FUNCTIONAL LONGEVITY IN FOUR SPANISH MATERNAL LINES OF RABBITS

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ABSTRACT

A comparative study among four maternal lines of rabbits (A, V, H and LP) was conducted. Data for this study were collected during the program of selection of these lines from September 1980 to March 2011. The main objective of this work was to compare doe longevity (length of productive life, LPL) in four lines selected for litter size at weaning but founded on different criteria. The analyzed traitwas defined as the time in days between date of the first positive pregnancy diagnosis and date of culling or death. The comparison has been done at their foundation time using the complete pedigree file and the complete data set of the performances from their foundation until March, 2011.The number of does with records was 12693 and the pedigree involved 14805 animals. The second objective of this study was to compare the lines at fixed times, during the last three year-seasons shared by at least three of them. The fixed times of comparison were from March, 1997 to September 1998 (period 1) for A, V and H lines, and from September, 2009 to March, 2011 (period 2) for A, V and LP lines. Survival analyses were carried out with a Cox proportional hazard model. The effective heritability for LPL was 0.16. The relative risk (RR) for the contrasts A*vs* V, A *vs* H and A *vs* LP was 3.40, 3.43 and 5.56 at foundation, respectively. RR for the contrasts A*vs* V and A *vs* H was 1.42 and 1.32, respectively, during the first fixed period of comparison. RR for the contrastsA*vs* V and A *vs* LP was 1.41 and 1.71, respectively, during the second fixed period of comparison. The line A had a risk of death or culling greater than the other lines in all comparisons. No significant differences either between V and LP lines or between V and H lines have been founded in any comparison.In general the differences between lines at fixed times were smaller than those at their foundation. Along the generations of selection for litter size, the differences of longevity between lines tend to decrease, due to the action of the natural selection in the lines of lower longevity. The foundation criterion is important to define the initial longevity of the lines.

Key words: Rabbits, longevity, maternal lines, survival analysis, Cox proportional hazard model.

INTRODUCTION

The annual replacement rate in meat rabbits is about 120% (Rafel et al., 2001) with near 50% of the dead or culled does replaced during their first 3 parities (Rosell, 2003). The main problems associated with this high replacement rate are the cost of the does, the greater frequency of less mature females, and sometimes the management and pathological problems related to introduction of animals from other farms (Piles et al., 2006a). Therefore selective breeding to increase the length of productive life could help to reduce costs attributed to replacements. Intensive meat rabbit production is based on the use of crossbred does, coming from the cross between two maternal lines. The length of productive life of the crossbred does will depend on both the longevity of the maternal lines involved in the cross and on heterotic effects that might

appear (Piles et al., 2006b). Consequently it is important to compare the longevity of lines involved in the cross and to assess how these differences evolve during the selection processes of the lines. Thus, the aims of this work were to compare four Spanish maternal lines of rabbits in terms of longevity, at their foundation and at different fixed periods during their selection process, considering that each line was founded on different criteria but all of these lines are being selected for litter size at weaning.

MATERIALS AND METHODS

Animals

Data used in the present study were collected from four Spanish maternal lines of rabbits (A, V, H, LP) reared at a selection nucleus located in the farm of the Department of Animal Science, Polytechnic University of Valencia. The records were collected along the generations of selection of those lines from September 1980 to March 2011. These lines are being selected for litter size at weaning and founded following different criteria(Ragab and Baselga, 2011). The last generations of selection considered from the beginning of selection were 41th, 37th, 10th (until May, 2004) and 7th for A, V, H and LP lines, respectively. Both males and females start reproduction, conducted by natural mating, at around 17 to 18 weeks, and in subsequence cycles animals are mated 11 days after kindling. On the day 12 post-mating a gestation test by abdominal palpation takes place.No cross fostering takesplace and weaningis done 28 days post-partum. Both breeding animals and progeny are fed ad libitum on a pelleted commercial ration.

Data and statistical models

The longevity of a doe (length of productive life, LPL) was measured as the difference between the date of first positive pregnancy diagnosis and date of death or culling.For appropriate genetic evaluations of animals, does were never culled on account of their production results, so LPL represented functional longevity. In addition to this information, the record of each animal included a censoring code (a binary variable indicating whether the animal died or it was culled because a pathological issue (uncensored) or either was alive or it was culled due to management practices (censored)) and all the information regarding physiological status of the female during herentire life, as well as all the prolificacy records during all the parturitions and the line to which the animal belongs. Date and reason for culling or death were systematically recorded. The number of does with records was 12693, 5132 censored, and the pedigree involved 14805 animals. The data set was analyzed with survival analysis techniques using the program Survival Kit 6.0 (Ducrocq et al., 2010). The model of analysis was a Cox proportional hazard model (Sánchez et al., 2004; Piles et al., 2006a). The hazard function of an individual i (i = 1….n) at time t is modelled as

$$h_i(t|\mathbf{x}'_i(t)) = h_0(t)*\exp\{ \mathbf{x}_i'(t)_{LYS} \beta_{LYS} + \mathbf{x}_i'(t)_{PS} \beta_{PS} + \mathbf{x}_i'(t)_{OPP} \beta_{OPP} + \mathbf{x}_i'(t)_{NBA} \beta_{NBA} + \mathbf{z}_i'\mathbf{u}\},$$

where $h_i(t|\mathbf{x}'_i(t))$ is the hazard of animal i at time t, affected by covariates indicated by $\mathbf{x}_i'(t) = \{ \mathbf{x}_i'(t)_{LYS}, \mathbf{x}_i'(t)_{PS}, \mathbf{x}_i'(t)_{OPP}, \mathbf{x}_i'(t)_{NBA}, \mathbf{z}_i \}$; $h_0(t)$ is the baseline hazard at time t. Fixed time dependent factors were: i. Line-year-season combination (LYS) with 151 classes, where the year-season is defined by 6 months time intervals. ii. Physiological status of the doe at mating time (PS), with 4 classes (pregnant, lactating, non-pregnant and pregnant and lactating). iii. Order of the positive palpation (OPP) which is categorized into 6 levels defined as 1, 2, 3, 4, 5 and 6 or > 6 positive palpation. iv. Number born alive (NBA), defined through 9 classes as follows: nulliparous, 0 to 1, 2 to 3, 4 to 5, 6 to 7, 8 to 9, 10 to 11, 12 to 13 or > 13 born alive. The only time-independent factor was the additive genetic effect of the animals (**u**), assumed to follow a multivariate normal distribution with mean zero and variance $A\sigma^2_A$, where A is the relationship matrix and σ^2_A is the additive variance. This is a parameter to be estimated, and from its value effective heritability was calculated as $h^2 = \sigma^2_A / \sigma^2_A + 1$ Yazdi et al. (2002).Using the estimated additive variance, the fixed and additive effects of the model were estimated, including LYS effects. Because the additive effects were considered, taking into account any possible genetic trend due to selection, the estimates of the difference between lines refer to the

line effects at foundation time. Thus, the contrast of the differences between each pair of lines at foundation is computed as the difference of the averages, for each line, of the line-year-season effects corresponding to the year-seasons common to both lines. Real differences between lines at different periods of time shared by some of the lines can be computed, without relying on the genetic model and by only using the records of the defined periods of the lines to be compared. To this end, the model of analysis should be the one previously defined, removing the additive genetic effect. In this case the line effects refer to the real genetic merit of these lines at the time of comparison. The difference between two lines at a defined period was computed as the difference between the averages for each line of the line-year-season effects of the period. These differences can be called observed differences. The periods chosen for comparison were arbitrarily defined by the last three year-seasons shared by three of the lines under the same managerial conditions. Between A, V and H lines this period was from March 1997 to September 1998, while between A, V and LP lines the period was from September 2009 to March 2011. It is possible to predict the differences between the lines at the defined periods using the results of the analysis with the complete model and complete data set. The predicted difference between two lines will be computed in the same way as the comparison at foundation but limited to the year-seasons corresponding to the period where both lines are present, adding the difference between the averages of the additive values of the animals of each line performing during that period. Then, the observed differences can be compared with the predicted ones as a way to check the adequacy of the complete model to explain the complete longevity data set.

RESULTS AND DISCUSSION

The estimated additive variance was 0.19 ± 0.03 which corresponds to an effective heritability of 0.16. Our estimate of effective heritability was larger than that one previously reported by Sánchez et al. (2004) (0.086, not presented in that paper). These two values should be compared with caution since the trait definition, the population studied, the physiological state categories, and the model are different. Other estimates of the heritability for longevity were reported by Garreau et al. (2001), who studied this parameter using different models, and the estimated value under the most realistic model was 0.05. Another estimate of heritability using a Bayesian methodology and the Cox animal model with residual was by Sánchez et al. (2006) who reported an additive variance of 0.25 (posterior mean) and a residual variance of 0.69 which corresponds to an effective heritability of 0.12, here the same population as Sánchez et al. (2004) was used, but the model of the analysis was different from the one used in our study. Our estimate of heritability is within the range of the different estimates of heritability reported by Piles et al. (2006a) (0.158 to 0.237). The comparison among lines at their foundation is shown in Table 1. Lines V, H and LP showed a significant superiority over line A. The greatest difference was observed between lines A and LP. LP line was created from does that had at least 25 parities as indicator of hyper-longevity and the longer productive life of LP females could partially be understood as an indicator of success of the selection procedure during the foundation of this line (Sánchez et al., 2008), thus it would be expected for this line to observe the lower risk of death or culling.

Table 1. Contrasts between the lines A, V, H and LP for longevity at foundation.

	A *vs* V	A *vs* H	A *vs* LP	V *vs* H	V *vs* LP
Estimate[1]	1.223[*]	1.232[*]	1.716[*]	-0.291	0.003
SE	0.259	0.287	0.327	0.267	0.289
Relative risk[2]	3.40	3.43	5.56	0.75	1.00

[1]Log-hazard ratios; SE : Standard error; [2]Hazard ratios; [*]significant difference (P<0.05).

On the other hand, Aline was founded by mating does and bucks of the New Zealand White breed belonging to commercial populations that primarily maintained the standard morphological characteristics of the breed, without attending to any productive criteria. Piles et

al. (2006b) found relevant differences in the genetic effects for functional longevity between maternal lines A, V and Prat and the crossbred females from them.They stated that an A doe was twice as likely to be replaced as a crossbred Prat × A doe, and in general the genetic types with the highest relative risks were those in which the A line participated. Sánchez et al. (2008) indicated the superiority of the line LP over the line V in survival ability, but this comparison was at foundation for line LP and at the generation 31st for line V.The relative risk describes how much more likely it is that culling or death occurs within a level of a given factor relative to another level of the same factor. Thus, relative risk in table 1 refers to the ratio between hazard of death or culling for the lines involved in the contrast.

The observed differences between the lines at periods 1 and 2 are presented in Table 2.A line had a risk of death or culling greater than V and H lines during the period 1, and also than V and LP lines during the period 2,similarly to what happened at foundation. This result is in agreement with those of Ragab et al. (2011) who demonstrated, with current records, that lines A and H lines have a similar ability to avoid risk factors and both of them are more sensitive than V and LP animals. No significant difference between V and LP lines has been found, contrarily to the result of Sánchez et al. (2008) who found that the LP line had a slightly longer reproductive life than the V line, but again the comparison is done at different moments of the selection process.

Table 2. Observed differences between lines for longevity during the different fixed periods of comparison.

	Period (1)			Period (2)		
	A *vs* V	A *vs* H	V *vs* H	A *vs* V	A *vs* LP	V *vs* LP
Estimate[1]	0.347[*]	0.278[*]	-0.069	0.347[*]	0.539[*]	0.192
SE	0.101	0.111	0.106	0.141	0.148	0.149
Relative risk[2]	1.42	1.32	0.93	1.41	1.71	1.21

Period (1): From March 1997 to September 1998; Period (2): From September 2009 to March 2011; [1]Log-hazard ratios; SE : Standard error; [2]Hazard ratios; [*]significant difference (P<0.05).

It deserves our attention that in general the differences between line A and the others as the selection process evolves get reduced. This result may be due to the fact that along the generations of selection for litter size, the differences of longevity between lines tend to decrease, due to the stronger effect of the natural selection in the lines of lower longevity. For animals with lower longevity (line A), the probability of dying before leaving progeny selected for litter size is higher than in animals having higher longevity, and also, the selected progeny of parents with low longevity would have a higher probability of dying before reaching maturity, thus long-lived animals tend to be those leaving more progeny during the selection process.

The corresponding predicted differences for both periods are presented in Table3; the predicted values of the log-hazard ratio between lines for the period 1 were 0.41, 0.22 and -0.18 for the contrasts between A*vs* V,A *vs* H, and V *vs* H lines respectively. For the period 2, the predictions for the contrasts between A *vs* V, A *vs* LP, and V *vs* LP lines were 0.36, 0.54 and 0.18 respectively. In both cases the observed differences (Table 2) and these predictions are similar, which is an indication of the adequacy of the model to explain the longevity data.

Table 3. Predicted differences between lines at fixed periods and their components.

Difference	Period (1)			Period (2)		
	A-V	A-H	V-H	A-V	A-LP	V-LP
At foundation[1]	1.52	1.23	-0.29	1.90	1.86	-0.04
Of additive averages[2]	-1.12	-1.01	0.11	-1.55	-1.32	0.22
Predicted	0.41	0.22	-0.18	0.36	0.54	0.18

[1]Computed using data performed at the periods (1) or (2); [2] Differences between averages of additive genetic values.

Table 3 shows that the differences between lines at foundation computed during the defined periods are similar to the values showed in Table 1, in addition it also shows how the selection process makes the averages of the breeding values for the line A to became more favorable than those from V and LP lines, which explains the observed reduction of differences between lines with selection.

CONCLUSIONS

The average longevity of a population greatly depend on the criteria followed for the foundation of this population, it seems thatthe breed criterion is less suitable than other criteria more closely related to production. Along the generations of selection for litter size, the differences of longevity between lines tend to decrease. The predicted differences between lines match well the current phenotypic differences between lines, indicating that the genetic model is suitable to describe the longevity records in this population.

ACKNOWLEDGEMENTS

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