GENETIC TREND FOR FLEECE TRAITS AND WORM RESISTANCE IN MERINO STUDS

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SUMMARY
Merino studs are able to monitor genetic trends for measured or assessed traits by the use of link sires across years. Lorehno Poll Merino stud and Ruby Hills Merino stud have estimated genetic trends for fibre diameter (FD), clean fleece weight (CFW) and faecal egg count (FEC) from 1991 and 1990, respectively. Average estimated breeding values for 4-5 consecutive drops of progeny are presented for each stud. The average proportion of offspring each year that had sire pedigree recorded was 56% at Lorehno and 91% at Ruby Hills. The proportion of progeny from link sires exceeded 30% for both studs but was highly variable across years. The genetic trend for FEC was in a downward direction in both studs and trends for CFW and FD varied over the period but in the last two years of recording were in the appropriate direction to increase dollar returns.

Keywords: Genetic trend, Merino sheep, worm resistance, genetic links.

INTRODUCTION
Genetic change in the performance of Merino sheep has been difficult to monitor because there has been little use of statistical techniques to separate genetic from year to year environmental variation. Several factors may contribute to changes in performance with time. Many planned changes on a property such as pasture development and improved husbandry practices are designed to increase current flock productivity, while land degradation, declining soil fertility or a cycle of drought years can lead to a downward trend in both the quality and quantity of production. The inability to identify genetic improvement in the midst of year to year variation has been frustrating. Many breeders have put their faith in selection practices which have been validated in research flocks, where genetic gain can be measured against a control, or in sheep classifiers with an accumulation of industry experience.

BLUP techniques (mixed model methodologies) allow the independent estimation of year effects and changes in genetic merit over time for any trait that can be assessed on a linear scale. Given a knowledge of pedigrees and that there are genetic links between years, i.e. some sheep are mated in more than one year, the average estimated breeding value (EBV) for each drop can be used to monitor genetic trends for traits under selection. How well the trend is estimated will depend on the reliability of the assumed parameters (heritability and the genetic and phenotypic correlations between traits) and the degree of linkage between years. Estimated genetic trends depend heavily on the assumed value of heritability (Blair and Pollack 1984; Thompson 1986; James 1987). If the heritability assumed is higher than the true value in the population then EBVs for the offspring are inflated and the genetic trends are over-estimated. This is particularly the case when genetic links between years are tenuous, as the separation of year effects from genetic change is not reliable. If
the numbers in each year's contemporary group are low, the estimates of year effects are also less reliable.

Because of the reliance on the prior assumed for heritability, mixed model methodology can be used as a monitoring device for a selection scheme but should be thought of as a sophisticated version of the predicted response rather than a measured response to selection (Thompson 1986). Research flocks usually have an added internal test for genetic change in that they have a control flock allowing parameters such as heritability to be validated independently. This highlights the importance of providing reliable genetic parameters for the evaluation of practical selection programs in studs where control lines are not feasible. Being able to monitor genetic trends for established breeding goals that include clean fleece weight (CFW), fibre diameter (FD) and wool quality is an extremely useful tool but this facility is especially useful when a new trait is introduced. This has been the case with the introduction of worm resistance into the breeding objective of studs in districts where worms are prevalent. This paper reports estimated genetic trends in two New England Merino studs that have included improved worm resistance in their breeding objective for the last 5-6 years, and also reports the structure of links between years.

MATERIALS AND METHODS

Data were from Lorelmo Poll Merino stud and Ruby Hills Merino stud, both located on the New England Tablelands of NSW. At Lorelmo rams and ewes are fleece tested at 14 months of age and faecal egg count (FEC) is measured at approximately the same age but only in the rams. The breeding goal is to reduce FD and FEC and to increase CFW. At Ruby Hills fleece measurements are made on rams at 22 months of age and FEC is measured in both sexes at 14 months of age. The breeding goal is to maintain FD, reduce FEC and increase CFW. Each stud has a proportion of progeny that have sire pedigrees recorded. Recording of dam pedigrees over the period reported was minimal and this information was ignored. Numbers of progeny, proportion of pedigreed and link progeny are given for each stud (Table 1 and 2). Numbers for each trait varied as some sheep were only fleece tested while others were fleece tested and measured for FEC.

Table 1. Number of link progeny (%) for each measured trait, and number of pedigreed progeny (%) in total drop for Lorelmo Poll Merino stud

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<tbody>
<tr>
<td>Link progeny for FEC</td>
<td>3/113 (3%)</td>
<td>42/88 (48%)</td>
<td>40/55 (73%)</td>
<td>54/188 (29%)</td>
</tr>
<tr>
<td>Link progeny for FD</td>
<td>3/113 (3%)</td>
<td>148/323 (46%)</td>
<td>154/220 (70%)</td>
<td>153/605 (25%)</td>
</tr>
<tr>
<td>Link progeny for GFW</td>
<td>3/113 (3%)</td>
<td>145/318 (46%)</td>
<td>154/221 (70%)</td>
<td>168/635 (26%)</td>
</tr>
<tr>
<td>Link progeny for CFW</td>
<td>3/113 (3%)</td>
<td>42/88 (48%)</td>
<td>53/71 (75%)</td>
<td>68/277 (25%)</td>
</tr>
<tr>
<td>Pedigreed progeny</td>
<td>113/156 (72%)</td>
<td>323/596 (54%)</td>
<td>221/660 (33%)</td>
<td>638/974 (66%)</td>
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Table 2. Number of link progeny (%) for each measured trait, and number of pedigreed progeny (%) in total drop for Ruby Hills Merino stud

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<tbody>
<tr>
<td><strong>Link progeny for FEC</strong></td>
<td>59/107</td>
<td>318/355</td>
<td>285/285</td>
<td>351/351</td>
<td>37/116</td>
</tr>
<tr>
<td>(55%)</td>
<td>(90%)</td>
<td>(100%)</td>
<td>(100%)</td>
<td>(32%)</td>
<td></td>
</tr>
<tr>
<td><strong>Link progeny for FD &amp; CFW</strong></td>
<td>59/106</td>
<td>89/102</td>
<td>91/91</td>
<td>85/85</td>
<td>35/107</td>
</tr>
<tr>
<td>(56%)</td>
<td>(87%)</td>
<td>(100%)</td>
<td>(100%)</td>
<td>(33%)</td>
<td></td>
</tr>
<tr>
<td><strong>Pedigreed progeny</strong></td>
<td>107/107</td>
<td>355/361</td>
<td>285/345</td>
<td>351/462</td>
<td>116/116</td>
</tr>
<tr>
<td>(100%)</td>
<td>(98%)</td>
<td>(83%)</td>
<td>(76%)</td>
<td>(100%)</td>
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Breeding values for each measured trait were estimated only for progeny with known sires in a multivariate analysis using PEST (Groeneveld 1990). Assumed heritability for FEC was 0.33 was 0.25 and genetic and phenotypic correlations between FEC and fleece traits were assumed to be zero. Genetic parameters for fleece traits are those currently used by Advanced Breeding Services (KD Atkins, pers. comm.). FEC (sunits), GFW (%), CFW (%) and FD (pm) were standardised to a variance of 1, 196, 196 and 2.25, respectively. EBVs were averaged for each drop and then expressed in standard deviation units so that all traits could be compared on the same scale.

RESULTS

The estimated genetic trends for measured traits are given for Lorelmo (Fig 1) and Ruby Hills (Fig 2). Since 1991 the trend at Lorelmo has been to increase fleece weight and reduce FD. The mean FEC EBV of offspring has shown a general downward trend in the two years where sires were selected using information on worm resistance. At Ruby Hills the estimated trend for FD showed little change while CFW initially decreased but then improved in the last two groups of progeny. Once again FEC has shown a downward trend since the testing of sires commenced.

DISCUSSION

Ram breeders and geneticists have been ready to support Merino improvement schemes without any efficient means of assessing realised progress. This has applied equally to schemes based on the conventionally measured traits such as CFW and FD as well as those based on “elite” wool quality attributes. With the development of methods to estimate genetic change this need no longer be the case and a critical evaluation of each scheme, in terms of where selection pressure is being applied, is now possible. The examination of genetic trends, although a retrospective picture of
estimated genetic change, is extremely useful in ensuring that the rams used as sires are resulting
in subsequent groups of progeny that demonstrate desirable attributes. While these results only
represent a small time frame in terms of the generation length within each stud they show a useful
pattern of change that breeders can use to monitor their selection program. The genetic trend for
FEC was in a downward direction in both studs. A reduction in FEC EBV of 0.3 is equivalent to a
reduction in mean FEC from 500 epg to 340 epg. Trends for CFW and FD varied over the period
but in the last two years of recording were in the appropriate direction to increase dollar returns.

The success of mixed model methodology in separating genetic and environmental effects is in
part dependent on genetic connectedness across environments or years. The partitioning of the
phenotypic performance of animals into year effects and genetic effects (breeding values) is also
dependent to some extent on the heritability assumed in the mixed model. The amount by which
the estimated genetic trend is affected by the assumed prior is related to the genetic connectedness
across years. If the only source of information for an animal is its own phenotypic measurement
then doubling the assumed heritability will double the estimated breeding value for that animal
(EBV = Phenotypic deviation x h²). When there are genetic links, information from relatives is
also used to determine an animal’s EBV. The better the genetic links across years the less the
estimate of genetic trend will be influenced by the prior assumed for heritability. Also the greater
the number of progeny per contemporary group, the better the year effects will be estimated.

With regard to genetic links, an allocation of one third of the progeny to reference sires will
normally be close to the optimum in terms of minimising prediction error variance (Ashtiani and
James 1992). As can be seen in Table 1 and 2 both studs have exceeded this optimum although
links were not uniform across years. For Lorelmo there were only 3% link progeny in 1991 with a
maximum of 75% in 1993. From these data it appears that some Merino studs have adequate
numbers of link progeny but the spread across years may be better optimised to allow genetic
trends to be estimated reliably. Balanced allocation of link progeny is advantageous because it
allows more accurate estimation of adjustments for fixed effects, in particular year effects
(assuming no significant sire x year interactions).

From the breeders perspective, since the 1970s the standard practice advocated by advisory
services has been to measure important economic parameters and then base selections on these
measured phenotypes. This has yielded good results as indicated, in general, by the position of
"measurers" in wether trials and central test sire evaluation. However, the rate of improvement can
be marginal even with measurement due to the multiple sources of inaccuracy in assessing an
individual’s phenotype and the "wastage" of selection emphasis on non-measured parameters. An
EBV based approach to selection, using information from all relatives, is capable of addressing
the problem of inaccurate selection for phenotype and the monitoring of genetic trends gives the
breeder good feedback on the selection emphasis being achieved for the measured traits as well as
an estimation of genetic progress. BLUP evaluation for Merino sheep is a logical development and
the stud breeders in this industry need to be convinced in the same way that stud cattle breeders
were (with the introduction of Breedplan) that there is merit in a system of sire selection based on

331
EBVs. However, this must be done properly with extensive validation work, or it too will be relegated to the “dud heap of failed academic ideas”.

ACKNOWLEDGMENTS

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REFERENCES