

ACROSS-FLOCK EVALUATION AND OPTIMISATION OF PEDIGREE RECORDING FOR MERINO SHEEP

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SUMMARY

Across-flock genetic evaluation in Australian Merinos has developed through (1) commercial product evaluation to provide commercial producers with production information on alternative ram sources and (2) central test sire evaluation to provide ram breeders with breeding values of sires from many sources. The constraints of these systems are the time delay in assessing average merit of ram sources and the limited numbers of sires that can be centrally progeny tested. While an across-flock evaluation scheme relying on on-farm data can be implemented or expanded, its utility will be restricted by inadequate pedigree recording within flocks and genetic links across flocks. Opportunities to reduce these limitations are reviewed.

INTRODUCTION

The Merino wool industry has been relatively slow to adopt across-flock genetic evaluation as a standard feature of its breed improvement program. In Australia, the other major livestock industries (dairy cattle, beef cattle, meat sheep and pigs) have all developed evaluation schemes which principally rely on on-farm data collection and centralised processing for across-flock (or -herd) solutions for breeding values of seedstock animals. The slower development of successful insemination with frozen semen in sheep and the relatively large size of Merino stud flocks and limited pedigree identification have been constraints to the development of across-flock evaluation in Merinos. Similarly, limited trade of rams among studs and the reliance of most commercial producers on a single source of ram purchases have limited the use of across-flock selection.

However, the potential exists for large gains in productivity by both ram breeders and commercial producers by exploiting across-flock genetic variation. The Merino breed contains both distinct strains and studs that have been maintained genetically isolated for long periods. Despite the lack of a single, integrated genetic evaluation scheme across Merino flocks there have been several developments over the last decade. Here, we review these developments and identify the prospects and limitations to implementing across-flock genetic evaluation within the Merino industry.

USE OF ACROSS-FLOCK SELECTION IN MERINOS

The Merino wool industry in Australia has a specialised ram breeding sector of large flocks (average of 700 breeding ewes) with limited pedigree recording. Across-flock selection is a regular feature of the ram breeding sector. In a survey of the larger ram breeding flocks (average flock size of 1200 breeding ewes but representing 80% of all flock rams sold) Casey and Hygate (1992) found that 90% of ram breeders had used sires bred outside the home flock during the previous 10 years. Of the total flock surveyed, 17% of all ewes were mated to rams bred outside the stud (14% to purchased sires and 3% to purchased semen). Another feature of the ram breeding sector is the

degree of pedigree recording. Casey and Hygate (1992) also found that, while 80% of ram breeders collected some pedigree information, only 6% of animals had sire + dam pedigrees, 28% had sire only pedigrees and a further 50% of animals had a sire syndicate identified.

Flock rams are purchased by commercial producers largely on the basis of within-flock assessment. Producers have chosen a single ram source and then have rarely changed that source. Across-flock selection has been limited to a choice among potential ram sources.

DEVELOPMENT OF ACROSS-FLOCK EVALUATION IN AUSTRALIA

Stimulating interest in across-flock selection was the recognition of substantial differences in performance between studs. Although large differences between strains had been reported by Dunlop (1962) and others, the genetic resource flocks established in the 1970's quantified large differences between stud sources within strains (Jackson and Roberts 1970, Mortimer and Atkins 1989, Lewer *et al* 1992). These resource flocks were established by purchasing ewes and rams from studs and testing their progeny in a common environment on research stations. But non-disclosure agreements between researchers and vendors meant that the across-flock information could not be reported to industry. What developed were specific forms of industry evaluation: firstly, flock evaluation for commercial producers to identify productive ram sources and secondly, sire evaluation for ram breeders to identify superior sires for their breeding programs.

Flock evaluation

While information from resource flocks was being generated, commercial production competitions for Merino producers became widespread. These competitions consisted of teams of wethers (5-30 per team) sampled from commercial flocks at a young age and then evaluated at a central site for 2 to 4 years. Between 8 and 80 teams were located at a single site. These competitions were originally designed as regional extension activities for commercial producers. Through their prolific growth and public naming of ram sources, implications for genetic evaluation of stud sources quickly became apparent. Between 1981 and 1995, there were 82 active wether comparisons in NSW and Victoria. Entered in these comparisons were 2025 teams with a total of 18366 animals, each with measurements of production and quality traits for an average of 3 annual records. An initial report on across-flock differences provided information on 53 ram sources that had standard errors of prediction of less than $\pm 3\%$ for fleece weight and $\pm 0.5\mu\text{m}$ for fibre diameter (Atkins *et al* 1992). More recently, Coelli *et al* 1996 provided information on 73 ram sources.

Information from wether comparisons has quantified genetic variation among Merino ram sources. From the analyses of Coelli *et al* (1996), between-flock variation in fleece weight and fibre diameter relative to expected within-flock genetic variation is shown in Table 1. These two traits, which dominate commercial returns from wool (Atkins and Coelli 1997), show substantial across-flock genetic variation despite their high heritabilities. Using market values from the previous 4 years, genetic variation in profitability ranged from 30% above to 25% below the mean among ram sources (Coelli *et al* 1996). Supporting information is designed to assist commercial producers set a breeding objective, benchmark their current genetics and identify potential ram sources on a combination of current production level and likely genetic progress in these ram sources. In the

past, 20% or fewer stud clients have been prepared to change ram source to capitalise on either short-term gains from superior sources (on current performance) or long-term gains from studs pursuing breeding programs delivering high genetic gain. A recent survey of NSW wool producers showed that 62% had changed their ram source at least once in the previous 10 years and 42% had changed in the previous 5 years. The dominant reason for change was genetic or performance level, indicating the high value that the commercial sector places on across-flock evaluation.

This form of commercial product evaluation still has limitations, particularly time delay in the information and its precision (Coelli *et al* 1996). Although analyses are restricted to wether comparisons that commenced within the previous 10 years, the ram source differences represent comparisons between rams bred in studs 10-15 years ago. Recent changes in breeding practices or objective will not be reflected. Precision of estimates is relatively low and the design of some comparisons include non-random selection of individuals and inaccurate description of ram source.

Table 1 Genetic variances for fleece weight (FW) and fibre diameter (FD) and the genetic correlation between them estimated within and across Merino flocks

	Literature values	Sire evaluation	Flock evaluation
Within (<i>across</i>) flock estimates			
FW variance (% ²)	97.8 (-)	86.9 (52.9)	- (50.3)
FD variance (μm^2)	1.29 (-)	1.25 (0.58)	- (0.84)
Correlation(FW/FD)	0.25 (-)	0.28 (0.27)	- (0.57)

Sire evaluation

In 1984, a sire referencing scheme was established in Western Australia (Lewer 1987). From an agreed list of reference sires, participating breeders chose semen from 2 reference sires to be used on-farm with at least 2 home sires and the resulting progeny evaluated. Scepticism by ram breeders over the integrity of on-farm comparisons and management difficulties associated with on-farm progeny testing have been advanced as problems with this scheme (MacLeod 1991). Central test sire evaluation quickly replaced sire referencing as the industry preferred means of sire evaluation.

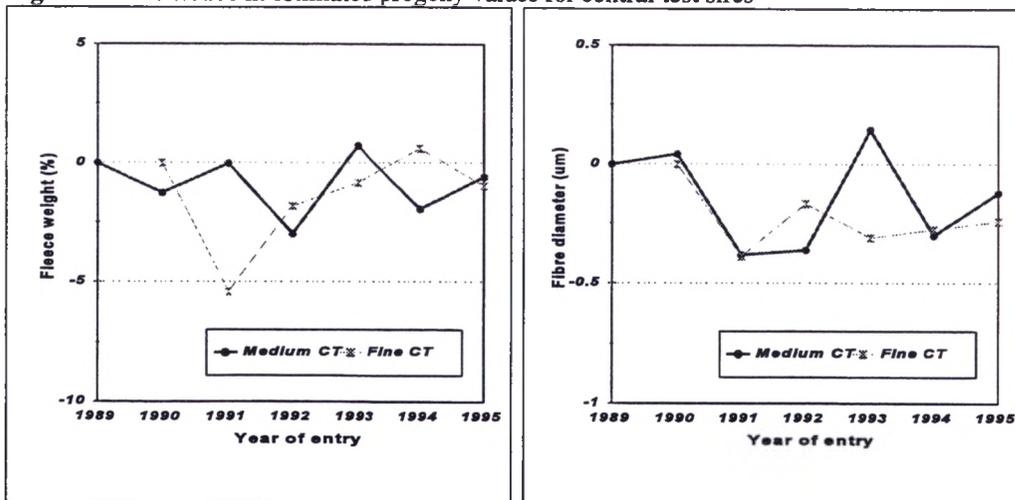
The first central test sire evaluation scheme commenced in NSW in 1987. Since then central test schemes have been initiated in 3 other States and in other regions of NSW. There are currently seven schemes operating covering the two major wool types, fine and medium wool. Guidelines have been set to ensure the integrity of the data collected (Roberts *et al* 1991). Each site evaluates 10-16 rams per year, at least 2 of which are rams that have been evaluated previously and provide genetic links between years within a site and between sites. Miraei Ashtiani and James (1991,1992) showed that 30% of total progeny from link sires was optimal for the moderately heritable wool traits, and current designs of central test evaluations closely match this optimum (Atkins and Casey 1994). Each site measures greasy and clean fleece weight, fibre diameter mean and variability, and body weight, while some sites also measure staple length, staple strength and

faecal egg count (Hickson 1997). Two sheep classers at each site visually assess conformation and additional wool quality characteristics (Atkins *et al* 1993).

Results from central test sire evaluation are reported as estimated progeny values from a sire model BLUP analysis in “Merino Superior Sires” (Casey *et al* 1995). The current data contains 305 sires from 132 source flocks. Estimates of between- and within-flock genetic variances for fleece weight and fibre diameter from central test data (Table 1) again emphasises the magnitude of across-flock variation available to the Merino seedstock industry. The similar within-flock genetic variances, compared with literature values, indicates that any prior selection applied to rams entering central test has been small or inconsistent in direction. Outstanding sires from central test have been used in many other studs (up to 70 reported by one ram breeder - A.E. Casey *pers. comm.*) to both capture superior genes and to compare the performance of home-bred rams with those in central test in on-farm evaluation. Thus, in choosing sires for the next generation, ram breeders have been able to compare the relative merit of home-bred sires with centrally tested sires, and have been able to identify rams that will perform well if entered in central test schemes (Hickson 1997).

The major limitation of central test evaluation is that available spaces are few compared with the number of rams used within studs. Further, the genetic merit of sires entered in central test has shown little improvement over the period of major activity since 1989 (Fig 1). In both medium and fine wool schemes there has been little change in fleece weight and only small reduction in fibre diameter among sires first entering central test.

Figure 1 Time trends in estimated progeny values for central test sires



FUTURE PROSPECTS AND LIMITATIONS

To make further advances in across-flock evaluation we need to overcome the time lag in assessing the genetic merit of flocks and to extend the number of rams evaluated across studs. A recent

initiative is the pilot development of Merino Benchmark, a group of 8 studs who have combined their on-farm data with central test data. The studs cover a substantial range in environments (representing all mainland states of Australia as well as high to low rainfall locations) as well as genotypes from superfine to medium wool types. The ram breeders all support central test sire evaluation and have an agreed protocol for the conduct and reporting of on-farm assessments. The group is not, then, a random sample of the ram breeding sector but does allow us to ask some questions on the likely operation of an across-flock evaluation scheme. In particular, the issues of data description, genetic linkage, genotype (sire) X environment interaction and the degree of pedigree identification were examined.

Data description

The data consisted of measurements on 24,815 animals which were the progeny of 516 sires. The animals were kept in eight studs and two central test groups (medium and fine wool). In the analysis, flock referred to this 10-way classification. Data from medium wool central test came from 5 sites and fine wool central test came from 3 sites, a total of 16 sites. There were records from up to eight years and a total of 120 management groups (year-site-sex combinations). Data analysis was restricted to fleece weight and fibre diameter records which were grouped into yearling (10-13 months), hogget (14-19 months) and adult (over 19 months) to allow for age effects on genetic parameters (Atkins 1990). Models were fitted in ASREML (Gilmour *et al* 1997) and included effects for management group (and its components flock, sex, site), sire and the interaction(s) between them. Substantial variation existed among management groups for both traits with a range in means of 2kg to 7kg for fleece weight and 16 μ m to 23 μ m for fibre diameter. The relationship between residual standard deviation and mean across management groups (Table 2) suggested that a log transformation would reduce the mean Vs standard deviation relationship and allow proportional sire effects to be fitted.

Table 2 Data records available for fleece weight (FWt) and fibre diameter (FD) according to age of measurement (yearling-y, hogget-h and adult-a)

yFWt	hFWt	aFWt	yFD	hFD	aFD
Numbers of animals with records					
17240	7020	8291	16206	6718	8371
†Regression of log (residual standard deviation) against log (mean)					
1.01 \pm .06	1.08 \pm .11	1.16 \pm .06	1.48 \pm .20	0.67 \pm .32	1.29 \pm .16

† A slope of 1 indicates a log transformation is appropriate.

Genetic linkage

Sire links across flocks were largely contributed by central test. In the absence of central test, only 18 sires were used in more than one stud. With central test data, 47 sires (9% of the total) provided links and their progeny represented 26% of the total data. Within studs, including central test data also improved the links between management groups.

Genotype X environment interactions

Sire X management group interaction (sire.mg) was a significant effect on all traits (Table 3). Part of this interaction reflects the wide variation across flocks so that the performance of sires depends on the genetic background in which they are used. Genetic groups were identified and fitted as fixed effects in the model. Each sire was classified according to its stud of origin: the 8 separate studs plus fine, fine-medium and medium wool flocks in the remaining central test sires giving a total of 11 genetic groups. Including genetic groups significantly improved the models fitted for all traits by reducing the contribution of sire.mg (Table 3). For fibre diameter, including genetic groups reduced the sire.mg component with little change to the sire component whilst for fleece weight, both sire and sire.mg components were reduced but sire.mg relatively more so.

Table 3 Values for sire and sire X management group (mg) components of variance (as a proportion of residual variance) for models with and without genetic groups

	yFWt	hFWt	aFWt	yFD	hFD	aFD
With Genetic Groups						
sire	0.051	0.099	0.086	0.141	0.207	0.127
sire.mg	0.059	0.011	0.049	0.019	0.003	0.036
Without Genetic Groups						
sire	0.068	0.114	0.105	0.134	0.221	0.129
sire.mg	0.075	0.017	0.082	0.032	0.168	0.051

Residual sire.mg (after genetic group) remained a significant source of variation particularly for fleece weight. Breaking this interaction into its components did not suggest a single source of interaction was evident across all traits. For yearling fleece weight, flock X genetic group was significant, possibly indicating non-additive genetic variance or heterosis (Mortimer *et al* 1994). In adult fleece weight, sire X location was the dominant contributor to the interaction. All we can conclude is that sire interactions were a feature of the data but the information was too sparse and confounded to adequately explain these departures from expectation in terms of consistent effects. But we can directly assess the impact on evaluation through the genetic parameters derived from these data (Table 4). The fitted model constrained the genetic correlations to be equal for the following groups: among fleece weights, among fibre diameters and between fleece weights and diameters. Literature values used for genetic evaluation are about 0.4 and 0.5 for the heritabilities of fleece weight and fibre diameter respectively with a genetic correlation of 0.25 between them. The internal estimates from the data were remarkably consistent with these, with the exception of a lower heritability for yearling fleece weight, the trait with the highest interaction estimate.

Degree of pedigree recording

The relative lack of pedigree records within Merino studs is illustrated in the Merino Benchmark data where 55% of the records were removed before analysis due to lack of sire pedigrees and/or lack of full pedigrees in the presence of selection of dams for sire mating groups. The result is that

estimated genetic merit of a flock based on available pedigree may poorly represent genetic merit of the whole flock. Opportunity exists to include information on syndicates of sires through the use of uncertain parentage (Kerr *et al* 1992). The principal benefit would be that links between years within a flock would be strengthened (by linking a young ram's own performance to its syndicate progeny performance) and most of a stud's on-farm data would be included in the analysis. The efficacy of such procedures as the sole pedigree information remains to be tested. The other potential area of improvement in pedigree recording may come from DNA fingerprinting provided the technology can be delivered at a cost-effective price (Barnett *et al* 1997).

Table 4 Heritabilities (on diagonal), phenotypic correlations (above diagonal) and genetic correlations (below diagonal) estimated from on-farm + central test data

	yFWt	hFWt	aFWt	yFD	hFD	aFD
yFWt	0.24±.03	0.63	0.60	0.19	0.13	0.11
hFWt	0.98±.04	0.43±.05	0.67	0.06	0.22	0.17
aFWt	0.98±.04	0.98±.04	0.39±.05	0.11	0.13	0.16
yFD	0.28±.06	0.28±.06	0.28±.06	0.55±.05	0.62	0.69
hFD	0.28±.06	0.28±.06	0.28±.06	0.95±.02	0.69±.07	0.71
aFD	0.28±.06	0.28±.06	0.28±.06	0.95±.02	0.95±.02	0.53±.05

CONCLUSIONS

Ten years ago, despite our knowledge of substantial variation among Merino ram breeding flocks in productivity, no public information was available to assist commercial producers or ram breeders to exploit it. The development of flock evaluation through analyses of wether comparisons and sire evaluation through central progeny tests have made significant contributions to breeding programs. The major constraints of these systems are the restricted numbers of sires in central test relative to the number used in studs and the delay in assessing genetic merit in flock evaluation.

Sire evaluation. Including on-farm information with central test is a natural extension of across-flock sire evaluation for ram breeders. The principle is already well accepted with more than 20 linked analyses between central test and individual flocks reported annually (A.E. Casey - *pers. comm.*) and the Merino Benchmark initiative. Concerns by some ram breeders over the integrity of on-farm comparisons and management procedures required (particularly equal allocation of ewes and non-selection of progeny prior to assessment) need addressing through agreed protocols. Technical concerns relate to genetic links across flocks and sire interactions. In the short-term, central test evaluation will be required to ensure adequate (if not optimal) genetic linkage. Using genetic groups in across-flock analyses will improve precision by reducing sire interactions, but the process of forming such groups needs attention. Similarly, improving the accuracy of assessment of fleece weight in young animals across flocks requires further work.

Flock evaluation. The use of across-flock analyses of studs to supply average flock (or genetic group) merit to replace information from wether comparisons would seem more difficult to achieve. Firstly, flock evaluation already provides estimates of flock differences on many more

ram breeding flocks than across-flock evaluation would provide in the medium term. Secondly, the incomplete pedigrees within-flock will result in estimated flock effects that poorly represent true flock effects. The use of uncertain parentage procedures to account for sire syndicates and the potential of DNA finger-printing to supplement within-flock pedigrees require urgent attention for both across-flock evaluation and estimating within-flock genetic trends.

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