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## SURVIVAL ANALYSIS OF LONGEVITY IN BREEDING DOES

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### ABSTRACT

This study aims to estimate the genetic variability of longevity in Hycole does from the line D. Reproductive longevity, measured by the number of artificial inseminations, is treated by survival analysis. The results of 20 410 rabbit does in the data set, inseminated from January 2005 to December 2012 are analyzed. The estimated heritability for longevity was 0.12. Genetic index correlations between longevity and selected traits on the D line are favorable. As a consequence, the genetic value of longevity could have been improved between 2005 and 2012. The genetic variability of longevity allows its use in a breeding program.

**Key words:** Rabbit, longevity, survival analysis

### INTRODUCTION

In a context of reduction use of drugs in meat rabbit breeding, selection schemes must continue to improve the productivity of their rabbits integrating this new constraint. The genetics selection company Hycole has implemented a project to compare different ways to improve does longevity in non-medicated feed conditions. The part of this project presented in this publication concerns the analysis of the productive life of the doe using the method of survival analysis.

The concept of longevity refers in breeding to the true or functional longevity of the animal, that is to say the duration of the reproductive career from the first mating to the death or culling (Garreau et al., 2008). The concept of true longevity applies when performance criteria are used as culling reason. The objective is therefore to improve the capacity of the animals to not succumb to disease or reproductive problems, while maintaining reproductive performances (Theilgaard et al., 2009). Heritability of functional longevity in rabbits is low to medium according to calculation method used and trait study, from 0.05 to 0.24 (Garreau et al., 2001; Sánchez et al., 2006; Piles et al., 2006).

In France, a divergent selection experiment on longevity using survival analysis was introduced in 2004 (Garreau et al., 2008). This selection experiment yielded a superior longevity of 0.92 artificial insemination (AI) for the high longevity line (Garreau et al., 2008). It was not shown significant differences on reproductive criteria. A Spanish study on the LP line selected on longevity, highlighted similar conclusions to the French study (Sánchez et al., 2008).

The objective of this study is to validate the method of survival analysis in non-experimental conditions and with the objective of improving true longevity in the D maternal line Hycole.

### MATERIALS AND METHODS

#### Data

Data studied correspond to the careers of does from the D maternal line breed in Ribecourt-la-Tour farm (59). This line is indexed on: the weight of the lightest rabbit at birth, number of born alive rabbits, litter weight at 28 days old, number of teats and adult weight of the female. This line is managed with a reproductive cycle of 42 days interval between each AI. A kindling group (birth) takes place weekly. Performance from each AI and birth are recorded as well as cause and release date (death or culling) for each doe.

Does are culled in priority for health reason and then for technical reason. The main causes of technical culling are: body condition, fertility (2 negative AI), prolificacy (<6 total born), an index value below 100... In this situation, the duration of the reproductive career can be defined as the true longevity. In this population, a

doe made a complete when it reaches the 11th AI, some does continue beyond depending on the situation. For this study, females performed more than 11 AI were censored.

Females retained for analysis are those with inputs into production between January 2005 and December 2012, whether 20 410 does. Animals are evaluated from their first fertilizing AI. The censure ate in the data file is 26%, which breaks down into 14% of does performed more than 11 AI and 12% of does with an undetermined culling cause. These females are from 913 sires and 850 maternal grandsires. Pedigree file includes 60 835 individuals, born between 2000 and 2012.

### Methods

Longevity data are studied by survival analysis method, using the "survival kit" (Ducrocq *et al.*, 2010). This method can process parametric or semi-parametric models, for continuous or discrete traits including time dependent factors. The hazard function of an individual  $i$  ( $i = 1 \dots n$ ) at time  $t$ , that is to say the likelihood of dying or culling at time  $t$  is modeled by:

$$\lambda_i(t) = \lambda_0(t) \cdot \exp [ \mathbf{x}'_i(t) \cdot \boldsymbol{\beta} + \alpha_i ]$$

where  $\lambda_0(t)$  is the baseline hazard function at time  $t$ ,  $\mathbf{x}'_i(t) \cdot \boldsymbol{\beta}$  represents fixed effects and  $\alpha_i$  random effects (Piles *et al.*, 2006).

The time variable analyzed is number of AI from the first fertilizing AI. This discrete variable was preferred to career duration because it allows a better model fitting (Piles *et al.*, 2006).

Three successive analyzes are performed. The first determines significant fixed effects ( $p < 0.001$ ). This analysis lets to estimate the risk assigned to each level of the effects. The second analysis consists in the estimation of genetic parameters of the trait using father / maternal grandfather model. The last analysis is realized with an animal model to estimate breeding value (BV) for each animal. In this case, variance parameters are fixed.

The model used includes as significant fixed time-dependent effects: the effect of year-season of AI, the effect of birth rank (1, 2, 3 and more), the effect of physiological status during gestation (milking or not), the effect of litter size at birth (TB). The model also takes into account an independent time covariate: age at the first birth in days. Random effects are also included in the model in the case of the sire/ maternal grandsire: sire additive effect and maternal grandsire additive effect and in the case of the animal model: individual additive effect.

Heritability is obtained taking into account the proportion of uncensored data  $p$  and sire variance  $\sigma_s^2$ :

$$h^2_{\text{equi}} = \frac{4\sigma_s^2}{\sigma_s^2 + \frac{1}{p}} \quad (\text{Yazdi et al., 2002}).$$

For the interpretation of results, each level of effects and BV are expressed in relative risk value, risk for an individual to die or be culled.

Survival analysis does not allow multi-criteria analyses, coefficients of correlations between longevity BV and BV of traits currently selected characters have been calculated using ASReml software (Gilmour *et al.*, 2009). The BV of selected criteria: number of born alive (NA), litter weight at 28 days old (WEA), number of teats (N), weight of adult female (P) and weight of the lightest rabbit at birth (MIN) are estimated by BLUP method with animal model using ASReml. The annual genetic trend is estimated by averaging the breeding values of reproductive females by year of birth and by calculating the regression of these breeding values on birth year.

## RESULTS AND DISCUSSION

### Survival curve

The female survival curve is shown in Figure 1. A high proportion of does disappears during the first AI, 45% of females are always in production at the 5<sup>th</sup> AI. Average career duration is 5.7 IA. This value is lower than that observed by Garreau *et al.* in 2001 (7.5 IA), due to a higher turnover rate applied to the selected population (120-140% per year) and to a stricter culling policy for infertility (2 negative AI vs 3) and for insufficient

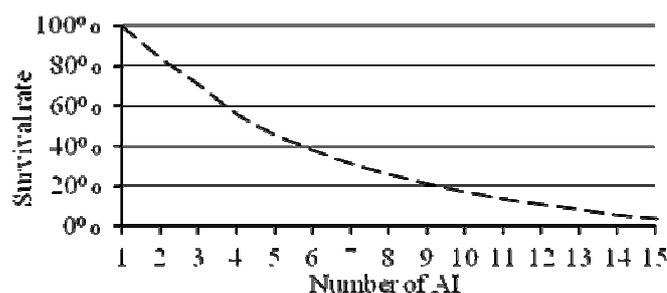


Figure 1 : Does survival curve

technical performance. The disappearance of females is caused in 80.2% of cases by culling and in 19.8% of cases by death.

### Risk evolution of time dependent effects

Risk for a female to die or be culled according to the factor Year/Season of the AI decrease between 2005 and the end of 2008 (reduction of 20%). This risk tends to increase slightly in 2009, with stronger seasonal variations and peak in 2011. This increase is explained by a gradual and continuous reduction of the medication in breeding farm, accompanied by stricter culling policy. Regarding the effect of the birth rank, the risk is 1.47 times greater for a female to die or be culled during the first birth than in third birth or above. This trend is consistent with the survival curve and the results of Piles *et al.* (2006). For litter size effect, risk decreases with the litter size increasing. A female with 13 rabbits or more has 2 times chance to stay in production than a female with less than 5 rabbits. The increase of litter size therefore has no negative effect on longevity, probably due to culling of less prolific does (12.5% of culled females). Small litter size and infertility increase the risk of death or culling and appear to result from pathological problems (Piles *et al.*, 2006).

### Genetic parameters

The estimated sire variance for this model is 0.04056, corresponding to a heritability of 0.116 for longevity. These parameters values are slightly less than those estimated in INRA1077 line in similar conditions by Piles *et al.* (2006,  $h^2 = 0.172$  and  $0.187$ ) but of the same order of magnitude as those estimated in other populations (from 0.05 to 0.24, Garreau *et al.*, 2001). Given the significant proportion of does culled for non-adaptation to the breeding objectives in these data (fertility, prolificacy and body condition), the studied trait is probably a little different from that studied in 1077 line. With this heritability, it is possible to consider an effective selection for longevity.

### Genetic indexes correlations

**Table 1:** Correlations between genetic indexes of selected criteria and longevity

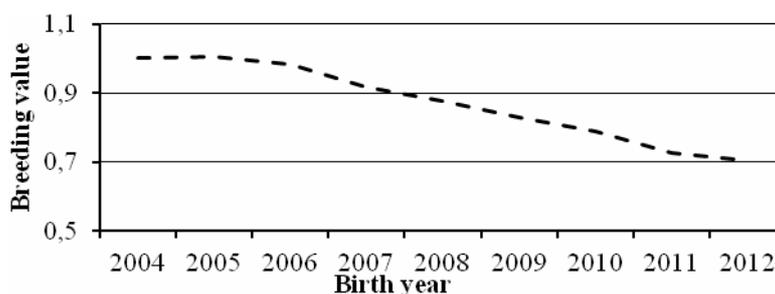
	Longevity
Born Alive	-0,72
Litter weight at weaning	-0,70
Teats number	-0,39
Adult weight	-0,20
Weight of lightest rabbit at birth	-0,37

All genetic indexes of selected traits are favorably correlated with the genetic index of true longevity (Table 1). The high proportion of does culled for low performances may in part explain these positive correlations, i.e. does do not meet breeding objective are culled earlier. Correlations are strong and favorable with the criteria born alive and litter weight at weaning, meaning these traits have an important effect on does longevity (early culling). This trend may also suggest that the longevity ability of a female is related to the improvement of reproductive and milking capacities. Publications of Tudela *et al.* (2003) and Sánchez *et al.* (2004) show independence between longevity and productivity criteria. According to Garreau *et al.* (2001), females with bigger litter size tend to realize a greater number of AI. In this case, longevity is directly associated to the animals' performances, but lower performances can indicate a poor health status or inadequate body condition.

### Estimated genetic evolution of longevity

The estimated genetic evolution of true longevity trait shows a positive trend (Figure 2). The risk of culling / death of females decreases by 30% between 2005 and 2012 (risk from 1 to 0.7). This trend may be interpreted as an indirect evolution due to the genetic indexes correlations estimated between longevity and selected traits.

This result may suggest an improvement of the adaptation of does to production targets under the conditions of reduction of drugs use and a reduction of risk of early culling for low performance.



**Figure 2:** Genetic evolution of longevity by year of birth

## CONCLUSIONS

This study highlights the possibility of direct selection of longevity using the method of survival analysis in line D, despite a strong culling rate in the population. The heritability estimated for this criterion is close to those observed in literature. The culling rate applied and confusion between voluntary and involuntary culling may explain lower heritability (0.116) than those obtained in 1077 INRA line (0.172 and 0.187). Genetic indexes correlations between longevity and the currently selected criteria are favorable. Genetic evolution of longevity indicates a better adaptation of females to the objectives of production and to the breeding conditions. These results show that it is possible to use the method of survival analysis in a selected population with a strong voluntary culling pressure to improve the reproductive longevity. In this study, analyzed longevity is an association between functional longevity and a better adaption to breeding objective. Introduction of the true longevity trait in selection objective could reduce risk of removal of the animals as well as their ability to adapt to breeding objective.

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