GENETIC EVALUATION FOR THE AUSTRALIAN SHEEP INDUSTRY

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SUMMARY
Sheep Genetics Australia (SGA) was established to deliver a national across-flock genetic evaluation system to the Australian sheep industry for terminal sires, maternal sires and Merinos. To achieve the aim of providing a single national genetic evaluation language for Australian sheep breeders, significant developments to existing systems were necessary and required various new innovations. These included the amalgamation of databases, data transformations, refinement of analysis models, genetic grouping methodology, updated genetic parameters, multiple trait across-flock linkage assessments, index development, and reporting changes. Since the establishment of SGA, research and development to further improve the system has continued. This paper describes SGA and the analysis used to estimate Australian Sheep Breeding Values (ASBVs). More information is located at www.sheepgenetics.org.au.

INTRODUCTION
Sheep Genetics Australia (SGA) was established in 2005 to deliver a nationally consistent across-flock genetic evaluation platform to the Australian sheep industry, generating information relevant for terminal, maternal and Merino sheep. SGA is a joint program of Australian Wool Innovations (AWI) and Meat and Livestock Australia (MLA). Historically, data in separate databases were evaluated by different organisations with different models, different genetic base points, and for different objectives. In addition, the results of these genetic evaluations were often presented in varying forms to the end-users, both ram breeders and commercial sheep producers. To achieve the aim of a single national genetic evaluation language, significant developments were necessary and a number of new innovations have been delivered to the Australian sheep industry.

Three years of research and development were required to produce the first SGA analysis. Since then research and development has been continual and has resulted in the SGA analysis as it is currently applied. Some of the early changes were superficial and did not impact on the ranking of animals, but others changed both animal and flock rankings. Independent of changes to models and parameters used for the analysis, the simple merging of Merino data to form the MERINOSELECT database had a major impact. This affected particularly the estimated breeding values of link sires with progeny across the various databases, and the ranking of flocks. Industry response to the single, combined analysis for Merinos, and the improved analysis for other breeds, has been very positive. Since the release of the first SGA analysis in November 2005 the membership of all three databases

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has increased; 11% for the terminal sires, 10% for the Merino database and 20% for the Maternal breeds (Apps, *pers. comm.*). This paper describes SGA and the analysis it uses to estimate Australian Sheep Breeding Values (ASBVs).

PARTICIPATING BREEDERS

The SGA databases consist of industry recorded data from three major breed types; 1) LAMBPLAN - terminal sire breeds, 2) LAMBPLAN - maternal / dual purpose breeds and 3) MERINOSELECT - Merino breeds. These are summarised in Table 1. The databases are managed by SGA on behalf of the breeders who submit regular updates as required. Approximately 1,827 breeders have supplied data to SGA spanning 48 years.

Table 1. Summary of the SGA databases at March 2007

	LAMBPLAN™ Terminal Sire	LAMBPLAN™ Maternal	MERINOSELECT™
Animals	1,332,643	313,989	1,138,266
Traits analysed	38	37	37
Flocks in pedigree	2,919	1,120	1,097
Flocks with data	1,711	425	254
Linked flocks (any trait)	522	123	225
Years	48	43	46
Sires	22,110	7,563	11,982
Dams	363,955	90,864	139,887
Weights records	2,176,972	470,956	997,977
Scan records	803,196	118,590	167,416
WEC[#] records	16,882	14,853	153,909
Wool records	17,231	82,997	1,112,419
Reproduction records	286,592	72,889	131,402
Av Generation Interval	2.9	3.0	3.3
Av CG[*] size	18.5	25.5	105.3
Av sires per CG	3.3	4.1	6.6

[#]WEC = Worm egg count   [*]CG = contemporary group

THE GENETIC EVALUATION

Models. SGA uses OVIS software (Brown *et al.* 2000) to estimate breeding values and accuracies. The analysis pre-adjusts for a range of systematic effects such as age of dam, age of animal, birth type, rearing type and live weight. The fixed effects of flock, year, sex, breeder-defined management group and day of measurement are all included in the definition of "contemporary group", which is fitted as a fixed effect in the OVIS model. To avoid potential errors in age adjustment or sudden changes in environmental conditions, OVIS also slices contemporary groups if the spread in age is greater than 35 days for birth and weaning weight and 70 days for all remaining traits. Early stage management groups are also maintained through to later stage measurements, such that animals will not be directly compared in the same group if they were in different groups at an earlier stage.

OVIS utilises an animal model which can include the following effects: direct genetic, maternal genetic, permanent environment effects due to the individual (repeated records) and the dam, and sire by flock-year interactions. Maternal effects are included for weight traits (birth, weaning, post-weaning, yearling and hogget) and fleece weight (yearling and hogget). Permanent environment effects due to the dam are also fitted for these traits. The genetic parameters used for this model were derived from a combination of estimates from the SGA database, published literature and results from research flocks.

Although OVIS can include sire by flock or sire by flock-year interactions in the model, they have not been included in SGA analyses yet. However recent research using SGA Merino data has established that the addition of sire by flock effects significantly improved the fit of the model for all traits investigated except staple strength (Brown 2007a). While the sire by flock effect only explained between 1 and 8% of the phenotypic variance, its inclusion consistently reduced the correlation between direct and maternal genetic effects and resulted in a significant reduction in the direct heritability for most traits, in some instances by up to 25%. Some of this reduction in heritability is likely due to the sire by flock effect absorbing genetic effects where data structure is not sufficient to partition these effects simultaneously.

Most traits analysed in SGA are subject to heterogenous variance across contemporary groups which affects the variance of breeding values if not correctly adjusted. SGA uses heterogenous residual variance adjustment (Reverter *et al.* 1997) for all traits except WEC (worm egg count) for which the residuals variance is homogenised across all contemporary groups (Brown and Tier 2003).

Traits. At present OVIS analyses up to 46 growth, carcase, wool, fitness and fertility traits simultaneously. Traits can be measured at 7 age stages or times of measurement: birth, weaning, post-weaning, yearling, hogget, adult and carcase. The range of traits which can be measured at these later ages include: live weight, ultrasonic fat depth, ultrasonic eye muscle depth, greasy and clean fleece weight, mean fibre diameter, fibre diameter variation, mean fibre curvature, staple length, staple strength, worm egg count, scrotal circumference and traits related to female reproduction.

As part of the research and development of the SGA analysis, the models, transformations and genetic parameters used for each trait were investigated. As a result of this work, body weight, fleece weight, fat depth and fibre diameter are analysed as a proportion of their contemporary group mean. This transformation produces more robust breeding values (Brown *et al.* 2005; Huisman and Brown 2006). New analysis models were also developed for WEC, based on a cube root power transformation and procedures to homogenise residual variance (Brown and Tier 2003).

There is scope for additional traits to be analysed and potential traits include visual assessments (such as conformation, wool style and maternal ability), temperament scores, gestation length, lamb survival and lambing ease. A range of visual wool and structural traits are commonly recorded by the Australian Merino Sire Evaluation Association (AMSEA) and ram breeders. While there is some inconsistency in scoring systems most of these traits have been shown to be heritable (Brown *et al.* 2006; Brown 2007b; Mortimer 2007). SGA has recently produced its first set of estimated breeding values for a subset of these traits using OVIS for AMSEA's 12th Merino Superior Sires report (Casey *et al.* 2007). SGA plans to expand this analysis to include data from industry ram breeding flocks and thereby produce ASBVs for a range of visual traits. MLA and AWI have also commissioned research to further investigate additional novel traits including temperament and additional wool quality

characteristics.

The 'information nucleus flock' newly established by the CRC for Sheep Industry Innovation (Banks *et al.* 2006; Fogarty *et al.* 2007) will progeny test annually up to 100 young industry sires, measuring an extensive range of traits which are not measured by ram breeders, including for example carcase and eating quality traits, and wool quality and processing performance. This information will flow back into SGA providing ram breeders with information on economic traits which are normally not observed in industry flocks, and potentially lifting the rate of genetic gain in the sheep industry through the application of advanced genetic technologies. This nucleus flock is also likely to generate additional information on difficult or expensive to measure traits such as carcase information. These traits will be included in the normal SGA analysis as soon as appropriate genetic parameters become available.

Across-flock linkage. Adequate genetic linkage between flocks and groups within flocks is vital to provide accurate and unbiased comparison of animals. Research by SGA resulted in a procedure that calculates the genetic linkages between any two flocks based on descendants from common sires, and quantifies these linkages as accuracies for across-flock comparisons. A detailed description of the linkage calculation can be found in Huisman *et al.* (2006).

Due to the fragmented data structure in the sheep industry, a single linkage estimate is not possible. Accordingly, calculations are performed for five different trait groups. Generally, traits within these different trait groups are moderately to highly genetically correlated ($r_g > 0.6$), while traits in different trait groups are more lowly correlated ($r_g < 0.5$). Within each trait group a multiple trait approach is applied. The 5 trait groups and the traits that are used to assess linkage are:

1. Body weight: post-weaning, yearling, hogget and adult weight
2. Wool: yearling, hogget and adult fibre diameter
3. Scan traits: post-weaning, yearling and hogget eye muscle depth
4. WEC: weaning, post weaning, yearling and hogget worm egg count
5. Reproduction traits: number of lambs weaned

ASBVs are only available for flock and trait groups which are linked. Breeding values for trait groups within each flock that are not linked are reported as within flock breeding values (FBVs). The linkage threshold requires at least one link with another flock in the main linkage group with 70% accuracy. At a between flock accuracy of 70% a difference of 0.86 genetic standard deviations would be significant at the 5% level. This accuracy value is dependent on the heritability of the trait group, so that for lowly heritable traits such as reproduction, more linked progeny are required. The results of these linkage analyses illustrate that the majority of flocks are linked for the trait groups which they measure (Figure 1).
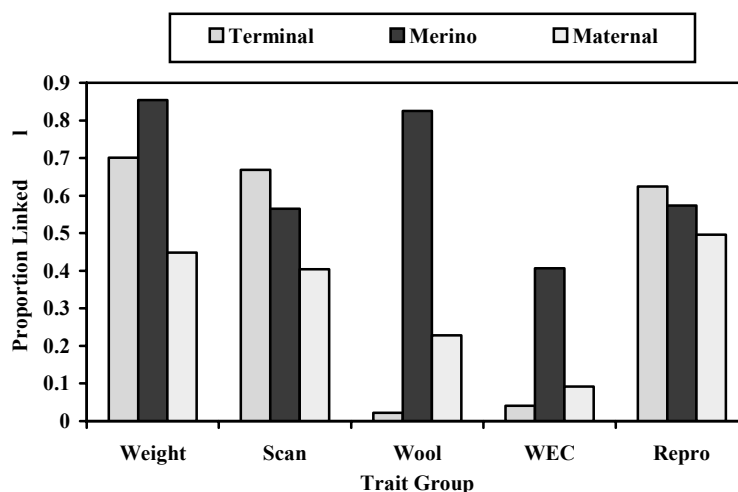
Figure 1. Proportion of linked flocks in each breed group

Genetic Grouping. An important capability of OVIS and SGA is the inclusion of genetic groups for base animals. One of the features of the MERINOSELECT database is a high level of incomplete pedigree, with many flocks recording only the sire for a proportion of progeny. In addition, the Merino is a very diverse breed, with a large range in the average performance of flocks represented in the database. Including both flock of origin and time as classifiers for genetic groups proved to be very important in order to more accurately estimate breeding values and genetic trends across flocks. As currently implemented, the MERINOSELECT analysis uses flock by period (5 years) genetic groupings. While this was not as critical for meat sheep breeds due to greater depth of pedigree, the LAMBPLAN analysis allocates base animals (animals with unknown sire and/or dam pedigree) to genetic groups based on breed and year. Recent research has confirmed the need to include genetic group effects in the SGA analysis and also highlighted the benefits obtained by including groups which accommodate changes in merit of base animals over time (Huisman and Brown 2007).

INDUSTRY OUTPUTS
Breeding Values. SGA reports 46 direct and 3 maternal breeding values and their accuracies. Flocks with sufficient linkage receive ASBVs, whereas flocks that are not sufficiently linked receive within-flock breeding values (FBVs). ASBVs are provided with an accuracy figure, while FBVs are not. Accuracy values are calculated as the correlation between true and estimated breeding value. Flock summaries are provided and include the flock and breed genetic trends for key traits. Inbreeding coefficients are also supplied, although in most cases these are underestimated due to incomplete pedigree. Research is currently underway to develop additional breeding values and reporting tools.

Selection Indexes. A range of selection indices have been developed by SGA to suit common markets in each breed type. These include;
- Wool production with a primary focus on reducing fibre diameter (10% micron premium).

191

- Merino wool, balanced emphasis on both reduced fibre diameter and increased fleece weight (7% micron premium).
- Dual purpose Merino wool and meat production (3.5% micron premium).
- For maternal breeds, dollar indexes are calculated on traits of current economic importance using economic weights derived from MLA data and customised for each breed group.
- Terminal sire breeds have three indexes, including CARCASE+, a 'desired gains' index with 60% emphasis on post weaning weight, 20% on post weaning fat depth and 20% on post weaning eye muscle depth, and two indexes specifically designed for the domestic (20-22 kg carcase weight) and export (24+ carcase weight) markets.

A wider range of indices are also available to suit more variable market segments. For example recently a 20% micron premium index has been developed (with options to include staple strength and worm egg count) to service superfine wool producers. More details about these indexes is available from www.sheepgenetics.org.au.

Further development of breeding objective software (SheepObject) will allow greater flexibility for developing customised objectives and selection indices (Swan *et al.* 2007).

VALIDATION OF ASBVS

As part of the ongoing research program the reliability of ASBVs in predicting the performance of progeny has been evaluated for a range of traits. Examples for WEC, body weight, wool traits and reproduction will be discussed here.

Worm egg count. SGA data were used to examine the reliability of WEC ASBVs as a selection tool. This was achieved by examining the predictive performance of ASBVs using a range of models and across different subsets of data from the SGA database. The result of these analyses illustrated that the worm egg count traits were more variable across years and environment compared to most other traits. This could also be a result of poor definition of the trait, differences in worm species, level of expression, age of measurement, drenching history and challenge history. However, ASBVs calculated using a model which includes terms to account for interactions between sires and flock-years, reliably predict progeny performance. That is, this model produced breeding values which more consistently predicted the differences between in the performance of progeny across a range of environments and ages.

Body weight. ASBVs estimated using the percentage transformation have been shown to reliably predict yearling and hogget weight in Merinos (Brown *et al.* 2005) and weaning weight in terminal sire sheep (Huisman and Brown 2006) across a range of environments. More recently Swan and Brown (2007) have shown that with a model that accounts for sire by flock-year interactions ASBVs reliably predict progeny performance in well recorded weaning weight data.

Wool. ASBVs estimated using the percentage transformation have also been shown to reliably predict yearling and hogget fleece weight and fibre diameter in Merinos across a range of environments (Brown *et al.* 2005). ASBVs for the wool quality traits of staple strength, staple length and fibre curvature were examined by Swan (pers. comm.) and also shown to reliably predict progeny performance across environments.

Reproduction. Recent research efforts have focussed on evaluating the reliability of reproduction ASBVs in all breeds. These analyses illustrated that with good quality data the breeding values reliably predict progeny performance using the SGA model. However when pedigree recording becomes sparse and or other factors such as fertility vary, the reliability of the ASBVs deteriorates. As a result SGA is developing a new evaluation model and data collection requirements.

FUTURE DEVELOPMENTS
SGA will evolve along with the needs of the ram breeders and enhancements in quantitative genetics. Improvements in computing technology have also allowed OVIS to utilise more advanced models for the SGA analyses. SGA is currently researching the following areas of possible improvements;
- Inclusion of sire by flock-year effects into routine evaluation
- Utilising sire information from multiple sire groups
- Enhancing the data collection and modelling of reproduction traits
- Developing an across breed analysis for the maternal breeds
- Producing ASBVs for additional traits
- Inclusion of genomic information in routine genetic evaluation

As a result of the large investment in Sheep Genomics (Oddy *et al.* 2005) it is likely that molecular information will be able to be utilised to improve the accuracy of selection in the near future. SGA is actively working to utilise molecular information in the routine genetic evaluation when it becomes available.

CONCLUSION
Sheep Genetics Australia has facilitated the development of a substantial new genetic evaluation system for the Australian sheep industry. Education of seed stock breeders and their clients on the use of SGA will ultimately determine the acceptance and value of SGA to the Australian sheep industry. Improvements in data quality and genetic linkage across flocks will also strengthen the accuracy of ASBVs. The capabilities of SGA are also being improved by the ongoing research and development program. More information can be found at www.sheepgenetics.org.au.

ACKNOWLEGMENTS
SGA is funded by Meat and Livestock Australia and Australian Wool Innovation, and SGA is made possible through the support of the Australian sheep industry. The database development by Stephen Field and David Rubie is gratefully acknowledged.

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Sheep 1

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