DIVERGENT SELECTION FOR LONGEVITY IN BREEDING DOES

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ABSTRACT

A divergent selection for functional longevity, based on genetic merit estimated through survival analysis techniques, was carried out in the INRA 1077 rabbit line. The experiment was carried out to estimate the efficiency of such a selection and to analyse the consequences on other reproduction traits. Given the herd management, length of productive life was measured as the number of artificial inseminations of rabbit does without any culling for infertility. A total of 48 males were progeny tested based on the longevity of ten daughters (5 in the INRA SAGA farm and 5 in the INRA EASM farm). Based on their estimated genetic merit, 5 “high longevity” and 5 “low longevity” males were selected and produced a new generation (5 sons/sire). These 48 males were similarly progeny tested to estimate the direct and correlated responses to selection. A significant difference in longevity (+0.92 AI i.e. 39 days) was observed between the two lines. The differences of survival between the 2 lines in the SAGA farm were mainly due to culling (26% in the low line vs. 14% in the high line) whereas the mortality was similar in the 2 lines. In the EASM farm, mortality and culling were both higher in the low line than in the high line (33% vs. 15% and 19% vs. 7%, respectively). Except for the total number born which was higher in the low line, there was no difference between the two lines for reproduction traits recorded for each kindling. Nevertheless, because of the difference in the number of litters between the 2 lines, the sum of young rabbits born alive per doe and the sum of young rabbits weaned per doe were higher in the high line (+5 kits).

Key words: Rabbit females, Longevity, Survival analysis.

INTRODUCTION

In French meat rabbit farming, the doe replacement rate is about 115%. This replacement rate is partly explained by the mortality of does (30% on average). The other causes of culling are varied but are often fertility troubles or a general difficulty to cope with several kindling. The main problems associated with high replacement rate are: the replacement cost of the does and the higher frequency of less mature females (young does are still growing and are less immunologically mature at parturition, showing lower litter size, and more health problems).

The longevity of does has been improved thanks to recent advances in sanitary management and the improvement of feeding programs. An other way of improvement is selection since several studies have showed the genetic variability of longevity (Sanchez *et al.*, 2004; Piles *et al.*, 2006). These studies were based on the use of a specific methodology for the treatment of time data: the survival analysis.

The aim of the present study was to verify the efficiency of selection for longevity in does and to study the consequences of such a selection on other reproduction traits. This study describes the results of a divergent selection experiment for functional longevity in does.

MATERIALS AND METHODS

First generation of selection

Forty eight bucks from the INRA 1777 strain were mated twice with 200 does from the same strain in order to produce, with a 4 months gap, 2 batches of 240 does by keeping 5 daughters per buck in each batch. Mating and kindling were performed at the SELAP INRA experimental farm. The young does of the first batch were transferred after weaning to the SAGA INRA experimental farm. The does of the second batch were transferred the day following their birth to the EASM INRA experimental farm; in this place, the young does were fostered by SPF lactating does.

Does were inseminated 7 times every 6 weeks from the age of 19 weeks in the farms of SAGA and EASM. The remaining still alive does were culled after the weaning of the 7th cycle. Replacement does were introduced regularly in the shed without any involvement in the experiment in order to keep the conditions of production constant.

In each farm the does were culled only for very bad body or health conditions. There was no litter standardization.

Selection of bucks

After the 7th AI of does, a survival analysis was performed using the Survival Kit (Ducrocq and Solkner, 1998), a FORTRAN package devoted to the analysis of survival data. Survival data are analysed using proportional hazards models. These models describe the hazard function of each individual as the product of a baseline hazard function and a positive exponential function of the covariates The number of AI was considered as the longevity measurement and a discrete model was applied. The following effects were included in the final model: season of mating within farm (8 classes), reproduction cycle (first, second or latter), litter size (8 classes), sire and maternal grand sire. The estimation of sire effect (genetic value of longevity) was used to rank sires according to their longevity index. The 5 bucks with the lowest longevity index and the 5 bucks with the highest longevity index, respectively, were selected to constitute the low line (L) and the high line (H), respectively. The average difference between the 2 groups of sires was equal to 3 standard deviations of index.
Each of the 5 bucks was mated with 4 INRA 1777 does in the SELAP experimental farm. 48 males resulting from this mating were randomly chosen in each buck family.

Selection response

As in the first generation, the 48 bucks of the second generation were mated 2 times with 200 does in order to produce 2 batches of 240 does. The does were transferred to the SAGA and EASM experimental farms in the same conditions as for the does of the first generation. The does were kept until the weaning of the 8th generation.

Measurements

The does were inseminated every 6 weeks with semen from a paternal heavy line. The young rabbits were weaned at 30 days. After each AI, fertility of does was recorded. For each litter the total number born, the number of born alive and the number weaned were also recorded. The sum of total born and born alive in a whole carrier was calculated for each doe. The longevity criterion was the number of AI. The does still alive after the 8th AI were considered as censored. A new survival analysis was performed on the does of the second generation. The model was the same as for the does of the first generation. Prolificacy traits and fertility were analysed using the GLM and the GENMOD procedures of the SAS software, respectively. The model included the fixed effects of line, farm and parity.

RESULTS

The survival curves for the 2 batches of the first generation are given in Figure 1. Mortality was higher in the batch housed in the SAGA farm than in the batch housed in the EASM farm.

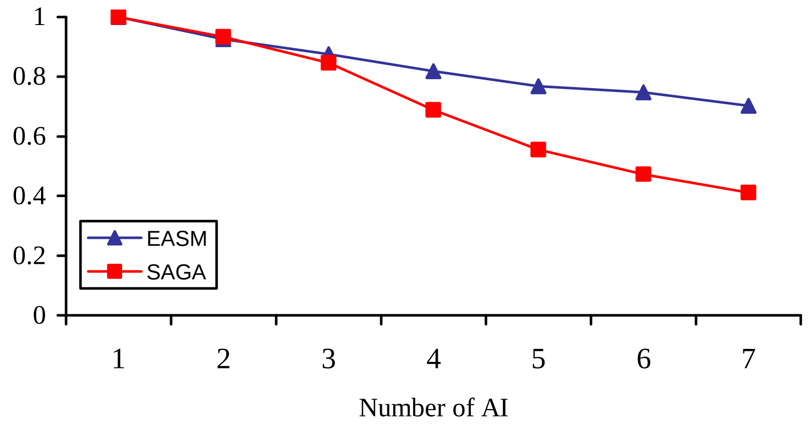

Figure 1: Survival curves for the 2 batches (SAGA and EASM) of the first generation

The survival curves for the two lines (B and H) and the 2 batches (SAGA and EASM) of the second generation are given in Figure 2. A survival analysis of this generation showed a significant effect of the line (P=0.001). The difference of longevity between the 2 lines was 0.92 AI i.e. 39 days. As in the first generation, mortality was higher in the SAGA farm than in the EASM farm. The Table 1 gives the proportion of mortality and culling in the 2 lines. The differences of survival between the 2 lines in the SAGA farm were mainly due to culling (26% in the low line vs. 14% in the high line) whereas the mortality was similar in the 2 lines. In the EASM farm, mortality and culling were both higher in the low line than in the high line (33% vs. 15% and 19% vs. 7%, respectively).

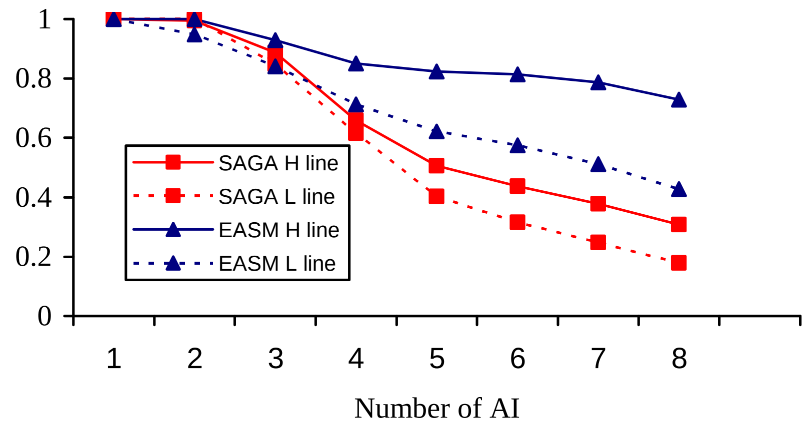

Figure 2: Survival curves for the 2 batches (SAGA and EASM) and the 2 lines (L and H) of the second generation

Concerning the reproduction traits, the number of litters was significantly higher in the high line than in the low line (4.26 in the high line vs. 3.64 in the low line). The total number born per litter was higher in the low line than in the high line (9.93 vs. 9.45) but there was no significant difference between the 2 lines for number born alive per litter and for number weaned per litter (Table 2). Nevertheless, because of the difference in the number of litters between the 2 lines, the sum of young rabbits born alive per doe and the sum young rabbits weaned per doe were higher in the high line (+ 5 kits).

Table 1: Mortality and culling in the second generation

	Low line		High line	
	SAGA	EASM	SAGA	EASM
Mortality (%)	56	33	54	15
Culling (%)	26	19	14	7

Table 2: Fertility, litter size per kindling and total number of born and weaned young rabbit per doe in their whole carrier in low line and high line in the second generation

	Low line	High line	Line effect
Fertility (%)	70.5	68.9	NS
Number of litters	3.64	4.26	***
Total number born/litter	9.93	9.45	*
Born alive/litter	8.88	8.79	NS
Weaned/litter	7.81	7.89	NS
Total number born/doe	32.3	37.0	*
Total weaned/doe	24.6	29.5	**

Significance test: NS: Non significant, *: $P<0.05$. **: $P<0.01$. ***: $P<0.001$

DISCUSSION

The difference in longevity between the 2 farms is mainly explained by disease: in the SAGA farm the does got sick of pasteurellosis after the 2nd AI. The antibiotic treatment applied to these does may have reduced the difference of longevity between the 2 lines. The health status of the EASM does was very good and no antibiotic treatment was used for them. This observation leads to the assumption that the difference between the 2 lines is stronger in a “favorable” environment (good sanitary status, no antibiotic treatment) than in an unfavorable environment.

The absence of difference between the 2 lines for prolificacy traits was expected. Even though genetic correlation between longevity and prolificacy is not well known, it seems to be low. Tudela *et al.*

(2003) demonstrated that selection for litter size did not increase the risk of culling. Sanchez *et al*. (2006) have estimated genetic correlations between longevity and litter size at birth and at weaning. Estimated correlations were weak and not significantly different from zero. Nevertheless, studying the evolution of litter size during successive parities in a line constituted for its high longevity, Theilgaard *et al.* (2007) showed the superiority of this line after the third parity.

CONCLUSIONS

This experiment aimed to validate previous results of survival analysis, to check the consequences of this selection on other traits and to propose a breeding program for genetic improvement of functional longevity in does. This experiment will allow a better characterization of the genetic determinism of longevity which could be of high interest for other species.

ACKNOWLEDGEMENTS

This experiment was financially supported by the French Ministry of Agriculture and Fisheries in the frame of the “actions innovantes” program financed by the “bureau de la génétique animale” of the DGPEI.

The authors thank the entire staff of the rabbit experimental farms (SELAP, IASM, and SAGA) and the IT staff of SAGA

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