Study of canalization in
an experiment of divergent selection for uterine capacity in rabbits

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Background

One of the most important traits in domestic prolific species is litter size. In recent years, homogeneity of litter size has become important, because it may influence economic efficiency. Here, we report the results of a 10 generation divergent selection experiment for uterine capacity in rabbits carried out at the Universidad Politécnica de Valencia.

Objectives

The objectives are first, to evaluate the response to selection for uterine capacity with two models: the classical infinitesimal model (additive genetic model with homogeneous environmental variance) and an additive genetic model with heterogeneous environmental variance. Secondly, to investigate whether it is reasonable to postulate that environmental variation is genetically regulated and whether these these genes are correlated with those affecting mean uterine capacity.

Material and Methods

Data

The data originate from a ten generation divergent selection experiment for uterine capacity in rabbits. In each selection line, there were approximately 40 female and 12 male parents each generation. Uterine capacity was defined as litter size of unilateral ovariectomized does.

Models Fitted and Implementation.

The following two models were fitted:

Model 1 is an additive genetic repeatability model. This was the model used during the selection stage of the experiment.

Model 2 postulates that the environmental variance is partly under genetic control. It assumes that, conditionally on vectors of location and dispersion parameters, the vector of phenotypes $y=(y_i)^n_{i=1}$ is Gaussian:

$$y|\ b, a, p, b^*, a^*, p^* \sim N(\mu, diag((\sigma^2_i)^n_{i=1}))$$

where $diag((\sigma^2_i)^n_{i=1})$ is a diagonal matrix with entries σ^2_i

$$\mu = Xb + Za + Wp \ \text{ and } (\log \sigma^2_i)^n_{i=1} = Xb^* + Za^* + Wp^*.$$

The vectors b and b^* contain effects associated with year-season (30 levels) and parity order (4 levels) and X, Z and W are known incidence matrices. The vectors p and p^* contain random permanent environmental effects (929 levels) and are assumed to be independent with

$$p \mid \sigma^2_p \sim N(0, \sigma^2_p),\ p^* \mid \sigma^2_{p*} \sim N(0, \sigma^2_{p*})$$

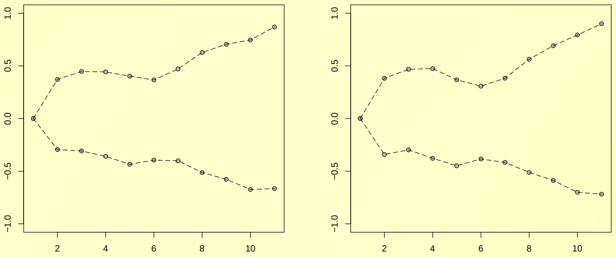
The genetic effects (a,a^*) *are assumed Gaussian*

$$\begin{pmatrix} a \\ a* \end{pmatrix} | G \ \ N\left(\begin{pmatrix} 0 \\ 0 \end{pmatrix}, G \otimes A\right), \ \text{where}$$

$$G = \left(\begin{bmatrix} \sigma^2_a & \rho\sigma_a\sigma_{a*} \\ \rho\sigma_a\sigma_{a*} & \sigma^2_{a*} \end{bmatrix}\right),$$

A is the additive genetic relationship matrix and ρ is the coefficient of genetic correlation. In our statistical analysis we use the Bayesian approach described in Sorensen & Waagepetersen (2003) where details about prior assumptions for b, $b*$, and the variance parameters σ^2_a, σ^2_{a*}, σ^2_p, σ^2_{a*} and ρ can be found. Posterior distributions are computed using the MCMC algorithm proposed by Sorensen & Waagepetersen (2003).

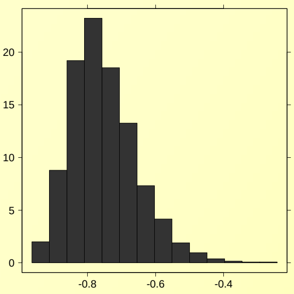
Results and Discussion



Estimated divergence in uterine capacity using Model 1 (left) and Model 2 (right)

Monte Carlo estimates of posterior means (first row for each model) and of 95% posterior intervals (second row for each model) of variance components for Models 1 and 2.

Model	σ^2_a	σ^2_p	ρ	σ^2_{a*}	σ^2_{p*}
1	0.59	0.51	-	-	-
	0.32;0.86	0.28;0.8	-	-	-
2	0.82	0.44	-0.74	0.16	0.12
	0.48;1.28	0.20;0.72	-0.90;0.52	0.10;0.25	0.07;0.18



Marginal posterior distribution of ρ (Model 2)

- ✓ Monte Carlo inferences for each model are based on a single chain of length 1,000,000 .
- ✓ For both models the estimated divergence after 10 generations of selection is symetrical.
- ✓ The 95% posterior interval of σ^2_{a*} provides evidence for the presence of genes affecting environmental variance .
- ✓ The correlation (ρ) is highly negative and the support of the posterior distribution is shifted away from zero.
- ✓ The models were compared using the deviance information criterion (DIC). The DIC for Models 1 and 2 are 7810 and 7720, respectively. This provides support for Model 2.

Conclusions

The inferred response from both models is similar.

The comparison based on DIC favours the model with a genetically structured environmental variance heterogeneity.

There is strong evidence of a negative correlation between the additive genetic values affecting mean uterine capacity and those affecting environmental variance.