

ESTIMATION OF GENETIC PARAMETERS AND GENETIC TRENDS FOR LITTER SIZE COMPONENTS USING BAYESIAN INFERENCE IN RABBITS

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INTRODUCTION

The heritability of litter size is low in rabbits and other prolific species. This is reflected in the low response to direct selection in closed populations (~0.1 rabbits per litter per generation) (Blasco, 1996). Selection on ovulation rate has been proposed as an alternative to improve litter size in pigs, but it has not produced a correlated response in litter size, suggesting uterine capacity as a limiting factor (Blasco *et al.*, 1993a). Blasco *et al.* (1994) proposed litter size in unilaterally ovariectomized does to evaluate uterine capacity.

Different techniques are used to estimate the genetic response. Least-squares with a control population and REML/BLUP procedures have been preferred. Response estimated by least-squares does not require the estimates of the genetic variance components, but has a higher variance. In REML/BLUP case, the sampling variance of the estimator of genetic response does not take into account the error of estimation of the variance components. A Bayesian solution to estimate selection response was proposed by Sorensen *et al.* (1994). The marginal posterior distribution of the response takes into account uncertainty about all other parameters of the genetic response. A multivariate Bayesian approach (Sorensen, 1996) was used to assess the response to selection for uterine capacity and litter size components in a divergent selection experiment for uterine capacity in rabbits.

MATERIAL AND METHODS

Animals. A divergent selection experiment on uterine capacity in rabbits was performed at the experimental farm of the Universidad Politécnica de Valencia. 80 does and 24 bucks from a synthetic line (V) selected for litter size, constituted the base generation. Unilateral ovariectomy was performed to remove the left ovary before puberty. The ovariectomized does (ULO does) were mated 10 days after farrowing. Selection was performed on litter size (i.e. uterine capacity), using a BLUP procedure under a repeatability animal model with generation and parity as fixed effects. Data included records up to fourth parity in most ULO does. Prior values ($h^2 = 0.10$ and $r = 0.15$) were estimated from the V population. The candidates, offspring of the ULO does, were selected on the average predicted breeding value of their parents for uterine capacity. Males were selected within sire families to avoid inbreeding. Each divergent line had approximately 40 females and 12 males per generation. The total number of records in both lines was 2997 during 10 cycles of selection.

Data. The following traits were analysed: ovulation rate (OR) evaluated as the number of corpora lutea, number of implanted embryos (IE) evaluated as the number of implantation sites, and uterine capacity (UC) evaluated as the litter size. All traits were measured on ULO does. OR and IE were measured by laparoscopy at day 12 of the second gestation, and UC was recorded over four parities.

Models and statistical inference. An animal model was used for OR and IE, and a repeatability animal model for UC. The repeatability animal model included environmental effects (what in a frequentist context are considered as “fixed effects”) of year-season with 30 levels (each class consisting of 3-month periods), lactation-parity with three levels (nulliparous does, pregnant and lactating does, pregnant and not lactating does), and common environment between parities (what in a frequentist context are considered as “permanent random effects”). The animal model included the same environmental effects but lactation-parity effect had only the two last levels because of OR and IE were recorded only in the second parity. *Data augmentation* approach was used (Tanner, 1996). The data vector was increased by generating the residuals for the missing data. The design matrices for OR and IE included rows with only zeroes for the augmented residuals in order to have the same dimensions in the three traits. Thus, the model for OR and IE was a repeatability animal model after data augmentation. Multivariate procedures are easier when the models for all traits have the same design matrices.

In a Bayesian analysis, inferences are based on marginal posterior distributions of the parameters. These are obtained from the joint posterior density of all unknowns by integrating out all nuisance parameters. All the full conditional posterior distributions of all the parameters of the model were derived and then the Gibbs sampler algorithm was used to estimate the marginal posterior distributions. The sampled breeding values in a particular round of the Gibbs sampling procedure were averaged according to the generation, line and trait in order to draw marginal inferences about response to selection. This average represented one sample from the marginal posterior density of the genetic mean. Exploratory analyses lead to run independent long chains of 800,000 iterations with a burn-in period of 200,000 and sampling interval of 60. The method of Johnson (1996), based on coupling chains, was used to assess convergence. The results presented here come from one of these chains.

RESULTS AND DISCUSSION

Genetic parameters. The estimated marginal posterior distributions of the genetic parameters are presented in figure 1. Often, the probability densities were not symmetric about their means; therefore, the values of the mean, mode and median were sometimes not similar. The marginal posterior distribution for the genetic correlation between OR and IE was highly asymmetric and its mode was very close to the parametric space border. This could have caused that, in preliminary analyses, REML algorithm did not reach convergence. Groeneveld (1994) stressed that, in situations where the true correlation between traits is expected to be high, the variance components proposed for the maximum of the likelihood lie often outside the parametric space.

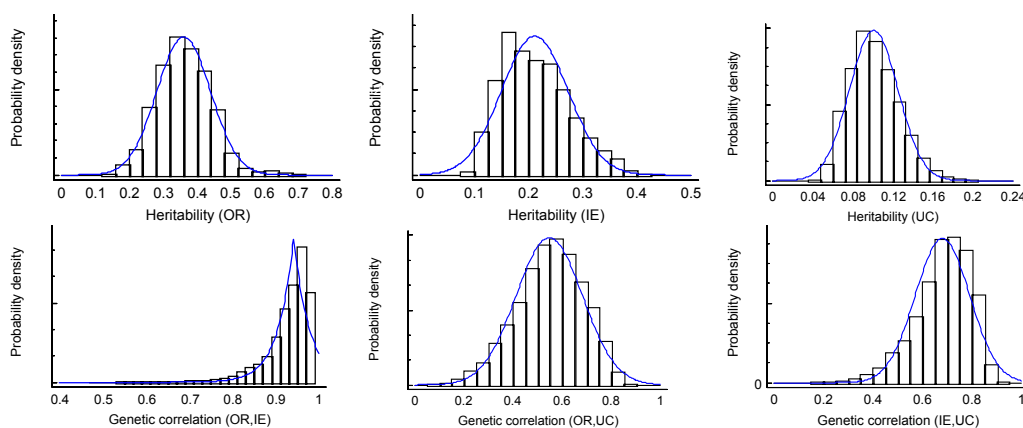


Figure 1. Marginal posterior distributions for the genetic parameters of OR (ovulation rate), IE (implanted embryos) and UC (uterine capacity)

Table 1 shows the means of the estimated marginal posterior distributions of the genetic parameters and residual correlations, with their highest posterior density regions at 95% (HPD_{95%}). In general, these intervals were not symmetric. Since the residual correlation between OR and UC was approximately equal to zero, the number ova were enough to overcrowd the uterine horn, and UC was expressed. The heritabilities for all traits are within of the ranges reported in the literature (see Blasco *et al.*, 1993a for a review). The heritability for OR was moderately high. The genetic correlation between OR and IE was very high. The remaining genetic correlations can be considered also relatively large. Genetic relationships between OR with IE and litter size, obtained by Blasco *et al.* (1993b) in intact does selected on litter size, seem to be lower (0.66 ± 0.22 and 0.36 ± 0.31 respectively). The relatively high genetic correlation between OR and UC and the heritability of OR indicate that selection on OR can be effective to improve UC in rabbits.

Table 1. Estimated marginal posterior means of the genetic parameters and residual correlations for OR (ovulation rate), IE (implanted embryos) and UC (uterine capacity) ^A

Traits	OR	IE	UC
OR	0.36 [0.16,0.53]	0.11 [-0.06,0.25]	-0.05 [-0.18,0.08]
IE	0.93 [0.79,0.99]	0.21 [0.10,0.36]	0.54 [0.45,0.62]
UC	0.55 [0.24,0.82]	0.68 [0.42,0.88]	0.10 [0.06,0.16]

^A Heritabilities (on the diagonal), genetic (below the diagonal) and residual correlations (above the diagonal) and HPD_{95%} in square brackets

Genetic trends. The selection on UC produced a slightly asymmetric response in favour of the high line with a final divergence of 1.45 young rabbits (Figure 2). The differences in UC between both lines were always positive, thus selection was successful. Around a half of this difference was observed in the first selection cycle, and the estimated response was not linear

until generation 6. The genetic trend of IE was close to the genetic trend of UC and produced a correlated divergence of 1.0 embryo. OR did not show a clear pattern but the divergence was 0.7 ova.

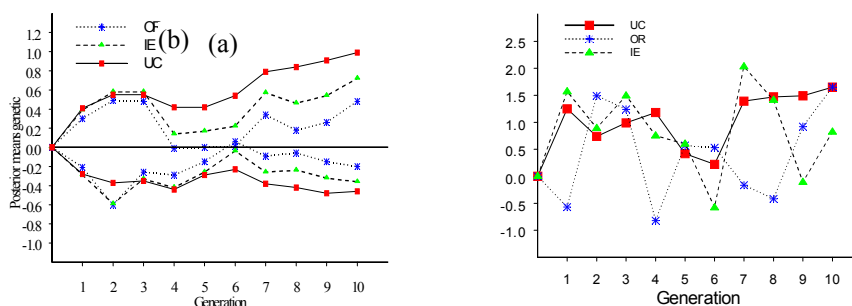


Figure 2. Genetic trends (a) and phenotypic differences (b) between both lines for OR (ovulation rate), IE (implanted embryos) and UC (uterine capacity)

CONCLUSION

Argente *et al.* (2000) showed that the genetic correlation between litter size in intact does and uterine capacity in ULO does of the same line was close to 1.0. Thus, the estimates of the genetic parameters in this population suggest that selection on ovulation rate can be effective to improve litter size, a result that seems to be different in pigs and mice. Uterine capacity differed around 1.4 young rabbits showing that the selection on UC was successful.

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