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Selection programmes for nematode resistant sheep in commercial flocks

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ABSTRACT

Evidence for multiple anthelmintic resistance has emerged rapidly. The need to investigate innovative alternatives to maximise nematode control is significantly more critical. Selection of sheep with above average natural or acquired resistance to infection is one such option that is being studied.

Progeny testing for faecal nematode egg count (FEC) has been evaluated following natural infection. Research involving 104 sires used on 4 commercial Romney studs over the last 2-5 years demonstrated considerable genetic variation. Heritability estimates for FEC ranged from 0.17 to 0.27. Moderate to strong positive genetic correlations (0.38-0.75) between FEC1 and FEC2 were observed. Furthermore, genetic correlations between FEC1 or FEC2 and production traits, including weaning weight, later liveweights and fleece weight were moderate.

Breeders face a philosophical dilemma whether to become involved in selection for nematode resistance or not in the face of the many unanswered questions, including why and how to undertake the work. Results to date indicate that breeders can adopt and apply a screening protocol to add to breeding trait records.

Keywords: nematode parasites, genetic, resistance, commercial, ram, breeders, production, FEC, correlations, sheep, Romney

INTRODUCTION

The future of sheep production in New Zealand depends on continued improvements in animal production. Until recently breeders have sought to generate genetic improvements in traits such as body and fleece weights which have direct economic benefits. Most have been easily quantified and associations have been characterised over extensive study and application in breeding flocks. Increasingly efforts are being directed towards farming efficiency and effectiveness. Developments in animal and pasture management have increased stocking rates and animal productivity. However, these seem to have been improved at the expense of certain aspects of animal health. Pressure to produce has meant that producers have become reliant on veterinary therapeutics to obviate sources of infection and disease. Currently, two of the best examples of this would be facial eczema and nematode parasites. In the case of the former, zinc salts are used to protect animals from toxicosis, with or without the application of chemicals to control fungal sources on pasture.

Since the 1960s modern broad-spectrum anthelmintics have been developed to control nematode parasites in ruminants. Little attention has been paid to the obvious fact that most parasite populations remain in the pasture. As a consequence, as land and animals have been pushed for production there has been a dramatic increase in the dependence which farmers have placed on these commercial products. By the mid 1980s it was estimated that one third of sheep production in this country was dependent on chemicals to control nematode infections (Brunsdon 1988). To this objective, in excess of 23 million dollars is spent on anthelmintics each year (Familton 1991) and the national average drenching frequency for lambs has been estimated to be almost 7 times per annum (Brunsdon 1982). Despite this, contamination of the

environment has continued with increased pressure to produce. There has been a general reliance on anthelmintics to control parasites with the expectation of maintaining growth rates. This combined with other factors has generated the drench resistance crisis now faced by producers.

The impact that the loss of one or more anthelmintic families could have on farm viability and animal production cannot be assessed accurately. As resistance to the milbemycins emerges as a threat through cross infection from goats, there is a high degree of urgency to prolong anthelmintic life expectancies, find new anthelmintics, and find alternatives to help sustain and enhance animal production through reduced parasite loading on pasture.

One alternative being investigated by various research groups is genetic selection to improve the natural ability of stock to resist or restrict infection. The aim is to effectively reduce and, in fact, minimise loading pastures with parasites. Ultimately the goal is to reduce dependence on anthelmintics and delay the emergence of drench resistance. Early studies have demonstrated that faecal nematode egg counts (FEC) generally correlate well with worm burdens. More recently FEC has been estimated to be moderately heritable with estimates not unlike those for a trait such as fleece weight. Since prospects for effective farming appear to be seriously compromised by factors such as anthelmintic resistance there has been significant interest to develop selection programmes and generate 'resistant' flocks. A number of issues remain to be resolved before such a trait can be included with accuracy and reliability in selection programmes. Reported herein are ongoing research studies designed to investigate opportunities for the introduction and application of FEC monitoring and selection programmes in various Romney stud flocks.

MATERIALS AND METHODS

Study Resources

Four Romney flocks (Studs A-D) from approximately 20 flocks currently involved in screening programmes have been included in this study. These were selected based on the duration of screening, the size and completeness of the data as well as the opportunity to use existing genetic links between 3 co-operators. These studs are located in Northland, Wairoa and Wairarapa and represent both registered and non-registered Romney breeders. Stud A is involved in a group breeding scheme, linked with reference sires.

All progeny were from single sire matings and this provided lambing and production records which consisted of sire, dam, sex, liveweights (LWT) and fleece weights (FWT). Where possible, attempts were made to ensure that each sire was represented by at least 20 progeny of any sex.

Data from Stud A consisted of records for progeny born between 1987 and 1991. Records were collected for 2503 progeny sired by 41 rams (Table 1). The FEC data include male and female progeny. Seasonal problems with facial eczema and viral pneumonia between February and May each year prevented a second FEC sampling until at least May. Generally, LWT1 and LWT2 correspond to January and May liveweights taken at FEC1 and FEC2 (14-16 weeks apart). These were only available for 1987 and 1988. FWT data were only available for the 1987, 1989 and 1990 born progeny.

Records for Studs B-D were of progeny born in 1990 and 1991. Lambing records and performance data were exported from the national database managed by the New Zealand Animal Breeding Trust (formerly Animalplan). FEC was recorded only on males from these 3 properties (Table 1). A total of 2262 individual records comprised the data set, generated using 63 sires in 1990 and/or 1991. FEC1 and FEC2 were generally recorded 5-8 weeks apart.

TABLE 1: Animal resource summary

Stud	Duration	Progeny ^a	Sires
A	1987-91	2503 (m/f)	41
B	1990-91	965 (m)	33(13) ^b
C	1990-91	919 (m)	48(26)
D	1990-91	378 (m)	29(24)

^a m = male; f = female

^b Total sires (unique sires)

Parasitology Protocols

Generally protocols were as described for similar research studies (Baker *et al.*, 1991). Progeny were run on each property from weaning (November-December) as single sex mobs. After treatment with anthelmintic at weaning all lambs acquired natural mixed nematode infections while grazing. From weaning, approximately 15 lambs at each location were monitored until mean faecal nematode egg counts rose to 800-1000 eggs/g. At that time, all lambs were faecal sampled to determine FEC1, weighed, given anthelmintic and the screening process repeated to provide FEC2.

Data Analysis

FEC was transformed using $\text{Log}_e(\text{FEC}+100)$ to stabilise variances prior to statistical analyses. Preliminary tests for significance among fixed effects were made using Genstat (1990). Stud A was analysed separately from Stud B-D. Fixed effects including year x sex contemporary groups, rearing rank and dam age (2-5+) were examined in both data sets. Birthday, birth rank and the flock x year of birth interaction were examined only for studs B-D. A mixed-model restricted maximum likelihood (REML) analysis was carried out including significant fixed effects and sire as a random effect. Genotypic and phenotypic correlations were obtained using REML on pairs of transformed traits and the sum of the pairs assuming equal design matrices for each pair (Thompson and Hill 1990).

RESULTS

Stud A

Half-sib heritabilities (h^2) for worm egg count were estimated to be 0.20 and 0.27 for FEC1 and FEC2, respectively (Table 2). *Nematodirus* egg count (NEM) heritability was estimated to be low (0.13). The estimates for the performance traits were 0.10, 0.17 and 0.25 for LWT1, LWT2 and FWT, respectively. Since birthday and birth rank were unavailable in Stud A, estimates of h^2 for production traits are biased downwards.

Positive genetic correlations were seen between FEC (1 and 2) and production traits (Table 3), but tended to be higher for FEC1. Corresponding phenotypic correlations were close to zero.

TABLE 2: Univariate half-sib heritability estimates.

Variate ^a	Heritabilities	
	Stud A	Studs B-D
$\text{Log}_e\text{FEC1}$	0.20 (0.04)*	0.17 (0.05)
$\text{Log}_e\text{FEC2}$	0.27 (0.08)	0.20 (0.06)
NEM1	0.13 (0.05)	-
LWT1	0.10 (0.05)	0.34 (0.08)
LWT2	0.17 (0.09)	-
FWT	0.25 (0.08)	0.35 (0.08)
WWT	-	0.36 (0.08)

^a FEC1 = faecal nematode egg count at 5-6 months; FEC2 = faecal egg count at 8-9 months; NEM = *Nematodirus* egg count at FEC1; LWT1 = liveweight at FEC1; LWT2 = liveweight at FEC2; FWT = greasy fleece weight at 10-12 months; WWT = weaning weight.

* (s.e.).

Studs B-D

Paternal half-sib REML estimates of h^2 were moderate for FEC1 and FEC2, 0.17 and 0.20, respectively (Table 2). Heritabilities were considerably higher for the production traits, weaning weight (WWT), LWT1 and FWT (0.36, 0.34 and 0.35, respectively).

The genetic correlation between FEC1 and FEC2 was high and positive (0.75) while genetic correlations between both estimates of FEC and the production traits were low to moderate (Table 3), similar to Stud A. Phenotypic correla-

TABLE 3: Estimates of genotypic (above diagonal) and phenotypic (below diagonal) relationships for various parasitological and production parameters.

Trait ^a	Stud	Trait						
		1	2	3	4	5	6	7
1 Log _e FEC1	A	-	0.38	0.62	0.40	0.65	0.14	-
	B-D	-	0.75	-	0.44	-	0.51	0.21
2 Log _e FEC2	A	0.18	-	0.34	0.05	-0.07	0.12	-
	B-D	0.20	-	-	0.40	-	0.17	0.03
3 NEM	A	0.36	0.09	-	-	-	-	-
	B-D	-	-	-	-	-	-	-
4 LWT1	A	0.03	-0.02	-	-	-	-	-
	B-D	-0.04	-0.01	-	-	-	-	-
5 LWT2	A	-0.04	-0.05	-	-	-	-	-
	B-D	-	-	-	-	-	-	-
6 FWT	A	0	-0.04	-	-	-	-	-
	B-D	-0.04	-0.04	-	-	-	-	-
7 WWT	A	-	-	-	-	-	-	-
	B-D	-0.03	0	-	-	-	-	-

^a Refer to Table 2 for explanation of traits.

Stud A: Average standard error for genetic correlations = 0.25; Average standard error for phenotypic correlations = 0.02.

Stud B-D: Average standard error for genetic correlations = 0.20; Average standard error for phenotypic correlations = 0.02.

tions between FEC and production traits were again close to zero.

DISCUSSION

Apart from contemporary groups and a small effect of birthday in Studs B-D, fixed effects were generally not significant for FEC1 and FEC2. Because of the assumption of equal design matrices for the bivariate REML procedure, all fixed effects were included in the model.

Heritability estimates (0.17-0.27) for log transformed FEC were moderate and fairly consistent between the 2 data sets but were slightly higher than the 0.13 estimated by McEwan *et al.*, (1992). Estimates made by other authors for Romney sheep in other commercial and experimental flocks in New Zealand (0.33-0.35) were somewhat higher (Baker *et al.*, 1991; Bisset *et al.*, 1992; Watson *et al.*, 1986).

The tendency for the h^2 estimate to increase between FEC1 and FEC2 has been shown previously (Baker *et al.*, 1991). This confirms that there may be some value in using more than one sample. In Studs B-D, FEC2 was generally determined 5-8 weeks after FEC1 when monitor counts demonstrated the 800-1000 eggs/g target. The increase in h^2 probably reflects divergence of FEC of resistant or susceptible genotypes following continued exposure to infective larvae. Morris C.A. and Bisset S.A. (unpublished, 1991) estimated the phenotypic correlation between FEC1 and FEC2 as 0.44 and the genetic correlation as 0.96, for egg counts made within a month of each other.

Although averaging across FEC has some statistical advantages it may be somewhat incorrect given the possible outcomes following continued exposure. There are clearly 2 outcomes at each sampling - high or low FEC. Obviously, animals that fall into the same level of FEC will be identified as 'resistant' or 'susceptible'. However, more weight should be given to FEC2 in differentiating animals that will acquire resistance between FEC1 and FEC2 from those which, for one reason or another, exhibit low FEC1 but high FEC2.

As in other studies, the relationship between FEC1 and FEC2 was positive in both data sets. It was unexpected that there was a weaker relationship between FEC1 and FEC2 on Stud A ($r_g = +0.38$). This was not the case on the other studs ($r_g = +0.75$). Strong associations between various FEC samples have been observed in most other experiments. Results on Stud A may reflect the longer time interval between samples. Consistently, egg counts on this stud have risen to presample target levels (800-1000 eggs/g) within a window 7 days either side of the last week of January over the duration of the study. However, the property has a history of facial eczema and viral pneumonia extending across the period of February to May. FEC2 has been recorded after this critical interval, 14-16 weeks after FEC1. This time span has generally been much shorter on the other properties (5-8 weeks).

The present data suggest that there are moderate genetic relationships between FEC and the various performance traits recorded. This was consistent across both data sets. The results agree with other studies where selection has been solely for high or low FEC or resistance to infection (Albers *et al.*, 1987; Woolaston 1990; Baker *et al.*, 1991; Bisset *et al.*, 1991).

Breeding for parasite resistance on the 4 properties included in this study is clearly recognised by the breeders as medium and longer term research investment for the future. Three options are represented by the breeders involved in the study. Stud A is specifically screening all male and female progeny to establish lines with lower FEC whereas B and C are screening all male progeny to identify likely stud ram candidates with lower FEC. Stud D is screening 20-30 male progeny per sire to estimate sire rankings for FEC. All believe that reducing parasite challenge from pasture is essential to effective parasite control. This is an epidemiologically and environmentally friendly objective that should support individual animal health programmes. The overall aim is to generate sheep which develop resistance to nematode parasites at a very early age with the wider objective to reduce contamination of pasture with worms. This is expected to

help minimise anthelmintic application frequency which, in turn, should delay the emergence of drench resistance throughout the national flock. Modelling has indicated that reducing contamination early in the season will have the most impact on drenching frequency and emergence of anthelmintic resistance (Leathwick *et al.*, 1992). The data presented here indicate that selection for lower FEC has a sound genetic basis but production will need to be monitored, possibly with index selection.

Additional benefits associated with animal management have also been realised on all 4 properties. Monitoring for FEC has increased awareness of the actual levels of infection in lambs at different times of the year. Parasitism is obviously not the only factor associated with poor or delayed lamb production. All have recognised the need to accurately differentiate the causes of ill-thrift and loss of condition.

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