ESTIMATION OF CROSSBREEDING PARAMETERS FOR AVERAGE DAILY
GAIN, FEED INTAKE AND FEED CONVERSION RATE IN FIVE RABBIT LINES

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INTRODUCTION
Post weaning average daily gain (ADG), feed intake (FI) and feed conversion rate (FCR) are economically important traits in rabbit production (Armero and Blasco, 1992), but mainly the last one, not very well known due to the high cost of data gathering. In order to increase the performances of young rabbits, during the fattening period after weaning, different sire lines are undergone selection for growth rate or body weight (Estany et al., 1992; Rochambeau et al., 1996; Gómez et al., 2000) to provide males to commercial farms, for matting with crossbred females following the three way crossbreeding scheme.

Five sire and dam rabbit lines are undergoing selection in Universidad Politécnica de Valencia (UPV) and Institut de Recerca i Tecnologia Agroalimentàries (IRTA) in Barcelona. In order to improve knowledge about the genetic determination of ADG, FI and FCR, the estimation of the crossbreeding parameters in a diallel crossbreeding plan (5 x 5) between all of them was done and the results are presented here.

MATERIAL AND METHODS
Animals. The experiment concerned the offspring produced crossing animals from five lines: Dam lines A, V and P : selected since 1980, 1982 and 1992 respectively for litter size at weaning using a family index with variable information (Baselga et al., 1984) for the line A and a repeatability animal model with BLUP methodology (Estany et al., 1989; Gomez et al., 1996) for lines V and P. Sire lines R and C : selected for ADG during the fattening period by individual selection since 1980 and 1993 respectively (Estany et al., 1992; Gómez et al., 2000). Line C had been previously selected on litter weight at 60 days from 1983 to 1993.

At two months of life, animals were allocated in the experimental farm of IRTA. They were bred under the same conditions of commercial farms in Spain. Does followed a semi-intensive reproductive rhythm. The offspring were weaned, weighed, identified and then, moved to collective cages (8 kids per cage) at 32 days of age until the end of the fattening period (60 days of life). Most of the cages contained rabbits coming from different litters, parity and different genetic types. A commercial diet was given ad libitum (16.5 % crude protein, 15.8 % fiber, 4 % fat). Individual weights and collective feed consumption were weekly recorded. The collective feed conversion was recorded as the ratio between collective feed intake and collective weight gain. Data from 360/326/277 cages (2773/2504/2127 individuals) were included in the analysis of ADG, FI and FCR respectively.

Statistical model and inference. Traits were analyzed separately in a set of univariate analyses. An animal model was used including the effects of batch (31 levels), parity (first,
second and third or more), litter size (with 7 levels: less than 5, five levels from 5 to 10, more than 10), genetic type (25 levels), the average weaning weight of the cage as a covariate, the environmental common litter effects and, the additive genetic values of the animals. Data were assumed to be generated from a normal distribution with residual (co)variance matrix

\[ R = R_e \sigma^2_e \]

where \( \sigma^2_e \) is the unknown variance of random residuals, and \( R_e \) is a N x N diagonal matrix (with N equal to the number of cages) whose elements are \( 1/n_i \), being \( n_i \) the number of individuals in cage \( i \). The assigned prior distributions for environmental common litter effects, additive genetic values and random residuals were respectively 

\[ a \mid A, \sigma^2_a \sim N(0, A \sigma^2_a) \]

\[ c \mid \sigma^2_c \sim N(0, I \sigma^2_c) \]

\[ e \mid \sigma^2_e \sim N(0, R_e \sigma^2_e) \]

where \( A \) is the additive genetic relationship matrix, \( \theta \) is a vector of zeros, \( \sigma^2_a \) is the unknown additive genetic variance in the base population, \( \sigma^2_c \) is the unknown variance of common environmental litter effects, \( \sigma^2_e \) is the unknown variance of residuals and \( I \) is the identity matrix. Prior distributions for environmental effects, \( \sigma^2_a \), \( \sigma^2_c \) and \( \sigma^2_e \) were uniform to convey lack of information about these parameters. The estimated marginal posterior distributions were obtained from the joint posterior density of all unknowns by integrating out all nuisance parameters using the Gibbs sampler algorithm (Gelfand and Smith, 1990). Details about this technique and the development of the fully conditional posterior distributions needed for its implementation can be found in Sorensen et al. (1994).

Samples from the marginal posterior distribution of the crossbreeding parameters (heterosis, direct and maternal genetic effects) were obtained from the samples of the marginal posterior distribution of the genetic type effects following the Dickerson model (Dickerson, 1969).

After some exploratory analysis, the implementation of the Gibbs sampler was made using a single long chain of 100,000 iterations. The first 25,000 iterations (warm up) of each chain were discarded, and samples of the parameter of interest were saved each 5 iterations. Gibbs samples were used directly to estimate features of the marginal posterior distribution. The method of Raftery and Lewis (1992) was used to estimate the number of iterations to be discarded and the method of Geweke (1992) was used to assess convergence. The autocorrelation between samples, the Monte Carlo error and the effective chain size were calculated using methods described by Geyer (1992).

RESULTS AND DISCUSSION

Visual inspection of the sample trace plots and the low correlation between samples found, indicated good mixing during the simulation process and determined the low Monte Carlo standard errors found (less than 0.05 % of the mean).

Table 1 shows summary statistics of the estimated marginal posterior distributions of direct genetic effects for FI, ADG and FCR. Table 2 shows the maternal genetic effects (on the diagonal) and the heterosis effects (above the diagonal) for the same traits.

Direct genetic effects for FI were distributed around zero, but differences between lines were appreciated (-5.39 g/d for line A versus 2.67 g/d for line V). Maternal genetic effects were also null, but differences between line A (3.71 g/d) and line C (-3.5 g/d) could be considered significant. Heterosis for the cross between lines R and V was 3.37 g (3.1 %), near to the
values reported by Jensen et al. (1996) but it wasn’t found any heterosis effect for crosses between the other lines.

Table 1. Mean and standard deviation (in brackets) of the estimated marginal posterior distributions of direct genetic effects of line for the traits: feed intake (FI), average daily gain (ADG) and feed conversion rate (FCR)

<table>
<thead>
<tr>
<th>Trait / Line</th>
<th>A</th>
<th>C</th>
<th>P</th>
<th>R</th>
<th>V</th>
</tr>
</thead>
<tbody>
<tr>
<td>FI (g/d)</td>
<td>-5.39 (3.08)</td>
<td>2.48 (3.00)</td>
<td>-0.099 (2.20)</td>
<td>0.33 (2.18)</td>
<td>2.67 (1.80)</td>
</tr>
<tr>
<td>ADG (g/d)</td>
<td>-3.28 (1.47)</td>
<td>2.26 (1.52)</td>
<td>-0.51 (1.31)</td>
<td>3.03 (1.18)</td>
<td>-1.49 (1.02)</td>
</tr>
<tr>
<td>FCR</td>
<td>0.009 (0.091)</td>
<td>-0.043 (0.089)</td>
<td>0.090 (0.066)</td>
<td>-0.181 (0.065)</td>
<td>0.125 (0.054)</td>
</tr>
</tbody>
</table>

Table 2. Mean and standard deviation (in brackets) of the estimated marginal posterior distributions of the genetic maternal effects (on the diagonal) of the lines and direct heterosis effects between lines for the traits: feed intake (FI), average daily gain (ADG) and feed conversion rate (FCR)

<table>
<thead>
<tr>
<th>Trait / line</th>
<th>A</th>
<th>C</th>
<th>P</th>
<th>R</th>
<th>V</th>
</tr>
</thead>
<tbody>
<tr>
<td>FI (g/d)</td>
<td>3.71 (2.56)</td>
<td>-2.56 (4.76)</td>
<td>-1.00 (3.69)</td>
<td>1.91 (2.15)</td>
<td>1.16 (1.85)</td>
</tr>
<tr>
<td>ADG (g/d)</td>
<td>-3.50 (2.54)</td>
<td>0.25 (1.42)</td>
<td>0.25 (1.49)</td>
<td>-0.07 (1.37)</td>
<td>-0.39 (1.13)</td>
</tr>
<tr>
<td>FCR</td>
<td>0.009 (0.091)</td>
<td>-0.043 (0.089)</td>
<td>0.090 (0.066)</td>
<td>-0.181 (0.065)</td>
<td>0.125 (0.054)</td>
</tr>
</tbody>
</table>

Main results for ADG were the clear difference between direct genetic effects of sire and dam lines: A (–3.28 g/d) vs R (3.03 g/d) and C (2.26 g/d) and, V (–1.49 g/d) vs R, as expected. No maternal genetic effects were found in any of the lines, in agreement with Gómez et al. (1999) who analysed data from three of the five lines of the present study. A negative heterosis effect (-5.06 g/d = -13%) was observed in the cross between lines A and P.

With respect to FCR, dam line V showed the highest value (0.125) of direct genetic effect. There were no differences with the other dam lines. Sire line R, selected for growth rate, showed the lowest value (-0.181 g/d) as expected according to the negative genetic correlation between ADG and FCR estimated by some authors (Baselga and Blasco, 1989). Direct genetic effect for line C was not different from zero, probably because this line has been selected for...
ADG during a shorter interval of time. It hasn’t been found maternal genetic effects or heterosis effects in the crosses between any lines for this trait.

CONCLUSION
Heterosis effects and maternal genetic effects were not relevant for growth, consumption and feed efficiency traits. Differences between the crossbreed animals seem to be due mainly to differences in direct genetic effects.

REFERENCES