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Romney male and female heritabilities and genetic correlations for weaning, autumn and spring body weights and hogget fleece weights

A.C. PARRATT

MAFTech, Ruakura Agricultural Centre, Hamilton

G.B. NICOLL AND M.J. ALDERTON

Land Corporation Ltd,
P O Box 1235, Hamilton

ABSTRACT

Often effective breeding programmes are dependent on the assumption that heritabilities and genetic correlations between traits are the same in both sexes and that the genetic correlation for the same trait measured on both sexes is unity. A total of 12 302 records from 149 sire groups were analysed using mixed model techniques to test these assumptions. The results provide an indication that genetic and phenotypic parameters differ for male and female sheep. Cognizance of this fact should be taken when considering alternative selection strategies.

Keywords Heritabilities; genetic correlations; sex; selection strategies; phenotypic parameters

INTRODUCTION

Little information is available on heritabilities, genetic and phenotypic correlations for economically important sheep traits either between the sexes or within sex independently. Baker *et al.* (1979) reported lower heritabilities for males than for females for body and fleece weights. Other authors (Kyle and Terrill, 1953; Young *et al.*, 1960; Pattie, 1965) found heritabilities tended to be higher in males than in females. Genetic correlations between the same trait measured on the two sexes were not reported. These correlations could be important in determining rates of progress when based solely on one sex or when selection indices derived from genetic parameters for one sex are applied to another. Although appearing trivial in the first instance, any marked divergence between parameter estimates would have implications for breeding programme design and subsequent selection responses.

The objective of this study was to estimate genetic and phenotypic parameters for male and female traits. Once these parameters had been estimated the second goal was to combine the information into selection indices and examine

predicted responses to selection.

MATERIALS AND METHODS

The data available were from the Land Corporation's large group breeding scheme central flock based at Waihora. A total of 12 302 complete records of lambs born from 1984 to 1986 was available. From 140 sires, 7056 males and 5246 females were analysed. Progeny were born on two adjacent blocks, Waihora and Otutira with a total of 9 sires repeat-mated across years. Once weaned all ram lambs from both blocks were transferred to a third adjacent block, Kakaho. Ewe lambs remained on their block of birth. Flock management was undertaken so as to ensure as far as possible, uniform treatment of animals between blocks and sexes to enable valid comparisons between sires, blocks and sexes.

Analyses

Data had been previously analysed using Restricted Maximum Likelihood (REML) procedures to obtain estimates of fixed effects for date of birth, birth/rearing rank and dam age. The dam age effect included ewe hogget adjustments

as well as 2-tooth and older ewes. Corrections to the database for these fixed effects estimates were undertaken before analyses for genetic parameters. Block of birth and year of birth were included as fixed effects in REML analyses undertaken for estimating genetic components. Although date of birth, dam age and birth/rearing rank effects were not estimated concurrently with variance components, failure to account for the associated degrees of freedom was considered trivial (Johnson, D.J. pers. comm).

Multivariate REML estimates of genetic parameters, on a within-sex basis, were provided by procedures incorporated in a suite of computer programmes elucidated by Meyer (1986a; 1986b). Genetic components for between-sex comparisons were undertaken using procedures described by Schaeffer *et al.* (1978) using pairwise comparisons for each trait combination. This technique permits simultaneous estimation of components of variance and covariance when different variables (traits) are observed in different experimental units, taking advantage of the fact that residual covariances do not exist. In this case pairwise comparisons were undertaken between body and fleece weights on males with body and fleece weights on females.

RESULTS AND DISCUSSION

TABLE 1 Heritabilities and standard errors (\pm) for male and female body weights and fleece weights.

	Male		Female	
Weaning weight	0.10	(0.02)	0.06	(0.02)
Autumn weight	0.17	(0.03)	0.14	(0.03)
Spring weight	0.27	(0.04)	0.22	(0.03)
Hogget fleece weight	0.21	(0.04)	0.23	(0.04)

Heritabilities and Variance Components

Heritabilities for male body weights were higher than those for females (Table 1). However, based on the standard errors, no two estimates on the same trait are significantly different between sexes. However, Baker *et al.* (1979) reported higher estimates of heritabilities for female body

and fleece weights when compared with males. Present estimates differ from previous Sheeplan estimates (Clarke and Rae, 1977) and the proposed Animalplan estimates of 0.12 for weaning weight, 0.25 for autumn weight, 0.35 for spring weight and 0.3 for hogget fleece weight (Callow C.F., pers. comm).

TABLE 2 Variance components for male and female body weights and fleece weights.

	Sire		Residual	
	Male	Female	Male	Female
Weaning weight	0.167	0.077	6.723	5.036
Autumn weight	0.723	0.311	15.931	8.064
Spring weight	0.762	0.583	10.675	10.235
Hogget fleece weight	0.009	0.008	0.160	0.135

An examination of the variance components, (Table 2), shows that in all instances, sire and residual components of variance were smaller for females than for males.

In contrast, Baker *et al.* (1979) reported both higher sire and residual components for females. The data in this analysis could have reduced variances as a result of a history of selection. Excluding autumn weight, the variances for both sexes were lower than the currently implied variances for Animalplan and Sheeplan. This result, in association with the lower heritabilities, has effects on predicted selection responses. This point is considered in more detail later.

Correlations

Genetic and phenotypic correlations between traits for each sex are important in determining correlated responses and for increasing the accuracy of predicting breeding values.

The estimates of within-sex genetic and phenotypic correlations (Table 3) are different from current Sheeplan and Animalplan estimates, especially for the genetic correlations with hogget fleece weight. Animalplan genetic correlation estimates between body weights and fleece weight are-

Hogget fleece weight and weaning weight	0.20
Hogget fleece weight and autumn weight	0.25

TABLE 3 Genetic and phenotypic correlations for body weights and fleece weight for males and females separately. Standard errors in parentheses¹.

	Weaning weight	Autumn weight	Spring weight	Hogget fleece weight
Females				
Weaning weight		0.41(0.01)	0.39(0.01)	0.13(0.01)
Autumn weight	0.29(0.14)		0.56(0.01)	0.26(0.01)
Spring weight	0.28(0.13)	0.80(0.06)		0.27(0.01)
Hogget fleece weight	0.20(0.15)	0.00(0.13)	-0.01(0.12)	
Males				
Weaning weight		0.58(0.01)	0.41(0.01)	0.21(0.01)
Autumn weight	0.54(0.11)		0.65(0.01)	0.41(0.01)
Spring weight	0.30(0.14)	0.84(0.04)		0.39(0.01)
Hogget fleece weight	-0.11(0.15)	0.18(0.12)	0.13(0.11)	

¹ Genetic correlations below the diagonals, phenotypic correlations above the diagonals

Hogget fleece weight and spring weight 0.30

The genetic correlations found in this study suggest indirect selection for fleece weight via body weight would have little impact on fleece weight. Although these results are different from current Sheepplan and Animalplan estimates they are similar to pooled estimates given by Baker *et al.* (1979).

It is commonly assumed that the genetic correlation between the same trait measured on both sexes is unity. The estimates derived in this study (Table 4) show that none of the diagonal elements was significantly different from 1.0. For the body weight traits, the correlations indicated that selection in one sex either on the same trait or on an indirect trait, would result in a correlated increase in the corresponding trait in the opposite sex. For hogget fleece weight, selection on indirect traits of one sex would be of little value in improving fleece weight in the other sex.

Predicted Responses

A major interest to animal breeders is the implication of changes in heritabilities, genetic and phenotypic correlations and variances on expected selection responses. The same generation interval and intensity of selection were assumed irrespective of the index or the traits compared.

The single trait expected responses within this population would be lower than those predicted Animalplan statistics. As Animalplan utilises within-flock phenotypic variances for calculations of breeding values, it is appropriate that comparisons of expected gain should also be on this basis. The only determinant of differences between predicted genetic gains would be the differences between heritabilities estimates. Therefore, the ratio of the heritabilities indicates the relative differences between predicted

TABLE 4 Genetic correlations for body weights and fleece weights between males and females. Standard errors in parentheses.

Males	Weaning weight	Autumn weight	Females	
			Spring weight	Fleece weight
Weaning weight	0.88(0.08)	0.38(0.15)	0.21(0.14)	-0.05(0.15)
Autumn weight	0.51(0.15)	0.88(0.08)	0.70(0.08)	-0.04(0.13)
Spring weight	0.29(0.15)	0.69(0.09)	0.75(0.10)	-0.02(0.12)
Fleece weight	0.01(0.16)	0.16(0.13)	0.01(0.12)	0.95(0.05)

responses for single trait selection. Comparisons are made with Animalplan statistics as the base (Table 5).

TABLE 5 Ratio of heritabilities ($\times 100$) for single trait selection.

	Weaning weight	Autumn weight	Spring weight	Hogget fleece weight
Animalplan	100	100	100	100
Male	83	68	77	70
Female	50	56	63	76

Although the within-flock rankings of animals will not change, the expected response to single trait selection will be lower in this population than predicted from Animalplan heritability estimates.

When combining information on each trait, selection indices can be derived to optimise responses in the overall breeding objective. If the intensity of selection, relative economic values, generation interval and phenotypic variances are the same for each alternative selection index, the determinants of response will be the heritabilities and genetic correlations between traits in the index and the objective.

The repercussions of utilising genetic parameters, estimated from this study, on expected genetic responses under index selection are presented in Table 6. Predicted responses for each trait of the index along with percentage contribution to overall economic gain and the

correlation between the index and breeding objective are presented. Phenotypic variances from each sex group were used in determining indices from the Animalplan genetic parameter set.

Expected responses for body weights and fleece weight are less when using parameters derived by this study. As with Animalplan, indices NLB and HFW account for over 70% of total gain. Lower heritabilities and genetic correlations for both male and female parameter sets result in lower correlations between the indices and the overall breeding objective.

The results obtained from this analysis serve to highlight some important issues. Firstly, as with previous studies, genetic and phenotypic variances can and will vary between sexes. The genetic bases for these differences could be simple (chromosomal) or complex (cytoplasmic inheritance, sex by environment interactions, epistasis). As we know these differences do exist, it is appropriate that emphasis be given to the various roles sex types can play in New Zealand production systems. Secondly, it is relevant to stress that differences between genetic parameters will exist between estimates proposed by such schemes as Animalplan and estimates derived from within-flock data; both are sample statistics. Problems arise when the indices or breeding values derived for individual animals have different rankings within a flock for the same breeding objective. Similarly, when comparisons are made across flocks, such as for sire referencing schemes, differences in genetic

TABLE 6 Expected responses to index selection with three alternative sets of genetic parameters.

Parameter	NLB ¹		WWT		ALW		SLW		HFW		r_{HI}
	ΔG^2	%	ΔG	%	ΔG	%	ΔG	%	ΔG	%	
Animalplan											
Female	0.03	28.9	0.17	4.1	0.49	17.7	0.70	0.0	0.08	49.3	0.42
Male	0.03	24.7	0.22	4.7	0.76	24.4	0.77	0.0	0.09	46.2	0.43
Female	0.03	41.2	0.05	1.6	0.03	3.0	0.03	0.0	0.06	54.2	0.32
Male	0.03	39.4	0.01	0.2	0.49	22.0	0.55	0.0	0.05	38.4	0.34

¹ NLB = number of lambs born; WWT = weaning weight; ALW = Autumn weight; SLW = spring weight; HFW = hogget fleece weight; r_{HI} = correlation between breeding objective and index

² ΔG = expected genetic response in each trait, standardised.

% = percentage contribution to overall objective.

covariances between flocks could produce altered rankings across flocks when breeding values are estimated by multivariate indices.

The results presented in this study provide an indication that genetic and phenotypic parameters differ for male and female sheep. Cognizance of this fact should be taken when considering alternative selection strategies.

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