GENETIC VARIATION IN RESISTANCE TO FLEECE ROT IN CSIRO'S FINE WOOL FLOCK

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SUMMARY

Genetic variation between- and within-bloodlines in resistance to fleece rot was investigated in the CSIRO's Fine-wool Flock with nine fine-wool bloodlines. There were significant differences in fleece rot incidence and severity among years, sexes, birth types. There was a considerable variation in fleece rot incidence and severity between bloodlines (6-7 % of the total variance). The estimated heritabilities of fleece rot incidence and severity were 0.17±0.02 and 0.24±0.02. Estimated heritability of liability to fleece rot was 0.11±0.02. Correlations of fleece rot incidence and severity with fleece and production traits were estimated. It was suggested that wool colour, which has both high heritability and high genetic correlation with fleece rot incidence and severity, has potential to be used as an indirect selection trait against fleece rot in breeding programs for fine-wool Merinos.

Keywords: Fleece rot, resistance, genetic variation, bloodlines, fine wool

INTRODUCTION

Fleece rot is a major factor predisposing sheep to blowfly strike (Belschner, 1937). It was found that there was a genetic correlation between fleece rot and blowfly strike (Atkins *et al.* 1980). Furthermore, due to low incidence of blowfly strike tolerated in commercial flocks, breeding sheep resistant to fleece rot is a long term measure to reduce susceptibility to blowfly strike in Merino (Raadsma *et al.* 1987).

A number of studies have been carried out on fleece rot in the Merino sheep industry. It has been found that there is considerable genetic variation of fleece rot within and between breeds, strains, bloodlines and studs. Heritabilities of fleece rot incidence and severity ranged from 0.13 to 0.41 and 0 to 0.52 respectively. There is considerable evidence that a number of fleece and skin characters are correlated with susceptibility to fleece rot and thus could be used as indirect selection criteria (Raadsma *et al.* 1987). To date the research on fleece rot has been carried out on three major flocks: a randomly bred medium Peppin flock, a South Australian strong-wool flock and a randomly bred multi-bloodline flock at Trangie in NSW (Raadsma *et al.* 1987). Although the Trangie study did include 2 fine-wool flocks, there is no other information about fleece rot genetic variation of fine-wool Merino sheep. This paper examines genetic variation in resistance to fleece rot and its correlation with other fleece traits in CSIRO's fine wool flock.

MATERIALS AND METHODS

The data were obtained from flocks of the CSIRO Fine Wool Project. The flock has been described in detail by Swan *et al* (1993,1995) and consists of nine fine-wool bloodlines chosen to represent the major Australian fine wool producing regions, including the tablelands of New South Wales, the western districts of Victoria, and Tasmania.

The data used in this analysis are from animals born in 1991-1996, with 6,213 progeny from 300 sires. Animals are visually scored prior to shearing at 10 months of age for fleece rot (0 to 9), colour (1 to 5), handle (1 to 5), crimp (1 to 5), dust (1 to 5), density (1 to 5) and staple size (1 to 5). The objectively measured wool traits from the shearing were greasy fleece weight (GFW), yield, clean fleece weight (CFW), mean fibre diameter (MFD), standard deviation of diameter (SD), staple length (SL), staple strength (SS).

The data were analysed with restricted maximum likelihood (REML), using ASREML (Gilmour *et al.* 1997). Fleece rot incidence and severity were initially analysed to identify significant sources of variation among fixed effects: bloodline, year, sexes (ewe and castrated hogget), birth types (single- and multiple-born), rearing type (single- and multiple-reared), flock and age of dam (2-10).

Heritability and correlation coefficients were estimated using the animal model. Bloodline was fitted as an additional random effect, giving estimates of between-bloodline genetic variance and its ratios to phenotypic variance, but it was fitted as a fixed effect when calculating heritibility and correlation.

Fleece rot incidence was analysed as an all-or-none trait. The heritability estimate of an all-or-none trait is reported to be incidence-dependent (Dempster and Lerner 1950, Hill and Smith 1977). The data were divided into three groups of cohorts of low, intermediate and high incidence according to the predicted least square estimate of incidence for a particular drop (McGuirk and Atkins, 1984). Four cohorts with incidence of less than 25 %, one drop with incidence of 56.4 %, one drop with incidence of 78.4 % were classed as low, intermediate and high. From these data, the heritability of liability to fleece rot was estimated.

RESULTS AND DISCUSSION

Mean fleece rot incidence and severity Mean fleece rot incidence and score were respectively 26.7 % and 0.58. The coefficients of variation were respectively 149 and 185 %. Fleece rot incidence and severity were significantly affected by year, sex and birth type ($P<0.05$). Incidence and severity of fleece rot varied widely among years, ranging with incidence from 0.46 % in 1991 to 75.2 % in 1996 ($P<0.01$) and with severity from 0.04 in 1991 to 1.82 in 1996 ($P<0.01$). Wethers had higher incidence and severity of fleece rot than ewes (29.2 v 24.3 %, 0.66 vs 0.51, $P<0.01$). Single-born animals had a higher incidence of fleece rot than twin-born and triple-born animals (32.6 vs 22.8, 23.5 %, $P<0.05$), and a higher severity of fleece rot (0.79 vs 0.50 and 0.35, $P<0.05$). There were no significant differences among rearing types, flocks and ages of dam in fleece rot incidence and severity ($P>0.05$).

Genetic variation between bloodlines There were significant differences in fleece rot incidence and score among bloodlines ($P<0.01$), with incidence ranging from 11.9 % to 39.1 % and with severity from 0.20 to 0.98. Phenotypic variances of fleece rot incidence and severity were 0.12 and

0.95, respectively. The ratios of between-bloodline variance to phenotypic variance were 6.6 % and 6 %, respectively.

Heritabilities of fleece rot traits and other traits The estimated heritabilities of fleece rot incidence and severity were 0.17±0.02 and 0.23±0.02 (Table 1). Estimated heritability of liability to fleece rot was 0.11±0.02. Heritabilities obtained from combined data or data of cohorts with different incidence were slightly lower than those reported by McGuirk and Atkins (1984) where the population had an average fleece rot incidence of 38 %. The heritabilities among cohorts with low, intermediate and high incidence of fleece rot were different. The low incidence cohorts had low heritabilities for incidence and severity score. The highest heritability estimate for fleece rot incidence was obtained in the cohorts of intermediate incidence, but the highest heritability estimate for fleece rot severity was obtained in the cohorts of high incidence. Heritability of liability to fleece rot was lower than those (0.35±0.12 for offspring-dam and 0.36±0.11 for offspring-sire) reported by Thompson *et al* (1985). Heritabilities of fleece trait scores were 0.20-0.31 with the exception of those of density and dust penetration scores being less than 0.1. Those of production traits were 0.34-0.65, while their genetic correlations with fleece rot traits were 0-0.20 (Table 2).

Table 1 Heritabilities of fleece rot incidence and severity (SE in parenthesis)

	Mean incidence (%)		Mean Score		Heritability			
					Incidence		Severity	
Low	9.0	(0.46)	0.15	(0.01)	0.10	(0.03)	0.11	(0.03)
Intermediate	52.7	(1.50)	1.22	(0.05)	0.26	(0.09)	0.12	(0.08)
High	75.5	(1.26)	1.83	(0.04)	0.13	(0.07)	0.24	(0.08)
Combined	26.7	(0.45)	0.58	(0.01)	0.17	(0.02)	0.23	(0.02)

Correlation of fleece rot traits with other traits Correlation of fleece rot traits with other traits were tabulated in Table 2. Clean fleece weight had positive genetic correlations with both fleece rot incidence and severity. Negative phenotypic and genetic correlations were observed between fleece rot traits and mean fibre diameter, standard deviation of diameter, staple length and staple strength. Because of these unfavourable associations between fleece rot traits and the economically important traits, further work is needed to identify the best strategy. The calculation of the economic values for fleece rot is an important first step in this process.

Wool colour had a positive phenotypic and genetic relationship with fleece rot. The whiter and brighter the wool the more resistant the animal is to fleece rot and was highly heritable. This supports previous findings of Holdaway *et al* 1934, Belschner 1937, Hayman 1953, Paynter 1961, James *et al* 1983 and James *et al* 1987, but not the results from Peppin sheep of Trangie (McGuirk *at al.* 1980 and Raadsma 1987). Staple size and character scores had negative genetic correlation with fleece rot incidence, which was the same trend found in other studies (Raadsma, 1987, James *et al.* 1983). Because of the relationships, selections aimed at reducing staple size and improving character will lead to unfavourable changes in fleece rot. The genetic correlations between fleece rot and assessed wool density and dust contamination were positive, and hence unfavourable. Despite this selection on density and dust will produce only small changes because of their low heritabilities.

In conclusion, several of relationships between fleece rot incidence and severity with the production traits examined were undesirable. This indicates that selection solely to reduce fleece rot incidence and severity will lead to a reduction in clean fleece weight, and an increase in mean fibre diameter. Further work needs to be conducted to clarify what are the optimum selection strategies. This result also suggests that wool colour, which has both high heritability and high genetic correlation with fleece rot incidence and severity, has potential to be used as an indirect selection trait against fleece rot in CSIRO's fine-wool flock.

Table 2. Heritabilities of fleece and production traits and their correlations with fleece rot traits (SE in parenthesis)

Traits	Heritability		Correlation with rot incidence				Correlation with rot severity			
			Phenotypic		Genetic		Phenotypic		Genetic	
Colour	0.31	(0.02)	0.18	(0.01)	0.47	(0.07)	0.16	(0.01)	0.38	(0.06)
Character	0.23	(0.02)	0.05	(0.01)	-0.15	(0.08)	0.02	(0.01)	-0.16	(0.08)
Density	0.09	(0.02)	0.08	(0.01)	0.16	(0.11)	0.10	(0.01)	0.25	(0.09)
Dust	0.05	(0.01)	0.10	(0.01)	0.27	(0.14)	0.09	(0.01)	0.45	(0.13)
Handle	0.21	(0.02)	0.02	(0.01)	-0.02	(0.09)	0.03	(0.01)	0.01	(0.07)
Staple	0.20	(0.01)	-0.03	(0.01)	-0.30	(0.02)	-0.01	(0.01)	-0.03	(0.00)
GFW	0.39	(0.03)	-0.04	(0.01)	0.02	(0.07)	-0.05	(0.01)	0.02	(0.06)
Yield	0.48	(0.04)	-0.04	(0.02)	-0.10	(0.08)	-0.01	(0.02)	-0.04	(0.07)
CFW	0.41	(0.02)	0.02	(0.02)	0.11	(0.09)	0.04	(0.02)	0.15	(0.08)
MFD	0.65	(0.02)	-0.12	(0.01)	-0.18	(0.06)	-0.15	(0.01)	-0.18	(0.05)
SD	0.50	(0.03)	-0.04	(0.01)	-0.17	(0.07)	-0.04	(0.01)	-0.14	(0.06)
SL	0.50	(0.03)	-0.04	(0.02)	-0.11	(0.08)	-0.08	(0.02)	-0.16	(0.07)
SS	0.34	(0.03)	0.07	(0.02)	-0.20	(0.09)	-0.08	(0.02)	-0.12	(0.09)

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