ADDITIVE MUTATIONAL VARIANCE FOR LITTER SIZE IN THE RIPOLLESA SHEEP BREED

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INTRODUCTION

During the last decades, the importance of new mutations on polygenic variability has been revealed in several experimental species. Nevertheless, little is known about mutational variability in livestock where only a few mutations with large effects have been reported.

OBJECTIVE

The main objective of the present work is to characterize the magnitude of the polygenic additive mutational variability for litter size in the Ripollesa sheep breed.

MATERIALS AND METHODS

Data Collection

- **1,765 litter size records (404 ewes).**
  - 1.49 ± 0.01 lambs per litter (53.8% single; 44.1% twins; 1.9% triplets; 0.2% quadruplets).
  - Records from years 1986 to 2008.
- **Pedigree.**
  - 22 rams (1 to 26 daughters with data), 541 ewes.
  - 98 founders (17.4%).
- **Ewes managed under standard semi-intensive farm conditions.**

Statistical Analysis

Bivariate (single *vs*. multiple lambing) threshold animal model

Liabilities (**u**) for litter size were modeled as:

$$\mathbf{u} = \mathbf{Xb} + \mathbf{Z}_1\mathbf{p} + \mathbf{Z}_2\mathbf{a} + \mathbf{Z}_2\mathbf{m} + \mathbf{e}$$

Where:

- **b** accounted for the systematic effects of parturition number and year of lambing.
- **p** was the permanent environmental effect of each ewe.
- **a** and **m** were the founder-related and mutational additive genetic effects, respectively.
- **X**, $\mathbf{Z}_1$ and $\mathbf{Z}_2$ were incidence matrices and **e** was the vector of residuals.
- **m** was modeled as $N(\mathbf{0},\mathbf{M}\sigma_m^2)$ were **M** was the mutational relationship matrix as defined by CASELLAS & MEDRANO (2008; Genetics 179:2147-2155).

This model was implemented under a standard Bayesian approach with 500,000 iterations.

RESULTS

The modal estimate for the mutational variance was 0.013 (0.007 to 0.044) and provided a mutational heritability of 0.9%. These value fell within the range of mutational heritabilities reported in experimental species.

Despite the small mutational variability, the model including mutational effects was clearly preferable when comparing with a competing model excluding the $\mathbf{Z}_2\mathbf{m}$ term (-5.3 deviance information criterion units). The genetic merit order for litter size suffered from moderate rearrangements between both models (Figure 1).

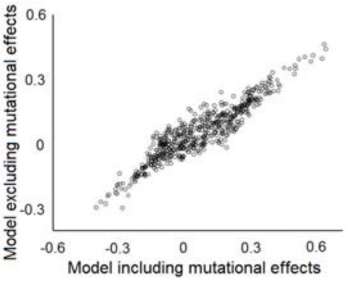

Figure 1. Plot of average estimates for predicted breeding values under models accounting for and excluding mutational effects.

CONCLUSIONS

A continuous uploading of new additive mutations was revealed for litter size in the Ripollesa ewe.

The mutational variance was small although moderately rearranged the genetic merit ranking.

Further studies are required to elucidate the relevance of polygenic mutations in livestock and current breeding programs.