

TRANS-TASMAN GENETIC EVALUATIONS OF SHEEP

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SUMMARY

Until recently it was not possible to compare the genetic merit of sheep between Australia and New Zealand in a technically valid manner. However some breeds now have sufficient sires with progeny in both countries to allow robust genetic evaluations based on performance and pedigree information from both countries. Corriedale and Coopworth breeders in the two countries have conducted across-flock, across-country evaluations using the Sheep Improvement Ltd (SIL) and Sheep Genetics (SG) genetic evaluation systems. Compared to within country evaluations, breeding values (BVs) from the across-flock evaluation were very similar ($r=0.96-1.00$) when the same system (SIL or SG) was used to estimate BVs. BVs generated from the combined data set by the two systems had lower but still strong correlations ($r=0.69-0.89$) for most traits. This variation was attributed to different analysis models, including genetic parameters, and performance being measured at somewhat different ages. Ultrasound scan traits were least well correlated ($r=0.14-0.65$), most likely due to SIL producing BVs adjusted to constant age while SG produces BVs adjusted to constant carcass weight. It was concluded that the best option for genetic evaluation of combined datasets from the two countries is to exchange and combine data but to conduct genetic evaluations and produce reports within-country.

INTRODUCTION

Genetic evaluation systems based on recorded performance measurements and pedigree, commonly use individual animal model BLUP (best linear unbiased prediction) methods for estimating genetic merit (*e.g.* Newman *et al.* 2000, Brown *et al.* 2007). Increasingly, breeders are using common sires to establish genetic connections on which to base across-flock genetic evaluations. These can extend to across-breed analyses *e.g.* LAMBPLAN Terminal Sire analysis (Brown *et al.* 2000; www.sheepgenetics.org.au/lambplan) or SIL-ACE (Young and Newman 2009; www.sil.co.nz) evaluations.

International genetic evaluations are well established for dairy and beef cattle (Schaeffer, 1994, Donoghue *et al.* 2007). To the author's knowledge, Dohne flocks in Australian and South African are the only sheep example of groups combining data for genetic evaluation from geographically separated countries. Many sheep breeders have sought improvements using overseas genetics through importation of "best bet" genetics from their current breed or "new" breeds to bring new or novel genetics into the industry. The true genetic merit of overseas animals relative to local animals is unknown prior to importation and takes time to estimate once used.

Local, specialized breeds of sheep occur in most countries but some breeds are common to a number of countries. Typically, such breeds have common selection objectives, albeit modified in response to local market signals. Modern methods used for across-flock genetic evaluation can lead to selection of highly related individuals and so to inbreeding in seedstock populations.

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Populations of the same breed from other countries offer one option when seeking genotypes that may lift performance and manage inbreeding. However, fair comparison of animals requires a common genetic evaluation of similar traits and relies on adequate genetic connectedness between populations (also called “linkage” - Newman 2003; Huisman *et al.* 2006). Table 1 summarizes options for comparing sheep from different countries for genetic merit. Robustness of comparisons made increases as you move down the table.

Table 1. Options for objective comparison of genetic merit of sheep across-country

Option	Factors to consider				Best options		
	<i>Traits measured</i>	<i>Connectedness between countries</i>	<i>Genetic analyses</i>	<i>Report features</i>	<i>Dataset</i>	<i>Genetic analysis</i>	<i>Report formats</i>
A	Different	<i>Not critical</i>	<i>Not critical</i>	<i>Not critical</i>	Separate	Separate	Different
B	Similar	Poor	<i>Not critical</i>	<i>Not critical</i>	Separate	Separate	Customize for each country
C	Similar	Good	Differ	<i>Not critical</i>	Combined	Separate	Customize for each country
D	Similar	Good	Similar	Different indexes	Combined	Common	Customize for each country
E	Similar	Good	Similar	Similar indexes	Combined	Common	Same format

GENETIC EVALUATIONS

At the request of Corriedale and Coopworth breeders in New Zealand and Australia, SIL and SG exchanged pedigree and performance datasets in order to determine the best approach to assessing genetic merit for sheep of each breed across-country. Such Trans-Tasman (TT) genetic evaluations can be provided by SIL and SG at the request of breed groups in each country, where there is good genetic connectedness.

Working with representatives of the breeder groups in each country, SIL and SG set up protocols for data protection and customer service. It was agreed that results of “trans-Tasman evaluations” be made available to both groups at a similar time and that the data could not be used for any purpose other than these genetic evaluations without permission of the breeders.

Within breed, the dataset from each country and the combined dataset were analysed by both genetic evaluation systems (SIL and SG). Table 2 details size of the Australian and New Zealand datasets for key traits analysed.

RESULTS AND DISCUSSION

There were very high correlations between breeding values for the same traits generated from analysis of a within country dataset and those from analysis of the combined dataset (0.96-1.00) within each evaluation system (SIL and SG). So breeders within each country should feel confident that the addition of overseas data will have little impact on their evaluations.

Comparison of SIL BVs with SG BVs using the same NZ data (Table 3) show a high correlations for body weight traits ($R^2=0.69$ to 0.86) where data and models are reasonably consistent but weaker correlations ($R^2=0.14$ to 0.32) for carcass traits, where models fitted in the analyses and data collected differ more. Similar results were seen for correlations between BVs generated by the two systems for the combined dataset.

Four factors led to less than perfect correlations between BVs estimated by the two systems.

1. Genetic parameters used in evaluations by the two systems were similar but not identical,

Breeding program design including MAS

2. Components of the genetic models fitted differ, including; fixed, maternal and permanent environment effects as well as adjustment for heterogeneous variance.
3. Weaker correlations seen for carcass traits occur because SIL adjusts these BVs to constant age whereas SG adjusts them to constant carcass weight,
4. Some measurements are collected at significantly different ages, or at a different site for carcass trait scanning, in each country (Young *et al.* 1992; Gilmour *et al.* 1994),

The greatest effects were seen for carcass traits. While we cannot determine the extent to which this was due to the adjustment to different bases (age or carcass weight) or to differences in scan site or age, we believe it is primarily due to different bases for adjustment of carcass traits.

Table 2. Number of animals and data counts for key traits in Corriedale and Coopworth datasets from Australia and New Zealand (NZ)

Trait	Corriedale		Coopworth	
	Australia	NZ	Australia	NZ
Total animals	46,875	128,014	74,223	826,661
Growth WWT – Weaning weight	23,421	90,084	56,952	637,468
Growth LW8 – Live weight at 8 months	10,984	23,384	30,270	378,163
Growth LW12 – Live weight at 12 months	14,078	14,857	29,683	90,314
Meat EMD – Eye muscle depth	7,513	5,312	21,930	27,735
Wool GFW - Greasy fleece weight	13,908	43,280	33,016	342,101

Table 3. Regression of BVs for NZ Corriedales between SIL and SG analyses.

Trait	All animals with records			Sires		
	Animals	R ²	Coefficient	Animals	R ²	Coefficient
WWT	132,439	0.86	0.56	5,749	0.81	0.53
LW8	130,960	0.69	0.90	1,851	0.64	0.75
LW12	131,060	0.81	1.00	2,269	0.79	0.99
FAT	66,507	0.14	0.42	2,628	0.23	0.36
EMD	83,747	0.32	0.73	144	0.51	0.87
GFW	130,989	0.82	0.03	37,633	0.84	0.03

Connectedness between countries was adequate to produce across country breeding values for each breed. Using current SG connectedness analyses, 27 of the 28 Corriedale flocks with recent data were sufficiently linked to report across flock breeding values. Twelve sires had recorded progeny in both countries and in excess of 100 sires had across country pedigrees. Approximately 10% of Australian born animals were from NZ sires where as only 1% of NZ born animals were from Australian sires. All active Australian flocks had direct sire connectedness with NZ flocks. Similar levels of connectedness were seen in the Coopworth dataset.

FUTURE INTERNATIONAL EVALUATIONS

Corriedale breeders involved in this evaluation have agreed to transfer updated datasets for trans-Tasman evaluations three times per year (January, May and October) to fit with data collection, selection and marketing decisions. In addition to routine reporting, top sires and young rams from both countries will also be reported to provide local breeders with the opportunity to identify new genetics to consider for importation. Coopworth breeders are considering how trans-Tasman evaluations can be best used for their breed.

Health concerns mean some countries will not accept live animals, semen, or embryos, from some other countries due to real and perceived disease risks. If such restrictions lie in only one direction, strong connections can be built by flocks in the less restrictive country using genetics from the other country. A downside is that genetics only flow in one direction so benefits to breeders in the country not allowing gene importation come only from sale of genes, as semen, embryos or live animals. If two countries do not allow importation of each others germplasm in any form, genetic connections cannot be created precluding across-country genetic evaluation.

Breeders in Australia and New Zealand can exchange sheep genetics to capture both genetic improvement and marketing opportunities. This should allow them greater flexibility when seeking high rates of genetic improvement while minimising inbreeding. Research and development will continue to enhance BVs effectiveness for across-country selection.

CONCLUSIONS

Across country genetic evaluation for sheep breeders in New Zealand and Australia is currently best achieved using a combined dataset with analysis and reporting from the local system breeders are familiar with. Differences in trait definition and analysis specification will cause minimal re-ranking of sires for non-carcass traits, between results of the two evaluation systems.

Breeding groups wishing to conduct across-country genetic evaluation should actively develop and maintain strong genetic links.

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