

ESTIMATION OF GENETIC TREND OF RABBIT GROWTH RATE BY
MIXED MODEL METHODOLOGY

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INTRODUCTION

When a control population is not available, mixed model methodology can be useful for estimating genetic and environmental trends of a selection process (HENDERSON, 1973). When the relationship matrix is used and under several assumptions, the average of genetic predictors is an unbiased estimate of the genetic mean (SORENSEN and KENNEDY, 1984).

Correlated response is also difficult to predict, but BLUP methods can remove some of the environmental effects which occurred during a selection process.

The aim of this paper is to estimate the genetic and environmental trend of growth rate in a line of rabbits individually selected on this trait. Also we examine the correlated response on growth rate of lines selected on litter size.

MATERIAL AND METHODS

Three lines of rabbit were used in the experiment. Two of them were selected on litter size at weaning, line A (White New Zealand) and line V (Synthetic line). The other one was selected on growth rate from weaning to slaughter time (28 to 77 days of life), line B (California). Table 1

shows the number of animals used.

The selection methods were familiar index for litter size and individual selection for line B. Selection started after several generations of random mating, which were used to estimate the genetic parameters.

All the animals were reared under the same conditions, but these conditions were improved little by little. Selection of lines A and B started in 1980, selection of line V started in 1984.

Data from seven generations of selection of the line A, from six of line B, and from one of line V have been used in the analysis. Also, data from three generations of random mating of line V have been used in the analysis and data from the foundation stock. Table 1 shows the structure of data.

TABLE 1

Total number of dams (D), sires (S) and parities (P), and minimal number of dams per generations (m).

LINE	D	S	P	m
A	764	143	1786	81 (A5)
V	572	108	1484	68 (V0)
B	507	118	988	50 (B1)

The traits analysed were: individual growth rate (GR), weaning weight (WW) and slaughter weight (SW).

BLUP was applied on the following mixed model:

$$Y_{ijklm} = L_i + E_j + a_K + a'_l + P_l + e_{ijklm}$$

- L_i is the parity effect (fixed)
- E_j is the year season effect (fixed)
- a_K is the sire additive effect (random)
- a'_l is the dam additive effect (random)
- p_l is the permanent non additive effect of the doe (random)
- e_{ijklm} is the residual (random)

Genetic parameters used to solve the model were previously estimated by BLASCO (1982) using data of former random mating generations.

The averages of the predicted additive individual values of males (2a) and females (2a') were calculated. Genetic trend was estimated by regression of these averages on generation number.

RESULTS AND DISCUSSION

TABLE 2

Averages of predictions of additive values of growth rate (GR), slaughter weight (SW) and weaning weight (WW) of a line selected for growth rate (line B) (grams).

Generation	DAMS			SIREs		
	WW	SW	GR	WW	SW	GR
1	3.3	12.7	10.0	11.7	44.3	34.9
2	9.6	50.5	47.3	17.9	88.5	79.0
3	15.7	92.4	88.9	22.8	137.9	136.4
4	24.4	129.6	121.7	35.5	164.6	145.4
5	33.2	166.1	151.3	31.4	164.4	152.3
6	31.9	183.9	174.3	29.0	176.7	171.5

Table 2 shows the evolution of genetic predictions averages. It seems that selection was effective and a correlated response is found in weaning and slaughter weight. Regression on generation number provides a trend of 33.32 ± 1.82 g.

TABLE 3

Weighted selection differentials of sires and dams (S_S and S_D), weighted additive value of sires and dams (A_S and A_D) and expected additive value of their offspring (A) for growth rate (grams).

Generation	A_D	A_S	A	S_D	S_S
1	32.4	67.4	49.9	22.5	32.5
2	71.8	102.7	87.2	24.5	23.6
3	102.7	146.6	124.7	13.8	10.2
4	131.7	158.6	145.2	9.9	13.2
5	168.2	179.7	173.9	16.8	27.4

By weighting the selection differential (FALCONER, 1981) the effective selection differential can be obtained. Table 3 shows the genetic prediction averages for sires (A_S) and dams (A_D) weighted according to the number of their offspring in next generation, the weighted selection differentials and the expected genetic mean of the generation (A). Selection differentials were poor in generation 4 because of pathological problems, selection in generation 5 was not very effective. Expected means agree with the observed in table 2, which is partially due to links and partially can confirm the validity of the model.

TABLE 4

Averages of prediction of additive values of growth rate of two lines selected on number of weaned rabbits (grams).

Generation	LINE A		LINE V	
	DAMS	SIRES	DAMS	SIRES
0	-	-	11.2	44.5
1	8.9	44.9	29.7	62.9
2	42.8	29.0	65.7	81.4
3	31.8	45.3	69.0	68.1
4	47.1	62.5	69.8	60.7
5	62.1	72.7	-	
6	86.1	91.5	-	
7	84.7	81.0	-	

Table 4 shows the evolution of growth rate in two lines selected for litter size. Only generation 4 was selected in line V whereas all the seven generations were selected in line A.

It can be observed some culling in random mating generations of line V (generative 0 to 3), at least at the beginning. Some improvement of growth rate can be observed in line A. It is difficult to assume that no culling was made, but if so, it was uncouscious. ESTANY et al. (1987) observed a certain improvement in litter size of line B, which leads to some positive relation between growth rate and litter size. Hitherto no estimates of that are available, but some results (ROUVIER et al. 1980) do not agree with our results.

Regression coefficients on generation number were 33.32 ± 1.62 , 13.12 ± 1.72 and 15.65 ± 2.93 g for line B, A and V respectively.

Errors of averages are not offered because of difficulties in computing them. Errors of regression coefficients are not the error of response because of the increase of the error variance with generation number. Nevertheless the results shows that selection was effective for growth rate and give some clues about some positive correlated response in other line selected for litter size.

REFERENCES

- BLASCO, A. 1982. Estudio genético y selección de caracteres de crecimiento en el conejo de carne. Tesis Doctoral. U.P.V. Valencia. pp. 203.
- ESTANY, J.; BASELGA, M.; BLASCO, A.; CAMACHO, J. 1987. Use of BLUP for the estimation of genetic response to selection in litter size of rabbits. 38th Annual Meeting of the E.A.A.P. Lisbon. Portugal 27th September. 1st Oct.
- FALCONER, D.S. 1981. Introduction to Quantitative Genetics. 2nd Edition Longman Ltd. London 340 pp.
- ROUVIER, R.; TUDELA, F.; DUZERT, R. 1980. Experimentation on selection sur la vitesse de croissance du lapin: résultats préliminaires. II Congreso Mundial de Cunicultura, I. Barcelona pp. 244-253.

ESTIMATION OF GENETIC TREND ON RABBIT GROWTH RATE
BY MIXED MODEL METHODOLOGY

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Two strains of rabbits (A and V) selected on litter size at weaning by an index (IX) were used to study the methodology of selection on litter size.

IX was an index containing records on the doe, her mother, full sibs and half sibs. All strains were under the same conditions and reproduction was organized in separate generations.

The accuracy of selection can be improved by considering the information of relatives and by removing non genetic influences. To assess the importance of adjusting data for environmental effects, BLUP method was compared with IX. BLUP was based on a simple repeatability model which included year-season of parity and state of the female (nuliparous, lactating or non nuliparous non lactating) as fixed effects.

On average, results concerning the use of BLUP were: (I) inbreeding coefficient can be disregarded when computing the inverse of the numerator relationship matrix; (II) despite the negative first parity effect and other environmental fluctuations, only 6% of the predicted BLUP response was lost when IX was applied; (III) BLUP was accurate enough when only the last two generations were used for prediction; and (IV) the efficiency of selection can be improved 25% by using sire information.

ESTIMACION DE LA TENDENCIA GENETICA EN VELOCIDAD DE CRECIMIENTO
USANDO EL MODELO MIXTO

A partir de dos líneas de conejos (A y V) seleccionadas por un índice (IX) sobre el tamaño de la camada al destete, se estudia la metodología de la selección del tamaño de la camada.

El índice IX se ha deducido combinando las observaciones de la hembra y las de su madre, hermanas completas y medias hermanas. Todas las líneas se han mantenido en idénticas condiciones y la reproducción se ha organizado en generaciones discretas.

La precisión de la selección puede mejorarse considerando la información de los parientes y eliminando las influencias no genéticas. Para contrastar la importancia de la corrección de los datos por los efectos ambientales, se ha comparado el método BLUP con el IX. La deducción del BLUP se ha basado en un modelo de repetibilidad simple que incluye como efectos fijos el año-estación del parto y el estado de la hembra (nulípara, lactante o no nulípara no lactante).

En promedio, los resultados que se derivan de la aplicación del BLUP son: (I) se puede prescindir del coeficiente de consanguinidad al calcular la inversa de la matriz de parentesco; (II) a pesar del efecto negativo del primer parto y de las fluctuaciones ambientales, solamente se pierde un 6% de la respuesta predicha por el BLUP cuando en su lugar se aplica el índice IX; (III) es suficiente considerar las dos últimas generaciones para calcular el BLUP, y (IV) la eficacia de la selección puede mejorarse en un 25% cuando se considera la información paternal.



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