

**THE EFFECT OF GENETIC PARAMETER ESTIMATES ON BREEDING VALUE ESTIMATION  
IN MERINO SIRE EVALUATION PROGRAMS**

**B.C.RUSSELL and D.J.COTTLE**

Department of Wool and Animal Science  
University of New South Wales  
PO Box 1, Kensington, NSW 2033, Australia.

**SUMMARY**

Multi-trait BLUP was used to estimate breeding values for 69 sires from a central test sire evaluation program. Three sets of genetic parameters were used and the correlations between the breeding value estimates for each parameter set were computed. The correlations were generally high, approaching unity, indicating that the sensitivity of the procedure to genetic parameter estimates may not be too great. This is discussed in relation to increasing the use of multi-trait BLUP in sire evaluation programs

**INTRODUCTION**

Merino sire evaluation programs are increasingly being recognised as a method of making both within- and across- flock genetic improvement. Programs are currently being undertaken at a number of central test sites in N.S.W, with private on-farm progeny testing being linked to the central tests via reference sires.

Sire evaluation may be analysed using a number of different procedures (Thompson 1979). In Western Australia, on-farm sire referencing schemes were analysed using the method of regressed least squares (contemporary comparison)(Lewer 1987). Here, the deviation from the mean of each sire's progeny is multiplied by a regression factor to account for the heritability of the trait and the number of progeny per sire. Currently, for central test sire evaluation in N.S.W, single trait Best Linear Unbiased Prediction (BLUP) is used to estimate breeding values. Potentially, BLUP offers more accurate comparisons of sheep, both within and across management groups provided adequate linkage is available. Single trait BLUP requires only an estimate of the heritability of each trait, and is therefore quite simple to apply using commonly available software such as SAS and Harveys LSMLMW (Harvey 1990). BLUP procedures also allow multiple trait evaluation, whereby information on progeny performance in one trait provides information for all correlated traits in the breeding objective. Multi-trait BLUP requires knowledge of the genetic and phenotypic correlations between traits as well as the heritabilities. The development of more specific software such as SIREBLUP (Gilmour 1990) has made the application of multi-trait BLUP to sire evaluation programs more practical.

Atkins (1991) recommends that multi-trait BLUP is the optimum method of analysis for sire evaluation. Although it is recognised that the differences between the available methods for breeding value estimation are insignificant (Mian 1991), multi-trait BLUP offers a number of advantages over contemporary comparison and single trait BLUP procedures, especially in the linking of on-farm and central test site data. For example, where on-farm progeny tests may measure greasy fleece weights only, multi-trait BLUP allows prediction of breeding values for clean fleece weight, allowing a more satisfactory link into central test site data. Two tooth and four tooth data may be combined more

easily and index values computed directly using multi-trait BLUP. In addition, the process fully utilises all information available and is, theoretically at least, a more accurate method. Despite these advantages, multi-trait BLUP has had limited use so far in central test sire evaluation.

There are two main problems associated with the use of multi-trait BLUP in sire evaluation programs. Firstly, the assumption that all sires are randomly selected from the same population is likely to be incorrect in most cases. Sires entered in evaluation programs do not originate from a single base population, and have almost always been subjected to a large range of selection strategies. If sires of different genetic origin are grouped together and regressed to a common mean, the breeding value estimates will be biased. The second problem, and the one to be addressed in this study is the choice of which genetic and phenotypic parameters to use in such a diverse population. The use of incorrect genetic parameters can lead to errors in breeding value estimation and the advantages of BLUP listed previously could be negated if this were to occur. This study takes a number of parameter sets and examines their effects on breeding value estimation using multi-trait BLUP in two different cases. Firstly, where direct information is available on all traits in the objective, as is generally the case when linking a number of central test sites. Secondly, where indirect breeding value estimation for one trait (clean fleece weight) occurs, as is often the case where on-farm programs are linked. Determining the sensitivity of the BLUP estimates to different parameters may lead to more confidence in its use in sire evaluation.

## MATERIALS AND METHODS

The data for this study were generated from two central test stations operated by the University of N.S.W, at Hay and Deniliquin in the Riverina region of N.S.W (Roberts et al 1991). Sire evaluation programs have been conducted there since 1987 with data being collected on 85 sires thus far. Breeding values for greasy and clean fleece weights, fibre diameter and body weight were estimated for 69 of these sires using SIREBLUP (Gilmour 1990). In the first case (direct estimation of all traits) information on all traits was included in the data file, while in the second case (indirect estimation of CFW) all information on CFW was deleted from the data file. Thus breeding value estimates for CFW are drawn from the other correlated traits. SIREBLUP requires heritabilities and genetic correlations as well as error variances and correlations between the traits.

Three sets of parameters were selected from the literature, and are shown in Table 1. The parameters were chosen so as to provide a reasonable range of values, and to represent the type of sheep evaluated in these programs. Those obtained by Brown and Turner (1968) were from medium wool Peppin Merino ewes, while those of Gregory (1982) were from the Bungaree family group of the South Australian strong wool strain. Estimates from Mortimer and Atkins (1989) were based on the four major Merino strains (fine, medium Peppin, medium non-Peppin and South Australian strong wool).

**Table 1. Genetic and phenotypic parameters used in the present study.**

a) Heritabilities.

Trait	1.Brown & Turner(1968)	2.Mortimer & Atkins(1989)	3.Gregory (1982)	Range
GFW	0.42	0.29	0.27	0.15
CFW	0.40	0.30	0.25	0.15
FD	0.47	0.48	0.75	0.28
BWT	0.65	0.34	0.40	0.31

## b) Genetic and Phenotypic Correlations.

Traits	1. Brown & Turner (1968)		2. Mortimer & Atkins (1989)		3. Gregory (1982)		Range	
	$r_g$	$r_p$	$r_g$	$r_p$	$r_g$	$r_p$	$r_g$	$r_p$
GFW-CFW	0.80	0.85	0.87	0.87	0.62	0.82	0.25	0.05
GFW-FD	0.13	0.13	0.27	0.21	-0.17	0.13	0.44	0.08
GFW-BWT	0.26	0.24	-0.03	0.32	0.03	0.37	0.29	0.13
CFW-FD	0.16	0.14	0.40	0.18	-0.06	0.13	0.46	0.05
CFW-BWT	0.27	0.27	-0.09	0.31	0.04	0.36	0.36	0.09
FD-BWT	0.12	0.13	0.12	0.12	-0.08	0.03	0.20	0.10

NB: GFW/CFW = greasy/clean fleece weight, FD = fibre diameter, BWT = bodyweight.

The data were pre-adjusted for the fixed effects of sex and birth status, with the fixed effect of group (location/year) being fitted by the SIREBLUP program. The Reduced Animal model was used to obtain BLUP solutions for the random effects (sires). In each case three estimates were made for the traits GFW, CFW, FD and BWT, with different parameters used each time. Correlation co-efficients were then computed between the estimates resulting from each set of parameters.

## RESULTS

The correlations between breeding values estimated using the three different parameter sets when information was available on all traits are presented in Table 2. All correlations were high and close to unity. They ranged from 0.86 to 0.99. The standard errors (not reported) were very low, due to the narrow distribution of high correlations. On the basis of these correlations it appears that the choice of genetic parameters did not have a very large effect on the breeding value estimates in this case, especially for bodyweight. When indirect estimation of breeding value for CFW occurs (Table 3) the correlations between the three estimates for CFW, while still remaining relatively high all decrease, while the correlations between the estimates for all other traits are either unaffected or increase.

Table 2. Correlations between estimated breeding values derived from three genetic parameter sets for four traits (direct estimation of breeding values for all traits).

Parameters		GFW	CFW	FD	BWT
1	2	0.98	0.97	0.93	0.99
1	3	0.86	0.93	0.99	0.99
2	3	0.92	0.96	0.93	0.99

Table 3. Correlations between estimated breeding values derived from three genetic parameter sets for four traits (indirect estimation of breeding value for CFW).

Parameters		GFW	CFW	FD	BWT
1	2	0.98	0.86	0.99	0.99
1	3	0.87	0.88	0.99	0.99
2	3	0.93	0.89	0.99	0.99

NB: Parameter sets 1, 2, and 3 correspond to those from Brown and Turner (1968), Mortimer and Atkins (1989) and Gregory (1982) respectively.

## DISCUSSION

It has previously been noted that if the genetic parameters used in the estimation of breeding values using multi-trait BLUP vary substantially from the true values, the errors will be greater than if the

correlated traits were not used at all (Henderson and Quaas 1976). In other words, if we cannot arrive at a set of genetic parameters that are appropriate for the population we wish to evaluate, the use of multi trait BLUP will be of little benefit, and we should therefore stick to the more simple evaluation procedures that do not require genetic correlation estimates. Genetic and phenotypic parameters used in the wool industry are usually produced from research flocks and then applied to the commercial and stud flocks that we wish to improve. The problem with central test sire evaluation is the genetic diversity of the sheep. There are almost as many genetic backgrounds as there are sires in the program, making the task of providing a single set of parameters that will be appropriate for all members of the population a very difficult one.

The results presented here indicate that it may not be of crucial importance to have a set of precise genetic parameters when data are available on all traits in the objective. When all traits have information available the contribution of the correlated traits to the breeding value estimate is minimal, and therefore the choice of which set of genetic parameters to use has less influence on the final estimates. When estimating breeding values for a trait with no direct information the choice of which parameter set to use is more important, although the correlations between the estimates are still high. The sires evaluated in the program are largely from medium wool strains, although sires from both fine and strong wool strains have been entered. The genetic parameters used to predict breeding values had quite a large range yet the results between all three parameter sets were highly correlated in both cases. The parameters from Gregory (1982) could be considered the most inappropriate as they were obtained from sheep that had little genetic connection to those that were evaluated here.

The risk of using very inappropriate parameters could be minimised by regulating the sheep that are entered in central test programs. By nominating whether the central test is for fine, medium or strong woolled sheep, more specific parameter sets could be developed for use in each evaluation. Likewise, breeders running a progeny test on-farm should be wary about linking to central tests or other on-farm programs where the sheep are from a distinctly different strain. This would reduce the likelihood of using parameters that are very different from the true values, and lead to more confidence in the use of multi-trait BLUP in Merino sire evaluation. Research into the magnitude of parameter differences between Merino strains would also be of use. These results suggest that the problem of an incorrect model is probably of greater magnitude than that of which set of parameters to use, especially in central test programs where the genetic diversity of the sheep is likely to be greater than on farm tests. This problem is still outstanding and must be overcome before BLUP of any type can be used routinely in sire evaluation

#### ACKNOWLEDGEMENTS

Thanks go to Prof. John James, Dr Kevin Atkins and the referee for valuable comments on the paper.

#### REFERENCES

- ATKINS K D (1991). In Merino Sire Evaluation in Australia (Ed F D Brien) (Australian Wool Corporation, Melbourne) In Press.
- BROWN G H and TURNER H N (1968). *Aust. J. Agric. Res.*, **19**, 303-22.
- GILMOUR A (1990). SIREBLUP. Instructions for use.
- GREGORY I P (1982). *Aust. J. Agric. Res.*, **33**, 363-73.
- HARVEY W (1990). Users Guide to LSMLMW.
- HENDERSON C R and QUAAS R (1976). *J. Anim. Sci.*, **43**, 1188-97.
- LEWER R P (1987). In Merino Improvement Programs in Australia (ed B J McGuirk) (Australian Wool Corporation, Melbourne) 413-420.
- MIAN B (1991). PhD Thesis, University of N.S.W.
- MORTIMER S I and ATKINS K D (1989). *Aust. J. Agric. Res.*, **40**, 433-43.
- ROBERTS E M, ATKINS K D, COTTLE D J, EPPLESTON J, JAMES J W, LOLLBACK M, SCHUMAN W and REED P (1991). *Wool Tech. Sheep Breed.* **39**, 1-9
- THOMPSON R (1979). *Biometrics*, **35**, 339-353.