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### Genetic selection for ovulation rate and litter size in rabbits: Estimation of genetic parameters and direct and correlated responses<sup>1</sup>

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**ABSTRACT:** The aim of this work was to estimate direct and correlated responses in survival rates in an experiment of selection for ovulation rate (OR) and litter size (LS) in a line of rabbits (OR LS). From generation 0 to 6 (first selection period), females were selected only for second gestation OR estimated by laparoscopy. From generation 7 to 13 (second selection period), a 2-stage selection for OR and LS was performed. In stage 1, females having the greatest OR at second gestation were selected. In stage 2, selection was for the greatest average LS of the first 2 parities of the females selected in stage 1. Total selection pressure in females was about 30%. The line had approximately 17 males and 75 females per generation. Traits recorded were OR estimated as the number of corpora lutea in both ovaries, number of implanted embryos (IE) estimated as the number of implantation sites, LS estimated as total number of rabbits born recorded at each parity, embryo survival

(ES) estimated as IE/OR, fetal survival (FS) estimated as LS/IE, and prenatal survival (PS) estimated as LS/ OR. Data were analyzed using Bayesian methodology. The estimated heritabilities of LS, OR, IE, ES, FS, and PS were 0.07, 0.21, 0.10, 0.07, 0.12, and 0.16, respectively. Direct and correlated responses from this study were estimated in each period of selection as the difference between the average genetic values of last and first generation. In the first selection period, OR increased 1.36 ova, but no correlated response was observed in LS due to a decrease on FS. Correlated responses for IE, ES, FS, and PS in the first selection period were 1.11, 0.00, -0.04, and -0.01, respectively. After 7 generations of 2-stage selection for OR and LS, OR increased 1.0 ova and response in LS was 0.9 kits. Correlated responses for IE, ES, FS, and PS in the second selection period were 1.14, 0.02, 0.02, and 0.07, respectively. Two-stage selection for OR and LS can be a promising procedure to improve LS in rabbits.

**Key words:** litter size, ovulation rate, rabbit, survival rates, two-stage selection.

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#### INTRODUCTION

Direct selection for litter size has not had the success expected in prolific species, which has led to searching alternative methods of selection. Several authors predicted greater response in litter size when

<sup>3</sup>Corresponding author: msantacr@dca.upv.es Received October 30, 2012. Accepted April 3, 2013. selecting for indexes of its components, because they are optimally weighted (Johnson et al., 1984; Bennett and Leymaster, 1989, 1990, in pigs; Ribeiro et al., 1997a,b, in mice). However, in 2 experiments of index selection, responses in litter size were less than expected (Kirby and Nielsen, 1993, in mice; Johnson et al., 1999, in pigs), probably due to the low precision of the estimated genetic correlations and the use of inappropriate economic weights (Falconer and Mackay, 2001).

Two-stage selection was proposed as an alternative to the index selection, which would be less affected by the precision of the genetic parameters. An experiment of 2-stage selection was performed by Ruiz-Flores and Johnson (2001) in pigs; selection was based on ovulation rate and litter size in a line previously

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**Table 1.** Means and SD (in parentheses) for ovulation rate (OR), litter size (LS), number of implanted embryos (IE), embryo survival (ES), fetal survival (FS), and prenatal survival (PS) in generations 0 to 13

|                   |        |        |        |        |        |        | Gener  | ation  |        |        |        |        |        |        |
|-------------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| Item <sup>1</sup> | 0      | 1      | 2      | 3      | 4      | 5      | 6      | 7      | 8      | 9      | 10     | 11     | 12     | 13     |
| n                 | 85     | 75     | 92     | 80     | 65     | 59     | 102    | 67     | 82     | 74     | 62     | 49     | 76     | 76     |
| $S_{OR}^2$        | 2.7    | 2.4    | 3.7    | 2.9    | 3.9    | 1.7    | 1.7    | 1.5    | 1.2    | 1.6    | 1.0    | 1.5    | 1.8    | _      |
| $S_{LS}^{3}$      | 0.4    | 0.7    | 0.7    | 0.4    | 0.1    | 0.2    | 2.1    | 2.3    | 2.4    | 1.9    | 2.6    | 1.9    | 2.5    | _      |
| $OR^2$            | 14.9   | 15.5   | 15.8   | 16.4   | 15.8   | 15.5   | 16.3   | 15.9   | 15.7   | 15.5   | 16.4   | 16.1   | 16.5   | 16.1   |
|                   | (2.2)  | (2.7)  | (2.6)  | (2.4)  | (2.7)  | (2.4)  | (2.3)  | (2.5)  | (2.4)  | (2.7)  | (2.4)  | (2.5)  | (2.9)  | (2.6)  |
| $LS^3$            | 8.1    | 8.5    | 9.1    | 9.1    | 8.6    | 8.7    | 9.3    | 9.1    | 8.8    | 9.4    | 9.4    | 9.6    | 9.1    | 9.6    |
|                   | (3.0)  | (2.6)  | (2.8)  | (3.0)  | (2.9)  | (3.1)  | (2.9)  | (3.3)  | (3.5)  | (3.0)  | (3.5)  | (3.1)  | (3.1)  | (3.2)  |
| $IE^4$            | 12.5   | 12.6   | 12.5   | 12.1   | 11.1   | 11.5   | 13.1   | 12.1   | 12.5   | 12.9   | 12.6   | 11.5   | 12.4   | 11.5   |
|                   | (3.1)  | (3.6)  | (3.6)  | (3.6)  | (4.1)  | (4.3)  | (3.4)  | (4.1)  | (4.0)  | (3.3)  | (4.5)  | (3.7)  | (3.7)  | (4.4)  |
| ES                | 0.82   | 0.81   | 0.79   | 0.75   | 0.71   | 0.74   | 0.79   | 0.75   | 0.76   | 0.82   | 0.76   | 0.73   | 0.76   | 0.71   |
|                   | (0.18) | (0.20) | (0.20) | (0.21) | (0.24) | (0.26) | (0.18) | (0.23) | (0.21) | (0.18) | (0.24) | (0.24) | (0.20) | (0.26) |
| FS                | 0.72   | 0.73   | 0.78   | 0.68   | 0.75   | 0.69   | 0.74   | 0.75   | 0.75   | 0.79   | 0.80   | 0.79   | 0.74   | 0.79   |
|                   | (0.19) | (0.20) | (0.17) | (0.22) | (0.16) | (0.18) | (0.14) | (0.19) | (0.18) | (0.15) | (0.15) | (0.14) | (0.16) | (0.17) |
| PS                | 0.59   | 0.57   | 0.62   | 0.51   | 0.58   | 0.55   | 0.58   | 0.58   | 0.57   | 0.66   | 0.61   | 0.58   | 0.57   | 0.63   |
|                   | (0.19) | (0.18) | (0.20) | (0.22) | (0.19) | (0.21) | (0.17) | (0.19) | (0.19) | (0.18) | (0.22) | (0.19) | (0.19) | (0.24) |

 $<sup>^{1}</sup>n$  = number of females at each generation.  $S_{OR}$  = selection differentials for ovulation rate.  $S_{LS}$  = selection differentials for litter size.

selected for an index to increase ovulation rate and embryonic survival. Response after 8 generations of selection was greater than the responses observed in other experiments of selection for litter size. Selection on litter size was also successful in a line of pigs previously selected for ovulation rate (Lamberson et al., 1991; Johnson, 1992).

An experiment of 2-stage selection for ovulation rate and litter size in rabbits is currently being performed. The objective of this experiment is to test whether 2-stage selection after previous selection for ovulation rate is successful for increasing litter size. Responses in ovulation rate, litter size, and survival rates were estimated for 6 generations of direct selection for ovulation rate and for 7 generations of 2-stage selection for ovulation rate and litter size.

#### MATERIALS AND METHODS

All experimental procedures involving animals were approved by the Universitat Politècnica de València Research Ethics Committee.

#### Animals and Experimental Design

Animals involved in this study came from a line (OR\_LS) whose origin was a synthetic line (V) first selected for litter size at weaning for 12 generations (García and Baselga, 2002) and then for high uterine capacity for 10 generations (Blasco et al., 2005), and then selection was relaxed for 6 generations. From

there, founders were chosen at random within sire families to create the line OR LS.

Line OR LS underwent 13 generations of selection. From generation 0 to 6 (first selection period), females were selected only for second gestation ovulation rate (OR) estimated by laparoscopy. From generation 7 to 13 (second selection period), a 2-stage selection for OR and litter size (LS) was performed. In stage 1, females having the greatest OR at second gestation were selected. In stage 2, selection was for the greatest average LS of the first 2 parities of the females selected in stage 1. There were no generations of relaxed selection between the 2 periods of selection. From generation 0 to 13, selection pressure in females was about 30%. From generation 7 to 13, selection pressure was about 65 and 49% for OR and LS, respectively. Males were selected within sire families from litters of best dams to limit inbreeding. One male was selected from each sire family. The number of females at each generation is presented in Table 1. The average number of males per generation was 17.

Does were mated for the first time at 18 to 20 wk of age and 11 to 12 d after each parturition. Females that did not accept males were mated again 1wk afterward. Pregnancy was checked approximately 13 d after mating by simple palpation of the abdomen. Animals were bred at the experimental farm of the Universitat Politècnica de València. Cages were "flat-deck," with extractable nest box with isolated plastic floor. Does were kept under a constant photoperiod of 16:8 h light:dark with controlled ventilation and fed a commercial diet.

 $<sup>^{2}</sup>$ Unit = ova.

 $<sup>^{3}</sup>$ Unit = kits.

 $<sup>^{4}</sup>$ Unit = embryos.

**Table 2.** Descriptive statistics for litter size (LS), ovulation rate (OR), implanted embryos (IE), embryo survival (ES), fetal survival (FS), and prenatal survival (PS)

| Trait | n     | Mean | SD   | Minimum | Maximum |
|-------|-------|------|------|---------|---------|
| LS    | 3,563 | 9.0  | 3.1  | 1.0     | 18      |
| OR    | 1,703 | 15.8 | 2.5  | 8.0     | 25      |
| IE    | 1,315 | 12.2 | 3.8  | 1.0     | 23      |
| ES    | 1,311 | 0.76 | 0.22 | 0.06    | 1.0     |
| FS    | 884   | 0.75 | 0.17 | 0.07    | 1.0     |
| PS    | 889   | 0.59 | 0.20 | 0.05    | 1.0     |

#### **Traits**

Ovulation rate, estimated as the number of corpora lutea in both ovaries, and the number of implanted embryos (IE), estimated as the number of implantation sites, were measured by using laparoscopy at d 12 of second gestation. Surgical technique is described by Santacreu et al. (1990) and Argente et al. (1997) and it was shown by Santacreu et al. (1990) to be an accurate technique for measuring OR without affecting LS. Litter size was measured as the total number of kits born per litter, embryo survival (ES) was estimated as IE/OR, fetal survival (FS) was estimated as LS/IE, and prenatal survival (PS) was estimated as LS/OR. Females from all generations had a second measurement of OR at last gestation and females from the first to the fifth generation and females from 12th and 13th generations had a second measurement of IE and ES. Second measurement of OR, IE, and ES were estimated postmortem at parities third, fourth, or fifth. Data from 969 laparoscopies and 4,370 parities were analyzed. Number of records for each trait is presented in Table 2. The number of animals in the pedigree was 1,289.

#### Statistical Analysis

Data from all 13 generations of selection were used in the analysis. Bayesian inference was used.

Bivariate and trivariate repeatability animal models were fitted to estimate the genetic parameters and genetic responses. Genetic parameters and correlations between OR and LS were estimated using a bivariate model. Trivariate analyses were used to estimate genetic parameters between traits different from OR and LS. Each 3-trait analysis included OR, LS, and 1 of the 4 remaining traits. The model assumed for OR, LS, IE, and ES was

$$y_{ijklm} = P_i + YS_j + L_k + a_l + p_l + e_{ijklm},$$

in which  $P_i$  is the effect of parity (5 levels for LS and 4 levels for the other traits because there were no records for them in the first gestation),  $YS_i$  is the effect of year–season (1 yr season every 3 mo: 38 levels for LS, 37 levels

for OR and IE, and 34 levels for ES),  $L_k$  is the effect of lactation state of the doe (2 levels: 1 for lactating and 2 for not lactating does when mated),  $a_l$  is the additive value of the animal,  $p_l$  is the permanent environmental and nonadditive effects of the doe, and  $e_{ijklm}$  is the residual of the model. The model for FS and PS had neither the parity effect nor the permanent environmental effect, because records came only from the second parity, and the year–season effect had 30 levels.

For the bivariate repeatability model, the traits were assumed to be conditionally normally distributed as follows:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} | \, \boldsymbol{b}_1, \boldsymbol{b}_2, \boldsymbol{a}_1, \boldsymbol{a}_2, \boldsymbol{p}_1, \boldsymbol{p}_2, \boldsymbol{R} \, \simeq \, N \Bigg( \boldsymbol{X} \begin{bmatrix} \boldsymbol{b}_1 \\ \boldsymbol{b}_2 \end{bmatrix} + \boldsymbol{Z} \begin{bmatrix} \boldsymbol{a}_1 \\ \boldsymbol{a}_2 \end{bmatrix} + \boldsymbol{W} \begin{bmatrix} \boldsymbol{p}_1 \\ \boldsymbol{p}_2 \end{bmatrix}, \boldsymbol{R} \Bigg)$$

in which  $b_1$  and  $b_2$  are random vectors including the effects of YS, L, and P,  $a_1$  and  $a_2$  are vectors of individual additive genetic effects,  $p_1$  and  $p_2$  are vectors of permanent environmental effects, X, Z, and W are known incidence matrices, and **R** is the residual (co) variance matrix. Between individuals, only the additive random effects are assumed correlated. Between traits, the additive, the permanent environmental, and the residual effects are assumed correlated. Sorting records by individual, and trait within individual, the residual (co)variance matrix can be written as  $\mathbf{R_0} \otimes \mathbf{I_n}$  with  $\mathbf{R_0}$ being the  $2 \times 2$  residual (co)variance matrix between the traits analyzed and  $I_n$  an identity matrix of appropriate order. Bounded uniform priors were used to represent vague previous knowledge of distributions of  $\mathbf{b_1}$  and **b**<sub>2</sub>. Prior knowledge concerning additive and permanent effects was represented by assuming that they were normally distributed, conditionally on the associated (co) variance components, as follows:

$$\begin{bmatrix} a_1 \\ a_2 \end{bmatrix} | \, G \sim N \big( 0, G \big) \qquad \qquad \begin{bmatrix} p_1 \\ p_2 \end{bmatrix} | \, P \sim N \big( 0, P \big)$$

in which  $\mathbf{0}$  is a vector of 0s,  $\mathbf{G}$  is the genetic (co) variance matrix, and  $\mathbf{P}$  is the (co)variance matrix of the nonadditive genetic plus permanent environmental effects of the doe. Sorting the data by individual as before, matrices  $\mathbf{G}$  and  $\mathbf{P}$  could be written as  $\mathbf{G}_0 \otimes \mathbf{A}$  and  $\mathbf{P}_0 \otimes \mathbf{I}_s$ , respectively, in which  $\mathbf{G}_0$  and  $\mathbf{P}_0$  are the  $2 \times 2$  genetic and permanent (co)variance matrices,  $\mathbf{A}$  is the known additive genetic relationship matrix, and  $\mathbf{I}_s$  the identity matrix of the same order as the number of levels of permanent effects. Bounded uniform priors were used for the components of the (co)variance matrices  $\mathbf{R}_0$  and  $\mathbf{G}_0$  and  $\mathbf{P}_0$ . For trivariate repeatability analyses the order of  $\mathbf{R}_0$ ,  $\mathbf{G}_0$ , and  $\mathbf{P}_0$  matrices was  $3 \times 3$ .

Marginal posterior distributions of all unknowns were estimated by using the Gibbs sampling algorithm. The data vector was augmented to have the same design

**Table 3.** Features of the marginal posterior distributions of the heritability  $(h^2)$  and the repeatability (r) of litter size (LS), ovulation rate (OR), number of implanted embryos (IE), and embryo survival (ES) and the heritability of fetal survival (FS) and prenatal survival (PS)<sup>1</sup>

|       |        | $h^2$              | r          |      |        |                    |
|-------|--------|--------------------|------------|------|--------|--------------------|
| Trait | Median | HPD <sub>95%</sub> | $P_{0.10}$ | k    | Median | HPD <sub>95%</sub> |
| LS    | 0.07   | 0.02, 0.12         | 0.16       | 0.03 | 0.16   | 0.13, 0.20         |
| OR    | 0.21   | 0.13, 0.29         | 1.00       | 0.14 | 0.27   | 0.21, 0.35         |
| IE    | 0.10   | 0.05, 0.17         | 0.60       | 0.06 | 0.20   | 0.14, 0.26         |
| ES    | 0.07   | 0.02, 0.12         | 0.19       | 0.03 | 0.14   | 0.08, 0.21         |
| FS    | 0.11   | 0.06, 0.21         | 0.69       | 0.07 | _      | _                  |
| PS    | 0.15   | 0.10, 0.20         | 0.99       | 0.11 | _      | -                  |

 $^{1}\text{HPD}_{95\%}$  = high posterior density interval at 95%;  $P_{0.10}$  = probability of the heritability being greater than 0.10; k = limit for the interval [k, +1) of the heritability having a probability of 95%.

matrices for all traits. Augmented data were not used for inferences but simplified computing by sampling from a predictive distribution of missing data (Sorensen and Gianola, 2002). The program TM developed by Legarra et al. (2008) was used for all Gibbs sampling procedures. After some exploratory analyses, chains of 1,000,000 samples were used, with a burn in period of 200,000. One sample each 100 for the bivariate analysis and 1 sample each 500 for the trivariate analysis were saved to avoid high correlations between consecutive samples. Convergence was tested using the Z criterion of Geweke (Sorensen and Gianola, 2002).

#### RESULTS AND DISCUSSION

Descriptive statistics for all traits are presented in Table 2. Values are in agreement with the ones published by other authors in maternal rabbit lines (Brun et al., 1992; García and Baselga, 2002; Piles et al., 2006; Theau-Clement et al., 2009). Realized selection differentials for OR and LS, means, and SD for all traits in generations 0 to 13 are presented in Table 1.

#### Genetic and Phenotypic Parameters

For all the traits analyzed, Monte Carlo SE were small. The Geweke test did not detect lack of convergence in any case, except for FS. Mean and median are similar for all the traits showing that, in all cases, the marginal posterior distributions were symmetric, and therefore only median values are given in the tables.

Features of the estimated marginal posterior distributions of heritability and repeatability for the traits studied are summarized in Table 3. In general, estimates of heritabilities were low with the exception of OR, which was moderate (0.21), with a probability of 95% of being at least 0.14 (*k* value; Table 3). Both

**Table 4.** Features of the marginal posterior distributions of the genetic correlation between the traits analyzed: litter size (LS), ovulation rate (OR), number of implanted embryos (IE), embryo survival (ES), fetal survival (FS), and prenatal survival (PS)<sup>1</sup>

| Trait  | Median | HPD <sub>95%</sub> | P                 | k                  |
|--------|--------|--------------------|-------------------|--------------------|
| LS, OR | 0.30   | -0.12, 0.71        | 0.92 <sup>a</sup> | -0.05 <sup>a</sup> |
| LS, IE | 0.68   | 0.34, 0.99         | 1.00 <sup>a</sup> | $0.34^{a}$         |
| LS, ES | 0.59   | -0.04, 0.95        | $0.94^{a}$        | $-0.04^{a}$        |
| LS, FS | 0.63   | 0.34, 0.96         | 1.00 <sup>a</sup> | 0.34 <sup>a</sup>  |
| LS, PS | 0.86   | 0.77, 0.91         | 1.00 <sup>a</sup> | 0.78 <sup>a</sup>  |
| OR, IE | 0.72   | 0.44, 0.93         | 1.00 <sup>a</sup> | 0.46 <sup>a</sup>  |
| OR, ES | -0.09  | -0.53, 0.34        | $0.67^{b}$        | 0.29 <sup>b</sup>  |
| OR, FS | -0.50  | -0.82, -0.27       | $1.00^{b}$        | $-0.30^{b}$        |
| OR, PS | -0.35  | -0.62, -0.09       | 0.99 <sup>b</sup> | $-0.12^{b}$        |

 $^{1}\mathrm{HPD}_{95\%}=$  high posterior density interval at 95%; P = probability of the genetic correlation being greater than 0 (superscript a) or less than 0 (superscript b); k= limit for the interval  $^{a}$  [k,+1),  $^{b}$  (-1,k], having a probability of 95%.

LS and IE had low heritability estimates (0.07 and 0.10, respectively). Similar estimates of heritabilities were obtained for ES and FS, 0.07 and 0.11, respectively. Heritability estimate of PS was 0.15 with a probability of 99% of being at least 0.10.

In general, our heritability estimates for the majority of traits were in agreement with other studies in rabbits (Blasco et al., 1993b; Argente et al., 2000; Garreau et al., 2004; Laborda et al., 2011, 2012a). In the case of OR, recent studies in pigs reported greater heritability estimates than in rabbits (Ruiz-Flores and Johnson, 2001; Rosendo et al., 2007) but causes were not clear although the process of ovulation is different between species because in rabbit, unlike in pig, ovulation occurs in response to coitus.

The repeatability estimate of LS was low (Table 3), which agrees with the estimates reported by Laborda et al. (2012a) and Khalil (1993) for a maternal line but was lower than the ones reported by Lukefahr and Hamilton (1997; 0.23) and Rastogi et al. (2000; 0.30). Ovulation rate and IE had moderate repeatability estimates (0.27 and 0.20, respectively), and ES showed a low repeatability estimate in agreement with Laborda et al. (2012a). The estimated ratios of the permanent environmental variance to the phenotypic variance (p²) were 0.09, 0.06, 0.07, and 0.07 for LS, OR, IE, and ES, respectively. Repeatability and p² estimates for the traits IE and ES are scarce in the literature in rabbits and pigs although these estimates are within of those published for LS in rabbits (reviewed by Garreau et al., 2004).

Features of the estimated marginal posterior distributions of the genetic correlations are summarized in Table 4. The estimate of the genetic correlation between LS and OR was positive (P = 0.92; Table 4) but imprecise (HPD<sub>95%</sub>: Table 4). Estimated genetic

correlations between LS and the remaining traits were positive (value P; Table 4) being moderate with IE, ES, and FS and high with PS with a probability of 95% of being at least 0.78 (k value; Table 4). Estimated genetic correlations of OR with FS and PS were negative (P = 1.00; Table 4), and nothing can be said about the sign of the estimated genetic correlation between OR and ES.

Estimated values of the genetic correlation between OR and LS found in literature were generally positive but they were reported without or with high SE (Johnson et al., 1999; Ruiz-Flores and Johnson, 2001; Rosendo et al., 2007, in pigs; Blasco et al., 1993b, in rabbits). Greater genetic correlations between LS and IE were obtained in other experiments, possibly because the number of fetuses was measured at a later point of gestation (Blasco et al., 1993b, in rabbits; Johnson et al., 1999, in pigs). The positive genetic correlations between LS and survival rates agree with estimates in the literature (Blasco et al., 1993b; Argente et al., 1997; Laborda et al., 2012a, in rabbits; Rosendo et al., 2007, in pigs). Besides, the genetic correlation between OR and IE was in accordance with the ones obtained in rabbits (0.58 by Laborda et al., 2012a), pigs (0.44 by Johnson et al., 1999), and mice (0.81 by Clutter et al., 1990).

Genetic correlations between traits were estimated with low precision, especially for the genetic correlations between LS with both OR and ES and between OR with ES, which had large credibility intervals. To obtain genetic parameters with greater precision, a larger set of data would be needed. Nevertheless, the nature of these kinds of experiments, which require techniques including laparoscopy or slaughter, prevents the collection of large data sets. Genetic correlations were estimated in this study with low precision, but they are within the range of the values reported in the literature.

Features of the estimated marginal posterior distributions of the phenotypic correlations are summarized in Table 5. Generally, phenotypic and genetic correlations have similar magnitudes and signs. The phenotypic correlation between LS and OR was positive (P = 1.00; Table 5) but low. The estimated phenotypic correlation between LS and IE was high and positive (P = 1.00; Table 5). The posterior mean of the phenotypic correlation between OR and IE (Table 5) had similar magnitude and sign as the ones obtained in pigs and mice. Estimated phenotypic correlations between OR and survival rates were negative (P =1.00; Table 5); however, they were of low magnitude, especially the phenotypic correlation between OR and ES. Phenotypic correlations between LS and survival rates were positive (P = 1.00; Table 5), being moderate with ES and FS and high with PS.

Positive correlations between LS and survival rates and negative correlations between OR and both FS and

**Table 5.** Features of the marginal posterior distributions of the phenotypic correlation between the traits analyzed: litter size (LS), ovulation rate (OR), number of implanted embryos (IE), embryo survival (ES), fetal survival (FS), and prenatal survival (PS)<sup>1</sup>

| Trait  | Median | HPD <sub>95%</sub> | P                 | k                 |
|--------|--------|--------------------|-------------------|-------------------|
| LS, OR | 0.20   | 0.13, 0.26         | 1.00 <sup>a</sup> | 0.14 <sup>a</sup> |
| LS, IE | 0.72   | 0.70, 0.75         | 1.00 <sup>a</sup> | $0.70^{a}$        |
| LS, ES | 0.68   | 0.64, 0.71         | 1.00 <sup>a</sup> | 0.65 <sup>a</sup> |
| LS, FS | 0.49   | 0.45, 0.54         | 1.00 <sup>a</sup> | 0.45 <sup>a</sup> |
| LS, PS | 0.88   | 0.87, 0.89         | 1.00 <sup>a</sup> | 0.87 <sup>a</sup> |
| OR, IE | 0.40   | 0.35, 0.45         | 1.00 <sup>a</sup> | $0.36^{a}$        |
| OR, ES | -0.09  | -0.15, -0.04       | 1.00 <sup>b</sup> | $-0.05^{b}$       |
| OR, FS | -0.23  | -0.30, -0.17       | 1.00 <sup>b</sup> | $-0.18^{b}$       |
| OR, PS | -0.25  | -0.31, -0.20       | 1.00 <sup>b</sup> | $-0.20^{b}$       |

 $^{1}$ HPD<sub>95%</sub> = high posterior density interval at 95%; P = probability of the genetic correlation being greater than 0 (superscript a) or less than 0 (superscript b); k = limit for the interval  $^{a}$  [k, +1),  $^{b}$  (-1, k], having a probability of 95%.

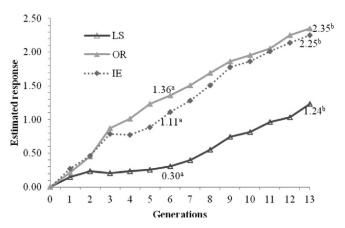
PS were in agreement with the estimates found in the literature (Blasco et al., 1993b, in rabbits; Blasco et al., 1993a, for a review in pigs and rabbits; Johnson et al., 1999; Rosendo et al., 2007, in pigs).

#### Response to Selection

Direct and correlated responses from this study were estimated in both periods of selection as the difference between the average genetic values of last and first generation. The estimated responses to selection for OR, LS, and IE are shown in Fig. 1. The correlated responses in ES, FS, and PS are shown in Fig. 2. We can distinguish 2 periods of genetic responses.

Selection for Ovulation Rate. From generation 0 to 6, OR increased in 1.36 ova, almost 1.5% per generation (0.22 ova/generation; Fig. 1). In this experiment, selection for OR did not practically modify LS; correlated response in LS was 0.30 kits in 6 generations (0.05 kit/ generation; Fig. 1). Implanted embryos increased 1.11 embryos in 6 generations (0.18 embryo/generation; Fig. 1). We did not observe any response in ES, but FS decreased consistently (0.038 in 6 generations, around 0.9% per generation; Fig. 2). Therefore, this decrease in FS seems to be responsible for the lack of correlated response observed in LS. Prenatal survival apparently showed a small decrease (0.013 in 6 generations; Fig. 2). Our results are in agreement with estimated responses published by Laborda et al. (2011, 2012a,b) using data of 10 generations of selection for OR (line OR).

Our estimated response of OR was similar to those reported in pigs by Leymaster and Christenson (2000) and in mice by Bradford (1969) but less than those obtained in other studies (Cunningham et al., 1979; Rosendo et al., 2007, in pigs; Land and Falconer, 1969,

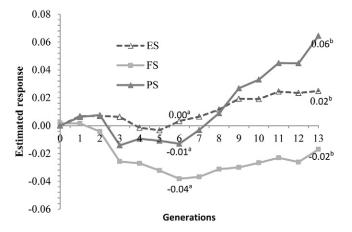


**Figure 1.** Genetic trends for ovulation rate (OR), litter size (LS), and number of implanted embryos (IE) of line OR\_LS. This line was selected for OR from generation 0 to 6 and for OR and LS from generation 7 to 13. Superscript <sup>a</sup> = mean of the EBV of the character at generation 6. Superscript <sup>b</sup> = mean of the EBV of the character at generation 13.

in mice). In these studies, the correlated response on LS was close to 0, except that observed by Cunningham et al. (1979) that was estimated with high SE (0.15  $\pm$  0.13 pig/generation). In all cases, an increase in prenatal mortality was observed. As in this experiment, Freking et al. (2007) in pigs and Bradford (1969) in mice observed that postimplantation losses were the main cause for a lack of correlated response in LS. Possible physiological causes were already discussed with details by Laborda et al. (2011, 2012a,b).

In conclusion, the results show that selection for OR could increase fetal mortality whereas embryo mortality does not seem to have been modified. This fetal mortality has been the main cause for the lack of correlated response observed in LS. Further studies are needed to explain the mechanisms that have increased fetal mortality in rabbits selected for high OR.

Two-Stage Selection for Ovulation Rate and Litter Size. Two-stage selection was proposed as an alternative to selection indexes that are sensitive to the precision of the genetic parameters. In the second period, 7 generations of 2-stage selection for OR and LS were performed. Ovulation rate continued increasing throughout the 2-stage selection but with a lower rate than during the first period of selection, due to a decrease in the selection differential applied (Table 1). In fact, from generation 6, the proportion of females with extremely high OR (more than 20 ova; i.e., twice the SD over the mean) increased 4.1% per generation in line OR against 0.9% in line OR LS. Response in OR was estimated to be 1 ovum, almost 0.9% per generation (0.14 ova/generation; Fig. 1). A change in LS was observed and the estimated response was approximately 0.9 kits (0.13 kit/generation; Fig. 1). The correlated response in IE was 1.14 embryos (Fig. 1). Thus, around 93% of the average increase in OR was realized as more



**Figure 2.** Genetic trends for embryo survival (ES), fetal survival (FS), and prenatal survival (PS) of line OR\_LS. This line was selected for ovulation rate (OR) from generation 0 to 6 and for OR and litter size (LS) from generation 7 to 13. <sup>a</sup> = mean of the EBV of the character at generation 6. <sup>b</sup> = mean of the EBV of the character at generation 13.

kits at birth, but only 22% was realized as more kits at birth in the first period of selection. It seems that both ES and FS have contributed with the same amount in the increase observed in prenatal survival. A small positive change in ES and FS was observed (approximately 0.020 in 7 generations; Fig. 2). Prenatal survival increased 0.077 in 7 generations, around 2% per generation (Fig. 2). The direct response in LS was similar to the response estimated in pigs by Lamberson et al. (1991) after direct selection for LS during 8 generations in a line previously selected to increase OR. A similar conclusion was obtained by Ruiz-Flores and Johnson (2001) in the 2-stage pig experiment although there was a greater direct response in LS at birth (0.33  $\pm$  0.06 pig/ generation). This greater response in LS could be due to a greater response in OR (0.26  $\pm$  0.07 ova/generation) because their estimate of correlated response in PS was the same as the one estimated in our study (0.01 per generation). Moreover, as it has been said before, estimates of heritability for OR were generally greater in pigs than in rabbits.

In pig populations selected for increasing OR, the total number of piglets born is expected to represent uterine capacity (i.e., PS that depends on the female) more closely than in unselected populations (Lamberson et al., 1991; Johnson et al., 1999; Ruíz-Flores and Johnson, 2001). In our experiment, OR was high enough to allow expression of uterine capacity due to the direct selection applied in both periods of selection. Therefore, 2-stage selection could indirectly improve uterine capacity, but LS is less expected to express uterine capacity in rabbits than in pigs due to the absence of embryo transmigration in rabbits. The observed changes in PS occurred either during pre- and postimplantation periods of gestation. In early stages of gestation, an

improvement in the quality of oocytes (Torres, 1982, in rabbits; Krisher, 2004, for a review in some species) and reduced variability of embryo development (Pope, 1988; Xie et al., 1990, in pigs) could explain the increase in ES. Laborda et al. (2012c) showed a greater number of better quality oocytes in the line OR\_LS than in a line of the same origin selected for OR during 10 generations (line OR). Both oocyte quality and variability of embryo development can also affect FS. Besides, in later stages of gestation, an increase in FS could be associated with availability of uterine space and resources (Adams, 1959; Hafez, 1969, in rabbits) and greater blood supply to the fetuses (Hafez, 1965; Duncan, 1969; Argente et al., 2008, in rabbits).

Results from first selection period show that, after 6 generations of selection for OR, OR responded to selection, but no correlated response in LS was observed. Results from second selection period show that 2-stage selection for OR and LS would be effective in improving OR and LS. Moreover, this increase has been due to reducing both pre- and postimplantation mortalities. Summarizing, the results obtained show that 2-stage selection for OR and LS could be effective to increase both LS and PS.

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