A GENETIC STUDY OF A LINE SELECTED ON LITTER SIZE AT WEANING

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Abstract - Line P was founded at 1992 and is being selected for litter size at weaning. Breeding values are predicted by BLUP method assuming a repeatability animal model. Genetic parameters have been estimated by REML: heritability 0.044 (s.e. 0.022) and 0.075 (s.e. 0.025) as proportion of variation due to permanent effect.
A comparison has been made between predicted genetic responses using the first genetic parameters used to evaluate the animals and the last obtained REML estimates. Difference on average predicted breeding values of females and of males between the start and the end of the period was 0.32 and 0.24 rabbits using the REML estimates.

INTRODUCTION

Numerical productivity of the doe is a very important economic trait in rabbit production (ARMERO and BLASCO, 1992). REML heritability estimates of litter size at weaning are low (BASELGA et al., 1992 ; FERRAZ et al., 1992 ; FERRAZ and ELER, 1994 ; GOMEZ, 1994 ; KROGMEIER et al., 1994 ; ROCHAMBEAU et al., 1994). Several experiments have been designed on, but the estimated genetic responses on litter size at weaning have been lower than expected (as in pig) (MATHERON and ROUVIER, 1977 ; MATHERON and POUJARDIEU, 1984 ; ESTANY et al., 1989 ; BASELGA et al., 1992 ; ROCHAMBEAU et al., 1994). Mixed model methodology has been used to estimate the genetic response without control population (SORENSEN and KENNEDY, 1984) despite the estimate depends on the heritability used (THOMPSON, 1986).
The aim of this work is multiple: first a brief description of line P and second, the genetic analysis of this population estimating the genetic parameters and the response to selection.

MATERIAL AND METHODS

Population

A base population with 178 crossbred animals (32 bucks and 146 does) was constituted. After two discrete generations without selection (first year), selection in overlapping generations has been carried out. Animals were divided in 8 selection groups.
Weaning records (3228) coming from 880 females and 183 males are involved in the analysis.
First mating was when females were around 4.5 months old. Dams were mated around 10 days after kindling (semi-intensive rhythm). Weaning of young rabbits was done around 30 days after birth. Breeding management is organised into fortnightly batches.

Selection process

Predicted breeding values were obtained by BLUP and the inbreeding coefficients were taken into account. A repeatability animal model was assumed (QUASS, 1984). Genetic parameters (CV1) were taken from GARCIA-XIMENEZ et al.(1982): heritability 0.13 and repeatability 0.20.
Sons were selected intrafamily of sire in order to minimise the rate of inbreeding. Matings among individuals with grandfather in common were avoided.
Selection was made on the predicted breeding values of the matings. Selected offspring from a mating or from a dam was limited.

Brief phenotypic description

The following variables have been studied :

- litter size at weaning as the most important trait because it is selected for
- number of records by doe, reflecting the individual information and the permanency
- average litter size at weaning by dam
- average litter size at weaning by fortnight batch.

Statistical analysis

Estimates of genetic parameters were obtained by REML on the repeatability animal model:

$$y_{ijkl} = AE_i + EF_j + a_k + p_k + e_{ijkl}$$

y = litter size at weaning (LSW).

AE = batch of kindling effect (69 levels). Minimum of 15 data was required by level. This effect was analysed as fixed.

EF = lactation effect (fixed) with seven levels. First level was for primiparous females (880 records). Other levels were assigned according to the lactation and pregnancy overlap and to the litter size at weaning of the previous litter of the doe (Table 1).

Table 1 : Description of lactation effects

level	Overlap (days)	previous LSW	records
2	>18	<5	188
3	>18	5-9	964
4	>18	>9	350
5	<7	<5	298
6	<7	5-9	405
7	<7	>9	143

a = individual (animal) genetic effect (random).

p = permanent effect associated with the doe (random).

e = residual effect (random).

The DFREML package (MEYER, 1991) was used to estimate variance components (CV2). All the pedigree information was available since the foundation of the line P (1063 individuals).

RESULTS AND DISCUSSION

Figure 1 : Number of records by litter size at weaning class

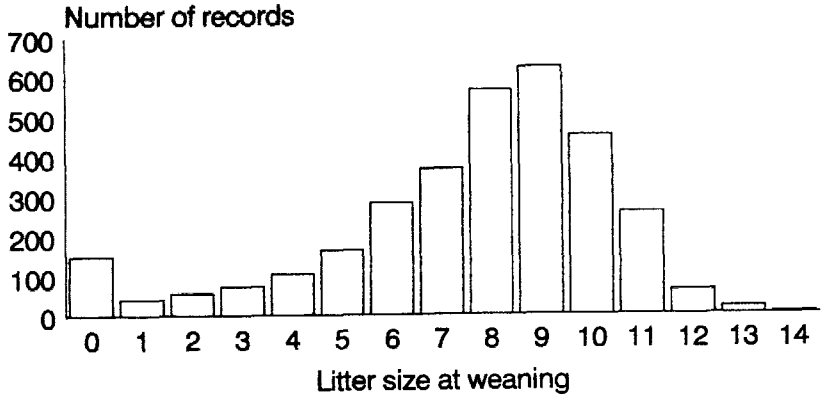
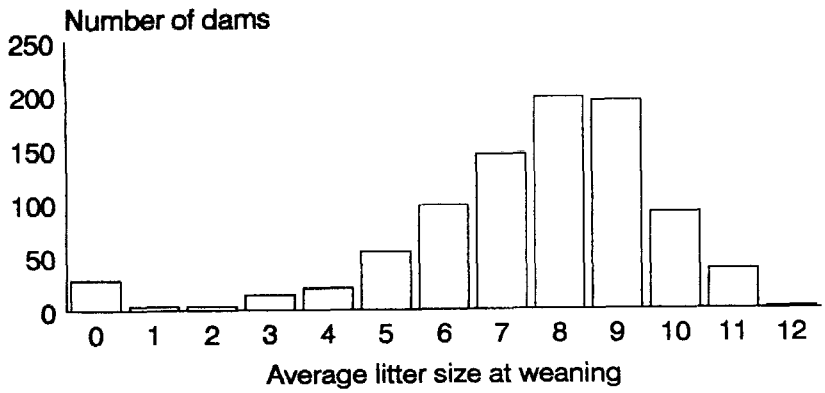


Figure 2 : Number of does by average litter size at weaning class



Phenotypic description

Distribution of litter size at weaning is showed in Figure 1. The mode is nine weaned young rabbits. Average and standard deviation are 7.57 and 2.84. 151 zero weanings were recorded. One fifth (22.5%) of them were at three batches (5%) due to digestive troubles on the nest.

Distribution of average litter size at weaning by dam is presented in Figure 2. Average and standard deviation are 7.23 and 2.18. In Figure 3, distribution of number of parity records by doe is showed. 629 females (71%) had three or more recorded parities.

Average litter size by batch is in Figure 4. Effect of high temperature in summer (August) is clearly reflected (batches 1, 27, 53, 79). High mortality on the nest due to pathological problems appeared in the batches 14-16 and 27-29.

Figure 3 : Number of does by number of parity records

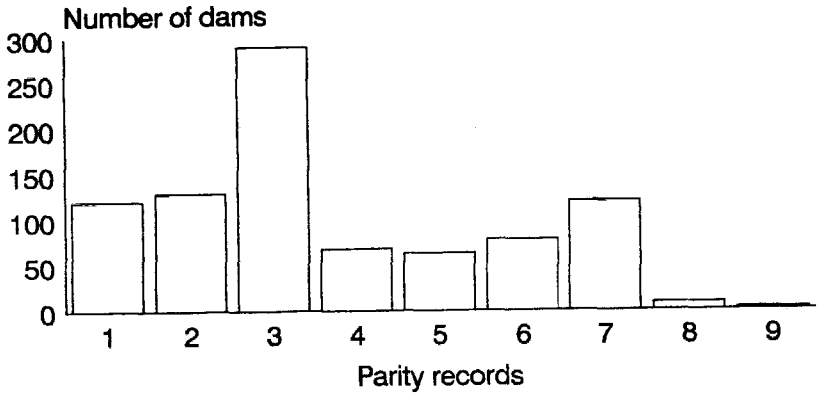
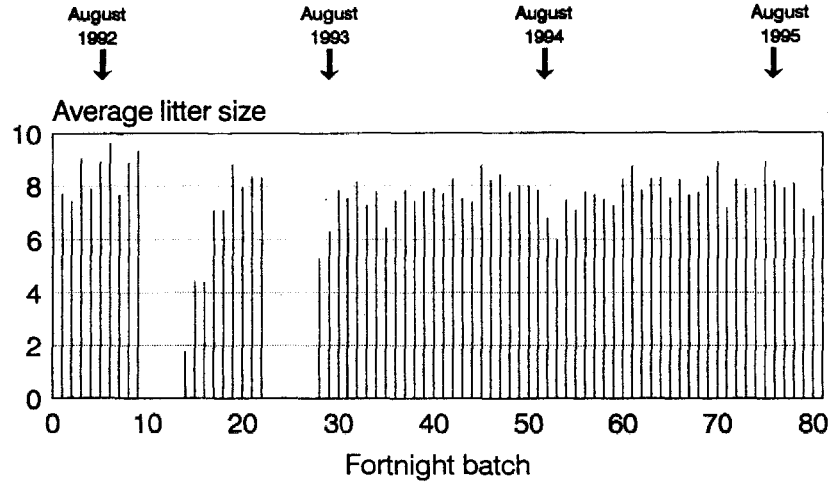


Figure 4 : Average litter size at weaning by kindling fortnight batch

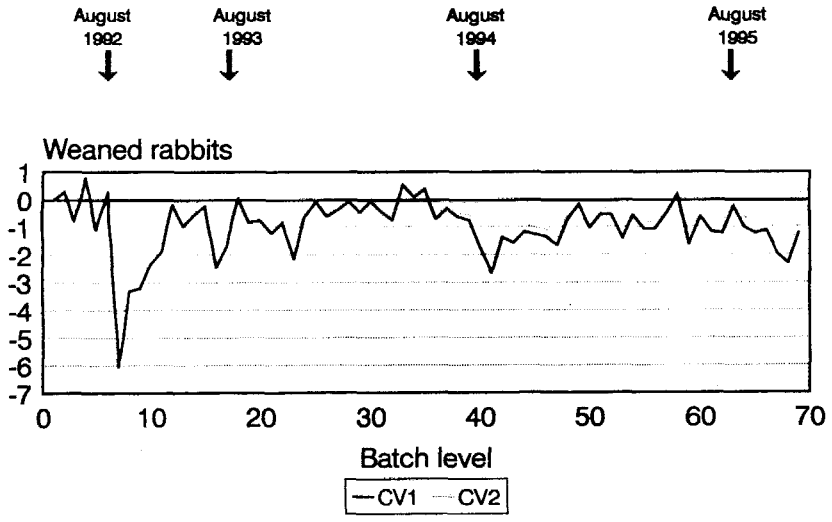


Genetic parameters

Reproductive traits had low heritabilities. Estimated heritability on line P for litter size at weaning was 0.044 (s.e. 0.022). Estimated proportion of phenotypic variance associated with the permanent effect was 0.075 (s.e. 0.025). These estimates are of the same magnitude than those recently reported in other selected populations (BASELGA et al., 1992 [h^2= 0.08 and 0.02, RE= 0.13 and 0.10] ; FERRAZ et al., 1992 [h^2=.14 and RE= 0.17] ; FERRAZ and ELER, 1994 [h^2= 0.10 and 0.00, RE= 0.12 and 0.14] ; GOMEZ, 1994 [h^2= 0.14 and 0.06, RE= 0.18 and 0.12] ; KROGMEIER et al., 1994 [h^2 = 0.09 and RE= 0.21] ; ROCHAMBEAU et al., 1994 [h^2= 0.03 and 0.04]).

Fixed effects

Figure 5 : Estimated batch effects by set of parameters as differences respect to batch 1



Estimated seasonal effects (by batch) appear in Figure 5. Magnitude of these effects was high. Correlation between estimates with different parameters (CV1 and CV2) is higher than 0.9.

The estimates of the lactation effects referred to primiparous effect are presented in Table 2. Litter size was the lowest at first parity. When females accepted the first mate postkindling, litter size at weaning was larger than remated females. The least number of weaned rabbits was when the previous litter size had been intermediate.

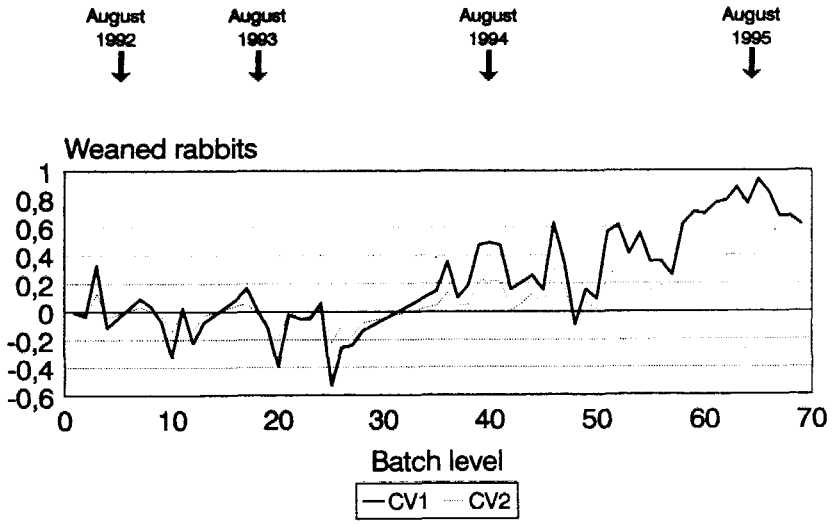
Table 2 : Estimates of lactation effect by BLUP using first (CV1) and REML (CV2) estimates as differences respect level 1

Level	2	3	4	5	6	7
CV1	2.06	0.97	1.12	0.65	0.16	0.19
CV2	1.85	0.94	1.22	0.58	0.16	0.35
S:E:*	0.21	0.10	0.15	0.16	0.16	0.24

*Standard errors of LSM estimates

Predicted breeding values

Figure 6 : Average predicted breeding values of primiparous does by batch level and by genetic parameter set



Average predicted breeding value of current females was 0.68 for CV1 parameter set and 0.32 for CV2 parameter set. These values were 0.53 and 0.24 for males. Thus, response was 0.09 young rabbits by year of selection using CV2 parameter set..

Estimated responses with mixed model methods without control population have been reported by ESTANY et al. (1989), BASELGA et al. (1992) or ROCHAMBEAU et al. (1994). Approximated yearly genetic responses lie in the range 0.20 (ROCHAMBEAU et al., 1994) - 0.04 (BASELGA et al., 1992).

Acknowledgements - The authors are thankful to Company A., Perucho O., Aloy N. and Catafau J. for their valuable assistance and support

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