DO WE NEED TO INCLUDE GENETIC GROUPS TO IMPROVE THE PRECISION OF MERINO SIRE EVALUATION?

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SUMMARY

The influence of genetic differences among Merino ram sources on sire evaluation was examined by estimating sire X dam flock interactions and including varying numbers of genetic groups to account for ram source differences. It was concluded that across-flock sire evaluation results will be biased (in some cases severely), if no account is taken of ram source through including genetic group in the model. Sire X dam source interactions were relatively small but indicated some heterosis between bloodline crosses that may also need to be included in evaluation models.

Keywords: Merino, sire evaluation, central test, genetic groups

INTRODUCTION

Genetic evaluation by BLUP relies on a knowledge of the genetic variation that exists within an unselected base population of animals. Performance records on individuals are used to estimate genetic values taking account of the association between phenotypic measurements and genetic value and the amount of information (or accuracy) contained in the data. In the presence of selection, the same principle can still be applied provided there is a pedigree that maps the genetic relationships among animals back to the base population and that the traits on which selection was based are part of the data. The process can also be extended across-flocks (or -herds) again based on the presumption that there is tight genetic linkage in the pedigree among the flocks and that the selection decisions are a function of the data.

The Australian Merino population consists of a number of distinct strains or bloodlines that are not highly related to each other either recently or historically. Some of these bloodlines have been maintained genetically isolated for many generations while the principal strains were based on mixtures of unrelated breed crosses. This is clearly reflected in the differences that exist among some traits in the between-flock and within-flock genetic correlations (Atkins and McGuirk 1976). Given this degree of unrelatedness, we need to consider the consequences of between-strain and bloodline differences on the effectiveness of across-flock genetic evaluation of sires. In this paper we examine the effects of including genetic groups in sire evaluation both where the sires were bred in a range of flocks and were mated with ewes that also come from a range of flocks.

MATERIALS AND METHODS

Description of sheep. The Merino bloodline crossing program at Trangie Agricultural Research Centre, described by Mortimer *et al* (1994), was based on 8 flocks from the multiple-bloodline project (Mortimer and Atkins 1989), 2 fine-wool, 2 medium-wool non-Peppin, 3 medium-wool Peppin and 1 broad wool bloodlines. From 1984, these bloodlines were mated in a complete diallel design to produce both purebred and two-way cross progeny. For this study, information is reported on 2003 hogget (15 months) ewes and rams measured during the period 1985-90. These animals were the progeny of 79 sires which had been selected at random from prior base populations at Trangie. On average, then, each bloodline flock had about 10 sires which each produced about 25 progeny, of which 7 were from dams of the same bloodline as the sire and 18 were from dams of the other 7 bloodlines. Progeny were recorded for greasy fleece weight (GFW), yield (Y), clean fleece weight (CFW), fibre diameter (FD) and off-shears body weight (OSWT) (see Mortimer and Atkins 1989).

Statistical analysis. Each trait was analysed separately in ASREML (Gilmour *et al.* 1997). Fixed effects were fitted for year, birth-rearing type, age of dam and date of birth plus any significant first order interactions. Dam-source (8 bloodlines) and sire as a random effect were also included in the model. Initially, we examined the effect of various models to account for sire-source by including an additional factor for genetic group:
Full Model: 8 genetic groups, 1 for each source bloodline
Model A: 3 genetic groups, fine (2 bloodlines), medium-low and medium-high (3 bloodlines in each group separated largely on fleece weight)
Model B: 2 genetic groups, fine (2 bloodlines) and medium (6 bloodlines)
Model C: No groups, all sires assumed to come from a single flock
Sire X dam-source was fitted as a random effect both in the presence and absence of a sire-source X dam-source interaction to account for non-additive effects of across-bloodline sire usage.

The impact of using the appropriate genetic parameters with an inappropriate model was examined by obtaining BLUP solutions from a single ASREML iteration using the sire variances obtained from the Full Model. For the incomplete genetic groups models we fitted group (sire-source) and sires plus fixed effects using the Full Model sire variance and then compared the sire solutions with those obtained from the Full Model analyses.

RESULTS

Variance estimates from genetic group models. The impact of alternative groupings of sire-source flocks on the estimates of variance components (Table 1) shows the bias that can occur in sire variances where sire-source is ignored (Model C) or poorly accounted for (Model B). The increase in apparent sire variance resulted from between-flock variance being added to the true within-flock sire variance. Sire X dam-source variances (where sire-source X dam-source was not fitted) were relatively small and consistent in all Models (Table 1). This interaction was only significant for GFW, CFW and OSWT. Where sire-source X dam-source was fitted, the sire X dam-source variance was substantially reduced for all traits and Models. From the Full Model, average heterosis estimates across all bloodline crosses were 3.6 %, 4.2 % and 2.6 % for GFW, CFW and OSWT respectively. The non-significant heterosis estimates for FD and Y were 0.1 % and 0.5 % respectively.

Sire solutions from genetic group models. Correlations among sire solutions from the various models were all very high (Table 2). Since the same sire variance was assumed, solutions within a sire bloodline group would rank very similarly leading to a high degree of association. It is only when we inspect the variances between BLUP solutions and the regression of the biassed estimate on the 'true' estimate that we can see the effect of reduced discrimination between the sire-sources (Table 2). Ignoring sire-source (Model C), reduced the regression of flock effects (averaged from the sire solutions) on flock effects estimated from the Full Model to 0.60-0.65, leading to the lower regression among sires shown in Table 2. The 3 genetic groups used in Model A had little effect on the sire solutions except for fibre diameter which was poorly discriminated in the medium-wool groups.

Table 1. Estimates of variances for sires, sire X dam-source and error from models with varying numbers of genetic groups

Trait	Full model (8 genetic groups)	Model A (3 genetic groups)	Model B (2 genetic groups)	Model C (1 genetic group)
GFW - sires	0.0331	0.0378	0.0458	0.0839
sire X dam-source	0.0032	0.0041	0.0044	0.0040
error	0.4507	0.4500	0.4498	0.4507
Y - sires	1.54	1.58	1.70	2.28
sire X dam-source	0.00	0.00	0.00	0.00
error	21.18	21.19	21.19	21.20
CFW - sires	0.0175	0.0195	0.0264	0.0569
sire X dam-source	0.0015	0.0020	0.0018	0.0015
error	0.2375	0.2370	0.2374	0.2379
FD - sires	0.2644	0.2887	0.3361	0.6094
sire X dam-source	0.0036	0.0043	0.0026	0.0008
error	1.4820	1.4810	1.4818	1.4819
OSWT - sires	2.13	2.04	2.53	2.79
sire X dam-source	1.09	1.08	1.09	1.09
error	22.62	22.63	22.62	22.63

DISCUSSION

Across-flock genetic evaluation in Merinos aims to provide ram breeders with information on the relative breeding values of alternative sires, often from alternative sources. If available data were used without identifying any source genetic group (Model C), the impact will be to seriously under-estimate above-average performing sources and over-estimate below-average sources. Central test sire evaluation operates both Fine- and Medium-wool schemes separately (Hickson 1997), akin to Model B. However, sire entries to both schemes represent a wide range of sources and several sires are entered in both schemes. Thus, biasses in sire solutions for extreme sires with modest numbers of progeny will occur. A more recent development in across-flock evaluation has been Merino Benchmark (Casey and Atkins 1999) which uses a genetic groups model similar to that of Model A. Provided the genetic groups account for the major differences in all traits, the Merino Benchmark model should provide nearly unbiassed estimates of breeding values.

Table 2. Effect of using sire variances from the full model on BLUP solutions from the incomplete models. Results are expressed as standard deviations (sd) among sires solutions and the regressions *[and correlations]* of sire solutions from the incomplete models Vs the full model

Trait	Full model (8 genetic groups)	Model A - 3 genetic groups	Model B - 2 genetic groups	Model C - 1 genetic group
GFW - sd	0.274	0.266	0.255	0.205
regression [*r*]		0.96 (*0.99*)	0.92 (*0.98*)	0.72 (*0.96*)
Y - sd	1.33	1.30	1.24	1.09
regression [*r*]		0.96 (*0.98*)	0.91 (*0.98*)	0.79 (*0.96*)
CFW - sd	0.228	0.224	0.213	0.162
regression [*r*]		0.98 (*0.99*)	0.92 (*0.98*)	0.68 (*0.96*)
FD - sd	0.75	0.72	0.71	0.65
regression [*r*]		0.87 (*0.91*)	0.87 (*0.92*)	0.77 (*0.90*)
OSWT - sd	1.48	1.46	1.37	1.30
regression [*r*]		0.98 (*0.99*)	0.91 (*0.98*)	0.85 (*0.97*)

The major implication of this study is the need to consider ram source genetic differences in across-flock sire evaluation. In particular, this would seem necessary in future analyses of central test sire evaluation. Substantial increases in progeny numbers may be one means of reducing bias arising from shrinkage to an inappropriate base population. Alternatively, the use of genetic groups in the analysis may be more practical. However, grouping highly selected sires from many sources is not a trivial task without additional information. An objective of grouping is to reduce the between-sire (within-group) variance to a value that is in line with the assumed within-flock sire variance. This may provide a test for the effectiveness of groups. The other issue of interaction between sire and dam-source on evaluation results was of secondary importance. Genetic groups and a more complex model may further reduce the relatively small impact of these interactions in genetic evaluation.

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