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sales for the flocks included and was beyond the scope of this analysis. Such an analysis based on the methodology of Meikle and Amer (2003) is being undertaken as part of a separate independent study. The industry benefits are expected to be substantial and to far outweigh the magnitude of industry funded investment in structures underpinning genetic improvement.

These results demonstrate substantial opportunities for further improvement. Of particular concern is the large number of flocks performing well within the potential rates of genetic progress demonstrated by other flocks. Another area of concern is the one-dimensional nature of genetic improvement, it being largely focused on growth rate, particularly in dual purpose type flocks. While genetic progress in litter size has contributed significantly, there are typically decreasing returns to additional incremental gains in litter size (Amer *et al.*, 1998) and there are significant numbers of sheep farmers that feel that they are at or approaching their optimal litter size. While increases in growth rate allow farmers to exploit seasonal price premiums and reduce lamb feed demand from times when pasture is most scarce, they also result in increases in breeding ewe mature weights, which offsets some of the benefits.

There is a need for new selection criteria that are not excessively costly and impractical in order to

broaden the directions of genetic progress. Research into genetic markers continues to hold much promise and the advent and recent rapid adoption of genome wide selection tools in dairy cattle suggests that new breakthroughs in this area for sheep may not be far away. This would provide sheep breeders with the option to select for a broader range of economically important traits at a young age, if genetic merit can be assessed using genetic markers with reasonable accuracy without detailed pedigree and performance recording, new models of sheep breeding programmes may evolve. In these, larger numbers of potential selection candidates might be generated, but the assessment of genetic merit via genetic marker tests would be restricted to those candidates that are deemed to be physically acceptable to commercial ram buyers. It is apparent from this study that selection for physical attributes remains a substantial drain on the genetic progress within a substantial proportion of performance recording breeder flocks under the current breeding structures.

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Trans-Tasman genetic evaluation of sheep – spreading the net wider

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ABSTRACT

At the instigation of local breed groups, Sheep Improvement Ltd. (SIL) and Sheep Genetics (SG) exchanged flock data and conducted genetic evaluations on the combined dataset. Results from each system show only modest changes in breeding values compared to analyses of their respective within country datasets. Correlations of breeding values (BVs) were 96 to 100% for weaning weight, autumn live weight, ultrasonic muscle, ultrasonic fat, fleece weight and number of lambs born. Correlations between BVs generated by the two systems from the same datasets were less strong but still good at 69 to 89%, for most traits. This was attributed to differences in parameters used by the two analysis systems and to some measurements being taken at different ages. The weakest correlations occurred for ultrasound scan traits at 14 to 65% since SG adjusts these to constant 'carcass' weight but SIL does not. It is concluded that the best option for breeders seeking superior genetics internationally is to facilitate data exchange and have analysis and reporting done within their own country.

Keywords: genetic evaluation; sheep; across-flock; international; Sheep Improvement Ltd; Sheep Genetics.

ACROSS-FLOCK GENETIC EVALUATIONS

Internationally, genetic evaluation systems based on recorded performance measurements and pedigree have settled on the use of individual animal model best linear unbiased prediction (BLUP) methods for estimating genetic merit. Increasingly, breeders with common breeding objectives share the use of sires and use the genetic connections these build to carry out across-flock genetic evaluations. In some cases this then extends to across breed analyses, for example the Sheep Improvement Ltd. - Advanced central evaluation (SIL-ACE) (Young & Newman, 2009; www.sil.co.nz) or LAMBPLAN Terminal Sires (www.sheepgenetics.org.au/lambplan) evaluations.

EXTENSION TO INTERNATIONAL DATASETS

The dairy cattle and beef industries routinely perform international genetic evaluations (Schaeffer, 1994, Donoghue *et al.*, 2007). However, we do not know of any international evaluations of sheep, certainly none where data are used from groups separated by major geographical features such as oceans. Genetic improvement using overseas genetics has been attempted through importations of 'new' breeds to bring new genetics into the industry or through use of sires either imported live or as semen. However, true genetic merit of these importations relative to local animals is seldom known prior to being sourced.

While many countries have local, specialized breeds of sheep, some breeds are common to a

number of countries and have similar selection objectives, albeit modified by local market signals. Some breeders seek new genetics from overseas populations of their breed to achieve their next lift in performance and to manage inbreeding by using genetic lines outside those they have available locally. Fair and effective comparison of animals, to better identify new genetics that will improve performance, requires a common genetic evaluation for similar traits and must be based on good genetic connections between flocks.

LOGISTICS AND SCALE

Powerful new computer systems and fast internet links now make it possible to routinely transfer large quantities of data between computer databases. At the request of breed groups in New Zealand and Australia, Sheep Improvement Ltd. (SIL) and Sheep genetics (SG) have exchanged data for several breed groups and the combined respective datasets have been subjected to genetic evaluation by both SIL and SG. Trans-Tasman genetic evaluations run by SIL and SG are provided at the request of breed groups in each country, where there is good genetic connectedness, sometimes termed 'linkage' (Newman, 2003).

Combining New Zealand and Australian datasets provides significant increases to both the number of animals and the number of records per trait. Tables 1 and 2 illustrate the size of the datasets and percentage increases for the Corriedale and Coopworth breeds respectively when Australian data is added to the New Zealand dataset.

TABLE 1: Number of animals, data counts for key traits and percentage increases in data for Corriedale dataset by adding Australian data to the New Zealand dataset.

Trait		New Zealand	Australia	% increase
Total animals		128,014	46,875	37
Growth	WWT – Weaning weight	90,084	23,421	26
Growth	LW8 – Live weight at 8 months	23,384	10,984	47
Growth	LW12 – Live weight at 12 months	14,857	14,078	95
Meat	EMD – Eye muscle depth	5,312	7,513	141
Wool	GFW - Greasy fleece weight	43,280	13,908	32

TABLE 2: Number of animals, data counts for key traits and percentage increases in data for Coopworth dataset by adding Australian data to the New Zealand dataset.

Trait		New Zealand	Australia	% increase
Total animals		826,661	74,223	9
Growth	WWT – Weaning weight	637,468	56,952	9
Growth	LW8 – Live weight at 8 months	378,163	30,270	8
Growth	LW12 – Live weight at 12 months	90,314	29,683	33
Meat	EMD – Eye muscle depth	27,735	21,930	79
Wool	GFW - Greasy fleece weight	342,101	33,016	10

COMPARISON OF RESULTS

Comparison of results show very high correlations between breeding values generated from evaluation of a within country dataset and those from evaluation of the combined dataset of between 96 and 100% within the SIL and SG systems.

Correlations between breeding values (BVs) generated by the two systems for the same datasets were weaker but still very good for most traits at between 69 and 89%. This is because genetic parameters used in BLUP evaluations of the two systems are similar but not the same. Additionally, some measurements are collected at significantly different ages or at a different site in the case of carcass trait scanning in New Zealand (Young *et al.*, 1992) to those collected in Australia (Meat and Livestock Australia, 2005). Weaker correlations were seen for carcass composition traits of between 14 and 65% since SIL currently produces age adjusted BVs whereas SG produces these BVs adjusted to a constant carcass weight.

While developed independently, both the SIL and SG analytical engines use the same underlying BLUP methodology (Newman *et al.*, 2000). Comparison of SIL results with results from SG using the same New Zealand data set show a high correlation of 82% where data and models are reasonably consistent (Figure 1) for a trait such as weaning live weight.

For a trait such as eye muscle depth, where the models fitted in analysis and the data collected are notably different the correlations are weaker at 60% (Figure 2).

CONSTRAINTS ON USE OF DATA

SIL and SG have conducted the trans-Tasman analyses in close collaboration with their respective breed group representatives. Agreements have been signed which mean each group will see results of the analyses at a similar time and that the data cannot be used for any purpose other than these genetic evaluations without the permission of the breed groups.

DATA UPDATING AND REPORTING

In consultation with SIL and SG, the breed societies determine when updated datasets will be exchanged and how animals from the other country will be reported. One group plans to transfer updated datasets for trans-Tasman evaluations three times per year in January, May and October, to fit with data collection, selection and marketing decisions. In addition to routinely reporting local animals, top sires and young rams from the overseas dataset will also be reported to provide local

FIGURE 1: Correlation of weaning weight breeding values (BVs) for New Zealand Corriedales from Sheep Improvement Ltd. (SIL) and Sheep Genetics (SG) analyses. The X-axis is the SG evaluation of the New Zealand dataset while the Y-axis is the SIL evaluation of the same dataset.

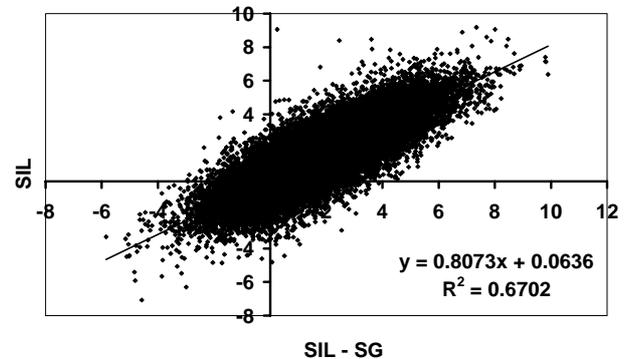
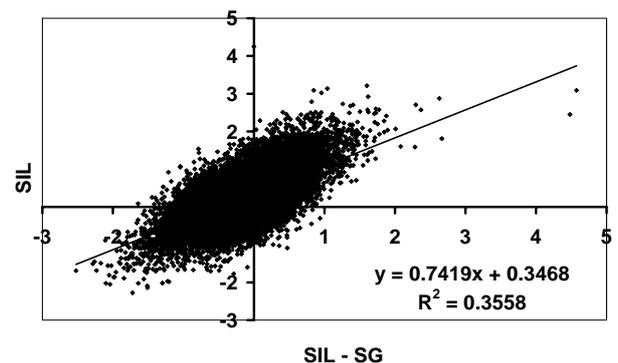


FIGURE 2: Correlation of post weaning eye muscle depth breeding values (BVs) for New Zealand Corriedales from Sheep Improvement Ltd. (SIL) and Sheep Genetics (SG) analyses. The X-axis is the SG evaluation of the New Zealand dataset while the Y-axis is the SIL evaluation of the same dataset.



breeders with the opportunity to identify new genetics to consider for importation. The other group is finalizing their initial look at how this can benefit their contributing breeders and how to manage this in future.

HEALTH AND QUARANTINE CONSTRAINTS

A number of countries will not accept either live animals, semen, or both from certain other countries due to real and perceived disease risks to their own industry. This may preclude building the genetic connections between some countries. Where such a restriction lies in only one direction, it is possible to build strong connections through flocks in the less restrictive area using genetics from the area where there are embargoes on gene importation. The downside is that superior genetics can only flow in one direction so the benefits to

breeders in the country that does not allow gene importation come only from sales of genes, as semen or as live animals and they miss-out on the opportunity to source superior genetics from the other group.

Fortunately, breeders in New Zealand and Australia can readily exchange genetics and capture both genetic improvement and marketing opportunities. One of the groups we are reporting on is discussing how to best establish ongoing transfer of genetics in both directions in order to strengthen genetic connectedness in the long-term.

CONCLUSIONS

Exchanging data and performing separate analyses on the combined dataset with each national system is most robust and appropriate for the breeders in each country. Breeders in both countries benefit from their Trans-Tasman genetic evaluations providing a wider pool of animals from which they can source genetics, with results being presented in familiar formats using selection indexes optimised for their industry.

Breeding groups wishing to spread the net wider than their own country in order to aid genetic progress should actively develop and maintain strong genetic links with like-minded groups in other countries.

Developments in the sheep meat industry: Genetic evaluation of meat yield

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ABSTRACT

Sheep Improvement Ltd. has a 'MEAT' Goal Trait Group which is used to select animals on their genetic merit for meat production. Breeding values are calculated for weight of carcass lean, carcass fat and carcass weight. These breeding values are estimated from live weight and ultrasonic eye muscle dimension data, with the option of incorporating computed tomography (CT) measurements. This served the sheep industry well while carcasses were graded on the basis of carcass weight and GR tissue depth. However, deregulation in the meat industry has seen individual meat processors developing carcass grading systems which not only improve estimates of lean and fat, but also estimate retail yield within individual cuts. SIL have developed a 'MEAT YIELD' module in response to these changes which estimates breeding values for lean weight in the shoulder, loin and hindleg primal cuts. Meat yield data collected from surplus slaughtered progeny are added to live weight and ultrasonic eye muscle data to predict the breeding values. Slaughter progeny should be randomly selected to avoid biasing the meat yield data. This module is likely to be developed further as additional grading systems are implemented, and equations to translate data into standardised measurements will be required.

Keywords: sheep; genetic evaluation; SIL; meat yield; VIAscan[®].

INTRODUCTION

The sheep meat industry in New Zealand has developed from humble beginnings with a shipment of frozen carcasses to London in 1882, through to 320,000 tonnes of lamb meat exported and around NZ\$2.38 billion in export earnings in the 2007/2008 season (Meat and Wool New Zealand, 2008b). Up until the 1970s, lamb meat had been exported in the form of whole carcasses, with around 92% of lamb meat exported as carcasses in the 1970/1971 season (Meat and Wool New Zealand, 2007). However, the proportion of the national kill exported in this manner has declined steadily over a twenty year period to fall below ten percent in the 1999/2000

season, and was around four percent for the 2005/2006 season (Meat and Wool New Zealand, 2007). Meat companies now further process almost all carcasses, with 81% of product being exported as cuts and 15% of product as boneless cuts in the 2005/2006 season.

While meat processors now sell a complex mix of further processed cuts, they purchase carcasses from farmers. In turn, 'quality' signals are sent to commercial farmers via their payment system. Carcass payment systems have until recently been based on a reward for weight of lean tissue in the carcass and a penalty for the weight of fat, with the weights of lean and fat estimated from carcass weight and GR tissue depth (Kirton *et al.*, 1999).