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GENETIC PARAMETERS FOR FAECAL WORM EGG COUNT AND OBJECTIVELY MEASURED WOOL TRAITS IN SOUTH AFRICAN MERINOS

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SUMMARY

Genetic parameter estimates for faecal worm egg count (FEC) and objectively measured wool traits were assessed, using data of Merino sheep from a selection experiment (four lines - a line selected for clean fleece weight, a fine wool line, an unselected control line and a line selected against rearing failure) maintained at the Tygerhoek research farm. Data consisted of between 3842 and 6822 (depending on the trait) records of animals born between 1989 and 2010. Rectal faecal samples were taken from individual sheep at 13 to 16 months of age after drenching was withheld for at least 10 weeks, generally in July to September. Nematode eggs were counted using McMaster technique, with a sensitivity of 100 eggs per gram of wet faeces. The heritability of FEC amounted to 0.16 after the data (with 100 added to account for zero counts) were transformed to logarithms to the power of 10. The genetic relationships of FEC with wool traits were favourable. Selection for a reduced FEC is unlikely to result in unfavourable correlated responses to wool traits in South African Merinos, in fact staple strength and the coefficient of variation of fibre diameter will benefit from it.

INTRODUCTION

Internal parasite infestations cost South African sheep producers hundreds of millions of rand each year arising from treatment costs, increased level of management and vigilance, a loss of production and even mortality in severe cases (Nieuwoudt *et al.* 2002). Resistance of gastro-intestinal parasites to anthelmintics has become more prevalent over the recent years to the stage that it has been described as rampant (Bath and Van Wyk 2009). In addition, consumers increasingly demand animal products that are free from contamination of chemicals (Khusro *et al.* 2004). Integrated parasite control measures (Nieuwoudt *et al.* 2002) may contribute to reduce the parasite burden in a variety of small ruminants. Several international authors reviewed genetic parameters for resistance to nematodes in sheep (Safari *et al.* 2005; Morris 2011). However, previous studies in South Africa is limited to those of Nieuwoudt *et al.* (2002), Cloete *et al.* (2007), as well as the work on the FAMACHA® system by Riley and Van Wyk (2009), The evidence of successful Australian (Woolaston and Piper 1996; Greeff *et al.* 2006) and New Zealand (Morris *et al.* 2005) breeding programs for resistance and resilience (Morris *et al.* 2010) to nematode infestation may also confer economic advantages in South African sheep. The objectives of this study were to estimate the (co)variance components and ratios as well as the genetic, phenotypic and environmental correlations between FEC and objectively measured wool traits in South African Merinos.

MATERIAL AND METHODS

Performance records were obtained from four lines (a line selected for clean fleece weight, a fine wool line, an unselected control line and a line selected against rearing failure) of Merino sheep maintained on the Tygerhoek experimental farm of the Western Cape Department of Agriculture, near Riviersonderend in the Western Cape Province of South Africa. Progeny born between 1989 and 2010 were used, with a pedigree from 1969 to 2010. The data included between 3842 and 6822 (depending on the trait; Table 1) records, the progeny of 554 sires and 2483 dams. The origin and initial selection in the flock were described by Heydenrych (1975). There was no selection for a reduction of FEC in any of the lines, and line effects were thus not considered. Flock maintenance, husbandry, experimental design and sampling procedures for FEC are described by Cloete *et al.* (2007). Rectal faeces samples were obtained under natural challenge from 1995 to 2010 (with the exception of 2004 when FEC data were not collected) from individual animals between the ages of 13 to 16 months. This was conducted after drenching was withheld for at least 10 weeks, generally in July to September. The pathogens present during this time of the year at Tygerhoek farm are *Teladorsagia*, *Nematodirus* and *Trichostrongylus* spp (Reinecke, 1994). Individual faecal samples were assessed for FEC using the McMaster technique, with a sensitivity of 100 eggs per gram of wet faeces (Cloete *et al.* 2007). Mean (±s.d.) untransformed FEC amounted to 694±1232, clearly showing a non-normal distribution. Transformation to logarithms, as described below, resulted in a data set with a normal distribution for the analysis of FEC.

Traits included in the analyses were thus the logarithm to the power of 10 of FEC (after 100 were added to account for zero counts; hereafter referred to as FEC), clean fleece weight (CFW), clean scoured yield percentage, (CY), fibre diameter (FD), staple length (SL), staple strength (SS) and coefficient of variation of FD (CVFD). Greasy fleece weight (GFW) was recorded at shearing in August-September each year after a wool growth period of approximately one year. Information on GFW was combined with CY data to derive CFW. Measures of wool quality were determined on a midrib wool sample taken from each animal at 14-16-months of age. It is conceded that heterogeneous variances between years may affect the outcome of the analyses on FEC, but these effects were adequately dealt with by the transformation.

Data of animals with information on pedigree, sex (male or female) dam age (2-6 years) and birth status (single or multiple) were included The statistical analysis was conducted using ASREML (Gilmour *et al.* 2009). The significance of fixed effects of sex, year of birth, birth type, selection line, dam age in years and sex*birth year interaction was tested leaving only significant effects in the final model. The best random effects models involving direct and maternal genetic variances, the correlation between direct and maternal effects, as well as maternal permanent environmental variances were tested for significance with ASREML, using log likelihood ratios derived from single-trait analysis on all traits. Variance component and heritability estimates were derived from single-trait animal models. The correlations were estimated by fitting a series of two-trait models, as it was impossible to include all traits in a single multi-trait model. Parameters stemming from the different models were all within a 0.02 range, and only two-trait analyses were reported.

RESULTS AND DISCUSSION

The fixed effects of birth type (single/multiple, $P<0.05$), sex (male/female), year of birth (1989-2003, 2005-2010) and the sex*birth year interaction had a significant ($P<0.01$) effect on FEC. These results are consistent with those reported by Cloete *et al.* (2007) on the same Merino resource flock. A similar set of fixed effects for FEC, with the addition of selection line (1-4) and age of dam ($2\text{-}7^+$) significantly affected all objectively measured wool traits, and were included in the models used for subsequent analyses. Models with only the direct additive effect fitted the data best for FEC, CY, SL, SS and CVFD. Maternal effects in addition to direct additive effect were present in the FD analysis, while the covariance between animal effects as well as dam permanent environmental effect contributed to the variation of CFW. FEC was heritable in this investigation at 0.16 (Table 1). The h^2_a in this investigation for FEC is consistent with a value of 0.18 reported by Cloete *et al.* (2007) on the same Merinos, slightly lower than those of 0.19 to 0.23 reported by

Riley and Van Wyk (2009) and lower than the average value of 0.27 derived from a mixture of data sets from naturally and artificially challenged flocks in Australia (reviewed by Safari *et al.* 2005). Estimates of h^2_a for objective wool traits ranged from 0.21 for SS to 0.68 for CVFD. Estimates of maternal heritability amounted to 0.08 for CFW and to 0.04 for FD. The dam permanent environmental effect accounted for 0.04±0.02 of the total phenotypic variance for CFW. The correlation between direct and maternal effects was high and negative at -0.58±0.08 for CFW

Table 1 Descriptive statistics for the data from the Tygerhoek Merino resource flock, also with appropriate direct and maternal heritability estimates

Trait	**n**	**Mean**	**SD**	**CV (%)**	**h^2 ± s.e**	**h^2_m ± s.e.**
FEC	5473	2.59	0.51	19.69	0.16±0.02	-
			Objective wool traits			
Clean fleece weight (kg)	6717	3.55	0.92	25.92	0.48±0.04	0.08±0.03
Clean yield (%)	6717	71.97	4.60	6.39	0.65±0.02	-
Staple length (mm)	6548	90.26	14.97	16.58	0.40±0.03	-
Staple strength (N/ktex)	3842	34.60	12.32	35.61	0.21±0.03	-
Fibre diameter (µm)	6822	19.33	1.99	10.29	0.66±0.04	0.04±0.01
CV of fibre diameter (%)	5683	19.62	2.84	14.48	0.68±0.03	-

n= number of records, SD=standard deviation and CV= coefficient of variation, FEC= log to the power of 10 transformed (FEC + 100), h^2_a= direct heritability, h^2_m= maternal heritability and se = standard error

Most of the correlations between FEC and objective wool traits were not significant (Table 2). The genetic correlation of FEC with CFW was unfavourable but did not reach a level of double the corresponding standard error. Animal model analyses by Pollott and Greef (2004) yielded an estimate of 0.13, which was in the same order of magnitude. The genetic relationships for FEC with CY, SL and FD were low to negligible. Pollott and Greeff (2004) accordingly reported genetic correlations of FEC that ranged from -0.02 to -0.05 for SL and from -0.03 to -0.08 with FD. Only staple strength and coefficient of variation of fibre diameter were significantly and favourably related to FEC on the genetic level. Similar findings were obtained previously on the current Merino resource flock (Cloete *et al.* 2007). The current genetic correlation of 0.33 between FEC and CVFD is higher than the values ranging from 0.06 to 0.13 reported for Australian Merinos (Greeff and Karlsson 1998). The negative, favourable genetic correlation of FEC with SS was comparatively high at -0.54 in the current study. Studies done on Australian Merinos yielded lower genetic correlation estimates, ranging from -0.05 to -0.17, depending on the model of analysis (Pollott and Greeff 2004). Cloete *et al.* (2007) also reported a similar genetic correlation estimate of -0.49 using a smaller data set of the current Merino flock. However, these results suggested that SS may be improved when animals are selected for a reduced FEC. Phenotypic and environmental correlations between wool traits and FEC were generally low and variable in sign.

CONCLUSIONS

The present study suggested that FEC is variable and heritable in South African Merinos, and that selection should result in additive gains in the ability of animals to resist natural nematode infestation. Selection for a reduced FEC is unlikely to result in unfavourable correlated responses in objectively measured wool traits in South African Merinos as suggested by low or negligible genetic relationships of most wool traits with FEC. The exceptions were favourable genetic correlations of FEC with SS and CVFD. Selection for resistance to nematode infestation may add to profitable sheep production in areas of Southern Africa with high levels of nematode challenge.

Table 2 Correlations (±s.e.) between log to the power of 10 transformed faecal worm egg count (FEC) and objectively measured wool traits in the Tygerhoek Merino flock

Trait	Genetic (r_g)	Environment (r_e)	Phenotypic(r_p)
Clean fleece weight	0.16±0.10	0.04±0.02	*0.06±0.02
Clean yield	0.05±0.07	-0.04±0.03	0.01±0.02
Staple length	-0.01±0.09	-0.01±0.03	-0.01±0.02
Staple strength	*-0.54±0.10	*0.08±0.03	*-0.04±0.02
Fibre diameter	-0.09±0.08	-0.00±0.03	-0.03±0.02
Coefficient of variation of fibre diameter	*0.33±0.07	*-0.06±0.03	*0.06±0.02

*** - significant (P<0.05) correlation**
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