ENDOPARASITE INFECTIONS IN ALPACAS (LAMA PACOS) IN RELATION TO THEIR GENETIC BACKGROUND

M. Gauly¹ and J. Vaughan²

¹Department of Animal Breeding and Genetics, University of Giessen, Germany
²PO Box 406, Ocean Grove, Victoria, Australia

INTRODUCTION
Alpacas (Lama pacos) are domesticated members of the Camelidae family and are found primarily in the Andean mountains of Bolivia and Peru where they form an important component of the agricultural economy. They are now also found in increasing numbers outside South America where they are mainly kept as pets (Gauly, 2001). However, in Australia, breeders are endeavouring to start a fibre industry based on alpacas imported from South America.

Parasitic infections may significantly limit the productivity of camelids (Fowler, 2002). The economic impact of endoparasites and the consequences of antiparasitic treatments from chemical residues in food products and the environment as well as the occurrence of drug resistance, has led to an increasing interest in genetic selection for parasite resistance in different host species as an alternative method of endoparasite control. Results of several studies have indicated that some species and breeds are genetically resistant to parasites. The trait of parasite resistance may be used for selective breeding purposes (Buchwalder et al., 1977; Gray, 1997; Kominakis and Theodoropoulos, 1999; Gauly et al., 2001; Gauly and Erhardt, 2001).

The aim of the present study was to evaluate the prevalence of endoparasites in an alpaca population in Australia and to estimate the genetic background of faecal egg counts.

MATERIALS AND METHODS
Animals and management. Individual faecal samples were taken from the rectums of 92 young alpacas (2 to 16 months of age) on two consecutive days in April 2000 at a commercial alpaca farm in New South Wales, Australia. The animals were kept on pasture. The alpacas descended from five different sires (numbers of offspring per male were 26, 11, 29, 7 and 19, respectively). No anthelmintic treatments had been administered in the previous two months prior to faecal sampling.

Faecal egg counts. Faecal egg counts (FEC), measured in eggs per gram, were determined by a modified McMaster technique with saturated sodium chloride solution using the MSD counting chamber, adapted to detect minimum egg counts of 50 eggs per gram of faeces. Trichostrongylidae eggs were not differentiated except for those of Nematodirus spp.
Statistical analyses. Statistical analyses were performed with the Statistical Package for the Social Sciences SPSS-PC Version 9.0.

RESULTS AND DISCUSSION

Prevalence and FEC values. Small numbers of eggs per gram of faeces from various endoparasites were found at different prevalences (Table 1). Low egg numbers may explain why no signs of clinical disease were observed in any animal.

Table 1. Faecal egg count (mean ± SD) and prevalence of endoparasites found in faeces of 92 young alpacas

<table>
<thead>
<tr>
<th>Parasite</th>
<th>Faecal egg count (eggs per gram)</th>
<th>Prevalence (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Trichostrongylidae*</td>
<td>99.5 ± 167.3</td>
<td>59.8</td>
</tr>
<tr>
<td>Nematodirus spp</td>
<td>20.7 ± 49.3</td>
<td>22.9</td>
</tr>
<tr>
<td>Trichuris spp</td>
<td>2.2 ± 10.3</td>
<td>4.3</td>
</tr>
<tr>
<td>Strongyloides spp</td>
<td>0.5 ± 5.2</td>
<td>0.9</td>
</tr>
<tr>
<td>Moniezia spp</td>
<td>21.7</td>
<td></td>
</tr>
<tr>
<td>Eimeria spp</td>
<td>91.5</td>
<td></td>
</tr>
</tbody>
</table>

*(excluding Nematodirus spp)

The prevalences of Strongyloides spp. and Trichuris spp. were very low but extremely high for Eimeria spp., as expected in young animals. There was no correlation between age and FEC (p > 0.05). The numbers of Trichostrongylidae and Nematodirus spp. eggs were correlated (r = 0.19, p < 0.05). The average Trichostrongylidae FEC was different among the offspring groups (p < 0.05). Mean FEC ranged from 71 (± 80) to 117 (± 142) eggs per gram (Figure 1).

Figure 1. Faecal egg counts (mean ± SE) of progeny from different alpaca sires
The prevalence between the offspring groups ranged from 47.4% to 65.5%. The differences in FEC and prevalence are probably caused by genetically-based resistance against endoparasites as described for other species (Gray, 1997; Gauly et al., 2001; Gauly and Erhardt, 2001).

CONCLUSION

The differences in FEC among the five offspring groups were probably caused by genetic differences. Heritabilities need to be estimated on a larger number of animals.

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REFERENCES