



Genetic parameters of rabbit semen traits and male fertilising ability



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ARTICLE INFO

Article history:

Received 21 July 2015

Received in revised form

21 December 2015

Accepted 22 December 2015

Available online 28 December 2015

Keywords:

Rabbit

Semen

Artificial insemination

Fertility

Heritability

ABSTRACT

This study aimed to estimate genetic parameters for rabbit semen production, semen characteristics and fertilising ability following artificial insemination. It involved five successive batches of 30–36 bucks each, 22 weeks of semen collection, and 11 weeks of semen recording per batch. Semen analyses were based on 2312 ejaculates. A total of 2019 inseminations were performed on 674 females with semen from 236 ejaculates from 128 bucks. Heritability estimates of semen traits ranged from 0.05 to 0.18. At approximately 0.05–0.06 for pH, volume and mass motility, they were higher for concentration (0.10) and the total number of sperms per ejaculate (0.12), and even higher for motility traits based on computer-assisted semen analysis. The percentage of motile sperms had the highest heritability (0.18) and appeared to be a good candidate criterion to select for both sperm number and motility. The heritability estimates were close to zero for all three criteria of fertilising ability: fertility (F), prolificacy (live births, LB) and their product (LB per insemination). A permanent environmental effect of the male seemed to be higher for LB (0.04) than for F (0.01). The rabbit does accounted for approximately 10% of the variance of the three criteria. With respect to the female, the male contribution was negligible for fertility and in a ratio of 4–10 for the number of live births. In our experimental conditions, prolificacy would thus be more highly influenced by the buck than fertility.

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1. Introduction

In intensive rabbit meat production, the use of artificial insemination (AI) is currently a widespread practice. Rabbit farmers are supplied with semen from specialised semen production centres. The efficiency of AI depends on male

and on female parameters. On the male side, it depends on the efficient production of potentially fertile doses, which, in turn, depends on quantitative semen production traits such as the sperm number per ejaculate and on quality characteristics that are potentially linked to the fertilising ability of the semen. The use of AI has increased the economic importance of male fertility (Alvariño, 2000) and breeders need information about the potential of genetic selection to improve semen traits and male reproductive performance, which depends on their heritability and genetic correlations. Current knowledge about the genetic determinism of traits involved in fertile dose production by

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AI centres has recently been reviewed by Piles et al. (2013). Concerning semen traits, this review states a small number of heritability estimations because of measurement difficulties inherent to these types of traits: some of them are time-consuming, such as the measurement of rabbit semen concentration; moreover, there is a high number of potentially measurable semen parameters. Such data are difficult to collect in an experimental context and authors generally collaborate with AI centres. Heritability estimates are generally found to be imprecise due to small datasets, and variable due to the diversity in environmental conditions (collection frequency, semen evaluation methods, semen treatment, time before evaluation), and to the definition of the trait. In some cases, the trait consists of the means of two consecutive ejaculates, whereas it corresponds to individual ejaculates in other cases. In some other cases, h^2 estimate was based on frozen rather than fresh semen (Lavara, 2013). Moreover, estimates of genetic correlations between semen traits are lacking. Concerning rabbit semen fertilising ability, heritability estimates are even scarcer (Piles et al., 2013) and are generally performed with sexually receptive does at insemination.

The present study aims to estimate genetic parameters for semen production, quality characteristics and fertilising ability based on experimental data, taking the physiological status of does at insemination into account.

2. Materials and methods

All procedures were conducted in accordance with the guidelines for the Care and Use of Animals in Agricultural Research and Teaching (French Agricultural Agency and Scientific Research Agency; approval number of the PEC-TOUL experimental farm: A 31 113 16).

2.1. Animals and experimental design

The bucks belonged to the experimental INRA1001 strain, descended from a commercial heavy sire line (Hypharm). The experimental design was based on the guidelines of Latter and Robertson (1960) and consisted of recording some 160 bucks from approximately 20 sires, *i.e.* eight bucks per sire. The parents of the bucks belonged to three successive generations of the INRA1001 strain. Bucks were distributed into five successive batches of 30–36 bucks each, and data was recorded between 2004 and 2008. Batches 1 and 2 had six sires in common; Batches 3 and 4 had five sires in common. Each batch was formed from about 80 bucks at the age of 28 d. At the age of 23 wks, from 30 to 36 bucks were selected according to their ability to respond to semen collection after a two-week training period. They were then solicited for semen collection every week, with two solicitations at a 15-min interval, resulting in ejaculate ranks 1 and 2. The absence of ejaculation within two minutes was considered as a failing solicitation. Semen traits were recorded every two weeks, resulting in 11 recorded series per batch. No sexual preparation was applied to bucks prior to collection. A total of 17 insemination series was performed to test the semen fertilising ability. Three successive cohorts of 220 rabbit does (INRA1777 strain) were used. They were inseminated every

42 days (single batch). Within a cohort, dead or culled rabbit does were replaced by rabbit does from INRA1777 or INRA2266 strains. After kindling, free nursing was applied. The animals were housed under a continuous photoperiod of 16 h light and 8 h darkness. They were fed a commercial diet containing 175 g/kg protein and 145 g/kg fibre *ad libitum*.

2.2. Semen evaluation

Immediately after semen collection, pH, volume and mass motility (ranked from 0 to 9) were estimated according to Brun et al. (2002). Sperm cell motility was analysed from a 2-mL sample after dilution (1:40) in Galap (IMV Technologies, France) by a Computer-Assisted Sperm Analysis (CASA) system (HTMA-IVOS, version 10, Hamilton-Thorne Research, USA) according to the set-up parameters of Brun et al. (2006). The minimum cell number counted was 50. For each ejaculate, two drops of 10 μ L each and three fields per drop were evaluated. The operating conditions and measurements are described in Theau-Clément et al. (1996a).

2.3. Inseminations

For each insemination series, only one ejaculate per buck was used. Only ejaculates without urine, with a volume greater than 0.4 mL and a mass motility greater than 5 were used for inseminations. Because of the difficulty to measure rabbit sperm concentration due to interactions with prostatic granules, we prepared insemination doses just like rabbit AI Centers do, using a fixed dilution rate, regardless of the concentration of ejaculates. Ejaculates were diluted (1:19) and stored in the extender (Galap, IMV Technologies, France) until insemination. Semen from each male was packaged in 0.5 mL straws in the late morning and stored at room temperature. Inseminations were performed within six hours after collection. One ejaculate made it possible to perform an average of seven inseminations. The receptivity of does was tested before insemination (exposure to a male; Theau-Clément et al., 2015) in order to assign a similar composition in terms of the physiological status of the does (receptive or non-receptive, lactating or non-lactating) to each buck. No hormonal treatment or biostimulation was used to induce sexual receptivity. Ovulation was induced by an intramuscular injection of 0.1 mL of Receptal (Intervet®).

2.4. Traits analysed

The traits analysed were pH, volume of the ejaculate, mass motility, concentration, total number of sperms per ejaculate (TSE = volume \times concentration), along with CASA traits: proportion of motile sperms (PMOT, %), average path velocity (VAP, μ /sec), and linearity of the sperm tracks (LIN, % deviation from rectitude). The choice of CASA parameters has been based mainly on the pattern of the phenotypic correlations between the numerous CASA parameters recorded in this experiment.

The fertilising ability of semen was evaluated after insemination using three criteria: fertility (all or none vari-

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