Genetic Parameters of Rabbit Semen Traits

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Introduction

With the generalization of artificial insemination, rabbit farmers are supplied with semen from specialized semen production centres. The profitability of these centres depends, among others, on the aptitude of the bucks to produce good quality semen, which also influences the success of the insemination and consequently, the profitability of the farmer. One can distinguish quantitative semen traits, such as the sperm number per ejaculate and qualitative criteria, potentially linked to the fertilizing ability of the semen. Breeders need information about the potential of genetic selection to improve semen traits, which partly depend on their heritability. Several studies indicate a genetic determinism of rabbit semen traits: between strain differences and heterosis effects have been evidenced (Brun *et al*., 2002 and 2006; Garcia-Tomas *et al*., 2006; Lavara *et al*., 2006). Within strains, the genetic factors have been less studied. Two experiments aimed at estimating heritability of semen traits (Panella *et al*., 1994 ; Lavara *et al*., 2008a et b) give contrasting estimates. Moreover, estimates of genetic correlations between semen traits are lacking. The present study aims at completing the knowledge of genetic parameters of semen traits in the rabbit.

Material and methods

Animals, management, semen collection and semen recording protocols. The bucks belonged to the experimental INRA1001 strain, descending from a commercial heavy sire line (Grimaud Frères sélection). The experimental design was based on the guidelines of Robertson (1959) and was to record about 160 bucks from around 20 sires, that is to say 8 bucks per sire. Bucks were distributed into 5 successive batches of 36 bucks each, and recorded between 2004 and 2008. The batches 1 and 2 had 6 sires in common; the batches 3 and 4 had 5 sires in common. A batch was formed from about 80 bucks at the age of 28 days. At the age of 23 weeks, 36 bucks were selected after a 2-week training period according to their ability to respond to semen collection. They were then solicited for semen collection every week, with two solicitations at a 15 min-interval, resulting in ranks 1 and 2 ejaculates. Semen traits were recorded every two weeks, resulting in 11 record series per batch. The semen recording protocol was described by Brun et al. (2006).

Traits analysed. The traits analysed were pH, volume of the ejaculate (mL), mass motility, concentration ($x10^6$ sperms/mL), total number of sperms per ejaculate (TSE=volume x concentration), along with Computer-Assisted Semen Analysis (CASA) traits: proportion motile sperms (PMOT, %), average path velocity (VAP, µ/sec), linearity of the sperm tracks (LIN, % deviation from rectitude).

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Statistical analyses. Genetic parameters were estimated with REML applied to an animal model with simple repeatability, using the version 4.2 of VCE (Neumaier et Groeneveld, 1998). The model took into account 2 fixed effects: 1) 'batch-series' (15 levels), after regrouping the 11 initial series within a batch into 3 classes (series 1 to 3, 4 to 7, 8 to 11). This effect also accounted for age and season effects; 2) ejaculate number (3 levels: 1, 2 or 3 for the ejaculates got from the 2nd solicitation after an unsuccessful first one). The two random effects were the additive genetic value and the permanent environmental effect of bucks. Pedigree was explored over 4 generations. Repeatability was estimated by adding the heritability and the proportion of permanent environmental effects.

Results and discussion

Table 1 gives base statistics of the studied traits. The performance file had 2313 ejaculates, but concentration was recorded on 1442 ejaculates. Overall, 172 bucks were recorded on 13 ejaculates on average. They came from 28 sires (6.1 bucks/sire) and 97 dams (1.8 bucks/dam and 3.5 dams/sire).

Table 1: Base statistics of the semen traits studied

	pH	Volume (ml)	Mass motility	Conc (10^6/ml)	TSE (10^6)	PMOT (%)	VAP (µ/sec)	LIN (%)
N	2196	2312	2225	1442	1401	2078	2078	2078
Mean	6.94	0.50	5.77	663	334	70.3	88.5	39,0
Std. dev.	0.36	0.30	1.88	390	279	26.9	26.4	10.4
Mini-maxi	5.86-8.40	0.10-2.00	0-9	0-2459	0-1304	0-99.0	0-157.3	0-71.5
Repeatability	0.15	0.22	0.24	0.31	0.18	0.28	0.30	0.25

Conc=concentration, TSE=Total number of sperms per ejaculate, PMOT=percent motile sperms, VAP=average path velocity, LIN=linearity of the sperm tracks

Repeatability estimates (table 1). Repeatability values, i.e. the correlation between repeated performance of a buck, are in the range from 0.15 (pH) to 0.31 (concentration).

Heritability estimates (table 2). Heritability estimates ranged from 0.05 to 0.18. At about 0.05-0.06 for pH, volume and mass motility, they were higher for concentration (0.10) and TSE (0.12), and even higher for motility traits from CASA (except LIN). Among the latter, the percent of motile sperms (PMOT) had the highest heritability (0.18). Overall, our heritability estimates are in agreement with those of Lavara *et al*. (2008, a and b), which were 0.10 for TSE and 0.16 for PMOT. Noticeable differences, however, concern concentration and LIN, estimated by Lavara *et al*. (2008) at 0.05 (vs. 0.10 in our study) and 0.19 (vs. 0.05), respectively.

Genetic correlations (table 2). The two components of TSE (volume and concentration) were positively correlated (rg=0.38), resulting in a higher heritability of TSE than that of its components. This positive correlation is not in agreement with the negative values found in sheep (David, 2008) and in beef (Basso et al., 2005).
Semen pH had a positive correlation with volume and with all the indicators of high sperm motility, but was not correlated with concentration.

Mass motility holds a key post due to its high genetic correlation with most of the other semen traits, whether quantitative or qualitative: it was highly correlated to concentration (rg=0.68) and TSE (rg=0.70) and particularly with motility parameters from CASA (rg=0.86 and rg =0.78 for VAP and LIN, respectively). Interestingly, mass motility, coded from 0 to 9 after a simple microscope observation had a genetic correlation close to 1 with PMOT, a variable from image analysis, indicating that both traits are determined by the same genes. The heritability difference between mass motility and PMOT can be explained by the information loss lead up by putting a continuous variable such as PMOT into classes. Due to its higher heritability, PMOT appeared as a choice criterion in order to select for semen quality, in terms of sperm number as well as in terms of sperm motility.

Table 2: Estimates of heritability (on the diagonal) and genetic correlations (above)

	pH	volume	Mass motility	Conc	TSE	PMOT	VAP	LIN
pH	0.06±0.02	0.70±0.28	0.58±0.32	-0.04±0.25	0.44±0.28	0.41±0.24	0.63±0.25	0.56±0.28
volume		0.06±0.03	0.45±0.43	0.38±0.45	0.82±0.18	0.41±0.23	0.38±0.26	0.32±0.28
massmot			0.05±0.03	0.68±0.19	0.70±0.19	0.99±0.01	0.86±0.24	0.78±0.16
conc				0.10±0.03	0.95±0.07	0.83±0.18	0.41±0.26	0.40±0.33
TSE					0.12±0.03	0.65±0.13	0.58±0.25	0.25±0.36
PMOT						0.18±0.04	0.76±0.08	0.75±0.15
VAP							0.14±0.03	0.44±0.16
LIN								0.05±0.03

See table 1 for the significance of the abbreviations

Permanent environmental effects (table 3). Along with the additive genetic effects, these effects contribute to the correlation between repeated performances of a buck. They are not strictly environmental as they may include a genetic component such as dominance. For most traits studied, their contribution to the variance was higher than that of the additive genetic value. Concerning the correlations between traits for these effects, they had often the same sign as the genetic correlation. The noticeable exceptions (inversion of sign) concerned the correlations with pH and the correlation between volume and concentration. In the case of pH, this correlation is explained by the decrease of pH caused by the accumulation of lactic acid into the seminal plasma, consequence of the metabolic activity of the mobile sperms.

Table 3: Permanent environmental effects: proportion of the total variance (on the diagonal) and correlations between traits (above)

	pH	volume	Mass motility	Conc	TSE	PMOT	VAP	LIN
pH	0.09±0.02	-0.36±0.13	-0.91±0.06	-0.53±0.10	-0.94±0.11	-0.90±0.07	-0.74±0.11	-0.68±0.10
volume		0.16±0.03	-0.06±0.12	-0.47±0.14	0.45±0.16	-0.07±0.16	0.07±0.12	0.09±0.09
massmot			0.19±0.03	0.79±0.07	0.78±0.16	0.98±0.04	0.83±0.06	0.78±0.04
conc				0.21±0.04	0.47±0.19	0.63±0.11	0.26±0.13	0.12±0.11
TSE					0.06±0.03	0.76±0.22	0.35±0.34	0.45±0.21
PMOT						0.10±0.03	0.79±0.07	0.74±0.09
VAP							0.16±0.03	0.99±0.02
LIN								0.20±0.03

See table 1 for the significance of the abbreviations

Conclusion

This study leads to estimates of heritability and genetic correlations of quantitative and qualitative rabbit sperm traits. Heritability estimates ranged from 0.05 to 0.18. Due to its fairly high heritability and to its favourable genetic correlations with the other sperm traits, PMOT appeared as a choice criterion to select for rabbit semen, at both the quantitative (number of sperms per ejaculate) and the qualitative levels, providing that PMOT influences the fertilizing ability of the semen.

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