RESISTANCE TO INTERNAL PARASITES IN DIVERSE LAMB GENOTYPES

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In Australia, more attention has been given to disease resistance of wool sheep genotypes than of meat sheep breeds. This paper reports the genetic variation of disease resistance in lamb genotypes derived from major terminal sire breeds and dam lines associated with meat sheep production.

Fresh faecal samples were taken in December 1995 from 425 cryptorchid lambs born between 1 and 3 1 July and maintained at the Agricultural Research Station, Cowra, N.S.W. Faecal worm egg counts (FEC, epg) were obtained using the McMaster method. Of the lambs, 262 were the progeny of Merino (M) and Border Leicester x Merino (BLM) ewes artificially inseminated (AI) by 4 Texel (T) and 3 Poll Dorset (PD) rams; 163 were the progeny of 5 M and 5 Border Leicester (BL) rams mated naturally with M ewes (Fogarty et *al*. 1995). Ewes lambed in separate paddocks according to dam breed, sire group and mating group (AI and natural). Lambs within each mating group were combined at marking and both mating groups were combined at weaning (4-5 October). Lambs received a combination clear/white drench at weaning and were then rotationally grazed as a single mob through paddocks with a predominance of luceme, subterranean clover and barley grass. Faecal samples were taken every 6 weeks post weaning on 20 lambs at random to time this sampling. Larval cultures indicated *Trichostrongylus* being the dominant genus of nematode (70%) followed by *Ostertagia* (25%). FEC was transformed in $\log_e(FEC+50)$ (denoted FECLN) prior to least squares analysis using the programme LSMLMW (Harvey 1990). Data of lambs born to T and PD sires were analysed separately to the progeny of M and BL sires, since the separate grazing of MxM and BLxM lambs to T and PD cross lambs until weaning may have led to different worm exposures and confound differences between these genotypes. Sire breed, dam breed, interaction of sire and dam breeds (symbolising genotype) and birth type were fitted as fixed effects, age and weaning weight as linear covariables and individual sire fitted as a random effect nested within sire breed, for T and PD lambs; as to M and BLM lambs, the model is the same as the former except deleting the interaction.

The least square means of FECLN for the lamb genotypes in the 2 analyses are shown in Table 1. In the first analysis, the differences between TxM, PDxM TxBLM and PDxBLM were not significant ($P>0.05$). Secondly, pure M lambs showed higher FECLN than BLxM lambs (Table 1, $P=0.15$). Contrasts between sire breeds showed no significant difference between T and PD breeds (6.15 ± 0.25 vs 6.22 ± 0.24, resp.). Nevertheless individual sire differences were highly significant ($P<0.001$) in both analyses. In sire groups, FECLN ranged from 5.68~6.34, 5.81~6.46, 5.96~6.84 and 6.32~7.24 within T, PD, BL and M sire breed, respectively. In addition the interaction between the individual sire (T and PD) and the dam breed (M and BLM) was highly significant ($P<0.05$).

Table 1. The least square means of FECLN for 6 lamb genotypes derived from 2 analyses

Genotype	T x M	PD x M	T x BLM	PD x BLM	M x M	BL x M
No. of Lambs	73	44	87	58	80	83
FECLN	6.17 ± 0.24[A]	6.28 ± 0.25	6.14 ± 0.22	6.16 ± 0.24	6.62 ± 0.17[B]	6.44 ± 0.20

[A] No significant difference between these 4 genotypes ($P>0.05$).
[B] No significant differences between MxM and BLxM ($P>0.05$).

The results indicate that there were no significant differences in FECLN between sire breeds, ewe breeds, as well as lamb genotypes; however the genetic variation was due mainly to individual sires.

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