

Between-flock genetic differences in 40 Merino studs

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Breeding values of production traits, relative to a genetic control flock, were estimated for 40 registered Merino studs. Breeding values, expressed as a percentage deviation from the control flock, varied from -16.7 to 31.2 for body mass, -6.4 to 28.1 for clean fleece mass and -3.7 to 13.2 for fibre diameter. The results indicate that some studs differed genetically. The correlations between stud phenotypic means and estimated breeding values for production traits were very low and statistically significant only for crimps per 25 mm (0.512) and total fold score (0.424). Overall means, standard deviations and correlations for the unselected two-tooth ewe and ram progeny of the 40 studs, are presented.

Teelwaardes vir produksiekenmerke, relatief tot 'n genetiese kontroletrop, is vir 40 geregistreerde Merinostoeterye bereken. Teelwaardes, uitgedruk as 'n persentasie afwyking vanaf die kontroletrop, het gevarieer vanaf -16.7 tot 31.2 vir liggaamsmassa, -6.4 tot 28.1 vir skoonwolmassa en -3.7 tot 13.2 vir veseldikte. Die resultate dui op genetiese verskille tussen sommige stoeterye. Die korrelasies tussen stoet fenotipiese gemiddelde en beraamde teelwaarde vir produksiekenmerke was baie laag en statisties betekenisvol vir slegs kartels per 25 mm (0.512) en totale plooitelling (0.424). Algehele gemiddeldes, standaardafwykings en korrelasies vir ongeselekteerde tweetand-ooie en -ramme van die 40 stoeterye, word gegee.

Keywords: Genetic differences, Merino sheep, phenotypic correlations, stud breeding values.

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Introduction

The breed structure of the South African Merino breed was analysed by Erasmus (1977). Two conclusions from his study were:

1. A few groups, which consisted of parent and daughter studs, seemed to exist in fair isolation from other studs within the breed due to limited exchange of genetic material between such groups and the rest of the population.
2. In many studs, genetic improvement depended mainly on within-stud selection, as few rams were purchased from other studs.

These two conclusions lead to the question whether genetic differences between certain studs exist.

From about 1970, an increasing number of breeders used within-stud performance testing for the selection of replacement sheep. Selection was based primarily on a selection index estimated from individual measurements of four traits, namely body mass, clean fleece mass, fibre diameter and skin fold development (Poggenpoel & Van der Merwe, 1975). These breeders were faced with the problem of finding a method to determine between-stud genetic differences so as to identify superior breeding material.

In an attempt to investigate between-stud genetic differences, a progeny test involving a control flock was developed. This method enabled a breeder to compare progeny of his home-bred selected sires with that of rams from a random-breeding, genetic control flock. As all participating studs were compared to the same genetic control flock, the relative genetic merit of different studs could be determined. Results of the first three studs tested were presented by Erasmus (1976) and Van der Merwe & Poggenpoel (1977) and results of a total of 25 studs by Poggenpoel & Van der Merwe (1984).

There are few published estimates of between-stud genetic differences in sheep. Jackson & James (1970) presented preliminary estimates of between-stud genetic variances and genetic correlations for seven Australian Merino studs from three different strains. Components of variance for only a few characteristics differed significantly from zero.

Data of 40 registered Merino studs compared against the genetic control flock are available at this stage. In this paper, estimates of relative breeding values of production traits for these 40 studs are given, together with the correlation data between stud relative breeding values and phenotypic means. Further estimates of phenotypic parameters such as means and correlations for the relative large data set of unselected two-tooth ewe and ram progeny are also presented.

Materials and Methods

A Merino genetic control flock is maintained by random replacement of a sire by a son and a dam by a daughter (Heydenrych *et al.*, 1984) at the Tygerhoek Experimental Farm of the Department of Agriculture. The flock initially consisted of 16 rams and 160 ewes and, since 1976, was increased to 20 rams and 200 ewes. Research work by Heydenrych *et al.* (1984) and Cloete *et al.* (1988) gave evidence of genetic stability of production traits in this control flock. Erasmus (1990), however, found that inclusion of body mass values of the 1987 and 1988 birth years, caused a significant positive genetic trend in this trait.

Surplus rams from this control flock were available for members of the Merino Breeders' Society of South Africa. Annually, one or two sets of 12 rams each were selected from the available control flock rams in such a way that the mean value of each set for each of the four traits of the selection

index did not deviate by more than *ca.* 2% from the mean of its contemporary group. The same set of control rams continued to be used, provided it consisted of a minimum of 10 rams. These sets of rams were circulated amongst breeders who wanted to participate in the control test.

A breeder would mate the set of control rams to a random sample of his breeding ewes. Simultaneously a selected group of about the same number of his own home-bred sires was mated to a comparable sample of ewes. The progeny of the two groups were identified, reared together and evaluated at approximately the two-tooth stage of growth. The difference between the progeny means of the breeder's home-bred sires and that of the control rams, was doubled to transform it to a breeding value deviation from the control flock. These breeding value deviations were then expressed as a percentage of the expected mean of the control flock on that particular farm. In this form, the deviations were not influenced by level of production. This test was essentially a breeding value evaluation of the group of home-bred sires and not of the breeding flock. However, on the assumption that approximately the same selection intensity was applied in the different studs for the selection of their breeding rams, these percentage breeding value deviations were in practice referred to as stud breeding values relative to that of the control flock. Different studs could therefore be compared on this basis.

Tests of significance for genetic differences were calculated according to Roux (1982). The procedure of Optimal Experimental Design was used in this study (Roux, C.Z., 1988, personal communication). Since progeny of individual rams was not identified in these commercial tests, as was required for the statistical test, only approximate standard errors based on average numbers of progeny per sire could be estimated. Tests of significance, therefore, only indicated approximate significance of estimated deviations.

The traits evaluated were greasy fleece mass, body mass and fold score at about two-tooth age, while a midside wool sample was sent to the Fleece Testing Centre for analysis. Fleece mass and staple length were corrected to a 12-month growth period. Folds on the neck, body and breech regions were scored to photographic standards of Turner *et al.* (1953). These three scores were summed to give the total fold score.

The control test also enables a breeder to estimate selection response in his stud by repeating the test after a number of years. Poggenpoel & Van der Merwe (1987) reported positive results in three closed studs after about seven years of index selection.

Results and Discussion

Breeding value deviations

The percentage breeding value deviations from the genetic control flock for six of the 40 studs tested are presented in Table 1. The three studs with the lowest deviation from the control for clean wool mass and the three with the highest deviations were selected for presentation. The rest of Table 1 presents results of all 40 studs. On average, 158 farm ram progeny and 118 control ram progeny were measured per stud. For the approximate tests of significance, the number of farm rams (N_f) and the number of control rams (N_c) were taken as 10. From these assumptions the average number of progeny per ram would be about 14. After consulting tables of heritabilities from Turner & Young (1969), Turner (1977) and Ponzoni (1987; 1988; values for Woolplan), the following values of heritabilities (h^2) were accepted for further calculations: greasy wool mass, $h^2 = 0.35$, body mass, crimps per 25 mm, fold score, staple length, clean yield and clean fleece mass, $h^2 = 0.40$ and fibre diameter, $h^2 = 0.50$. Absolute values of deviation in breeding value from the control were used for tests of significance, and the percentage deviations are given in Table 1. The relatively large numbers in progeny groups gave more confidence in the results although, as mentioned, tests of significance were approximations. It could nevertheless be deduced that deviations for the economically more important characteristics should have reached significance at values of the following order: body mass, 7%; fibre diameter, 4%; clean fleece mass, 9%. As can be seen from the ranges of the minimum to the maximum deviations in Table 1, there were large differences between studs. The total range from the minimum to the maximum deviation for all characteristics was four times or more the approximate value of significance. It was therefore concluded that the breeding value of many studs deviated significantly from that of the control flock and, consequently, that

Table 1 Percentage breeding value deviations of home-bred stud rams from the genetic control flock in six selected Merino studs¹

Test no.	Number of progeny		Body mass	Greasy fleece	Crimps per 25 mm	Fold score total	Staple length	Fibre diameter	Clean yield	Clean fleece
	Farm rams	Control rams								
7	362	58	4.1	-2.6	9.7*	-28.9**	11.1	2.3	0.4	-2.1
8	244	231	9.6*	1.9	-3.6	-36.7**	5.3	5.0*	-3.4	-1.6
13	124	140	-1.3	-4.2	-4.8	-18.8	-1.8	-3.7	-1.8	-6.4
22	152	106	22.8**	16.0**	-11.9	16.1	8.0**	8.4**	4.5*	21.4**
26	120	80	20.8**	26.0**	1.3	-12.6**	9.6*	3.6	-1.0	24.7**
39	189	158	14.4**	22.1**	-18.8**	-31.7*	6.2*	6.2**	3.8*	28.1**
Mean	158	118	9.71	10.01	-5.23	-11.98	7.17	4.11	-0.76	9.13
Minimum value			-16.7	-4.2	-22.4	-63.9	-10.7	-3.7	-8.4	-6.4
Maximum value			31.2	26.0	10.4	37.8	30.2	12.2	9.3	28.1
Significant value ²			7	8	8	16	7	4	4	9

* $P < 0.05$; ** $P < 0.01$. Approximate tests of significance.

¹ The rest of the table are results of all 40 studs.

² Order of value of percentage deviation needed for possible significance at the 5% level.

genetic differences between studs were identified.

The reasons for the large differences between certain studs can only be speculated on. Most of these studs had a history of limited purchasing of breeding material and quite a number of them were even closed flocks for a few years preceding the control test. It seems as if these and other practices in the past caused real genetic differences between some studs. This conclusion will probably not apply to the whole stud industry. It is expected that there will be smaller genetic differences between studs with a policy of regular purchasing of rams from different sources. Atkins *et al.* (1991) found a high migration rate of rams between flocks in the Australian Poll Dorset Sheep breed and no significant variation due to flock in their analyses.

Correlation between stud phenotypic mean and breeding value

To investigate the relationship between stud phenotypic means and their estimated breeding values, the correlation between the progeny mean of home-bred rams and its percentage breeding value deviation from the control was estimated for each trait of the 40 studs. The squared value of this correlation gave the proportion of variation in stud breeding value that could be attributed to its relationships with stud phenotypic mean for a particular trait. The estimated correlations (r) are given in Table 2 together with the overall means of farm ram two-tooth progeny means (stud means of both sexes) and the standard deviations of individual stud means.

Table 2 Correlations (r) between stud phenotypic means and estimated breeding values and the overall means and standard deviations of individual stud means

Characteristic		Overall mean	Standard deviation
Body mass (kg)	-0.023	34.76	6.09
Greasy fleece mass (kg)	0.243	5.11	1.47
Crimps per 25 mm	0.512**	9.83	0.97
Fold score total	0.424**	6.33	2.03
Staple length (mm)	0.064	98.67	15.09
Fibre diameter (μ)	0.267	20.08	1.27
Clean yield (%)	0.075	67.23	3.83
Clean fleece mass (kg)	0.015	3.43	0.97

** $P < 0.01$.

Only two of the eight correlation coefficients in Table 2 were statistically significant. Consequently it appears that only for crimps per 25 mm ($r = 0.512$) and total fold score ($r = 0.424$) were there significant relationships between the measured stud mean and its estimated breeding value. The values for the rest of the characteristics were extremely small and not significantly different from zero.

The question of a possible effect of level of production of clean fleece mass on these correlation estimates was investigated by ranking the 40 studs on their phenotypic means for clean fleece mass and dividing them into three groups. The correlations between flock means and percentage breeding value deviations were then estimated within the three clean fleece groups. The correlation coefficients in the group with

the lowest clean fleece mass (Group 1) and the group with the highest clean fleece mass (Group 3) were -0.12 and 0.35 respectively for greasy fleece mass and -0.05 and 0.20 for clean fleece mass. These results seem to indicate a higher correlation at higher levels of wool production. However, in the same Groups 1 and 3 respectively, the correlations for body mass (0.53 and -0.04) and staple length (0.34 and -0.17) were lower at the higher level of production. There were small differences between the other correlations of the two groups. Because of the small number of studs (13 and 14 in the two groups), and the contradictory results, no conclusion was possible from this analysis.

It is clear that in this study, stud mean was a poor indicator of stud breeding value, with the exception of crimps and total fold score. Jackson & James (1970) found a between-stud genetic variance component of *ca.* 10% of the total variance for body mass, greasy and clean fleece mass. Although other traits had higher values, the standard error of all estimates was large. Pirchner & Lush (1959) found for dairy cattle in the United States that the heritability of herd differences was 6.5% for both milk and butterfat production. The present results indicated that the general conception of low heritabilities of flock means is also applicable to South African Merino studs.

Means, variances and correlations

As these studs were located in all of the major Merino production areas, these values may be fairly representative of the South African Merino industry. Data of unselected progeny without any preliminary culling were used for the control tests. This is generally not the case with other performance testing data. Furthermore the data from this study were used to obtain values for the overall means, standard deviations and correlations of unselected two-tooth Merino ewes and rams in the 40 studs. Inspection of estimated stud means, variances and correlations showed large variations, with many outlier values. It was therefore decided that the best way to obtain an overall mean from the different sets of data, would be to find the median value for each desired estimate (Van Aarde, I.M.R., 1988, personal communication).

The estimated median values for stud means, standard deviations and the calculated coefficients of variation for progeny of home-bred rams are presented in Table 3. The age at measurement ranged from 12 to 18 months with an average of 16 months. Fold score values of the neck, middle and breech for ewes were based on estimates in the first 12 studs measured, total fold score standard deviation was based on estimates in the remaining 28 studs, and total fold score mean on estimates in all 40 studs. This was due to a change in the output format of the results by the Fleece Testing Centre. Consequently the means of fold score neck, middle and breech did not add up to the figure for total fold score. Unselected two-tooth ram progeny were only available in 28 of the 40 studs. Fold score values for neck, middle and breech for ram progeny were from 10 studs and values for total fold score from 20 studs. Data from a total of 4298 unselected two-tooth ewes from 40 studs and 2633 unselected two-tooth rams from 28 studs were available for these estimates. The average wool growth at the time of measurement was 9.3 months. Means for rams were slightly higher than ewe means; for body mass 35.84 vs. 32.35 kg and for clean wool mass 3.42 vs. 3.21 kg respectively.

The means and standard deviations for crimps, fibre diameter and clean yield percentage of this study, were very

Table 5 Means and standard deviations of unselected two-tooth Merino ewes in three groups of studs arranged according to clean fleece mass

Stud group (ascending)	Clean fleece mass (kg)		Greasy fleece mass (kg)		Staple length (mm)		Body mass (kg)		Fibre diameter (μ)		Crimps per 25 mm		Fold score total		Clean yield (%)	
	\bar{x}	s.d.	\bar{x}	s.d.	\bar{x}	s.d.	\bar{x}	s.d.	\bar{x}	s.d.	\bar{x}	s.d.	\bar{x}	s.d.	\bar{x}	s.d.
1	2.48	0.36	3.84	0.49	84	9.53	28.9	3.28	19.06	1.20	10.33	1.33	6.61	1.45	66.5	4.60
2	3.19	0.49	4.73	0.68	96	10.21	29.6	3.58	20.32	1.32	9.36	1.25	4.87	1.51	68.2	4.64
3	3.98	0.54	5.84	0.69	102	10.21	35.4	3.79	21.29	1.30	9.10	1.20	6.74	1.80	69.2	4.62
Overall median value	3.21	0.47	4.73	0.62	97.0	10.21	32.35	3.58	20.22	1.30	9.59	1.25	6.61	1.56	67.7	4.74

\bar{x} = mean; s.d. = standard deviation of individual values.

1.95 to 6.54 kg. To obtain further information on the variation of stud means, the 40 studs were ranked on clean fleece mass of two-tooth ewe progeny of farm rams and grouped into three groups of 13, 13, and 14 studs respectively. The range of clean fleece mass means for Group 1 varied from 1.95 to 2.83 kg, for Group 2 from 2.93 to 3.44 kg and for Group 3 from 3.47 to 6.54 kg. The means and standard deviations of clean fleece mass and the other traits of these three groups are presented in Table 5. The traits are roughly ranked from left to right in Table 5 according to the degree to which their means were influenced by grouping into clean fleece groups. As can be expected, greasy fleece mass and staple length means differed markedly between the three groups with smaller differences in the other traits. The standard deviations tended to show a positive association with the means.

The median values of correlations between traits of two-tooth ewes were also estimated within each of the three clean fleece mass groups. Only some correlations showed a tendency to be influenced by clean fleece mass grouping. In each case the numeric value of the correlation was greater in the low producing Group 1 than in the high producing Group 3. The relevant correlations in Group 1 and Group 3 were respectively: clean fleece mass \times crimps -0.21 and -0.09 , clean fleece mass \times fibre diameter 0.28 and 0.10 , greasy fleece mass \times body mass 0.44 and 0.29 , greasy fleece \times staple length 0.24 and 0.11 .

In general it appeared that level of clean fleece production had little effect on correlations between production traits.

The 40 studs of this study were geographically scattered mainly over the north-western, middle and eastern Karoo, eastern Orange Free State, eastern Transvaal and south-western Cape. Flocks from all regions were found in all three clean fleece groups (Table 5) with the exception of flocks from the south-western Cape which were all to be found in Group 3, *i.e.* the highest producing group. These results indicate that the level of production was, in general, more influenced by the feed supply and management on a particular farm than the geographical region.

Conclusions

The results of this study must be seen against the background of possibly large experimental errors since measurements were taken under uncontrolled conditions by different people on different farms. There are, however, strong indications that the following two conclusions can be drawn. Firstly, there are genetic differences for production traits between some Merino

studs. Secondly, stud phenotypic mean is a poor indicator of stud breeding value.

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