GENOTYPE X MANAGEMENT INTERACTION ON WOOL PRODUCTION TRAITS AND BODY WEIGHT IN WESTERN AUSTRALIAN MERINO SHEEP

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SUMMARY

The importance of a genotype x environment interaction in Merino sheep was investigated in two management groups, high versus low feeding level, which were designed to create two levels of production. The heritabilities for wool production and wool quality traits did not differ significantly between the two management groups, only for body weight. The genetic correlations between the two management groups were not significantly different from unity for yield, CV of fibre diameter, staple length and body weight. The genetic correlations between management groups for greasy fleece weight, clean fleece weight, mean fibre diameter and staple strength were significantly different from 1, but not from 0.8. That is showing a GxE interaction, which is not considered to be of practical importance.

Keywords: Genotype x environment interaction, Merino, genetic parameters, Western Australia

INTRODUCTION

Most wool production areas in Western Australia (WA) are located in Mediterranean climates. Winter rainfalls and dry periods in summer result in seasonal fluctuations in feed supply that impact negatively on wool quality and weight gain in sheep (Belotti *et al.* 1992). Within this climate, the management systems can form quite different environments for sheep production depending on stocking rate and level of supplementary feeding during the dry season.

The reaction of a genotype (sire, strain, breed) to the environment, referred to as genotype x environment interaction (GxE), can change the phenotypic ranking of a genotype from one environment to the other (Dickerson 1962). Selection based on the phenotype in one environment can lead to erroneous selection decisions for performance in other environments. The same trait expressed in different environments can be considered as two correlated traits (Falconer 1952). The magnitude of the correlation indicates the importance of the interaction of a genotype with the environment.

The aim of this study was to investigate through Falconer's (1952) approach, the existence of genotype x management interactions for body weight, wool production and wool quality traits. Some authors have published results of analysis performed on parts of the data set (MacLeod *et al.* 1990; Howe *et al.* 1991; Lewer and Ritchie 1992). The analysis for this paper was based on the complete data set of the project.

MATERIAL AND METHODS

Experimental design. The data were collected within the Wool Tenderness project (MacLeod *et al.* 1990, Lewer and Ritchic 1992), conducted by Agriculture Western Australia at Katanning, WA, from 1984 to 1991. Two management groups were established each with 320 Collinsville ewes. One group was run under low stocking rate and high level of supplementary feeding whereas the other group was managed with high stocking rate and low level of supplementation. The management regimes resulted in a difference of 7 - 10 kg in body weight in favor of the ewes in the high nutrition group. The rams (n = 63) were sourced from 12 studs and used over both groups. Four studs contributed to each of three sire strains (Collinsville, Bungaree and Peppin). The ewes were mainly Collinsville, except 2% were Collinsville x Peppin crosses. From the progeny, 14 % were used as ewe replacements in the high nutrition group, 10% in the low nutrition group.

Lambing occured in May and weaning in September. Weight at birth was recorded, as was body weight approximately 1.5 years of age (BWT), corrected for birth weight. The wool production and quality data were collected after 12 months of wool growth. It comprised: greasy fleece weight (GFW), yield (Y), clean fleece weight (CFW), staple length (SL), staple strength (SS), mean fibre diameter (MFD) and coefficient of variation of fibre diameter (CVFD). The complete hogget data set consisted of 1490 records in the high and 1395 records in the low nutrition group.

Statistical analysis. Least squares means were calculated with SAS (SAS Institute Inc. 1985). Testing of fixed effects, estimation of variance components and heritabilities and the calculation of correlations were performed via bivariate analysis of an animal model using ASREML (Gilmour 1998). The fixed effects tested in the model were dam birth year, weaning type and sire stud nested within strain. Hogget birth year, sex and flock were fitted together as contemporary group effects. September age (in days) was fitted as a covariate. Fourteen outliers, defined as records of which the residuals were four standard deviations or more from the contemporary mean, were rejected from the analysis to reduce the risk of accepting wrongly recorded data. However this still enabled inclusion of records in the analysis, which were, for biological reasons, not fully explained by the model.

RESULTS AND DISCUSSION

Least squares means. Table 1 shows that the animals in the high nutrition group had higher least squares means for CFW, MFD, SS, SL and BWT, while for CVFD they were higher in the low nutrition flock. All differences were statistically significant ($P > 0.01$) except for Y.

Table 1. Least square means for high and low nutrition group

	GFW (kg)	Y (%)	CFW (kg)	MFD (μm)	CVFD	SS (N/ktex)	SL (mm)	BWT (kg)
High	3.8	72.2	2.7	19.8	23.7	31.8	81.0	40.6
Low	3.0	72.5	2.2	18.4	24.9	25.4	75.7	33.5

Heritability. Table 2 shows the heritability estimates for the high and low nutrition groups. They were moderate to high. In comparison to heritabilities from previous work (MacLeod *et al.* 1990, Howe *et al.* 1991, Lewer and Ritchie 1992) they were within the same range. The heritability estimates for traits obtained for the high nutrition group were not significantly different from the corresponding estimates for the other group, which agrees with the results of Lewer and Ritchie (1992). Howe *et al* (1991) found some significant differences between the heritability estimates of BWT and SS calculated for the different management groups, but some of the results were not in the expected parameter range. Table 3 shows that the phenotypic variances were higher in the high nutrition environment than in the other management group. This did not impact on the heritability estimates, as the ratio between genetic and phenotypic variance remained relatively constant. An explanation could be that the restricted feeding conditions limit the expression of the phenotype, as a scale effect.

Table 2. Heritabilities of high versus low nutrition group and the correlation between the same trait in different environments

	Heritability ^{A}		Correlation
	High	Low	
GFW	0.33	0.40	0.82 ± 0.13^B
Y	0.66	0.61	0.95 ± 0.05
CFW	0.27	0.27	0.62 ± 0.20^B
MFD	0.55	0.55	0.77 ± 0.11^B
CVFD	0.55	0.51	0.93 ± 0.07
SL	0.46	0.44	1.00 ± 0.07
SS	0.32	0.37	0.80 ± 0.13^B
BWT	0.46	0.61	1.00 ± 0.05

^{A} standard errors from 0.05 – 0.07.

^{B} significantly different from 1.

Correlations. Table 2 shows that the genetic correlations between the two environments were significantly different from 1 for GFW, CFW, MFD and SS. These correlations had higher values than those reported by MacLeod *et al* (1990). The differences in the findings could have arisen from a more rigorous method used in the current study and approximately double the number of records were included in the analysis. Robertson (1959) suggested that correlations below 0.8 indicate the presence of a GxE interaction of agricultural importance. Most correlation estimates were higher than or at least close to 0.8, except CFW. It had an estimate of 0.62, which was through the associated standard error not significantly different from 0.8.

The genetic correlation between the high and low nutrition group indicates that a GxE was present for some traits, but not to an extent likely to be of practical importance on body weight, wool production or wool quality traits. Scale effects caused by the different feeding level were the main cause of differences in the phenotype, while the genetic differences remained relatively constant across the two feeding levels.

Table 3. Genetic and phenotypic variances of high versus low feeding level group

	Genetic variance		Phenotypic variance	
	High	Low	High	Low
GFW (kg)	0.10	0.07	0.29	0.17
Y (%)	11.83	9.35	17.88	15.26
CFW (kg)	0.04	0.03	0.16	0.10
MFD (μm)	1.03	0.81	1.89	1.46
CVFD	3.99	3.59	7.28	6.99
SL (mm)	32.56	25.86	70.58	58.73
SS (N/ktex)	26.70	21.81	82.04	57.51
BWT (kg)	11.08	9.59	23.96	15.83

ACKNOWLEDGEMENTS

Special thanks to Agriculture WA for excess to the database that was used in the current study. Thanks to Agriculture Western Australia, the Wool CRC for the support and AGBU for the assistance of this work. Greatly appreciated was the advice from Ron Crump (AGBU) on the analysis.

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