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## An investigation of sire by location interactions for faecal nematode egg counts in lambs

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### ABSTRACT

An experiment was carried out at Tokanui (Te Awamutu) and Wallaceville (Upper Hutt) over 4 years to test for the presence of sire by location interactions for faecal nematode egg count (FEC), using Romney rams from the flocks at these locations selected for high (H) or low (L) FEC.

A total of 14 Tokanui rams (8H and 6L) and 12 Wallaceville rams (7H and 5L) were used in their flock of origin in the mating years 1986-90 and then in the other location in 1988-91. There were 491 lambs recorded for FEC at Tokanui, and 875 at Wallaceville. A test of the sire by location interaction was obtained by treating records from the two locations as different 'traits', and estimating the genetic correlation between them. Estimates were made on log transformed FEC from lambs recorded in January and again in March. Fixed effects were included for sire source and contemporary group (genetic group of dam, year of birth of lamb, sex of lamb), and sire was fitted as a random effect. For FEC in January, heritabilities for the two locations averaged  $0.39 \pm 0.13$ , and the genetic correlation was  $0.78 \pm 0.25$ . For corresponding data in March, heritabilities averaged  $0.46 \pm 0.14$  and the genetic correlation was  $0.86 \pm 0.21$ . The analyses showed that the sire rankings for FEC were fairly robust across locations.

**Keywords:** Internal parasites, sheep, faecal egg count, genetics, interaction.

### INTRODUCTION

The use of a sire reference scheme to provide genetic links between locations generally assumes that there are no sire by location interactions. Experimental data were available to test this for faecal nematode egg count (FEC) in lambs, using two AgResearch locations, Tokanui (Te Awamutu) and Wallaceville (Upper Hutt).

### MATERIALS AND METHODS

#### Experimental design

Selection flocks for high (H) and low (L) FEC in lambs were established with Romneys by Ruakura staff in 1985 at Rotomahana, later (December 1988) transferred to Tokanui, and by Wallaceville staff in 1979 at Wallaceville. The histories of these flocks were described respectively by Baker *et al.* (1990) and by Bisset *et al.* (1991). A total of 14 Tokanui rams (8H and 6L) and 12 Wallaceville rams (7H and 5L) were used for this experiment in their flock of origin in the mating years 1986-90 and then in the other location in 1988-91.

In the home environment the H and L rams were single-sire mated to random samples of H and L selection flock ewes respectively, whilst in the other location the same rams were allocated in single-sire mating groups in a subsequent year to random samples of tester-flock Romney ewes.

#### Recording

Lambs were born in spring (mainly in September) and were identified to dam at birth. At Tokanui, H and L selection

ewes and the tester ewes were run in one management group until weaning, whilst at Wallaceville H and L selection ewes were run in one management group and tester ewes in another. After weaning (generally November), lambs of each sex remained in contemporary management groups similar to those already described, but with the minor exceptions given in the data analyses below.

After weaning, a monitor group of lambs from each management group was faecal sampled weekly until average FECs rose above about 1500 eggs/g, at which time all animals were faecal sampled, drenched with anthelmintic, and the monitor group was then followed again. In this way two faecal samples for FEC were obtained from each animal, FEC1 generally in January and FEC2 generally in March.

At Tokanui, 323 and 168 lambs by home and Wallaceville rams were recorded for FEC, giving average progeny group sizes of 23 and 14 respectively. At Wallaceville, 470 and 405 lambs by home and Tokanui rams were recorded for FEC, giving average progeny group sizes of 39 and 29 respectively. These group sizes contained, in some cases, animals born in 2 or more years.

#### Data analyses

All FEC records were transformed using the function  $\log_e(\text{FEC}+100)$ . The BIREML mixed-model computer programme of Meyer (1986) was used to estimate genetic (co)variances, treating records from the two locations as different 'traits'. This programme estimates (co)variance components when different traits are measured on different experi-

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mental locations, assuming that environmental covariances are zero. Genetic source of sire and contemporary group were fitted as fixed effects. The genetic source of sire was defined as Tokanui or Wallaceville. Contemporary group was defined as the genetic group of dam x year of birth of lamb x sex of lamb, where there were three genetic groups of dam at each location: H selection flock, L selection flock or progeny tester flock. All lambs from H and L sires were grazed together, except for the 1990-born and 1991-born Wallaceville female selection-line lambs.

## RESULTS

### Heritability and correlation estimates

Table 1 shows estimates of heritability for log FEC1 and log FEC2 for each location, and the genetic correlations between locations for each trait.

**TABLE 1:** Heritability of the logarithm of faecal egg count (FEC) in January and March, and the genetic correlations estimated across two locations.

Parameter	January		March	
	Tokanui	Wallaceville	Tokanui	Wallaceville
Phenotypic SD <sup>1</sup>	0.88	0.78	0.84	0.82
Heritability : estimate	0.43	0.34	0.38	0.54
: s.e.	0.22	0.14	0.21	0.18
Genetic correlation				
: estimate		0.78		0.86
: s.e.		0.25		0.21

<sup>1</sup> Units:  $\log_e(\text{FEC}+100)$  where FEC were in eggs/g.

Neither genetic correlation was significantly smaller than unity, where unity indicates complete correspondence between the ranking of the progeny of all sires at both locations. The estimated progeny differences (EPD, = half the sire breeding value derived from the mixed model analysis) at Wallaceville and the corresponding EPDs at Tokanui are shown for log FEC1 and log FEC2 (Figure 1). For log FEC1, EPDs overall ranged from 0.49 to -0.36  $\log_e$  FEC units (eggs/g), whereas for log FEC2 they ranged from 0.48 to -

0.37  $\log_e$  units. In Figure 1, 2 out of 26 sires had different progeny performance for log FEC1 at the two locations (arbitrarily taken as a difference in EPDs between locations of  $>0.135 \log_e$  units or half a genetic standard deviation), and 2 sires were also in this category for log FEC2.

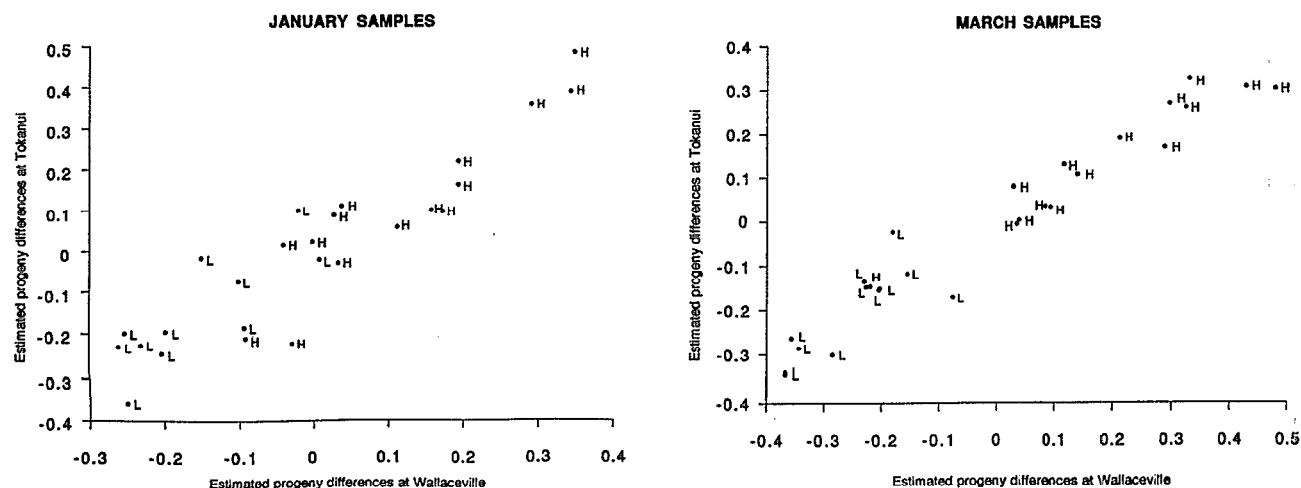
Further subdivision of the genetic grouping of sires into H and L selection flocks reduced the estimates of genetic (co)variation, particularly the genetic variance for log FEC1 at Wallaceville. The genetic correlation estimate was out of bounds ( $1.04 \pm 0.63$ ) for log FEC1 and was  $0.61 \pm 0.75$  for log FEC2. The corresponding heritabilities averaged  $0.16 \pm 0.12$ .

## DISCUSSION

The results of this sire by location experiment showed reasonably high genetic correlations between log FEC at home and at a second location. When the model including sire selection flock was used, the genetic correlations had 3-fold larger standard errors than the estimates in Table 1 because there were few sires in each sire source. The within-source analyses also removed over half of the variance attributed to sire in Table 1, giving heritabilities averaging 0.16 compared with an average of 0.42 in Table 1. This was the result of progeny testing sires from an FEC selection experiment, so that overall genetic variance was partitioned into genetic differences between and within flocks.

Our overall heritability estimate of 0.42 was similar to the value of 0.35 in the review by Baker *et al.* (1991) and in an additional data set reported by Bisset *et al.* (1992). With ram selection based on performance testing, and a heritability of about 0.35 for this trait, it is inevitable that some rams will be misclassified on performance test. Figure 1a included two such rams which were classified on phenotype as H at Wallaceville, shown in the L/L sector of the Figure, and Figure 1b included a similar example from a Tokanui-bred ram. Possibly maternal effects can change the lamb's own performance for FEC; this has been investigated in more detail in a companion paper (Morris *et al.*, 1993). The performance selection criterion in practice however was a combination of log FEC1 and log FEC2.

**FIGURE 1:** Relationship of estimated progeny differences  $\log_e$  faecal egg count (eggs/g) for high (H) or low (L) breeding value sires used at Tokanui and Wallaceville; (a) January samples, (b) March samples.



Baker *et al.* (1991) reported on preliminary lamb crops of data (the first two progeny test years) from this sire by location experiment. With hindsight, results from their sire groups which appeared to show an interaction did not persist in the larger bank of data evaluated here.

In conclusion, genetic correlations between locations were 0.78 and 0.86. Thus, sire by location interactions in this experiment were small and not significant, and any sire re-ranking observed generally affected only a small proportion of sires.

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