Proc. Assoc. Advmt. Anim. Breed. Genet. ***16****: 389-392*

MERINO BREEDING VALUES – HOW DO THEY COMPARE?

J.E. Hocking Edwards, N.J. Edwards and T.M. Starbuck
SARDI Livestock Systems, Struan Research Centre, Naracoorte, SA 5271

SUMMARY
There is a question in some sections of the Merino industry whether the methods used to describe the genetic value of a ram provide a true and unbiased representation of his genetic merit if the information is collected in the field, or if it does not take into account the performance of his progeny. This paper compares Estimated Progeny Values calculated in the Central Test Sire Evaluation, based solely on the performance of his progeny, with Estimated Breeding Values calculated through the Merino Validation Project, based on the ram's own performance plus that of all of his recorded relatives. The data used was from rams evaluated in the South Australian Central Test Sire Evaluation over 3 drops. There are very good relationships between the estimated genetic values for all the hogget wool, carcass and health characteristics evaluated. As there was common data used in each of the databases, it would be expected that the correlations would be high. Nevertheless, the results demonstrate that the Merino industry can have confidence that genetic evaluation of a ram provides reliable information on his genetic merit whether the information is gathered from the performance of his progeny or his own performance together with that of his relatives.
Keywords: progeny test, wool, selection, EBV, EPV

INTRODUCTION
Performance recording and genetic evaluation in the Australian wool sheep industry has, until recently, had a slow rate of implementation and uptake due to industry concerns about accuracy and repeatability of objective measurement of wool, the ability of objective measurement to describe all wool quality characteristics and incomplete understanding of measurements (Rogan, 1995). These concerns have been addressed by research into objective measurements that can be used to describe wool quality and the accreditation of wool testing laboratories. In addition, the use of programs such as RAMPOWER to obtain genetic performance information within flocks has increased the awareness of the measurement of genetic merit. It appears that confidence in, and understanding of, the use of objective assessment of a Merino's genetic potential is now increasing, since one of the genetic analysis services, Merino Genetic Services (MGS), currently has 180 Merino flocks participating and now with 500,000 pedigreed and recorded animals (R. Banks, 2005; *pers. comm*.).

To enable higher rates of economic gain, it is important that breeders are able to access accurate and reliable across-flock genetic information. Currently there are three main databases that provide across-flock genetic comparisons – MGS; Central Test Sire Evaluation (CTSE); and Merino Benchmark – and several smaller datasets. A joint initiative between Australian Wool Innovation Ltd and Meat & Livestock Australia Ltd seeks to combine information from each of these into a single database(Sheep Genetics Australia - SGA) to maximise the power and reliability of breeding values for across flock breeding information.

At present the existing analyses use different genetic parameters, models and reporting descriptors that may cause differences in breeding values. This leads to confusion amongst people using the information. Estimated Breeding Values (EBV) produced by MGS are calculated using measured performance of the individual sheep and all its recorded and pedigreed relatives. Estimated Progeny Values (EPV) calculated in the CTSE estimates the breeding value of the ram based on the performance of progeny recorded within the central test and comparisons are made between sites using link rams. EPVs are equivalent to ½ EBV since EPVs describe the performance of the progeny (who receive only half their genes from their ram).

As the understanding of breeding values improves, there is now a concern by some breeders and wool producers that the methods used to describe a ram's breeding value are not a true representation of his genetic merit if it does not take into account the performance of his progeny and therefore does not represent his "true breeding value". Also, some people place more trust in data collected by an "independent source", such as in the CTSE, rather than that collected in the field by the possibly "biased" ram breeder. This paper compares EPVs calculated in the CTSE, that are based on the performance of a rams progeny, with EBVs calculated as part of the Merino Validation Project. The EBVs include data collected in the field by the ram breeders regarding the ram's performance, his relatives and progeny's performance plus the data from the South Australian CTSE (SACTSE)

MATERIALS AND METHODS

Progeny from the 2001, 2002 and 2003-drop SACTSE were managed at Struan Research Centre as part of the national sire evaluation scheme for Merino sheep according to the guidelines provided by the Australian Merino Sire Evaluation Association (2000). South Australian Merino ewes were artificially inseminated with semen from Merino rams entered by ram breeders from SA, Vic, NSW and WA. A total of 30 rams were evaluated, with two link rams per year. The number of rams entered and the total number of progeny for each drop in the SACTSE are shown in Table 1. Birth and rear type of the progeny were recorded. The progeny were weighed at eight-week intervals from birth to hogget shearing at 16 months of age. Faecal egg counts (HFEC) and ultrasound measurements of eye muscle (HEMD) and fat depth (HFAT) were performed close to hogget shearing.

Table 1. The number of rams evaluated (including link rams), the total number of hoggets for each drop and range in number of hoggets per ram evaluated in SACTSE and the total number records and range of number of records per ram evaluated in MGS

Drop	2001	2002	2003
N rams	10	15	8
Hoggets in SACTSE (range)	468 (73 - 120)	755 (27 – 69)	560 (56 – 107)
Records in MGS (range)	1080 (53 – 264)	1934 (29-578)	2794 (74 – 1114)

EPVs based on progeny data were calculated for the SACTSE (Gilmour, 1993). SACTSE progeny data and all available relative data were used to calculate EPVs for the national Merino Superior Sires (MSS) analyses. Only rams entered into the 2001 and 2002 drops were evaluated in MSS. All of this data was collected in centralised progeny tests and these EPVs have been reported previously (Hocking Edwards *et al*., 2003; Hocking Edwards *et al*., 2004; Hocking Edwards *et al*., 2005; Swan *et al.,* 2004; mss.anprod.csiro.au). EBVs calculated by MGS (OVIS software www.mla.com.au/mgs) included all progeny data collected in SACTSE as well as any progeny and relative data collected in the field by ram breeders. EBVs for the rams entered into the 2001 and 2002 drop were calculated in the June 2004 MGS analysis and the EBVs for rams assessed in the 2003 drop were calculated in the February 2005 MGS analysis. Pearson correlation coefficients and the slope of the regression equations between EBVs with the EPVs from MSS and SACTSE were calculated (SAS 8.02). Body weight (HWT) and clean fleece weight (HCFW) EPVs are expressed as percentage deviations whereas HWT and HCFW EBVs are expressed as kg deviations, thus the slopes of these regression equations have not been reported

RESULTS AND DISCUSSION

All of the correlations between the hogget EBVs and EPVs were significant (P<0.05; Table 2) with most correlations being highly significant (P<0.0001). This was true for both the site analysis (SACTSE) that only calculates EPVs based on single-drop data and the National CTSE analysis (MSS) that calculates EPVs across sites and years. This indicates that whatever analysis is used, the ranking of rams within the evaluation is highly comparable across analyses. In simple terms the breeding values and the ram rankings for all traits are highly consistent for all 3 analyses.

As the SACTSE, MSS and MGS analyses contain common progeny data, from statistical principles it would be expected that the correlations would be high between the analyses. These results support this. Breeders and producers who are not geneticists or statisticians can see from the current results that similar ranking of rams occurs, regardless of whether SACTSE, MSS or MGS is used to derive genetic information about rams. This supports the validity of measurements made by ram breeders compared to independent assessment and the combination of field data plus central test progeny agrees very well with central test progeny alone. The high correlations also demonstrate that the combination of field data from many flocks is as unbiased as the independent data collected from central progeny tests.

Table 2. Pearson correlation coefficients for EBVs calculated by Merino Genetic Services (MGS EBV) and EPVs calculated by the SA Merino Central Test Sire Evaluation (SACTSE) and Merino Central Test Sire Evaluation (MSS) and slope of the regression of EPV against EBV

EPV	MGS EBV								
	HWT	HCFW	HFD	HFDCV	HSL	HSS	HFEC	HFAT	HEMD
SACTSE	0.906*	0.705*	0.948*	0.967*	0.956*	0.956*	0.912*	0.725*	0.487
Slope			0.60±0.04	0.44±0.02	0.46±0.03	0.50±0.03	0.26±0.02	0.06±0.01	0.29±0.1
MSS	0.987*	0.905*	0.982*	0.910*				HFAT	HEMD
Slope			0.48±0.05	0.42±0.04				0.725*	0.487

* Significance of correlation (P<0.0001); ** Significance of correlation (P=0.006)

The slope of the regression equation between EBVs and the EPVs would be expected to approximate 0.5 given that EPV = ½EBV. This was the case for fibre diameter (HFD), fibre diameter variation (HFDCV), staple length (HSL) and staple strength (HSS). In this analysis, the slope of the regression of EPV and EBV HFAT and HEMD differed from 0.5 (Table 2) and HFEC differed from 1 (both SACTSE and MGS express HFEC as an EBV). These EBVs and EPVs are all expressed as absolute units and are thus describing the same genetic value. However, the models used for each of the traits in the SACTSE and MGS analysis are not identical as there are some differences in the methods of fitting fixed effects and the genetic parameters. Also, some traits are expressed differently between analyses. This demonstrates that absolute EBVs and EPVs can not be compared to anything other than the EBVs or EPVs calculated in the same analysis.

CONCLUSIONS

The results presented in this paper demonstrate the expected outcome that EPVs and EBVs provide similar ranking of Merino rams across analyses. It is likely that ranking of rams will not significantly change when data from MGS and CTSE are combined and analysed as a single dataset. This is also confirmed by results of analyses being conducted in the development of the SGA (D. Brown, 2005, *pers. comm*.). SGA is aimed at combining different sources of data to maximise the power and reliability of breeding values. These results demonstrate that this approach will be successful. Central progeny tests will continue to have value in providing linkage between flocks, years and environments and can potentially focus on harder to measure traits such as temperament, maternal ability, feed efficiency and meat eating quality.

Breeding values are affected by the data and statistical models used to calculate them and by the genetic parameters used in those models. With care, all sources of data relating to an animal can, and should be, included in its breeding value as using all available data will give the most accurate and widely relevant indication of genetic merit. These results confirm that it is incorrect to say that only centrally collected data is useful – however all data must be collected carefully and analysed. It is important that this is recognised and accepted by all participants (breeders and researchers) in genetic evaluation of the Merino industry so that confusion is minimised and the Merino industry can use breeding value information with confidence.

ACKNOWLEDGEMENTS

This work is funded by the prime lamb industry through Meat and Livestock Australia Ltd, Merino ram breeders, South Australian Stud Merino Breeders Incorporated, Australian Wool Innovation Ltd through funding of link rams and Allflex®. Editorial comment from Rob Banks is greatly appreciated.

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