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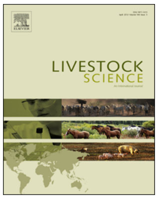

Estimates of genetic parameters for worm resistance, wool and growth traits in Merino sheep of Uruguay

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ABSTRACT

The genotype of an individual and the environment as the maternal ability of its dam have substantial effects on the phenotype expression of many production traits. The aim of the present study was to estimate the (co)variance components for worm resistance, wool and growth traits in Merino sheep, testing the importance of maternal effects and to determine the most appropriate model for each trait. The traits analyzed were Greasy Fleece Weight (GFW), Clean Fleece Weight (CFW), average Fibre Diameter (FD), Coefficient of Variation of FD (CVFD), Staple Length (SL), Comfort Factor (CF30), Weaning Weight (WWT), Yearling Body Weight (YWT) and Faecal worm Egg Count (FEC). The data were recorded during a 15-year period from 1995 to 2010, from Uruguayan Merino stud flocks. A Bayesian analysis was performed to estimate (co)variance components and genetic parameters. By ignoring or including maternal genetic or environmental effects, five different univariate models were fitted in order to determine the most effective for each trait. For CVFD and YWT, the model fitting the data best included direct additive effects as the only significant random source of variation. For GFW, CFW, FD, SL and CF30 the most appropriate model included direct-maternal covariance; while for FEC included maternal genetics effects with a zero direct-maternal covariance. The most suitable model for WWT included correlated maternal genetic plus maternal permanent environmental effects. The estimates of direct heritability were moderate to high and ranged from 0.15 for log transformed FEC to 0.74 for FD. Most of the direct additive genetic correlation (rg) estimations were in the expected range for Merino breed. However, the estimate of rg between FEC and FD was unfavourable (-0.18 ± 0.03). In conclusion, there is considerable genetic variation in the traits analyzed, indicating the potential to make genetic progress on these traits. This study showed that maternal effects are influencing most of traits analyzed, thus these effects should be considered in Uruguayan Merino breeding programs; since the implementation of an appropriate model of analysis is critical to obtain accurate estimates.

1. Introduction

In Uruguay, the Merino National Genetic Evaluation has been developed since 1995. Most of Merino Stud Breeders have as their principal selection objectives decreasing Fibre Diameter, maintaining or increasing Clean Fleece Weight and increasing Yearling Body Weight.

A multi-trait genetic evaluation requires accurate estimates of genetic parameters. The precision of the estimation of (co)variance components can be essentially affected by two sources of bias: the choice of the genetic model to analyze data and data structure (Clément et al., 2001). Regarding the first point, the genotype of the individual and the maternal nurturing provided by its dam (the milk supply and the maternal care she provides) have substantial

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effects on growth in young animals (Lewis and Beatson, 1999). When traits are governed by both direct and maternal effects, fitting only direct effects leads to an overestimation of direct heritability, being sometimes more than double (Clément et al., 2001). With sufficiently large data sets, ewe's relatively prolific and ancestral relationships sufficient to link grandparent–offspring performance, complex maternal-effect models can be reliably fitted (Lewis and Beatson, 1999). The relative part of direct and maternal effects (genetic or environmental) and the nature and magnitude of the relationship between these effects are determining conditions for the effectiveness of a selection scheme (Clément et al., 2001).

Moreover, the absence of connectedness and poor genealogical information are also responsible for biases and loss of accuracy in the prediction of genetic values by an animal or sire model (Hanocq et al., 1996). Maniatis and Pollott (2003) suggested that both the number of progeny per dam and the proportion of mothers with recorded performance considerably influence the parameter estimates. With a small size of progeny group per dam and limited information from recorded dams, the direct-maternal correlation had the highest (negative) value (Maniatis and Pollott, 2003). Besides this, it has been shown that estimates of (co)variance components are subject to large sampling variances and high sampling correlations, even for a “reduced” model ignoring dominance effects and family structures, providing numerous types of (co)variances between relatives which have been specifically designed for the estimation of the maternal effects (Meyer, 1992).

The aim of the present study was to estimate (co)variance components for worm resistance, wool and growth traits in Merino sheep, testing the importance of maternal effects and determining the most appropriate model for each trait. Direct additive correlations between all traits were estimated based on the selected model.

2. Material and methods

2.1. Data and traits

The data were recorded during a 15-year period from 1995 to 2010, from Uruguayan Merino studs flocks, which integrate the National Genetic Evaluation for sheep. The Rural Association of Uruguay (ARU) provided pedigree information and the Uruguayan Stud Merino Breeders Society (SCMAU) the performance data. The analyzed traits were grouped in

- Wool traits: Greasy Fleece Weight (GFW), Clean Fleece Weight (CFW), average Fibre Diameter (FD), Coefficient of Variation of Fibre Diameter (CVFD), Staple Length (SL) and Comfort Factor 30 (CF30) (percentage of fibres lower than 30 μm). These traits were recorded at first shearing, that was on average, at 12.5 months of age.
- Growth traits: Weaning Weight (WWT) measured on average at 4.2 months of age and Yearling Body Weight (YWT) recorded at first shearing.
- Worm resistance: measured as Faecal worm Egg Count (FEC). Animals were recorded on average at 9.5 and 11.6 months of age (for FEC1 and FEC2, respectively) under natural mixed-species challenge, according to the protocol to evaluate the genetic resistance to gastrointestinal parasites in Uruguay (Goldberg et al., 2011). The genetic evaluation is performed by a repeatability animal model and the genetic merit is published as FEC estimated breeding value (Ciappesoni et al., 2010).

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 observations with more than three standard deviations outside the mean of the contemporary group, were deleted of the data set. An unlinked flock is one which has not been sharing a common ram with another flock, or which has less than 20 lambs registered to a common sire. Summary statistics and data structure for all the traits analyzed are presented in Table 1.

2.2. Models

Faecal egg counts were transformed to $\log_e(\mathrm{FEC}+100)$ (log FEC) to produce approximately normally distributed data.

The variance and covariance components for the random effects of each trait were estimated fitting a univariate animal model using the Bayesian method. Direct additive correlations between all traits were estimated with a bivariate analysis using the most appropriate model for each trait (see below). Bayesian methods have the advantage of obtaining the posterior standard deviation (PSD) and the 95% credibility interval for the (co)variances estimates and their ratios (e.g. heritability). The analysis was performed with the GIBBS2F90 computer package (Misztal et al., 2002). For all traits, after preliminary analysis, it was decided to run a single chain of 600,000 iterations. The first 200,000 iterations were discarded and the sampling interval was 30, so that a total of 13,334 samples were kept to estimate features of posterior distributions. The posterior mean, the PSD, highest posterior density interval at 95% (95%HPD) and effective sample size (ESS) of the estimated marginal posterior distribution were calculated.

The full model was defined as

$$y = Xb + Z_1 a + Z_2 c + Z_3 m + Z_4 mc + e$$

where y is the record of the animal, b, a, c, m, mc and e are the vectors of the systematic effects, direct genetic effects, permanent animal environmental effects, maternal genetic effects, permanent maternal environmental effects and random residual effects, respectively; and X, Z_1, Z_2, Z_3 and Z_4 are the incidence matrices relating the respective effects to y.

The variance and covariance structure for the random effects are $\mathrm{var}(a)=A\sigma_a^2$; $\mathrm{var}(m)=A\sigma_m^2$; $\mathrm{var}(c)=I\sigma_{mc}^2$; $\mathrm{var}(mc)=I_m\sigma_{mc}^2$; $\mathrm{var}(e)=I\sigma_e^2$; $\mathrm{cov}(a,m)=A\sigma_{am}$; where A is the numerator relationship matrix, I and I_m are the identity matrices for individuals and dams, respectively; σ_a^2, σ_m^2, σ_c^2, σ_{mc}^2 and σ_e^2, are the direct additive genetic, maternal additive genetic, permanent animal environmental, maternal permanent environmental and residual variances, respectively; and σ_{am} is the direct-maternal covariance.