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THE EFFECT OF GENOTYPE X ENVIRONMENT INTERACTION ON DIFFERENT TRAITS IN DIFFERENT ENVIRONMENTS

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SUMMARY

The effect of genotype x environment (GxE) interaction on different traits in different environments was investigated. If the genetic correlation (r_G) between different traits is significantly different between environments, the underlying genetic relationship between different traits depends on the environments in which they are expressed. The experimental data were collected for the Wool Tenderness Project conducted at Katanning, Western Australia. The two environments were different feeding levels (low – "l" and high – "h") and the traits investigated included clean fleece weight (CFW), fibre diameter (CVFD), staple strength (SS), staple length (SL) and body weight (BWT). Significant differences were found between the correlations r_G(lSS – hFD) and r_G(lFD – hSS) and between r_G(lBWT – hFD) and r_G(lFD – hBWT). These results show a possible effect of GxE interaction on different traits expressed in different environments.

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

INTRODUCTION

In situations where effects of genotype x environment (GxE) interactions are considered, the focus is set on estimates of genetic correlation between the same trait expressed in different environments (Falconer 1952; Dickerson 1962; Yamada 1962). Via and Lande (1985) postulated that the covariance of the same trait expressed in two environments is due to pleiotropy and the genetic correlation gives an estimate of the extent that the same alleles act in the same way in different environments. It is usually neglected that there might also be an influence on the genetic correlations between different traits in different environments. For illustration purposes, assume A and B to be correlated traits in one environment. A_1 and A_2 are correlated expressions of the same trait in environments 1 and 2, with a genetic correlation < 1. If this deviation from 1 is caused through the same alleles acting in different ways in different environments, it could be assumed that the correlation between B_1 and A_2 or A_1 and B_2 would be affected as well and the genetic correlations could deviate from what is found within a given environment.

A study on Western Australian Merino sheep investigated the genetic relationships between clean fleece weight (CFW), fibre diameter (FD), staple strength (SS) and coefficient of variation of fibre diameter (CVFD) expressed at different times of shearing (autumn (a) and spring (s)) (Greeff 2000). It was found that the genetic correlations between the same traits expressed at autumn and spring shearing were not significantly different from one. Therefore, it was concluded that genetically they are the same traits. However, the genetic correlations between staple strength and the coefficient of variation of fibre diameter was different within and across different times of shearing, e.g. aSS vs

aCVFD showed a genetic correlation of r_G = -0.30, whereas the genetic correlation for aSS vs sCVFD was r_G = -0.59. This might indicate that either the genetic basis is different for the expression of different traits in different environments and / or that the same alleles act differently under different environmental conditions.

The aim of this study was to determine effects of GxE interaction between different traits expressed in different environments.

MATERIAL AND METHODS

The project. The data for this study were collected on hoggets within the Wool Tenderness Project (MacLeod *et. al.* 1990). Agriculture Western Australia at Katanning, WA conducted the project from 1984 to 1991. Two management groups were established each with 320 Collinsville ewes, which were mated to Collinsville, Bungaree and Peppin rams. One group was run under a high level of nutrition ("high nutrition group", 1490 records) whereas the other group was managed at a lower nutrition level ("low nutrition group", 1395 records). The analysed traits comprised body weight at approximately 1.5 years of age (BWT), clean fleece weight (CFW), SL (staple length), SS (staple strength), fibre diameter (FD) and coefficient of variation of fibre diameter (CVFD).

Statistical analysis. The existence of a genotype x environment interactions in Merino sheep subjected to different feeding levels was investigated using Falconer's (1952) approach. Different traits expressed in two different environments were treated as two genetically correlated traits. If the correlation (r_G) is below unity, this indicates an effect of GxE interaction. Details about the data preparation and the model that was used in the analysis were described by Dominik *et. al.* (1999). Testing of fixed effects, estimation of variance components and the calculation of correlations was performed using bivariate analysis of an animal model. Genetic and phenotypic correlations were calculated between different traits within flocks (e.g. between clean fleece weight and fibre diameter within the high nutrition group). Furthermore, the genetic correlations between different traits in different environments (e.g. between clean fleece weight expressed in the high nutrition group and fibre diameter in the low nutrition group and vice versa) were calculated to investigate the effect of genotype x environment interaction on them.

RESULTS AND DISCUSSION

The genetic (r_G) and phenotypic (r_P) correlations for the traits within nutrition group can be seen in Tables 1 and 2. Table 3 presents the genetic correlations between different traits across environments.

The phenotypic correlations for the traits within the high and low nutrition group (italic – Table 1 and Table 2) were similar. The strongest phenotypic relationship was found for SS and CVFD expressed within the high (r_P = -0.43) and the low nutrition group (r_P = -0.41) respectively. The weakest for CFW and CVFD with r_P = -0.05 in both groups.

A comparison of the genetic correlations between different traits within the two groups (lower triangle - Table 1 and Table 2) showed that the estimates were not significantly different from each

other, assuming no error covariance between estimates, because some had moderate standard errors associated with them.

Table 1. Genetic (below diagonal) and phenotypic (above diagonal – italic) correlations with standard error (in brackets) for the high (h) nutrition group

	lCFW	lFD	lSS	lCVFD	lSL	lBWT
hCFW	1	*0.27*	*0.13*	*-0.05*	*0.36*	*0.39*
		(0.03)	*(0.03)*	*(0.03)*	*(0.03)*	*(0.03)*
hFD	0.29	1	*0.26*	*-0.16*	*0.25*	*0.28*
	(0.12)		*(0.03)*	*(0.03)*	*(0.03)*	*(0.03)*
hSS	0.23	0.40	1	*-0.43*	*-0.13*	*0.07*
	(0.15)	(0.11)		*(0.03)*	*(0.03)*	*(0.03)*
hCVFD	0.11	-0.18	-0.71	1	*-0.17*	*-0.07*
	(0.13)	(0.10)	(0.08)		*(0.03)*	*(0.03)*
hSL	0.31	0.33	0.35	-0.11	1	*0.13*
	(0.13)	(0.10)	(0.12)	(0.11)		*(0.03)*
hBWT	0.48	0.45	0.16	0.09	-0.05	1
	(0.13)	(0.12)	(0.15)	(0.12)	(0.13)	

Table 2. Genetic (below diagonal) and phenotypic (above diagonal – italic) correlations with standard error (in brackets) for the low (l) nutrition group

	lCFW	lFD	lSS	lCVFD	lSL	lBWT
lCFW	1	*0.26*	*0.07*	*-0.05*	*0.37*	*0.36*
		(0.03)	*(0.03)*	*(0.03)*	*(0.03)*	*(0.03)*
lFD	0.44	1	*0.19*	*-0.12*	*0.25*	*0.21*
	(0.12)		*(0.03)*	*(0.03)*	*(0.03)*	*(0.03)*
lSS	0.16	0.31	1	*-0.41*	*0.11*	*0.10*
	(0.16)	(0.12)		*(0.03)*	*(0.03)*	*(0.04)*
lCVFD	-0.07	-0.01	-0.72	1	*-0.18*	*-0.12*
	(0.14)	(0.11)	(0.08)		*(0.03)*	*(0.04)*
lSL	0.44	0.14	0.26	-0.25	1	*0.14*
	(0.12)	(0.11)	(0.13)	(0.11)		*(0.04)*
lBWT	0.18	0.36	0.27	-0.13	0.04	1
	(0.14)	(0.10)	(0.13)	(0.11)	(0.12)	

The genetic correlations between different traits across different environments (Table 3) were associated with high standard errors. Even though the estimates were different between reciprocal correlations (e.g. r_G (lCFW-hSS) = -0.38 vs. r_G (lSS - hCFW) = -0.18), they were mostly not significantly different from each other when the standard errors were taken into account, and assuming no error covariance between estimates. Significant differences were found in the correlations r_G (lSS-hFD) and r_G (lBWT-hFD) and their corresponding correlations for opposite environments.

Table 3. Genetic correlations with standard error (in brackets) between traits of the high (h) and low (l) nutrition group

	lCFW	lFD	lSS	lCVFD	lSL	lBWT
hCFW		0.15	-0.38	0.31	0.37	0.62
		(0.22)	(0.22)	(0.22)	(0.20)	(0.12)
hFD	0.19		-0.05	0.08	0.16	0.84
	(0.22)		(0.21)	(0.19)	(0.19)	(0.10)
hSS	-0.18	0.39		-0.74	0.17	0.29
	(0.24)	(0.19)		(0.14)	(0.21)	(0.21)
hCVFD	0.001	-0.08	-0.70		-0.16	-0.06
	(0.22)	(0.19)	(0.14)		(0.19)	(0.20)
hSL	0.41	0.34	0.03	-0.19		0.48
	(0.21)	(0.18)	(0.23)	(0.19)		(0.17)
hBWT	0.55	0.47	-0.10	0.20	0.15	
	(0.20)	(0.18)	(0.24)	(0.20)	(0.22)	

In comparison to the genetic correlations that were estimated within groups (Table 1 and 2), the genetic correlations for the trait expressions across environments (Table 3) yielded somewhat different estimates. However, they were not significantly different from each other. It is difficult to draw conclusions about the effect of GxE interaction on the expression of different traits in different environments. Only the estimates and the standard errors were available to determine the significance of the results. However, the statistical significance of the differences between the estimates can be expected to be greater than the results imply, because the error covariance is unknown. The findings of Greeff (2000) suggest different genetic relationships between different traits across environments. This can be confirmed in the current study. The results in this study suggest that different traits expressed in different environments are influenced through GxE interaction, which manifests itself in different genetic correlations. However, the number of progeny per sire in the two environments was not large enough to give significant results.

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