PRELIMINARY RESULTS IN A DIVERGENT SELECTION EXPERIMENT ON VARIANCE OF LITTER SIZE IN RABBITS. I. GENETIC PARAMETERS

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ABSTRACT

Data from a single generation divergent selection experiment for the phenotypic variance of litter size in rabbits were analysed to estimate genetic parameters on the environmental variance of litter size using a model which postulates that environmental variance is partly under genetic control. Selection was based on the phenotypic variance of litter size for each doe after correcting litter size for the fixed effects of year-season and lactation status. Selection pressure on does was approximately 30% in each line. Males were chosen within sire families in order to avoid the increase in inbreeding. The total number of records for litter size was 1929. The posterior mean of additive variance at the variance level was 0.12 and the highest posterior interval at 95% did not include zero. The estimated genetic correlation between the additive genetic effects on the mean and those on the variance was -0.74 with a posterior interval far away from zero. The first preliminary results of this study support the model postulating that environmental variation for litter size is partly under genetic control, and it would suggest that selection for environmental variance can be successful on both the mean and variance of litter size.

Keys words: Selection, Variance, Litter size, Bayesian methods.

INTRODUCTION

Over the last decade, breeding programmes in pigs and rabbits have emphasized selection pressure on litter size, a trait with low heritability. Besides, there is increasing awareness that homogeneity of litter size is an important factor of economic efficiency. Thus, a challenging selection goal would be to manipulate both the mean and environmental variance of litter size by selection. SanCristobal-Gaudy *et al.* (1998) proposed an infinitesimal model with a genetically structured environmental variance. Recently, Sorensen and Waagepetersen (2003), Gutiérrez *et al.* (2006) and Ibañez-Escriche *et al.* (2007) provided model testing evidence in support for this model using litter size data from pigs and mice, and uterine capacity in rabbits, respectively. Moreover, Garreau *et al.* (2004) showed a successful response to selection for homogeneity of litter weight at birth in rabbits.

The objective of this work is to estimate the genetic parameters of environmental variance of litter size in a divergent selection experiment on phenotypic variance of litter size in rabbits.

MATERIALS AND METHODS

Animals

The data originate from a divergent selection experiment on phenotypic variance of litter size. Animals were derived from a synthetic population of the experimental farm at the Universidad Miguel

Hernández de Elche. The females were first mated at 18 weeks of age and thereafter 10 days after parturition, producing an average of 2.5 parities per doe. Reproduction was organized in discrete generations and mating of close relatives was avoided to reduce inbreeding.

The criterion of selection was phenotypic variance of litter size for each doe after correcting litter size for the fixed effects of year-season and lactation status (PVc). The effect of year-season included seven levels and the effect of lactation status included three levels (nulliparous, lactating and nonlactating does with more than one parity). PVc within doe was calculated as $\frac{1}{n+1}\sum_{i=1}^{n}(e_i - \bar{e})^2$, where e is the phenotypic litter size after correcting for year-season and lactation status and n is the number of parities of each doe (n varying from 2 to 6). Selection pressure on does was approximately 30% in each line. Males were chosen within sire families in order to avoid inbreeding.

Data from the base generation and the first generation of selection were used in the analysis. The total number of records for litter size was 1929. The total of number of individuals included in the pedigree was 835. The number of does was 265 in the base population, 141 in High line and 128 in Low line.

Model Fitted

The model proposed by SanCristobal-Gaudy *et al.* (1998), which postulates that environmental variance is heterogeneous and partly under genetic control, was used to analyze litter size. The sampling model for the data is Gaussian:

$$\mathbf{y} \mid \mathbf{b}, \mathbf{a}, \mathbf{p}, \mathbf{b}^*, \mathbf{a}^*, \mathbf{p}^* \quad \sim \quad N\left(\boldsymbol{\mu}, diag\left(\left(\sigma_i^2\right)_{i=1}^{n}\right)\right),$$

Where y is the vector of data for litter size and $diag\left(\left(\sigma_i^2\right)_{i=1}^{n}\right)$ is the diagonal matrix with diagonal entries σ_i^2,

$\left(\log \sigma_i^2\right)_{i=1}^{2} = \mathbf{Xb}^* + \mathbf{Za}^* + \mathbf{Wp}^*$ and $\mu = \left(\mu\right)_{i=1}^{n} = \mathbf{Xb} + \mathbf{Za} + \mathbf{Wp}$

The vectors **b** and **b*** contain effects associated with year-season and lactation status. **X**, **Z** and **W** are known incidence matrices. Vectors **p** and **p*** contain permanent environmental effect for litter size and are assumed to have independent normal distributions

$\mathbf{p} \mid \sigma_p^2 \sim N\left(\mathbf{0}, \mathbf{I}\sigma_p^2\right)$

$\mathbf{p} \mid \sigma_{p*}^2 \sim N\left(\mathbf{0}, \mathbf{I}\sigma_{p*}^2\right)$

Vector (**a**$^\mathbf{T}$, **a**$^{*\mathbf{T}}$) contain normally distributed additive genetic effects

$$\begin{pmatrix} \mathbf{a} \\ \mathbf{a}^* \end{pmatrix} \Bigg| \quad \mathbf{G} \quad \sim \quad N\left(\begin{pmatrix} \mathbf{0} \\ \mathbf{0} \end{pmatrix}, \quad \mathbf{G} \quad \otimes \quad \mathbf{A}\right) \quad \text{Where} \quad \mathbf{G} = \begin{pmatrix} \sigma_a^2 & \rho\sigma_a\sigma_{a*} \\ \rho\sigma_a\sigma_{a*} & \sigma_{a*}^2 \end{pmatrix}$$

A is the additive relationship matrix, ρ is the genetic correlation coefficient between **a** and **a***, and $\left(\sigma_a^2, \sigma_{a*}^2\right)$ are additive genetic variances associated with the distribution of (**a**, **a***). Briefly, a priori, **b**, **b*** were assigned normal distributions with zero mean vector and diagonal matrix with very large diagonal elements. The variance parameters σ_a^2, σ_{a*}^2, σ_p^2, σ_{p*}^2 were assigned scaled inverted chi-squared distributions ($\nu = 4$ and $S = 0.45$) and ρ was assigned a uniform prior bounded between -1 and 1. The implementation was based on the MCMC (Markov chain Monte Carlo) algorithm proposed by Sorensen and Waagepetersen (2003).

The results reported from each model are based on MCMC runs consisting of 1,000,000 iterations. Convergence was tested using the Z criterion of Geweke (Sorensen and Gianola, 2002) and Monte Carlo sampling errors were computed using time-series procedures described in Geyer (1992).

RESULTS AND DISCUSSION

Table 1 shows Monte Carlo estimates of posterior means and of 95% highest density posterior intervals for variance components derived from the Model. The permanent environmental variance σ_p^2 is a little higher than the additive variance σ_a^2. However, the posterior means for σ_{a*}^2 and σ_{p*}^2 were similar and their 95% highest posterior intervals did not include the zero. The posterior mean of the correlation coefficient was -0.75; the Monte Carlo estimate of the 95% highest posterior density interval indicates that the support of the posterior distribution is shifted a long way from zero.

The posterior additive variance at level of the variance σ_{a*}^2 achieved from this model would indicate a genetic control on the environmental variance, therefore the variance of litter size could be manipulated by means of selection. Moreover, the variability can be depending of resistant diseases, witch is partly controlled by genes. Thus, the negative correlation coefficient obtained would indicate that does with higher values of additive genes for litter size would be more resistant to diseases and as a consequence with less variability.

The negative correlation obtained is in perfect agreement with the results of Ibañez-Escriche *et al.* (2007) for uterine capacity in does, Sorensen and Waagepetersen (2003) for litter size in pig, Gutiérrez *et al*. (2006) for litter size in mice and Ibáñez-Escriche *et al*. (2008) for weight gain in mice. Furthermore, Ibáñez-Escriche *et al*. (2008) found sings of correlated response on the coefficient of variation for weight gain in mice. However, these changes on the environmental variance depend on the functional relationship between mean and variance (Ros *et al.*, 2004). In these studies, the model postulates a linear stochastic relationship between mean and log-variance, and incorrect choice of functional relationship could give the wrong results for the genetic correlation between mean and log environmental variance.

Table 1: Monte Carlo estimates of posterior means and of 95% highest posterior density intervals (HPD95%) of variance components. $\sigma_a^2 \left(\sigma_{a*}^2 \right)$: additive variance at the level of the mean (variance); $\sigma_p^2 \left(\sigma_{p*}^2 \right)$: permanent environmental variance at the level of the mean (variance); ρ: genetic correlation

	σ_a^2	σ_{a*}^2	P	σ_p^2	σ_{p*}^2
Posterior Mean	0.77	0.12	-0.75	1.08	0.11
HPD$_{95\%}$	0.17 , 1.46	0.06 , 0.18	-0.36 , -0.99	0.37 , 1.66	0.06 , 0.17
k*	0.29	0.07	-0.37	0.52	0.07

* Limit of the interval [k, +∞) containing a probability of 95% for variance parameters, ρ [k, -1) limit of interval

CONCLUSIONS

The first preliminary results of this study support the model postulating that environmental variation for litter size is partly under genetic control, and its would suggest that the selection for environmental variance has been successful on both, the mean and variance of litter size.

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