

## GENETIC RESPONSE TO SELECTION FOR REPRODUCTIVE PERFORMANCE IN A MATERNAL LINE OF RABBITS

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**ABSTRACT:** An evaluation of genetic response on reproductive traits was carried out in a line of rabbits selected for litter size at weaning. The evaluation was performed comparing contemporary does of generation 17 and 26, using cryopreservation techniques. The direct response to selection between both generations was  $0.77 \pm 0.27$  rabbits weaned/litter and there were favorable correlated responses in total litter size at birth and born alive. There was a

non-significant response in prenatal traits, but the litter size results imply response probably in foetal survival. The genetic trends were also estimated using mixed model methodology and were higher than the previous ones. Therefore, the repeatability animal model and the genetic parameters used are unsuitable. Models taking into account effects such as dominance need to be investigated.

**RÉSUMÉ:** Progrès génétique pour la fécondité dans une souche femelle de lapin.

La réponse à la sélection a été estimée dans une souche de lapin sélectionnée pour la taille de la portée au sevrage. L'estimation a été obtenue en comparant des femelles issues des générations 17 et 26, et rendues contemporaines par la cryoconservation. La réponse directe à la sélection est égale à  $0.77 \pm 0.27$  lapin sevré par portée. Les réponses corrélées sur les nombre de lapereaux nés totaux et nés vivants sont favorables. La réponse sur les

caractères mesurés avant la naissance n'était pas significative, mais les résultats observés sur la taille de la portée impliquent une réponse probable sur la survie prénatale. L'évolution génétique a aussi été évaluée en utilisant le modèle mixte et l'estimation est alors plus élevée. En conséquence, le modèle animal avec répétabilité et les paramètres génétiques utilisés semblent ne pas convenir. Il faudrait tester des modèles intégrant par exemple la dominance.

### INTRODUCTION

It is common that data from selection experiments in rabbits are analysed by mixed model methodology in order to estimate the genetic trend as an evaluation of selection response. Significant genetic trends have been reported for litter size in rabbits (ESTANY *et al.*, 1989; ROCHAMBEAU *et al.*, 1994; GÓMEZ *et al.*, 1996). It is less common the evaluation of the response was based on a control population (POUJARDIEU *et al.*, 1994) or comparing contemporarily two separate generations using cryopreserved embryos (GARCÍA and BASELGA, 2002). The objective of this paper is to evaluate the direct and correlated response in litter size traits and components of litter size comparing contemporarily two different generations of a maternal line of rabbits. A secondary objective is the comparison of the results

with the genetic trends obtained using mixed model methodology.

### MATERIAL AND METHODS

#### Animals

Estimation of response with control group (cryopreserved embryos). Line A was selected for litter size at weaning since 1980 evaluating the animals by a family index (BASELGA *et al.*, 1984). A control group (CG), representing generation 17 of selection was made up by 237 does. This group was compared to another one, called the selected group (SG), made up by 634 does pertaining to generation 26. The details of the cryopreservation (vitrification) process, thawing and embryo transfer can be found in GARCÍA *et al.*, (2000). To record the components of litter size between ovulation and birth, a total of 205 laparoscopies were performed on day 12 of the 2<sup>nd</sup> and 3<sup>rd</sup> pregnancies. The traits studied with this technique were ovulation

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rate (OR), number of implanted embryos (NIE), number of dead foetus (NDF), implantation rate (NIE/OR), foetus survival (LS/NEI) and prenatal survival (LS/OR). After birth, total litter size at birth (LS), number of young rabbits born alive (NBA), number of rabbits weaned (NW) and number of rabbits at 63 days of age (NS) were recorded. A total of 2468 parities were recorded from birth to weaning and only 1424 until 63 days of age.

### Statistical analyses

Data were analysed by solving a mixed model that for all traits had the same fixed and random effects. Fixed factors were: group (CG and SG), vitrification effect (2 levels), farm-year-season (5 levels for OR, NIE, NDF, IR, FS, PS; 23 levels for LS, NW, NBA; 11 levels for NS), physiological state of the doe: second and third gestation for OR, NIE, NDF, IR, FS and PS, and five levels for the other traits: nulliparous, primiparous (lactating and non-lactating) and multiparous (lactating and non-lactating). Random factors were the additive and non-additive permanent effect of the doe. Does were related only through their parents. All models were solved using the PEST software package (GROENEVELD, 1990) and the variance component ratios were estimated by Restricted Maximum Likelihood (REML) procedure (NEUMAIER and GROENEVELD, 1998), with the information of all generations and complete relationship matrix for the traits recorded after birth. The heritabilities were 0.35, 0.20, 0.15, 0.10, 0.05 and 0.15 for ovulation rate, number of implanted embryos, number of dead foetus,

implantation rate, foetus survival and prenatal survival, respectively, and the ratio of non-additive permanent doe effects to phenotypic variance were 0.05 for ovulation rate and 0.10 for the other traits.

### Genetic trends

Data from 26 generations from line A were used in the analysis. A total of 9842 parities from 1980 to 1999 were involved. Traits studied were LS, NBA, NW and NS. The model was the same for each trait. The year-season in which the parity took place had 78 levels and the physiological state of the doe had 3 levels as fixed effects. The additive value of the doe and the non-additive genetic effect plus the permanent environmental effect associated with the doe were the random effects. Variance and covariance components were estimated using the derivative-free multiple trait Restricted Maximum Likelihood (REML) procedure (NEUMAIER and GROENEVELD, 1998), with litter size at weaning included in all the analyses.

## RESULTS AND DISCUSSION

### Estimation of response with control group

The selected group did not show significant differences with the control group in implanted embryos, number of dead foetus, implantation rate, foetus survival and prenatal survival (Table 1). The high difference obtained in foetus survival and prenatal survival is remarkable, although the contrast was not significant. The insufficient number of

**Table 1:** Contrasts between selected group (SG) and control group (CG). Standard error between brackets.

	OR	NIE	NDF	NIE/OR (%)	LS/NIE (%)	LS/OR (%)	LS	NBA	NW	NS
SG - CG	0.03	-0.15	-0.63	-1.44	5.7	3.7	0.78*	0.74**	0.77*	0.50
	(0.49)	(0.54)	(0.51)	(2.87)	(3.7)	(4.6)	(0.30)	(0.32)	(0.27)	(0.42)

Ovulation rate (OR), number of implanted embryos (NIE), number of dead foetus (NDF), implantation rate (NIE/OR), foetus survival (LS/NEI), prenatal survival (LS/OR), total litter size at birth (LS), number of young rabbits born alive (NBA), number of rabbits weaned (NW) and number of rabbits at 63 days of age (NS). \*\*P<0.01; \* P<0.05.

**Table 2:** Genetic parameters. Estimates of heritability in the diagonal, genetic correlations above the diagonal and correlations between non-additive permanent plus environmental effects below the diagonal,  $\pm$  standard error.

	LS	NBA	NW	NS
LS	0.153 $\pm$ 0.017	0.964 $\pm$ 0.008	0.855 $\pm$ 0.025	0.818 $\pm$ 0.030
NBA	0.930 $\pm$ 0.014	0.130 $\pm$ 0.017	0.934 $\pm$ 0.014	0.920 $\pm$ 0.018
NW	0.768 $\pm$ 0.050	0.822 $\pm$ 0.038	0.114 $\pm$ 0.016	0.982 $\pm$ 0.014
NS	0.728 $\pm$ 0.064	0.751 $\pm$ 0.053	0.922 $\pm$ 0.021	0.120 $\pm$ 0.016

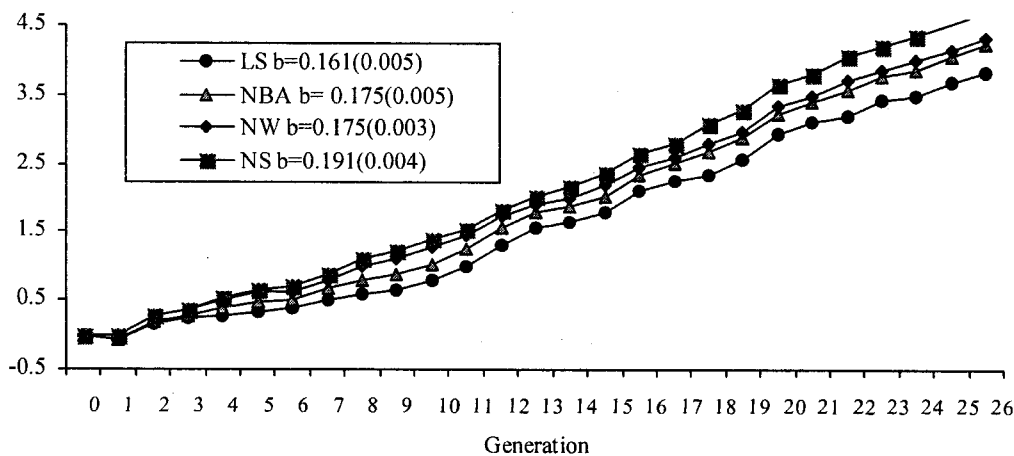
Total litter size at birth (LS), number of young rabbits born alive (NBA), number of rabbits weaned (NW) and number of rabbits at 63 days of age (NS).

laparoscopies carried out could be the explanation of this result. Direct response for litter size at weaning was significant (0.085 weaned young/litter per generation) because the number of weaned rabbits was significantly higher for the selected group than for the control group (difference of  $0.77 \pm 0.27$ ) and the difference between both groups involved nine generations of selection. The superiority of the selected group was also significant for total litter size at birth and number of young rabbits born alive. These results imply that a response was based on the prenatal components of litter size, presumably in foetus and prenatal survival. In a companion experiment, using the same methodological approach to estimate

response to selection, but involving a different maternal line, line V, it was found that selection of line V for litter size was effective, and a significant difference of 0.08 weaned young/litter and generation was reported (GARCÍA and BASELGA, 2002). This line showed a significant correlated response to selection in ovulation rate (0.18 ova more per generation).

**Estimation of genetic parameters**

Heritabilities of litter size between birth to slaughter ranged between 0.114 and 0.153, estimates being a little higher than the estimates commonly obtained for these traits (Table 2). Repeatabilities ranged between 0.171 and 0.236 for the same



**Figure 1:** Genetic trends for total litter size (LS), number born alive (NBA), number weaned (NW) and number of rabbits at 63 days of age (NS). b: coefficient of regression of the mean of the predicted additive values by generation on generation number, standard error within brackets.

characters because the ratio between the variance of non-additive permanent plus environmental effects and the phenotypic variance was  $0.083 \pm 0.011$  for LS,  $0.081 \pm 0.012$  for NBA,  $0.061 \pm 0.012$  for NW and  $0.051 \pm 0.011$  for NS. The genetic correlations were positive and near 1 and they were higher than correlations between non-additive permanent plus environmental effects

### Genetic trends

The genetic trend, calculated as the regression of the mean of the predicted additive values by generation on generation number, is plotted in Figure 1 for litter size at birth, weaning and slaughter. All regression coefficients were significant. The estimated response to selection for litter size at weaning did not agree when we compared both methodologies, using a control population (0.085 weaned per generation) or a mixed model approach (0.175 weaned per generation). The dependency on the model and genetic parameters of the mixed model methodology questions the adequacy of this approach to evaluate genetic progress. Several explanations can be envisaged for this result. MEYER (1992) investigated the effect of ignoring the maternal effect and found that the variances estimated were biased if this effect is important and the genetic correlation between maternal and direct effects is close to 1. However, for line A, GÓMEZ (1994) reported a maternal variance of  $0.0022 \pm 0.0100$ , an additive variance was  $0.1392 \pm 0.0381$ , and a correlation of  $-0.0164$ . Another explanation considers that dominance variance was not included in the model, so the heritability could be overestimated (JOHANSSÓN *et al.*, 1994; CULBERTSON *et al.*, 1998; MISZTAL and BESBES, 2000).

### CONCLUSION

Direct selection for litter size was successful and the response was estimated as 0.085 weaned young per generation. When we compared two methods of

estimation, control population and mixed model approximation, the results were different, indicating that the model used for genetic trends may be inappropriate. Additional studies need to be conducted to analyse the relative genetic improvement in prediction of additive effects by accounting for dominance.

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