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# PRELIMINARY ANALYSIS OF SIRE EFFECTS ON RESISTANCE TO GASTROINTESTINAL NEMATODE INFECTION IN ANGORA AND CASHMERE GOATS

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## SUMMARY

Genetic resistance to gastro-intestinal nematode infection (GIN) in Angora and Cashmere goats is being investigated on two properties in northern NSW, Australia. Results from natural infections during the first year of a 5-year investigation are presented. Data consists of faecal egg counts (FEC) after natural infection (predominantly with *Haemonchus contortus*) of 222 and 220 progeny of 6 Angora and 9 Cashmere bucks, respectively. $FEC^{0.33}$ measured at 5 (FEC5) but not 3 (FEC3) months of age differed significantly among sires in both breeds. Oral vaccination of kids at 1 and 2 months of age with irradiated $L_3$ larvae of *Trichostrongylus colubriformis* did not influence FEC3 or FEC5. Heritability estimates for $FEC5^{0.33}$ were $0.25 \pm 0.21$ and $0.23 \pm 0.19$ for Angora and Cashmere goats respectively. The phenotypic correlation between FEC5 and weight at 5 months was -0.21 ($P<0.05$) in Angora goats and non-significant in Cashmere goats. These preliminary findings are encouraging and broadly consistent with other studies in sheep and some other breeds of goat.

**Keywords:** Heritability, gastro-intestinal nematodes, genetic resistance, irradiated larvae.

## INTRODUCTION

In high rainfall areas of Australia, gastrointestinal nematodiasis (GIN) caused by *Haemonchus contortus, Trichostrongylus colubriformis* and *Ostertagia circumcincta* is the major health problem of Angora and Cashmere goats (Adams 1995). The most important effect of GIN is decreased productivity although mortality occurs in severe cases. Control of GIN rests primarily on the use of anthelmintics but resistance to anthelmintics is widespread and has been documented in dairy, meat and fibre goats (Jackson 2000). Because of this, alternative control measures for inclusion in integrated parasite control systems need to be identified.

There have been reports on between and within breed differences in resistance to GIN in goats (Baker *et al.* 1998). Studies with Creole goats showed significant sire effects on resistance to natural infection in 6 and 8 months old kids (Aumont *et al*. 1998) and breeding for resistance to natural mixed infection had no unfavourable effects on their production capacity (Mandonnet *et al*. 2000). Jackson *et al*. (1999) showed that it is possible to reduce FEC by about 33% after 5 generations of selection in Scottish Cashmere goats. However, in Fijian goats under natural infection FEC was neither heritable nor repeatable (Woolaston *et al*. 1995).

The inclusion of host genetic resistance to GIN as an additional control measure is already being used in the Australian sheep industry under the Nemesis program. However, the breeding principles involved can not be transferred directly to the goat industry because the basic genetic information on resistance to GIN is not yet available. The major aim of this study is to provide the parameter

estimates needed for implementation of selection for gastrointestinal parasite resistance, and to determine whether early vaccination of kids with irradiated larvae of *Trichostrongylus colubriformis* will induce resistance to future GIN infection in Australian fibre goat populations. This paper is based upon natural infection data from the first year (2000/2001) of a proposed five- year study.

**MATERIALS AND METHODS**

The study involved the testing of 222 and 220 progeny of 6 Angora and 9 Cashmere bucks respectively, for host resistance to gastrointestinal nematodes. The animals were raised and managed separately on two commercial farms on the New England Tablelands of New South Wales, Australia. Kids of both breeds were weaned at about 5 months of age. On the Angora farm all kids were born and raised to weaning in one management group, and kids of both sexes were available for the study. On the Cashmere farm, kids were born and raised to weaning in 9 management groups each containing progeny from every sire. Only female kids were available for the study on this farm.

At approximately 26 days and one month of age respectively, half of the Angora and Cashmere kids received an oral dose of 5,000 attenuated $L_3$ larvae of *T. colubriformis* of the CSIRO McMaster strain (Vaccinated group) while the remaining kids served as controls. The kids in the Vaccinated group were given a booster dose of 14,000 attenuated $L_3$ larvae of *Trichostrongylus colubriformis* 4 weeks after the first challenge. Individual faecal samples were collected from all Angora kids at average ages of 87 and 127 days and Angora kids at approximately 3 and 5 months of age for FEC. Live weights were recorded at 1, 2, 3 & 5 months of age. Individual FEC was determined using the modified McMaster floatation technique. At each FEC measurement pooled faecal samples were cultured for larval differentiation to determine the species of nematode involved.

The importance of each source of variation was determined by univariate analysis using ASREML (Gilmour *et al.* 1999). Data was analysed separately for each breed (farm). For the Angora data the factors considered were sire, birth type, irradiated larvae, sex and age fitted as covariate. The effects fitted for the Cashmere data were sire, birth type, irradiated larvae and management group. In both models, all effects were considered fixed, except for the effect of sire, which was considered random. Heritabilities were estimated from the sire variance and the variance between progeny within sire. The traits considered for analysis were FEC at 3 (FEC3) and 5 (FEC5) months of age, and live weight at 5 months of age. The FEC data were cube root transformed to normalise the data.

**RESULT AND DISCUSSION**

Larval differentiation results showed *Haemonchus contortus* (91%) to be the predominant nematode species for FEC5 at both properties (Table 1). For Angora goats the least squares means (± se) for $FEC3^{0.33}$ and $FEC5^{0.33}$ were 3.2 ± 0.9 epg and 9.6 ± 1.0 epg, respectively while for Cashmere goats these means were 7.4 ± 1.1 epg and 9.6 ± 1.0 epg respectively (Table 2). At 3 months of age, none of the effects in the model had a significant influence on FEC3 for the Angora kids except for the age, while management group and birth type had significant effects in Cashmeres. There were no significant effects of sire or vaccination on FEC3 in either breed. However, analysis of FEC5 revealed significant variation between sires for both breeds. Other factors considered in the model for Angoras were non-significant. In addition to the sire effect in the Cashmeres, management group

**Table 1. Proportion (%) of different nematode species in faecal samples of Angora and Cashmere kids at 3 (FEC3) and 5 (FEC5) months of age**

| | Angora kids | | Cashmere kids | |
|---|---|---|---|---|
| Worm Spp | FEC3 | FEC5 | FEC3 | FEC5 |
| *Haemonchus contortus* | 9 | 91 | 91 | 91 |
| *Trichostrongylus colubriformis* | 15 | 6 | 9 | 7 |
| *Ostertagia circumcincta* | 76 | 3 | 0 | 2 |

(paddock) was also a significant effect. The progeny of the most resistant sire in each breed produced on average 452 and 526 epg less than the mean of the population in Angora and Cashmere respectively, (Figure 1). The kids in this study showed a lack of response to vaccination similar to that described in lambs in similar conditions (Windon 1991). Although Windon and Dineen (1984) described a response to vaccination with irradiated *T. colubriformis* larvae in young lambs that varied between sire groups, vaccination in that case was carried out under highly controlled conditions in pens.

**Table 2**. **Least squares means (± se) of cube root transformed faecal egg count in 3 (FEC3) and 5 (FEC5) month old Angora and Cashmere kids, classified by sire**

| Breed | | Least squares means (± se) | | Breed | | Least squares means (± se) | |
|---|---|---|---|---|---|---|---|
| Angora | No of kids | FEC3 | FEC5 | Cashmere | No of kids | FEC3 | FEC5 |
| 1 | 35 | 3.1±0.9 | 10.4±1.0 | 1 | 24 | 6.5±1.0 | 9.9±0.9 |
| 2 | 35 | 2.8±0.9 | 7.6±1.0 | 2 | 24 | 6.7±1.0 | 9.0±0.9 |
| 3 | 37 | 3.6±0.9 | 10.5±1.0 | 3 | 29 | 6.8±0.8 | 9.2±0.8 |
| 4 | 38 | 2.8±0.9 | 9.8±1.0 | 4 | 20 | 5.8±1.1 | 7.3±1.0 |
| 5 | 32 | 2.8±1.0 | 9.3±1.0 | 5 | 7 | 10.9±1.7 | 9.8±1.5 |
| 6 | 45 | 3.9±0.8 | 9.6±0.9 | 6 | 30 | 7.7±1.0 | 10.7±0.9 |
| | | | | 7 | 33 | 6.9±0.9 | 9.9±0.9 |
| | | | | 8 | 19 | 8.2±1.1 | 9.8±1.0 |
| | | | | 9 | 31 | 8.1±0.9 | 10.9±0.9 |
| Overall | 222 | 3.2±0.9 | 9.6±1.0 | Overall | 220 | 7.4±1.1 | 9.6±1.0 |

Paternal half-sib heritability estimates (±se) for $FEC5^{0.33}$ were 0.25 ± 0.21 and 0.23 ± 0.19 for Angora and Cashmere goats, respectively. This agrees with the heritability estimate of 0.23±0.05 for FEC in 6 months old Creole goats (Mandonnet *et al*. 2000), but is lower than the estimate of 0.31±0.08 for the mean of repeated $FEC^{0.33}$ in Scottish Cashmere goats (Vagenas *et al*. 2000). The phenotypic correlation between $FEC5^{0.33}$ and weight at 5 months was -0.21 in Angora and -0.02 in Cashmere. The moderate estimates of heritability for FEC5 in both Cashmere and Angora goats suggest that resistance measured at 5 months of age is heritable and that genetic improvement for parasite resistance should be possible in a goat breeding program. However, the standard errors of the estimates are large and further data are required to increase the precision of the estimates.

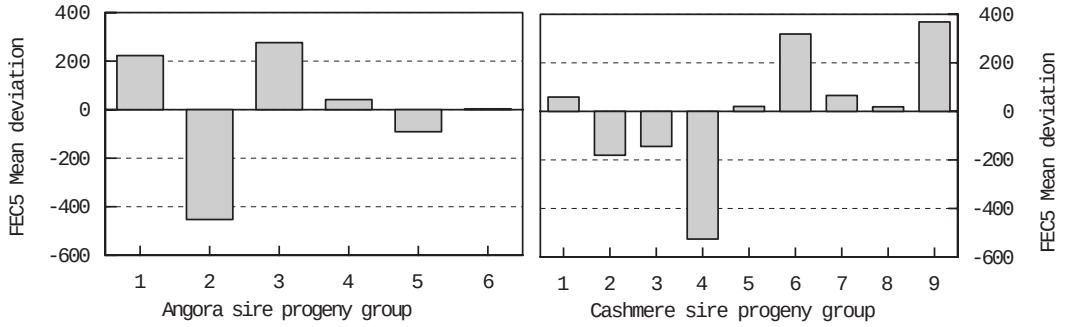


**Figure 1. Back transformed progeny mean deviation of $FEC5^{0.33}$ from the population mean of Angora and Cashmere goats.**

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