THE GENETIC CONTROL OF GASTROINTESTINAL NEMATODE INFECTIONS IN RUMINANTS

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SUMMARY

Infection with gastrointestinal nematodes is a major constraint on ruminant production throughout the world. There is an urgent and increasing need to develop additional methods of nematode control. One approach is to use genetically resistant stock. Resistance to some nematode infections is under moderate to strong genetic control in cattle and sheep. Some progress has been made in identifying the genes involved. In particular, the major histocompatibility complex appears to be one of the genetic systems contributing to the variation in resistance to infection.

INTRODUCTION

Nematode parasitism is arguably the most serious constraint affecting ruminant production world-wide. Economic losses are caused by loss of production, by costs of prophylaxis, by costs of treatment, and by the death of infected animals. In 1976 the United States Department of Agriculture (USDA) National Program Staff estimated that annual losses due to parasitism in ruminants exceeded $420,000,000 for the United States alone (USDA, 1976a,b).

The control of gastrointestinal nematodes traditionally relies on grazing management or anthelmintic treatment or both. However, grazing management schemes are often impractical due to expense or to the hardiness of infective larvae on pasture. In addition, the evolution of anthelmintic resistance in nematode populations threatens the efficacy of drug treatment programs. There is an urgent and increasing need to develop alternative strategies for control of nematode infections.

One approach is to use genetically more resistant stock as an adjunct to current methods of control. Not only would these animals be more resistant to infection and its effects, but their use would reduce pasture contamination with eggs and infective larvae. The reduced need for drug treatment should slow the evolution of drug resistance in nematodes. Also, increasing consumer pressure makes it desirable to pursue methods of decreasing drug residues in meat and meat products. There are two other advantages. The identification of genetically susceptible animals should improve progress in vaccine and drug development because it will be possible to test the efficacy of new products in susceptible
individuals. The identification of the genes involved in regulating resistance or susceptibility should lead to a better understanding of the mechanisms of host defense against infection. This improved understanding should lead to more efficient development of vaccines and anthelmintic drugs for veterinary and medical use.

It may not be possible to identify animals which are totally immune to nematode infection, but there is considerable evidence that part of the natural variation in resistance to nematode infection in ruminants is under genetic control (reviewed by Wakelin, 1978; Barger, 1989).

Breed differences

A comparison of different breeds has shown that some breeds are more resistant than others to the effects of nematode infection. For example, Scottish Blackface sheep are more resistant than Finn-Dorset sheep to *Haemonchus contortus* infection (Altaif and Dargie, 1978). The indigenous Kenyan Red Maasai sheep are more resistant than imported breeds (Preston and Allonby, 1978, 1979a). In France, Gruner et al (1986) showed that Romanov sheep were more susceptible than Lacaune sheep to *Nematodirus spathiger* and *Ostertagia circumcincta*. In the United States, Courtney et al (1985) showed that St. Croix lambs were more resistant than Florida Native and Barbados Blackbelly lambs which in turn were more resistant than domestic crossbred (Suffolk, Finn-Dorset, and Rambouillet) lambs, while Radhakrishnan et al (1972) showed that Florida Native lambs were more resistant to *H. contortus* infection than Rambouillet lambs. Also, Miller and Stear (manuscript in preparation) have shown that Louisiana Native sheep are more resistant than Suffolk sheep. In cattle, Frisch and Vercoe (1984) found that post-weaning nematode egg counts were lower in Brahman and Brahman-cross cattle than in Hereford x Shorthorn cattle.

Heritability of resistance to infection

Further evidence for genetic control comes from studies looking at the heritability of resistance to nematode infection. Albers et al (1987) challenged 882 lambs with 11,000 *H. contortus* larvae and estimated the heritability of faecal nematode egg counts four weeks after challenge as 0.34 ± 0.10 (mean ± standard error). Dineen and colleagues (personal communication) have estimated the heritability of faecal nematode egg counts following challenge of lambs with *Trichostrongylus colubriformis* as 0.41 ± 0.19. Interestingly, the response to challenge was bimodal and after three generations of selection the high responders (resistant lambs) were also more resistant to *H. contortus* infection.

In cattle, Stear et al (1988b) found that the heritability of faecal worm egg counts following natural mixed infection was 0.31 ± 0.11 for a single count and 0.63 ± 0.27 for the mean of four counts. In an independent trial at another location (Stear et al, 1990) the heritability of the mean of five faecal nematode egg counts was 0.51 ± 0.26. These high estimates are consistent with other reports from Australia (Seifert, 1977; Esdale et al, 1986). They imply that resistance to natural nematode infection is under stronger genetic control than growth rate in beef cattle or milk production in dairy cattle.
Identification of genetic systems involved

One half-sibling group in the study by Albers et al (1987) had extremely low egg counts following challenge and the sire was postulated to be the carrier of dominant allele with a major effect on resistance to infection with *H. contortus* larvae. Whitlock and Madsen (1958) also proposed the existence of a gene with a major effect on *H. contortus* infection to explain their observations.

Sheep have two alleles (A and B) for haemoglobin and several studies have suggested that animals with the A allele are more resistant to infection with *H. contortus* and its effects (Allonby and Urquhart, 1976; Altaif and Dargie, 1978; Preston and Allonby, 1979). However, other studies have been unable to confirm this association (Albers, personal communication).

The major histocompatibility complex (MHC) regulates resistance to nematode infections in experimental mice, guinea pigs, and swine (Wassom et al, 1979; Bell et al, 1982; Wakelin and Donachie, 1983; Geczy and Rothwell, 1981; Lunney, personal communication). Outteridge et al (1985, 1986, 1988) have reported an association between Class I antigens of the ovine MHC and response to challenge with *T. colubriformis*. However, Cooper et al (1989) found no evidence for an association between Class I antigens of the ovine MHC and susceptibility to *H. contortus* infection in the progeny of six rams. Stear et al (1988a, 1990) showed that the bovine MHC is one of the genetic systems regulating resistance to nematode infection. After allowing for the effects of sex and sire, cattle with resistant MHC haplotypes had approximately half the concentration of eggs in their faeces as cattle with other MHC haplotypes. Larval differentiation showed that these associations were strongest for *Haemonchus placei*. There were five groups of nematodes present: *Bunostomum phlebotomum*, *Cooperia spp*, *Haemonchus placei*, *Oesophagostomum radiatum*, and *Trichostrongylus axei*. Among worm species, *O. radiatum* egg counts showed the strongest correlation with postweaning weight gain. One Class I antigen w20 had an association with increased postweaning weight gain and calves with this antigen shed 40% fewer *O. radiatum* eggs than calves lacking this antigen. The results suggest that some of the variation in growth rate can be explained by variation in nematode burdens and the observed association of the MHC with growth rate in this study is due to the role of the MHC in regulating the response to nematode infection.

REFERENCES


