DETECTION OF A QUANTITATIVE TRAIT LOCUS ASSOCIATED WITH A REDUCTION OF FAECAL EGG COUNT IN MERINO SHEEP

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SUMMARY

Data consisting of 4,397 animals with approximately 2,500 records for faecal egg count at 28 days (FEC1) and 35 days (FEC2) post-infection with *Haemonchus contortus* were analysed for detection of quantitative trait loci (QTL) and polygenic variances. The estimate of polygenic variance for FEC1, FEC2 and the mean of FEC1 and FEC2 (FECM), cube-root transformed, was 9.4, 9.2 and 8.1 respectively, equating to a polygenic heritability of approximately 0.20. A QTL conferring resistance to *Haemonchus contortus* infection was detected with variance 3.8, 4.4 and 2.9 for cube-root transformed FEC1, FEC2 and FECM respectively, accounting for approximately one third of the total genetic variance of each trait. Individuals homozygous for the favourable allele are expected to have faecal eggs counts that are one half of that in individuals carrying no copies of the favourable allele.

Keywords: Quantitative trait locus, host resistance, sheep, nematode parasites

INTRODUCTION

Resistance to internal parasites is a trait of major economic importance to the sheep industry (Gray 1997). Previous studies have shown that sufficient genetic variation exists for improvement of resistance to parasite burden (Albers *et al.* 1987, Woolaston and Piper 1996). Segregation of a putative major gene for resistance to *Haemonchus contortus* was suspected in the University of New England's Golden Ram flock but previous attempts to detect a major gene were inconclusive (Woolaston *et al.* 1990). Recent advances in methodology for the detection of quantitative trait loci (QTL) have become available, and are used here to detect the presence of a QTL conferring resistance to *Haemonchus contortus* infection.

METHODS

The data, spanning the years 1981 to 1992, consisted of 4,397 Merino sheep, many of which were descended from a single base sire, known as 'the Golden Ram' (Table 1). Two faecal egg count records were available; faecal egg count at approximately 28 days following infection (FEC1), and at approximately 35 days following infection (FEC2). There were 2,666 records for FEC1, 2,601 records for FEC2 and 2,518 records for the mean of FEC1 and FEC2 (FECM). A cube root transformation was performed on each of FEC1 (CFEC1), FEC2 (CFEC2) and FECM (CFECM) since the distributions of observed faecal egg counts were highly skewed. The means of the

transformed egg counts were 20.4, 21.9, and 21.8 for CFEC1, CFEC2 and CFECM respectively. Fixed effects included in the model were year-group subclasses, sex and birth type.

Table 1. Number of lambs born, sires used, progeny of Golden Ram, and faecal egg count records at 28 days (FEC1), 35 days (FEC2) and mean of 28 and 35 days (FECM)

Year	Lambs	Sires	Golden Progeny	FEC1	FEC2	FECM
1981	347	21	20	332	334	324
1982	325	21	0	310	316	310
1983	483	27	49	421	332	321
1984	85	2	40	0	0	0
1985	239	15	42	211	234	209
1986	529	15	107	358	361	348
1987	370	20	0	364	355	351
1988	352	20	0	350	350	348
1989	199	18	0	186	182	174
1990	321	18	0	83	85	83
1991	224	17	0	16	16	15
1992	194	19	0	35	36	35
Total	3,668		258	2,666	2,601	2,518

The data were analysed using "The Gene Detective" (TGD) software of Tier and Henshall (pers comm). This software applies a Markov Chain Monte Carlo (MCMC) algorithm to estimate error, polygenic and QTL variances in complex pedigrees. Fixed effect estimates, polygenic breeding values and genotype probability estimates for each animal in the pedigree, and an estimate of the magnitude of the effect of the QTL, are also produced. In addition, simulations were performed to assess the validity of the results.

RESULTS AND DISCUSSION

Results presented (Table 2) are means of the last 2,000 of 4,000 MCMC samples. The total genetic component equates to a heritability of approximately 0.27 for all three traits, consistent with the studies of Woolaston and Piper (1996) and Albers *et al* (1987). Partitioning the total genetic variance for CFEC1 into polygenic and QTL components results in an estimate of polygenic heritability of 0.20 and a QTL heritability of 0.07.

The distribution of QTL variances sampled support the hypothesis of a QTL explaining between one quarter and one third of the total genetic variance. Converting the estimated QTL effect for CFEC1 to an egg count on the observed scale suggests that homozygous individuals carrying two copies of the allele conferring resistance are expected to have faecal egg counts of 6,128 eggs. Individuals carrying no copies of the favourable allele are expected to have faecal egg counts of 11,391 eggs, resulting in a difference of the two genotypes of approximately 5,000 eggs.

Validation. Two simulations were performed to establish whether some aspect of the data structure may have influenced the results.

In simulation 1, the Golden Ram was removed from the data, with each of his progeny assigned a different dummy base sire. The remainder of the pedigree was unchanged, and TGD analysis was performed on CFEC1. The variance component estimates obtained with the modified pedigree for CFEC1 (Table 3) were not significantly different to those obtained for CFEC1 with the original pedigree

Table 3. Estimates of variance due to error, polygenic effects and QTL effects, of cube root transformed faecal egg counts at 28 days (CFEC1), 35 days (CFEC2) and the mean of 28 and 35 days (CFECM), and effect (α) of the QTL (standard deviations in brackets)

	Error Variance	Polygenic Variance	QTL Variance	α^1
CFEC1	33.7 (1.7)	9.4 (1.7)	3.8 (1.4)	4.2 (1.5)
CFEC2	39.8 (2.0)	9.2 (1.9)	4.4 (1.5)	3.6 (1.3)
CFECM	29.3 (1.7)	8.1 (1.7)	2.9 (1.2)	3.0 (1.3)

[1]α is defined as the magnitude of the difference between homozygous classes

In simulation 2, the pedigree and record structure for FEC1 were retained, but new CFEC1 values were simulated for each animal. An error variance of 33.7 and a polygenic variance of 12.0 were used to simulate the CFEC1 records, being similar to the estimates from CFEC1 if the QTL variance is added to the polygenic variance. The breeding value of the golden ram was artificially set at -9.0, which is 2.6 standard deviations from the mean. No QTL effect was simulated, and no significant QTL effect was found using TGD (Table 3). The simulation was repeated with the breeding value of the golden ram artificially set at -15.0, which is 3.5 standard deviations from the mean. No QTL effect was simulated, and again no significant QTL effect was found using TGD (Table 3).

Table 3 Estimates of variance due to error, polygenic effects and QTL effects of cube root transformed faecal egg count at 28 days (CFEC1), and effect (α) of the QTL (standard deviations in brackets) for a) Sim1; Golden progeny assumed unrelated, b) Sim2a; simulated CFEC1 with no QTL and Golden Ram genetic value simulated 2.6 standard deviations from the mean, c) Sim2b; simulated CFEC1 with no QTL and Golden Ram genetic value simulated 3.5 standard deviations from the mean

	Error Variance	Polygenic Variance	QTL Variance	α^1
Sim1	33.2 (1.8)	10.7 (1.5)	4.2 (1.6)	3.5 (1.4)
Sim2a	31.7 (2.1)	15.3 (2.3)	0.85 (0.75)	1.2 (1.3)
Sim2b	32.8 (1.9)	15.6 (2.1)	0.64 (0.52)	1.4 (1.3)

[1]α is defined as the magnitude of the difference between homozygous classes

Implications. It has been recognised that genetic variation in resistance to parasites allows selection for the genetic improvement of parasite resistance. If some of this genetic variation is due to a single region of the genome, then opportunities for new approaches become available. Prediction of the genotypes of animals available for use as sires allows more informed selection and mating decisions.

This may occur within flock to increase the frequency of the desirable allele(s), or as an aid to introgression of the desirable allele(s) into industry flocks.

Another approach to the utilisation of desirable allele(s) is to attempt to locate the region of the genome involved, using molecular techniques. Once markers associated with the QTL are identified, then marker assisted selection (MAS) and marker assisted introgression (MAI) become feasible. Since faecal egg count is both difficult and expensive to measure in the field, a direct measure for a gene with an effect on faecal egg count offers the potential to save on measurement costs. Introgression of a desirable allele from an otherwise inferior population into an elite population is more effective through the use of MAI (Visscher *et al.* 1996).

Interest in parasite resistance has increased in recent years due to increasing drench resistance of parasites and the recording of faecal egg count is becoming more common. This offers scope for analysis of the type performed here on industry flocks. The effect of QTL found for parasite resistance on other traits of economic importance would also need to be established.

CONCLUSION

The analyses performed here suggest that genetic resistance to *Haemonchus contortus* infection in the Golden Ram flock is due to both a polygenic and a QTL component. The magnitude of the QTL effect is sufficiently large to be of economic importance. The existence of a QTL conferring resistance to internal parasites has important implications for the Australian sheep industries.

ACKNOWLEDGEMENTS

Support from the Australian Meat Research Committee (1981-1986), the Wool Research and Development Fund (1986 -1992) and Australian Centre for International Agricultural Research PN9422 is acknowledged. Many staff at the University of New England and the CSIRO Pastoral Research Laboratory contributed much to the experimental program that generated the data used in this study. Advice and comments on the manuscript by Dr. Rob Woolaston are gratefully acknowledged.

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