

Genetic Relationships between Faecal Worm Egg Count and Production Traits in Merino Sheep of Uruguay

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Introduction

The existence of genetic variation among individuals for resistance to gastrointestinal parasites is well documented (e.g. Safari *et al.*, 2005; Morris 2009). The most commonly used selection criterion is the Faecal worm Egg Count (FEC), which have moderate heritability (Safari *et al.*, 2005). Estimates of genetic correlation between FEC and production traits (i.e. wool and growth) appear to vary with breed and country. Morris (2009) considered that breed is confounded with management, grazing conditions, parasite species involved in the parasitism, and with method of challenge. In general, New Zealand studies cited that FEC is genetically correlated unfavourably with lamb growth and with fleece weights (Morris 2009). In Australia, the Merino data reviewed by Safari *et al.* (2005) and Safari and Fogarty (2003) suggest no significant genetic correlations of FEC with fleece weight and diameter and favourable low correlations with lamb growth.

Some countries include the genetic evaluation of FEC in industry programs (e.g. WormFEC in New Zealand, Nemesis in Australia). Since 1995 to 2001, the evaluation of FEC was included in the Central Progeny Centres of the Merino Breed in Uruguay. In 1998, the Association of the Uruguayan Merino Breeders of Uruguay (SCMAU), the Uruguayan Wool Secretariat (SUL) and the National Agriculture Research Institute (INIA) start with the Fine Merino Project of Uruguay. This was the pioneer seed for the implementation of the Merino National Genetic Evaluation. In 2009, the 8th National Genetic Evaluation was performed (progeny 2008), including wool and growth data from 14 studs, 5 of them with FEC (not mandatory) data. The purpose of this study is to estimate the genetic correlation between FEC and the main production traits for the Merino in Uruguay.

Material and methods

Records and measurements. The *Asociación Rural del Uruguay* (ARU) provided pedigree information and SCMAU the performance data recorded at stud level. FEC were recorded after weaning in two independent natural challenges (in average at 8.7 and 10.9 month of age). In addition with FEC, six traits of economic importance for wool production were recorded: Greasy Fleece (GFW), Clean Fleece Weight (CFW), mean Fibre Diameter (FD), Staple Length (SL), Body Weight (BW) and Coefficient of Variation of Fibre Diameter (CVFD) (at 12.2 month of age in average). The data analyzed had been recorded during the

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period 1995-2009. Several quality controls on performance records were carried out in order to exclude logical inconsistencies and biological improbabilities. Unlinked flocks, animals with unknown sires, contemporary groups with less than three observations or with less than two sires, and trait values beyond three standard deviations of the contemporary group were deleted of the data set.

Statistical analyses: The faecal egg count (FEC) was adjusted through $\text{Log}_e(\text{FEC}+100)$ transformation, so as to normalize data. Heritabilities for the sixth productive traits and their genetic correlations with FEC were estimated with a bivariate analysis (FEC parameters were estimated with FD) with the model (1) for wool traits and (2) for FEC:

$$(1) y_{ijklm} = \text{CG}_i + \text{BT}_j + \text{DA}_k + \text{age}_m + a_l + e_{ijklm}$$

$$(2) y_{ijklm} = \text{CG}_i + \text{BT}_j + \text{DA}_k + \text{age}_m + a_l + \text{pe}_1 + e_{ijklm}$$

where:

y_{ijklm} ...m-th performance record of animal l,

CG_i ...fixed effect of the contemporary group i (flock-year-sex-management group),

BT_j ... fixed effect of birth type j (2 levels),

DA_k ... fixed effect of dam age k (4 levels),

age... age at m measurement of animal l as a co-variable,

a_l ...random additive genetic effect of animal l (15,828 animals),

pe_1 ...random permanent environmental effect of animal l (11,311 levels), and

e_{ijklm} ...random residual.

A Bayesian analysis was performed with the GIBBSF90 computer package (Misztal *et al.*, 2002). The number of iterations after burn-in used for posterior inferences was 360,000. The sampling interval was 40, so that a total of 9000 samples were kept to estimates features of posterior distributions. The posterior mean, median, standard deviation (PSD) and 95% highest posterior density interval (HPD) were calculated.

Correlated and Direct Response in FEC (CR_{FEC} , DR_{FEC}): The annual change in FEC resulting from genetic selection of each production trait or by the FEC itself was calculated with the formulas (Falconer and Mackay, 1996):

$$\text{CR}_{\text{FEC}} = i \mathbf{h}_X \mathbf{r}_A \sigma_{\text{A FEC}} / \mathbf{L}$$

$$\text{DR}_{\text{FEC}} = i \mathbf{h}_{\text{FEC}} (2/(1+r))^{0.5} \sigma_{\text{A FEC}} / \mathbf{L}$$

where: i is the selection intensity, \mathbf{h}_X and \mathbf{h}_{FEC} are the square root of heritabilities of the production trait and FEC, respectively, \mathbf{r}_A is the genetic correlation between traits, $\sigma_{\text{A FEC}}$ is the additive standard deviation of FEC, r is the repeatability of FEC, and \mathbf{L} is the generation interval. It was assumed i equal to 0.97 (proportion selected = 40%) and a \mathbf{L} of 3.1 years. The probability of increase, by correlated response, from an average of 500 to 600 and to 625 FEC in ten years of FD selection was calculated.

Results and discussion

A description of dataset utilized for the estimation is presented in Table 1. The results of the main statistics of marginal posterior distributions of genetic parameters are presented in Table 2. The FEC heritability is slightly lower than values reported by Safari and Fogarty (2003), but in this review only two papers included the permanent environmental effect (in Scottish Blackface breed) (i.e. Bishop *et al.* 1996, Bishop and Staeer 2001, cited by Safari and Fogarty, 2003). The magnitude of permanent effect cited by these authors is similar to our estimations. The back-transformed direct response to selection for resistance would be equivalent to a reduction from an average of 500 to 274 or from 1000 to 548 FEC in ten

years. According to Bishop (2009) the benefits from selection differ for disease data compared to productive data. In our case, the total benefits would be larger by improved performance due to decreased larval challenge (Bishop 2009).

Table 1. Descriptive statistics of Faecal Worm Egg Count, wool and live weight traits

Traits	N°	Mean	SD	Min	Max
FEC1	10994	1214.84	1915.34	0.00	36800
FEC2	9124	1293.48	1907.32	0.00	27400
Log _e (FEC1+100)	10994	6.61	1.07	4.61	10.52
Log _e (FEC2+100)	9124	6.69	1.07	4.61	10.22
GFW (kg)	10930	3.09	0.72	1.00	6.11
CFW(kg)	10848	2.34	0.55	0.78	4.60
FD (micron)	10978	17.24	1.85	12.60	24.90
BW (kg)	10933	36.21	9.56	15.00	73.74
SL (cm)	10454	8.14	1.57	3.50	13.50
CVFD (%)	8072	18.52	2.77	0.10	37.10

Table 2. Estimated statistics of marginal posterior distributions of genetic parameters (heritability, h^2 , permanent environmental effect, pe^2 , and genetic correlations, r_A) for Faecal Worm Egg Count, wool and live weight traits

Trait	Parameter	Mean	Median	PSD	95%HPD _L	95%HPD _U
Log _e (FEC+100)	h^2	0.183	0.182	0.017	0.151	0.216
	pe^2	0.108	0.109	0.016	0.077	0.139
	DR	-0.060	-0.060	0.006	-0.071	-0.050
GFW	h^2	0.447	0.447	0.030	0.390	0.508
	r_A FEC	0.027	0.027	0.033	-0.038	0.092
	CR	0.002	0.002	0.002	-0.003	0.007
CFW	h^2	0.459	0.459	0.030	0.398	0.517
	r_A FEC	0.062	0.061	0.033	-0.001	0.128
	CR	0.005	0.005	0.002	0.000	0.010
FD	h^2	0.732	0.732	0.023	0.689	0.776
	r_A FEC	-0.177	-0.176	0.026	-0.230	-0.128
	CR	0.017	0.017	0.002	0.012	0.022
BW	h^2	0.487	0.487	0.027	0.433	0.538
	r_A FEC	-0.143	-0.142	0.030	-0.200	-0.081
	CR	-0.011	-0.011	0.002	-0.016	-0.007
SL	h^2	0.440	0.440	0.028	0.386	0.497
	r_A FEC	-0.101	-0.101	0.033	-0.163	-0.033
	CR	-0.008	-0.008	0.003	-0.013	-0.003
CVFD	h^2	0.541	0.542	0.034	0.474	0.607
	r_A FEC	0.037	0.037	0.033	-0.029	0.101
	CR	0.003	0.003	0.003	-0.002	0.009

PSD: posterior standard deviation; 95%HPD: 95% highest posterior density interval Lower (L) -Upper (U) bound; CR, DR: Correlated and Direct response in FEC.

Posterior marginal means and medians of heritabilities for the production traits (GFW, CFW, SL, BW and CVFD) are close to those reported in the literature (Fogarty, 1995; Safari *et al.*, 2005). Conversely, heritability estimates for FD was slightly higher than found by Fogarty (1995) and Safari *et al.* (2005) for wool breeds. All heritabilities were slightly higher than previous estimations (Ciappesoni *et al.*, 2006). The 95% Bayesian credibility region for the genetic correlations of FEC with GFW, CFW and CVFD included the zero value, and the probability of unfavourable correlation is 0.80, 0.97 and 0.13, respectively. The posterior mean correlations with BW and SL are negative (favourable) with a low magnitude. The posterior mean FD-FEC correlation was unfavourable (probability $<0=1$ and $<-0.5=0$) and with a higher magnitude than the reported by Safari *et al.* (2005) and Fogarty, (1995). The probabilities of an unfavourable change in FEC, caused by ten years of fibre diameter selection, from an average of 500 to 600 and to 625 were 0.31 and 0.02, respectively.

Conclusion

The resistance to gastrointestinal parasites measured as FEC presents a moderate heritability which shows that a relevant genetic progress can be achieved. In Uruguay in general, the Merino Stud Breeders put more emphasis on decreasing FD, with increasing BW and maintaining or increasing CFW. This fact, together with the unfavourable genetic correlation between FD and FEC would cause a decrease in the animal resistance to nematodes. Although the correlated unfavourable response is of low magnitude, it is predicted using quantitative genetic theory that ignores disease epidemiology. For this reason, the true total negative effect of FD selection on FEC could be greater than predicted. Therefore, it is recommendable to take into account the FEC EBV together with other production traits EBV in the moment of selection of breeding animal.

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