

GROWTH TRAITS IN FOUR MATERNAL RABBIT LINES

Mínguez C^{1*}, Sánchez J.P.², Ragab M.^{1,3}, El Nagar A.G.^{1,4}, Baselga M.¹

¹Dept. of Animal Science, Polytechnic University of Valencia, Camino de Vera S/N, 46022, Valencia, Spain

²Institut de Recerca i Tecnologia Agroalimentàries. Av. Alcalde Rovira i Roure 191, 25198, Lleida, Spain

³Poultry Production Department, Faculty of Agriculture, Kafr El-Sheikh, Kafr El-Sheikh University, Egypt.

⁴Department of Animal Production, Faculty of Agriculture at Moshtohor, Benha University, Egypt.

*Corresponding author: carminba@posgrado.upv.es

ABSTRACT

This study compares growth traits (weaning weight, slaughter weight and average daily gain) in four maternal lines of rabbits, A, V, H y LP, founded under different criteria, but all of them selected for litter size at weaning at the nucleus of the Polytechnic University of Valencia, until generations 41th, 37th, 10th (only until May 2004) and 6th respectively. A Bayesian approach was used for inference. Two types of comparisons were performed. One was carried out at the origin of the lines, using the complete data set (data from June 1980 to November 2010) and a two-trait analysis. Each growth trait was analysed together with litter size at weaning to avoid bias due to selection. The model used for the growth traits was a mixed model that includes as random effects, the additive, the maternal and the litter of birth. The consideration of the complete data set and the inclusion of the additive effects allow the comparison between the lines at their origin and allowed to predict the differences for given periods (expected differences). The other type of comparisons, at fixed periods of time, was done from March 1997 to August 1998 for comparisons between the lines A, V and H (period 1), and from December 2009 to November 2010 for comparisons between the lines A, V and LP (period 2). Each period of comparison corresponded to the last period when all the lines of each set were housed together at the nucleus, having the same management. These analyses used only the data corresponding to each period and one-trait models for the growth traits. These models were the same than the ones referred for the comparisons at the origin, but the additive effects were excluded. These comparisons allow estimating the actual differences between the lines at the given periods (observed differences) and comparing them to the expected differences for the same periods. A similarity between observed and predicted differences can be interpreted as an indication of the suitability of the complete model to explain the traits.

The estimates of the genetic correlations between litter size at weaning and growth traits were positive but low. At the origin, significant differences were observed for growth traits between the different lines. The contrast between H and LP lines was not done because they only shared two years-season. The results showed that at the origin, the H and LP lines were the heaviest. These differences may be due to different criteria and processes used to establish these lines. In period 1, the results showed that the H line was the heaviest. In period 2, the results showed that the LP line was the heaviest. In both periods, the observed (computed with the records of each period) and the expected differences (computed with the complete model and data set) were very similar for all traits in the two periods, indicating the suitability of the used models. At each period, the differences between lines for growth traits were smaller than at the origin. This result could be due to a correlated response to the selection for litter size at weaning and to the direct response to a concomitant, non-programmed selection for the growth traits themselves different in intensity between the lines.

Key words: Growth traits, Foundation, Genetic lines, Rabbit.

INTRODUCTION

The litter size is an important component in rabbit production and its genetic improvement is considered an effective way to improve economic efficiency in this production (Armero y Blasco, 1992). In general, meat production in rabbits is based on a three-way crossbreeding scheme (Lebas *et*

al., 1996) that needs maternal and paternal lines. The criteria of selection for maternal lines used are litter size at birth or at weaning (Rochambeau *et al.*, 1998, Garreau *et al.*, 2004) and for paternal lines post-weaning daily gain or some weight close to slaughter time (Nagy *et al.*, 2006), traits that are also economically important (Armero y Blasco, 1992). Therefore, it is important to take into account how the growth traits will be affected by the foundation of the maternal lines and by their selection for reproductive traits, because the crossbred does provide to the rabbits for slaughter 50% of their genes. The males of the paternal lines provide the other 50% and these males have very high genetic value for growth and, consequently, is also necessary than the maternal lines have an acceptable level for these traits, and if possible, from their foundation.

The objective of this study was to compare growth traits (weaning weight, slaughter weight and average daily gain) at the origin and at fixed periods during the selection process of four maternal lines of rabbits, founded under different criteria but all of them selected for litter size at weaning.

MATERIALS AND METHODS

Animals and experimental design

This study was carried out in four maternal lines of rabbits housed in the nucleus of the Polytechnic University of Valencia (Spain). These lines are A, V, H and LP and the analysis included all the data recorded from the 1st generation to the current generation at November 2010 (41th, 37th, 10th (only until May 2004) and 6th respectively). These lines have remained as closed populations since the foundation to the present and selected for litter size at weaning. Line A was generated in 1980 from New Zealand White rabbits. This line had been selected by a family index (Baselga *et al.*, 1984, Estany *et al.*, 1989). Line V was generated in 1984 from four different synthetic populations. This line has been selected by through BLUP under a repeatability animal model (Estany *et al.*, 1989), as for lines H and LP. Line H was founded by applying hyperprolific selection and embryo cryopreservation techniques from a large commercial population (Cifre *et al.*, 1998). The LP line was created by selecting females from commercial farms that showed an extremely long productive life, associated with prolificacy near or above the average of the Spanish commercial rabbit population (Sánchez *et al.*, 2008). The line H was housed on the same farm until its 10th generation of selection (May 2004) when it was moved to another farm.

The reproductive management was semi-intensive, the does were mated for first time at 17 weeks of age. After first parturition does were serviced 10-12 days post-kindling and a pregnancy test was carried out by an abdominal palpation on day 12 after mating. The does that did not accept the buck were presented to the male 1 week later and does that were not pregnant were also returned to repeat mating. Matings between close relatives were avoided and mates did not have common grandparents. Litters were reared by their dams, without fostering, until weaning at 28 days. At weaning, rabbits were individually identified by a number tattooed on the ear and placed into collective cages of about eight rabbits until marketing at 63 days. Rabbits were fed a standard commercial pellet diet, offered *ad libitum*

The growth traits studied were: weaning weight (WW), slaughter weight (SW) and average daily gain (ADG). The numbers of records were 323,208 for WW, 300,553 for SW and ADG coming from 46,708 litters with their number of born and weaned rabbits recorded. The pedigree file included 346,638 animals.

Statistical Analysis

To avoid bias in the estimates due to the selection process (Sorensen and Johansson, 1992), the analyses of WW, WS and ADG were carried out together with litter size at weaning, i.e. the selection criteria. Two-trait models were used, one for each of the growth traits and the other for litter size at weaning; thus considering the complete data set, the variances components and the differences between lines at origin were estimated. The model for each growth traits was:

$$Y_{ijklmn} = LAE_j + OP_k + bNV_n + a_l + m_m + co_n + e_{ijklmn}$$

Where: Y_{ijklmn} is a record of the trait of animal l ; LAE_j is the effect of line-year-season combination, line of animal l and the year-season in which the animal l was born (one year-season every 3 month: 298 levels for all lines); OP_k is the effect of the order of parity (5 levels: 1st, 2nd, 3rd, 4th, and >4th), NV_n is a covariate including the number of born alive in the litter in which the animal was born, being b the regression coefficient; a_l is the random additive value of animal l ; m_m is the random effect of its dam (animal m is the dam of the individual l); co_n is the random effect of the litter in which the animal was born and e_{ijklmn} is the residual effect.

The model for litter size at weaning was:

$$NW_{jkl} = LAE_j + EF_k + a_l + p_l + e_{jkl}$$

Where: NW_{jkl} is the litter size at weaning of a parity of dam l , EF_k is the effect of the physiological state of the doe (5 levels: nulliparous, primiparous lactating, primiparous non-lactating, multiparous lactating and multiparous non-lactating), p_l is the random, permanent effect of the doe l . Other components of the model were defined above.

The correlation structure between the random effects was: between the additive effects of the two groups of traits related through the numerator relationship matrix and the maternal effect of growth traits (m_m) with the permanent effect of the litter size at weaning (p_l). Also, to specify the environmental covariance structure between each of the growth traits and NW , the term e_{jkl} of the NW model was divided in two parts, c and e^* , The first effect was assumed to be correlated with the effect of the litter on growth trait model (co_n) and the second uncorrelated (García y Baselga, 2002). For solving these two-trait models (variance components, systematic and random effects estimation) gibbs2f90 (Miszta *et al.*, 2002) was used, assuming flat priors for systematic effects and variance components, and normal priors for random effects.

Contrasts between lines at their foundation: As in Ragab and Baselga (2011), the differences between pair of lines at foundation were calculated from the estimates of the LAE effects. To do this, we considered the difference between the averages for each line of the pair of the LAE effects corresponding to the levels shared by the two lines under the same environmental conditions. Because the effect of selection is considered in the models by the additive effects, the line effect refers to the time of foundation of the lines.

Contrasts between lines at fixed times: The times chosen for the comparisons were the more recent periods when different sets of three of lines were housed together at the nucleus having the same type of cages and management. They were from March 1997 to August 1998 (period 1) for lines A, V and H, and from December 2009 to November 2010 (period 2) for lines A, V and LP. For estimating observed differences, the additive genetic effects were excluded from the models and only the data recorded during the shared times of comparison were used. Thus, the line effects refer to the real genetic merit of the lines at the time of comparison as a consequence of selection and genetic drift. Thus, the statistical models used in these analyses were the same as described for the differences at the foundation, but the additive genetic effects were not considered. Expected differences between the lines at fixed times using the complete model and data set can be computed as the contrast between lines during the times shared (period 1 and period 2), plus the difference between the averages of the additive genetic values of the animals of each line having data in this period. These expected estimates were computed and their comparison to the observed differences provides evidence of the appropriateness of the genetic models used.

RESULTS AND DISCUSSION

Table 1 shows the contrasts between the lines A, V, H and LP for the traits WW (g), SW (g) and ADG (g/day) at foundation. The contrasts A-V showed that line A was superior to line V, with a probability of this contrast to be greater than 0 of 0.99 for WW, 0.97 for SW and 0.75 for ADG, although the HPD

95% (highest posterior density region at 95 %) of SW and ADG included the 0. The contrasts between the lines H and LP with the lines A and V (A-H, V-H, A-LP and V-LP) pointed out that the lines H and LP were the heaviest with a probability of zero or near zero of these contrasts to be greater than 0.

Table 1: Contrasts between the lines A, V, H and LP for WW (g), SW(g) and ADG (g/day) at foundation. (Posterior means \pm posterior standard deviations).

Trait	A-V	A-H	V-H	A-LP	V-LP
WW(g)	28 \pm 12	-24 \pm 14	-59 \pm 14	-66 \pm 16	-120 \pm 16
SW(g)	70 \pm 38	-142 \pm 33	-214 \pm 49	-217 \pm 34	-372 \pm 57
ADG(g/d)	0.51 \pm 0.78	-3.99 \pm 0.77	-4.19 \pm 1.12	-5.18 \pm 0.8	-6.93 \pm 1.33

Table 2 shows the contrasts between the lines A, V, H and LP for the growth traits at fixed times (observed differences). In period 1, the contrast A-V showed that line A was superior for WW, with a probability of 1.00 of this contrast to be greater than 0, but the line V was superior for SW and ADG, being 0.17 and 0.00 respectively, the probability that the contrasts were positive. However, the HPD 95% of SW included the 0. The contrasts involving line H (A-H and V-H), indicated that this line was the heaviest with a probability of 0 that all these contrasts were positive, excepted the A-H contrast for WW that had a probability of 0.25 (its HPD 95% included 0).

Table 2: Contrasts between the lines A, V, H and LP for WW(g), SW(g) and ADG (g/day) at fixed time (Observed differences). (Posterior means \pm posterior standard deviations).

Trait	Period 1			Period 2		
	A-V	A-H	V-H	A-V	A-LP	V-LP
WW (g)	17 \pm 5	-4 \pm 5	-20 \pm 5	-7 \pm 8	-53 \pm 7	-46 \pm 6
SW (g)	-8 \pm 9	-59 \pm 10	-51 \pm 9	-17 \pm 13	-88 \pm 13	-71 \pm 11
ADG (g/day)	-0.87 \pm 0.18	-1.71 \pm 0.20	-0.85 \pm 0.18	-0.44 \pm 0.28	-1.18 \pm 0.22	-0.74 \pm 0.22

Table 3: Contrasts between the lines A, V, H and LP for WW (g), SW (g) and ADG (g/day) at fixed time (Expected differences) (Posterior means \pm posterior standard deviations)

Trait	Period1			Period 2		
	A-V	A-H	V-H	A-V	A-LP	V-LP
WW (g)	22 \pm 5	2 \pm 5	-20 \pm 5	0 \pm 7	-44 \pm 6	-45 \pm 6
SW (g)	-6 \pm 8	-56 \pm 9	-50 \pm 8	-20 \pm 10	-80 \pm 10	-61 \pm 8
ADG (g/day)	-1.00 \pm 0.15	-1.82 \pm 0.17	-0.82 \pm 0.16	-0.58 \pm 0.20	-1.19 \pm 0.20	-0.60 \pm 0.16

In period 2, the contrast A-V showed that, for all the studied traits, the line V was the heaviest and the probabilities of the contrasts to be greater than 0 were 0.17 for WW, 0.09 for PS and 0.05 for ADG. However, the corresponding HPD 95% included the 0. The contrasts for line LP (A-LP and V-LP) showed that this line was the heaviest with the probability that these contrasts were greater than 0 were zero for all. The expected differences between lines (Table 3) are similar to the observed differences (Table 2). This similarity possibly indicates the appropriateness of the models used to analyse the traits. It should be noted that the observed differences at different times of the process of selection follow the same trend as the differences estimated at the origin of lines but their magnitude decreased. The lines differ in the number of generations of selection and this factor could explain part of the decrease as a correlated response (positive genetic correlation between NW and growth traits: 0.29, 0.13 and 0.15 respectively for WW, SW and ADG) and for the effect of a concomitant, non-programmed selection tending to partly benefit the selection of animals with heavier weight, mainly in the V line.

CONCLUSIONS

The results showed that at the origin there are important differences between the lines in growth traits that could be partly explained by the different procedures used for establishing the lines. In general, the differences at the origin are kept along the process of selection, but their magnitude tend to

decrease, due to differences in the number of generations of selection and to the effect of a concomitant, non-programmed selection for the growth traits. The similarity, between observed and predicted differences at fixed times for all traits and pair of lines, is an indicator of the suitability of the genetic model used to analyse the data.

ACKNOWLEDGEMENTS

This study was supported by the Spanish research project (CICYT AGL2008-03274). C. Mínguez Spanish was supported by a research grant from the Spanish Ministry of Education (BES-2009-015378).

REFERENCES

- Armero Q., Blasco A. 1992. Economic weights for rabbit selection indices. *J. Appl. Rabbit Res.* 15:637-642.
- Baselga M., Blasco A., Estany J. 1984. Índice de selección de caracteres reproductivos con información variable. *IN: Proc. 3rd World Rabbit Congr., 1984 June, Rome, Italy* 1:62-65.
- Cifre J., Baselga M., García-Ximénez F., Vicente J.S. 1998. Performance of a hyperprolific rabbit line I. Litter size traits. *J. Anim. Breed. Genet.* 115: 131-138.
- Estany J., Baselga M., Blasco A., Camacho J. 1989. Mixed model methodology for the estimation of genetic response to selection in litter size of rabbits. *Livest. Prod. Sci.* 21:67-76.
- García M. L., Baselga M. 2002. Estimation of correlated response on growth traits to selection in litter size of rabbits using a cryopreserved control population and genetics trends. *Livest. Prod. Sci.* 78:91-98.
- Garreau H., Piles M., Larzul C., Baselga M., Rochambeau H. de 2004. Selection of maternal lines: last results and prospects. *In: Proc. 8th World Rabbit Congress, 2004 September, Puebla, Mexico.*
- Lebas, F., P. Coudert, H. Rochambeau, and R. G. Thébault. 1996. Le Lapin. Elevage et Pathologie. *FAO, Rome, Italy.*
- Misztal I., Tsuruta S., Strabel T., Auvray B., Druet T., Lee D. H. 2002. BLUPF90 and related programs (BGF90). *In: Proc. 7th World Congress on Genetics Applied to Livestock Production, 2002 Montpellier August, France. Commun. No. 28-07*
- Nagy I., Ibáñez N., Romvári R., Mekkawy W., Metzger Sz., Horn P., Szendrő Zs. 2006. Genetic parameters of growth and in vivo computerized tomography based carcass traits in Pannon White Rabbits. *Livest. Sci., 104: 46-52.*
- Ragab M., Baselga M. 2011. A comparison of reproductive traits of four maternal lines of rabbits selected for litter size at weaning and founded on different criteria. *Lives. Sci.* 136: 201-206.
- Rochambeau H. de., Duzert R., Tudela F. 1998. Long term selection experiments in rabbit. Estimation of genetic progress on litter size at weaning. *In: Proc. 6th World Congress on Genetics Applied to Livestock Production, 1998 January, Armindale, Australia, Vol., 26:112-115*
- Sánchez J. P., Theilgaard P., Mínguez C., Baselga M. 2008. Constitution and evaluation of a long-lived productive rabbit line. *J. Anim. Sci.* 86:515-525.
- Sorensen D. A., Johansson K. 1992. Estimation of direct and correlated responses to selection using univariate animal models. *J. Anim. Sci.* 70: 2038-2044.