DIMINISHED DISCRIMINATION IN MERINO GENETIC EVALUATIONS

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SUMMARY

Many Merino studs use across-year Best Linear Unbiased Predictor (BLUP) evaluations performed with incomplete pedigree but with common sires providing links between successive years – commonly in the form of linked sire evaluations. Simulation results are presented which show that sire-only pedigree structures under BLUP analysis lead to significant underestimation of the genetic differences between years. This would have some impact on the efficiency of selection across age groups, and would cause severe underestimation of genetic trends within a flock. An optimal solution to this problem is also likely to be found by such simulation studies.

Keywords: BLUP, accuracy, pedigree, genetic trend, simulation

INTRODUCTION

Casey and Hygate (1992) reported that pedigree records are relatively sparse in Australian Merino studs. While some improvement might be expected over the time since their report, less than 6 % of animals had full pedigree recorded. With 20 % of studs recording full pedigree on at least some animals, clearly either small studs were over-represented in this category, or many studs recorded full pedigree on only a few animals.

A much larger proportion of studs (78 %) and animals (28 %) had sire pedigree available (Casey and Hygate 1992). There are several reasons why sire-only pedigree is more common:

i) sire evaluation may be the prime reason for pedigree recording
ii) sire pedigree recording is less demanding or expensive
iii) sire information is seen as more valuable in selection decisions
iv) sire information is seen as more valuable in marketing rams.

Sire evaluation itself is used to compare young rams to proven performers; to evaluate rams from other flocks; or to identify entrants for central test sire evaluation. The simplicity of breeding design and ease of interpretation of results give sire evaluation an enduring appeal to many breeders. As an important part of across-flock comparisons, on-farm sire evaluations are encouraged as a key factor in sustained genetic improvement in the industry. While pedigree recording in general is encouraged, the cost of dam recording is likely to lead to increasing prevalence of sire-only pedigree. Considerable attention has been given to adequate linkage between central test sire evaluations. (Miraei Ashtiani and James 1991, 1992). Whilst still an important issue, less emphasis has been given to the quantity or quality of linkage among on-farm sire evaluations.

Many breeders are interested in demonstrating genetic change in their flocks – to assess their own performance and directions of genetic change, and as a marketing tool. Breeders with several years of data available are routinely provided with across-year BLUP analyses, and some have received the derived estimates of genetic trend, based on mean breeding values by year of birth. Some geneticists who have attempted to estimate genetic trends in Merino stud flocks have been concerned by the irregular results. In the author's experience, these estimates often exhibit high year-to-year variability of mean performance, and the estimated genetic trends rarely keep pace with the changes predicted by selection differentials. Accounting for selection is a fundamental requirement of BLUP, but this is regularly not met, either due to the increasing genetic merit of the ewe flock or because highly selected rams are introduced from other sources for evaluation.

This investigation set out to determine whether the failure to account for all selection represents a serious problem, or whether it may be conveniently ignored for practical purposes.

METHODS

A Merino flock was simulated by computer, with 16 rams and 512 ewes mated per year over 17 years of breeding. A single trait was simulated and measured once prior to the first breeding at 19 months. The single trait simulated had phenotypic variance, VP=1.0 and additive genetic variance, VA=0.4. There were no environmental or sex effects simulated; year of birth was the only effect fitted in BLUP evaluations. The simulation was an adaptation of that described by Brash *et al* (1996).

The first breeding groups were drawn by mass selection from 800 ewes and 200 rams in 4 and 1 age groups respectively. Thereafter, BLUP was performed each year with complete pedigree information available. Five of the first ram group became link sires and were used in all subsequent years, while the 11 other rams were selected from available ram hoggets each year and culled after one joining. Ewe selection was across age-groups, with 5 % annual wastage of adults due to death or culling. Progeny of the link sires were included in evaluations but were not available for selection.

Three genetic analyses were performed after measurement of the 17th cohort:
Scheme A: Animal Model BLUP. Full pedigree information.
Scheme B: Sire Model BLUP without pedigree. All dam pedigree was discarded, and sire identities were re-coded so that there remained no link back to their breeding and hogget measurement records in the flock, but the sire linkage across years was preserved.
Scheme C: Sire Model BLUP with link sires fixed. BLUP was performed on each single year with sire pedigree only, and the results for link sires equalised to provide solutions for all sires.

One such population was analysed in detail. The realised reproduction rate was 94 % progeny reaching hogget measurement per ewe joined, with an average of 30 progeny per sire group and range 22 to 40. The link sires had an average total of 514 progeny and range 494 to 527. A separate run of 10 populations was performed to demonstrate that the outcome is repeatable.

The linkage arrangement was chosen to meet the criteria of 30 % of progeny by link sires (Miraei Ashtiani and James 1992). The universal use of five sires also seemed to represent an ideal situation, to put the adequacy of linkage beyond doubt and remove linkage per se from the possible causes. BVEST software calculates coefficients of linkage between each group and all other groups in an analysis (Gilmour 1996), with a value below 10 considered suspect (AR Gilmour, pers. comm.). For Scheme B the average was 74.5 (range 71 to 78), emphasising the high level of sire linkage.

RESULTS

Figure 1 shows the breeding values for all 192 sires used. True breeding values (TBVs), Scheme A estimated breeding values (EBVs) and Scheme B EBVs are shown standardised to a mean of zero.

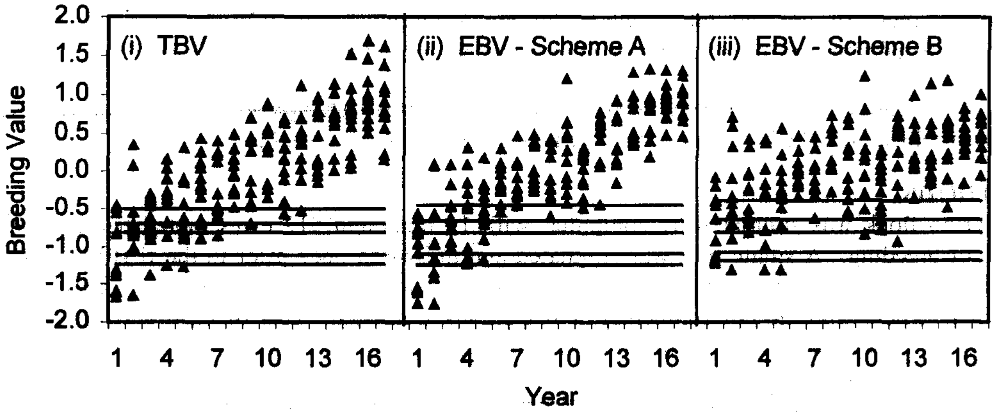

Figure 1. (i) True breeding values and (ii) estimated breeding values for Scheme A and (iii) Scheme B respectively, for all sires by year of use. The horizontal bars indicate the link sires.

The correlations between EBVs and TBVs for link sires were greater than 0.99 for all schemes. For the sires used together (ie the link sires plus a cohort of 11 single-use sires) these correlations were high in all years and for both schemes. The range was 0.85 to 0.98 for Scheme A and 0.77 to 0.98 for Schemes B and C, with A showing higher correlations than B and C in all but two of the 17 years.

When all sires were included, the correlation between EBVs and TBVs for Scheme A was 0.94, but for Scheme B dropped to 0.82, and to 0.87 for Scheme C. As consistent genetic improvement is being made, the single-use sires show a regression on TBVs of 0.114 units per year. For Scheme A (animal model) this regression on EBVs was 0.119 units/yr, but for Scheme B (sire model) was 0.057 units/year – only 50 % of the real genetic trend. This was underlined by a closer analysis of residuals for Scheme B EBVs on single-use sires which showed that 46 % of error variance was explained by a linear regression on year. For Scheme C, the result was intermediate at 0.087 units/yr.

For the run of 10 replicate simulations, the TBV genetic trend averaged 0.112 units/yr and ranged from 0.094 to 0.127 units/year. The EBV trend for Scheme A averaged 0.116 units/yr and ranged from 0.107 to 0.124 units/year (range 93 to 120 % of TBV trend) and for Scheme B average 0.054 units/yr and ranging from 0.044 to 0.064 units/year (41 to 55 % of TBV trend).

DISCUSSION

As expected, within each year a high accuracy is achieved, and this is little affected by other factors. With full pedigree information (Scheme A), accuracy of combined evaluations was still very high. However, it is clear that the BLUP is incapable of correctly estimating the genetic differences between years when it has incomplete pedigree information. The EBVs are biased with respect to TBVs because for a given EBV, animals born in later years will predictably perform better on average. The overall accuracy is still quite good, and the best few sires would be identified with a high level of reliability. There would be a high probability of moderate errors in the ranking of the middle-range sires tested, but this would have a relatively small impact on genetic improvement.

The linkage was deliberately idealised so that any bias would be attributed elsewhere. However, it is likely that any deficiency of linkage may aggravate the problem in Merino studs. The simulated linkage ensures that the years most remote in time are linked as strongly as adjacent years, and this is unlike the linkage observed in stud flocks, where even the best performing sires are discarded after several years. This means that while successive years are well linked, years remote in time have only weak linkage through sire comparisons in several other years. The greatest risk of poor trend estimation comes from comparing animals born (or used) in different years. This is rarely done for ewes but is increasingly relevant for sire selection. Whereas combined analyses have tended to replace single year genetic analyses, the latter may well be more informative at times.

The presence of selection which is not accounted for in a data set will render BLUP EBVs biased. Knowledge of the extent and effect of such bias, and the influence of other factors, are important steps towards a more complete understanding of the problem and its implications, and towards its practical resolution. The treatment of link sires as “fixed” seems to offer some hope. However, this may be less effective if a lower proportion of ewes were allocated to link sires, and may be unreliable when link sires are turned over rapidly.

There is a possibility that the bias shown may also impact on the combined analysis of central test sire evaluation results. Although the test dams are a random selection, those used at different sites are drawn from diverse populations, and therefore have different levels of genetic merit.

Industry players should ensure that greater emphasis is placed on comparisons between sires in the same progeny test, than on comparisons between sires in different tests. It is also critical that methodological research is continued in the short term to devise techniques that improve the accuracy of combined analyses and genetic trend estimates. Incorporating a genetic grouping strategy into BLUP is likely to provide a partial solution, but requires testing and tailoring to practical situations.

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