed analysis, as mentioned above. In addition, some high content Border Leicesters also had East Friesian breed content. However, there appears to be relatively little crossing otherwise between the breeds of interest.

Generally, the high level of mixed genotype data and multi-genotype flocks implies that breed composition should be included in the genetic evaluation system to ensure accurate comparison amongst individuals expressing different levels of heterosis. However, there is considerable variation in breed content which will potentially make it difficult to form breed content groups in which the performance can be reliably estimated for genetic evaluation. Further, there is likely a variable distribution of breed composition across flocks.

Other results suggest that there are several large Border Leicester flocks containing non-purebred animals (based on the OVIS breed designation) who are obtaining EBVs not corrected for differential heterosis, and who are presumably selling non-purebred animals to industry as purebreds. The accuracy of OVIS breed designation needs to be reviewed and the parentage of animals confirmed with the breeders where possible. Following this clarification, these results would suggest that strategies need to be developed for more accurate genetic evaluation in the presence of non-purebred animals.

A full report is attached in the December 2009 Technical Committee report. This work is continuing with the aim of developing an across breed maternal analysis by the end of 2010.

8.13 Index accuracy

Methodology and software has been developed by AGBU to calculate approximate accuracies for Sheep Genetics indexes. A detailed description of this work was prepared for the December 2009 Technical Committee meeting.

Since this meeting an additional program has now been implemented into the routine runs so that index accuracies for each of the standard Sheep Genetic indexes are now calculated after each analysis.

These accuracies are available for publication with indexes, and are being used to set thresholds for reporting of indexes, in the same way that thresholds are set for breeding values.

8.14 Adjustment of wool traits using weaning weight

Weaning weight has been suggested as a potential adjustment factor for fleece weight in genetic evaluations for Merinos following earlier published work. The idea is that fitting weaning weight accounts for some of the variation in fleece weight caused by effects such as birth/rearing type and wool growth period in the interval between birth and first shearing. In addition, the direct heritability for fleece weight can be higher and random maternal effects lower after making the weaning weight adjustment. As a consequence there has been interest in using weaning weight as a proxy for birth/rearing type and age in Merinos because these are often not recorded, particularly in flocks which do not have full pedigree.

A study was performed to investigate the value of the weaning weight adjustment based on three research flock data sets.

Detailed findings are included in the report to the December 2009 Technical Committee meeting, but the recommendation from the study was not to adjust fleece weight for weaning weight in MERINOSELECT for the following reasons:

- After adjusting for weaning weight the trait is not the same
- Across flock effects may lead to over adjustment of fleece weight
- The adjustment does not remove all of the effects of birth/rearing type and age
- In addition it would be difficult to implement in MERINOSELECT where there are a mixture of data with and without birth/rearing type, age and weaning weight.

8.15 Maternal effects for embryo transfer and fostered animals

OVIS contains functionality carried over from BREEDPLAN to allocate maternal genetic and environmental effects to different dams for Embryo transfer and fostered animals. Where the animals are known to be ET or fostered but the recipient or foster dams are not know then a dummy dam is created to allow for the maternal effects to be fitted.

This functionality has not previously been used in OVIS. The code was modified and tested to utilise this feature. It is now used routinely in the Terminal Sire and Dohne analyses.

8.16 Marker assisted breeding values

A prototype version of OVIS has been developed to handle genomic data in the form of marker estimated breeding values (MEBV). These MEBV have been developed using the Sheep CRC's Information Nucleus Flock as a discovery population, and are predictions of breeding value given genotypes derived from a 50K SNP panel.

MEBV are included in OVIS as correlated traits and a major part of the research has been to estimate genetic covariances between MEBV traits and standard OVIS traits. This was achieved for 8 MEBV traits in Merinos, and will be extended to terminal sires and maternal breeds in the near future. The prototype model will be tested as further MEBV's become available through the pilot project.

8.17 Unlinked management groups

The technical committee had some concern that there could potentially be a significant number of unlinked management groups in the SG analyses. Thus the linkage software was slightly modified to calculate linkage based on management groups instead of flocks. As there are many more management groups than flocks only data from 2004 onwards was included in the analysis. The results show that there are very few management groups that are completely unlinked. The number of animals in completely unlinked management groups is very small compared to the total number of animals.

8.18 Diagnostics

Diagnostics were performed routinely for changes in breeding values of individual animals. Unusual genetic trends have been observed for several flocks which required detailed investigations. One such flock is GRASS Merinos and more detail can be found in the appendices.

Flocks were identified for further study and consultation. Meetings and phone hook-ups have been conducted to discuss data quality issues. Most of these meetings required data analyses and documentation prior to the meetings as well as follow up analyses.

A more detailed description of this work included in the May 2008 Technical Committee papers attached to this report.

8.19 National Sheep Improvement Program development

AGBU has worked with SG and David Notter from the National Sheep Improvement Program in the United States to develop new OVIS analyses to suit their system. New parameter files and routine analyses have now been development for 3 breeds, Targhee, Suffolk and Polypay. This has proved to be a very successful international collaboration.

9 Improved diagnostic tools and reporting tools.

Additional diagnostic files were developed and are now produced on a routine basis for the SG database to import. They will provide an on-line tool for SG staff.

The diagnostic tools used by AGBU staff were also further refined to produce additional and more informative reports.

10 Upgrade software to reduce runtime and allow larger data sets to be processed.

This work was completed and reported in previous milestone reports.

11 Additional analytical software to judge data quality and provide KPI’s for genetic change at flock level

This work has not commenced as the Technical Committee agreed that the other worked described in this Milestone had a higher priority.

12 Develop a base model using minimum performance recording using breeding objectives

Due to high priority matters arising, work addressing the milestone has not commenced.

13 Calculate cost benefit parameters for additionally recorded traits

Due to high priority matters arising, work addressing the milestone has not commenced.

14 Staff, Students and Supervision

During the course of the project there were some significant changes to the AGBU staff who worked on this project. Dr Abe Huisman resigned from his position at AGBU and ceased work in Feb 2007. In September 2006 Dr Andrew Swan was appointed to the research team.

In February 2007 Ms Christie Iker commenced employment as a Junior Research Fellow under the SGA.005 project. A significant amount of time was devoted to assisting Christie to understand the data, analysis systems and programming languages used in these projects. Christie then resigned from her position in January 2009. To overcome this staffing shortfall AGBU was able to temporarily re-prioritise staff and provide Dr Li Li as an additional full time scientist to work on this project from April to July 2009. From July 2009 Dr Kim Bunter, a senior scientist at AGBU, also spent 40% of her time assisting with this project. The addition of these two staff members showed immediate benefits in terms of the research results achieved by this project.

At the start of this project Mr Mohammad Khusro join the team as a PhD student. Khusro submitted this PhD thesis in May 2007 and graduated in October 2009. The title of the thesis is; The effect of linkage and genetic grouping on the accuracy of across-flock genetic evaluation in Australian Merino sheep.

15 Communication

15.1 Scientific Publications

15.1.1 Refereed Journal Papers

Brown, D.J., Swan, A.A., and Gill, J.S. (2010). Genetic Relationships between Indicator Traits for Fly Strike Resistance and Production Traits in Merino Sheep, *Animal Production Science* (Sumbitted)

Banks, R.G. and Brown, D.J. (2009). ‘Genetic improvement in the Australasian Merino – management of a diverse gene pool for changing markets.” *Animal Genetic Resources Information* 45:29-36.

Huisman, A.E. and Brown, D.J. (2009) Genetic parameters for body weight, wool, and disease resistance and reproduction traits in Merino sheep: 3. Genetic relationships between ultrasound scan traits and other traits, *Animal Production Science* 49(4): 283-288

Huisman, A.E. and Brown, D.J. (2009) Genetic parameters for body weight, wool, and disease resistance and reproduction traits in Merino sheep: 4. Genetic relationships between and within wool traits, , *Animal Production Science* 49(4): 289-296

Huisman, A.E., Brown, D.J., Ball, A.J. and Graser, H.-U. (2008) Genetic parameters for body weight, wool, and disease resistance and reproduction traits in Merino sheep: 1. Description of traits, model comparison, variance components and their ratios, *Australian Journal of Experimental Agriculture* 48(9): 1177-1185

Huisman, A.E. and Brown, D.J. (2008) Genetic parameters for body weight, wool, and disease resistance and reproduction traits in Merino sheep: 2. Genetic relationships between body weight traits and other traits, *Australian Journal of Experimental Agriculture* 48(9): 1186-1193

Brown, D.J., Mortimer, R.L., and Mortimer, M.L. (2006). Genetic aspects of greasy wool colour assessments in Merino sheep, *International Journal of Sheep and Wool Science,* **54**(3), 1-16.

Huisman, AE; Tier, B and Brown, DJ (2006). “On assessing contrasts between groups of animals.” Livestock Science 104(3): 254-267.

15.1.2 Conference Papers

Brown, D. J., Swan, A.A., and Graser, H.U. (2010). Genetic Relationships between Indicator Traits for Fly Strike Resistance and Production Traits in Merino Sheep, *Proceedings 9th World Congress on Genetics Applied to Livestock Production*, Leipzig, Germany (In Press).

Banks, R G; Brown, D J and Field, S R (2009). "Meta-analysis of cross-bred progeny data for Australian terminal sire sheep." Proceedings of the 18th Conference of the Association for the Advancement of Animal Breeding and Genetics. Barossa Valley, South Australia. September 28-October 1. pp.480-483.

Brown, D J; Swan, A A; Johnston, D J and Graser, H-U (2009). "Sire by flock-year interactions for body weight in Poll Dorset sheep." *Proceedings of the 18th Conference of the Association for the Advancement of Animal Breeding and Genetics*. Barossa Valley, South Australia. September 28-October 1. pp.48-51.

Swan, A A; Brown, D J and Banks, R G (2009). "Genetic progress in the Australian Sheep Industry." *Proceedings of the 18th Conference of the Association for the Advancement of Animal Breeding and Genetics*. Barossa Valley, South Australia. September 28-October 1. pp.326-329.

Whelan, M B; Cottle, D J; Geenty, K G and Brown, D J (2009). "Classifying sheep grazing environments using satellite data to quantify genotype by environment interactions." *Proceedings of the 18th Conference of the Association for the Advancement of Animal Breeding and Genetics*. Barossa Valley, South Australia. September 28-October 1. pp.52-55.

Young, M J; Newman, S-A N; Apps, R; Ball, A J and Brown, D J (2009). "Trans-Tasman genetic evaluations of sheep." *Proceedings of the 18th Conference of the Association for the Advancement of Animal Breeding and Genetics*. Barossa Valley, South Australia. September 28-October 1. pp.212-215.

Young, M J; Newman, S-A N; Apps, R. and Brown, D J (2009). "Trans-Tasman genetic evaluations of sheep – spreading the net wider." *Proceedings of the New Zealand Society of Animal Production*. 69, 212-215.

Brown, D.J. (2007). Variance components for lambing ease and gestation length in sheep, *Proceedings of the Association for the Advancement of Animal Breeding and Genetics* **17**, 268-271.

Brown, D.J., Huisman, A.E., Swan, A.A., Graser, H-U., Woolaston, R.R., Ball, A.J., Atkins, K.D. and Banks, R.B. (2007). Genetic evaluation for the Australian sheep industry, *Proceedings of the Association for the Advancement of Animal Breeding and Genetics* **17**, 187-194.

Johnston, D.J., Brown, D.J. and Graser, H-U. (2007). The effect of age slicing interval on the variance components and data effectiveness for birth and 200day weights in Angus cattle, *Proceedings of the Association for the Advancement of Animal Breeding and Genetics* **17**, 344-347

Huisman, A.E. and Brown, D.J. (2007). What genetic group structure to fit? A Bayesian approach applied to yearling worm egg count data in Merino sheep, *Proceedings of the Association for the Advancement of Animal Breeding and Genetics* **17**, 399-402.

Mohammad, K.. Brown, D.J., Graser, H-U. and Tier, B. (2007). The effect of linkage and flock size on the accuracy of estimated genetic group effects, *Proceedings of the Association for the Advancement of Animal Breeding and Genetics* **17**, 545-548.

Piper, L.R., Swan, A.A., and Brewer, H.G. (2007). Is increased fleece weight associated with reduced reproduction rate? Results from long term multi-trait selection flocks, *Proceedings of the Association for the Advancement of Animal Breeding and Genetics* **17**, 103-106.

Robinson, D.L., Mortimer, S.I., Swan. A.A. and Purvis, I.W. (2007). Genetic parameters for subjectively scored traits in yearling and adult fine wool Merinos, *Proceedings of the Association for the Advancement of Animal Breeding and Genetics* **17**, 336-339.

Swan, A.A. and Brown, D.J. (2007). A simple bootstrapping procedure to validate the MERINOSELECT model for weaning weight, *Proceedings of the Association for the Advancement of Animal Breeding and Genetics* **17**, 395-398.

Swan, A.A., van der Werf, J.H.J. and Atkins, K.D. (2007). Developments in breeding objectives for the Australian sheep industry, *Proceedings of the Association for the Advancement of Animal Breeding and Genetics* **17**, 483-490.

Woolaston, RR; Brown DJ; Atkins, KD; Casey, AE and Ball, AJ (2006). “Genetic changes in the Australian Merino since 1990.” Agribusiness Sheep Updates 2006, Perth, Australia, West Australian Government – Department of Agriculture and Food. Ed. Sue-Ellen Shaw.

Huisman, A.E. and Brown, D. J. (2006). Predictive ability of sire weaning weight breeding values estimated across environments in Terminal sire sheep breeds, *Proceedings 8th World Congress on Genetics Applied to Livestock Production,* Communication No 04-07, Belo Horizonte.

Brown, D. J., Ball, A., Huisman, A.E., Swan, A.A., Atkins, K.D., Graser, H.U., Banks, R., Swan, P. and Woolaston, R. (2006). Sheep Genetic Australia: A national genetic evaluation system for sheep, *Proceedings 8th World Congress on Genetics Applied to Livestock Production*, Communication No 05-03, Belo Horizonte.

15.1.3 Book Chapters

Greeff, J; Kinghorn, B P and Brown, D J (2010). Breeding and Selection. In International Sheep and Wool Handbook, Cottle, D J (Ed). Nottingham University Press

15.2 Presentations

- Prepared and submitted an 9th WCGALP paper.
- Prepared and presented an 8th WCGALP paper.
- Prepared and presented 9 2007 AAABG papers.
- Prepared and presented 5 2009 AAABG papers.
- SG Technical Committee – numerous presentations on research and development outcomes
- SG Advisory Committee – numerous presentations on research and development outcomes
- Numerous seminars at AGBU

15.3 Extension Activities

- Advising breeders about a range of issues including;
- EBV understanding
- Measurement strategies
- Data entry and software issues
- Management group issues
- Sale Catalogue preparation and EBV display
- Diagnostic work

16 Other Activities and Outcomes

- Participation in CRC meetings.
- Participation in SG Meetings.
- Attendance at AAABG conference in Armidale (2007) and Adelaide (2009).
- Attendance 8th World Congress of Genetics Applied to Livestock Production in Brazil (2006)
- Participation in meetings with LAMBPLAN and MERINSELECT clients.
- Participated in discussions with MLA, LAMBPLAN, AWI staff about future project proposals
- Produced shedding EBVs for a Wiltshire Horn breeder in each year (2003, 2004 and 2005)
- Refereed papers for Wool Technology and Sheep Breeding, Animal Science, Journal of Animal Science, Australian Journal of Agriculture Research, Australian Journal of Experimental Agriculture, Animal Production Science, Livestock Science, and Genetics Selection and Evolution.

17 Impact on Meat and Livestock Industry

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 index accuracy and selection indexes assisted to improve selection accuracy.

18 Conclusions and Recommendations

The objectives for this project have been achieved. The system developed for the routine genetic evaluations continues to work well. This is also strengthened due to the excellent cooperation between AGBU and SG staff. More recently, facilitated by SG, there has been a large 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.

19 Appendices

19.1 Appendix 1: List of Milestone reports

These Milestone reports are included in the CD provided;

MLA_SHGEN_113_Milestone_2_Report.pdf
MLA_SHGEN_113_Milestone_4_Report.pdf
MLA_SHGEN_113_Milestone_5_Report.pdf
MLA_SHGEN_113_Milestone_7_Report.pdf
MLA_SHGEN_113_Milestone_9_Report.pdf
MLA_SHGEN.113 Milestone 11 report.pdf
MLA_SHGEN.113 Milestone 12 report.pdf
MLA_SHGEN.113 Milestone 14 report.pdf

19.2 Appendix 2: List of Technical Committee reports

These TC meeting reports are included in the CD provided;

AGBU TC report 19 July 2006.pdf
AGBU TC report 7 Nov 2006.pdf
AGBU TC report 5 March 2007.pdf
AGBU TC report 5 June 2007.pdf
AGBU TC report 27 Nov 2007.pdf
AGBU TC report 13 Feb 2008.pdf
AGBU TC report 14 May 2008.pdf
AGBU TC report 11 Sep 2008.pdf
AGBU TC report 3 Dec 2008.pdf
AGBU TC report 4 March 2009.pdf
AGBU TC report 1 July 2009.pdf
AGBU TC report 2 Dec 2009.pdf
AGBU TC report 17 May 2010.pdf

19.3 Appendix 2: List of other reports attached

These reports are also included in the CD provided;

SO Workshop 31Mar2009.pdf
Terminal Sire Validation.pdf