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GENETIC PARAMETERS OF FERTILITY
IN TWO LINES OF RABBIT OF DIFFERENT APTITUDE

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ABSTRACT

A Bayesian analysis with a threshold model was performed for fertility defined as a binary trait (1, successful mating, 0, unsuccessful mating) in two populations of rabbit of different reproductive potential: Line P selected for litter size and Line C selected for growth rate. There were 20793 records (86.2% successful) of natural mating in line C from 1983 to 2003 and 17548 records (80.5% successful) in line P, from 1992 to 2003. Data concerned 5388 and 3848 females and 1021 and 685 males in lines C and P. The pedigree included 6409 and 4533 individuals in lines C and P respectively. The binary response was modeled under a probit approach. The model for the latent variable included male and female additive genetic effects, male and female permanent environmental effects and year-season and physiological status of the female as systematic effects. Means (standard deviation) of the estimated marginal posterior distribution (EMPD) of male heritability were 0.013 (0.006) and 0.010 (0.008) in lines C and P respectively and of EMPD of female heritability were 0.056 (0.013) and 0.062 (0.018) in lines C and P. Means of the EMPD of the proportion of the phenotypic variance due to environmental male and female effects were 0.031 (0.007) and 0.128 (0.018) in line C and 0.053 (0.010) and 0.231 (0.024) in line P. Means (posterior standard deviation) of the EMPD of genetic correlations between male and female were 0.733 (0.197) in line C and 0.434 (0.381) in line P. Results indicate that little genetic variation exists for female fertility but not for male fertility and, that genetic control of these traits could be close, but this need to be confirmed. Therefore, it would be possible to improve reproductive performance by including female fertility in a breeding program but response to selection would be very small.

Key words: Bayesian Theory, fertility, genetic parameters, rabbit, threshold model.

INTRODUCTION

In meat rabbit production, efficiency of production and profitability of farms depends highly on the reproductive success conditioned to fertility and litter size. Fertility can be considered a trait of the female, of the male or of both. It depends on a great number of environmental and genetic factors. In other species, several authors have shown that there is little, almost null, genetic variation in mating or conception rate (in cattle:

JANSEN, 1986, WELLER and RON, 1992, BOICHARD and MANFREDI, 1994, WEIGEL and REKAYA, 2000; in pig: VARONA and NOGUERA, 2001), but in rabbit, the information in the literature about variance components of these traits is very scarce. There is just one study concerning repeatability of female fertility measured as number of presentations to the male (BLASCO et al., 1979) and there is no any estimate of variance components of male fertility. Selection efforts have been focused on litter size and just a low intensity selection by culling sterile individuals is practiced.

Male fertility may have economic interest since a male can influence success on conception of a high number of females, especially when artificial insemination is practiced. It could be improved by direct or indirect selection through its components, like parameters defining semen quality. From a selection point of view, knowledge of variance components of male and female fertility and their genetic relationship has a great importance to evaluate future strategies of selection.

Fertility can be evaluated as a continuous (conception rate, mating rate) or a discrete trait (success or failure to mating or conception). Success to mating or to conception shows a binary expression (1, successful, 0, unsuccessful). The threshold model postulates that the observed binary response is related to an underlying normal variable, often called "the latent variable", and to a fixed threshold that divides the continuous scale in two intervals delimiting the two categories of response (WRIGHT, 1934). Thus, if the "latent variable" exceeds the threshold the observation would be in the second class. Procedures developed by SORENSEN et al., (1995) and MORENO et al., (1997) based on Markov Chain Monte Carlo methods allow the analysis of categorical traits with this model. VARONA et al., (1999) also developed models that allow including continuous correlated traits.

The aim of this job was to estimate variance components of male and female fertility defined as success or failure to mating, and their genetic relationship in two populations of rabbit with different reproductive potential.

MATERIAL AND METHODS

Animals and data

Animals belong to the lines C and P of rabbits selected for growth rate and litter size at weaning respectively (RAFEL et al., 1998). They were housed in the two farms of the Institut de Recerca i Tecnologia Agroalimentàries (IRTA) which follows the same management system. Does follow a semi-intensive reproductive rhythm: first mating at about four and half months of life and reproductive cycles of 42 days. Males start their reproductive life at 6 months. Diagnostic of gestation was made 14 days after mating by palpation. The assigned fertility score was 1 if the female was diagnosed positive and 0 otherwise. There were 20793 records (16740 successful, 86.2 %) of natural mating in line C from 1983 to 2003 and 17548 records (15134 successful, 80.5 %) in line P, from 1992 to 2003. Data concerned 5388 and 3848 females and 1021 and 685 males in lines

C and P. They were analyzed separately in each line. The pedigree included 6409 and 4533 individuals in lines C and P respectively.

Model and statistical analysis

The model assumed for the underlying variable (*l*), was:

$$l = X\beta + Z_1 u_m + Z_2 u_f + Z_3 p_m + Z_4 p_f + e$$

Where β is the vector of systematic effects, u_m and u_f are the vector of male and female genetic additive effects respectively, p_m and p_f are the vectors of male and female permanent environmental effects, e is the vector of random residuals and X, Z_1, Z_2, Z_3 and Z_4 are incidence matrices relating the underlying variable with systematic, genetic and permanent environmental effects. Systematic effects included in the model were: the physiological status (phs) of the female and year-season (ys) at mating day. Physiological status of the female was considered to have 3 levels: 1 for nulliparous does, 2 for multiparous does in lactation at mating day and, 3 for multiparous does not in lactation at mating day. Year-season was defined as intervals of 6 months length (April to September and October to March) between November 1983 to June 2003 in line C and, between July 1992 to November 2003 in line P.

Given β, u_m, u_f, p_m and p_f, the elements of the vector l are conditionally independent and distributed as: $l \mid \beta, u_m, u_f, p_m, p_f, \sigma_e^2 \sim N\left(X\beta + Z_1 u_m + Z_2 u_f + Z_3 p_m + Z_4 p_f, \, I\sigma_e^2\right)$ being σ_e^2 the residual variance (set to 1).

The observed data (success or failure to mating) are conditionally independent, given β, u_m, u_f, p_m and p_f. Therefore the conditional distribution of the data given the parameters can be written, following SORENSEN *et al.,* (1995), as:

$$p\left(y \mid \beta, u_m, u_f, p_m, p_f, l, G\right) = \prod_{i=1}^{n}\{I(l_i > 0)I(y_i = 1) + I(l_i \le 0)I(y_i = 0)\}$$

where y={y_i} (i=1,2,…,n) denote the vector of observed data and $I(y_i = j)$ is an indicator function taking the value 1 if response fall in category j and 0 otherwise.

A Bayesian framework was adopted for inference. The joint posterior distribution of all parameters was:

$$p\left(\beta, u_m, u_f, p_m, p_f, l, G \mid y\right) \propto$$

$$p\left(l \mid \beta, u_m, u_f, p_m, p_f\right)p\left(u_m, u_f \mid G\right)p(G)p\left(p_m \mid \sigma_m^2\right)p\left(\sigma_m^2\right)p\left(p_f \mid \sigma_f^2\right)p\left(\sigma_f^2\right) x$$

$$p\prod_{i=1}^{n}\{I(l_i > 0)I(y_i = 1) + I(l_i \le 0)I(y_i = 0)\}$$

with the following prior densities: $p(\beta) \sim U(-5,5)$, $p\left(u_m, u_f \mid G\right) \sim N(0, A \otimes G)$, $p\left(p_m \mid \sigma_m^2\right) \sim N\left(0, I\sigma_m^2\right)$, $p\left(p_f \mid \sigma_f^2\right) \sim N\left(0, I\sigma_f^2\right)$, where A is the numerator relationship matrix, **G** is the matrix of (co)variance components and σ_m^2 and σ_f^2 are the permanent environmental variances of male and female respectively. Prior densities for *G*, σ_m^2 and σ_f^2 were vague proper distributions to convey lack of information about these

parameters: $p(\boldsymbol{G}) \sim IW(\boldsymbol{S}_g, 5)$, $p(\sigma_m^2) \sim \chi^{-2}(s_m, 5)$, $p(\sigma_f^2) \sim \chi^{-2}(s_f, 5)$, with $s_m = 0.1$, $s_p = 0.1$

and $\boldsymbol{S}_g = \begin{bmatrix} 0.1 & 0 \\ 0 & 0.1 \end{bmatrix}$.

Statistical inferences were derived from the samples of the marginal posterior distributions obtained by using the Gibbs sampler algorithm (GELFAND and SMITH, 1990). The Gibbs sampler is an updating sampling scheme, which requires random draws from all the full conditional distributions. These distributions had been derived for the models used by SORENSEN et al., (1995). Implementation of the Gibbs sampler was made using two chains of 2,000,000 iterations. The first 250,000 iterations of each chain were discarded, and samples of the parameters of interest were saved for each of 5 iterations. The sampling variance of the chains was obtained computing Monte Carlo standard errors (GEYER, 1992). The effective sample size was estimated by using the algorithm of GEYER (1992). GELMAN and RUBIN's (1992) diagnostic test was used to assess convergence. Statistics of marginal posterior distributions were calculated directly from the samples.

RESULTS AND DISCUSSION

Trace plots (not shown) of different chains completely overlapped for all unknowns suggesting convergence. Table 1 shows summary statistics of marginal posterior distributions of male and female heritabilities, percentage of environmental variation due to the male and female, and genetic correlation between male and female fertility. The GELMAN and RUBIN test (1992) indicated convergence for all the parameters since the calculated "Shrink" factors were all close to 1. As expected, the highest value of the correlation between samples and the lowest value of effective sample size corresponded to the genetic correlation between male and female fertility and heritability of male fertility in both lines indicating poor mixing, but the Monte Carlo standard errors were small (always lower than 2% of the posterior mean). Thus, estimates could be considered accurate enough.

Heritability of male fertility and percentage of environmental variation due to the male were practically null in both lines being the repeatability for these traits 4.4% in line C and 6.3% in line P. This result indicates that most of the phenotypic variance of this trait can be explained by sources of variation non-related with the male. Female heritabilities were low in both lines (about 5%) and the percentage of environmental variation due to the female 13 and 23%, being the repeatability of female fertility 18.4% and 29.3% in line C and P respectively. These results indicate that genetic variation exists for female fertility and therefore it could be possible to improve reproductive performance by including this trait in a breeding program. However, direct response to selection would be very small. Posterior mean of genetic correlation between male and female fertility was high and positive in line C (0.73 with probability of a positive value equal to 0.999 from the marginal posterior density) indicating that genetic control of fertility could be close for males and females. In line P, the posterior standard deviation was higher possibly due to the lower amount of mates, being the probability of a positive value 0.87.

Estimates of heritabilities are in agreement with the values reported by VARONA and NOGUERA (2001) in pigs for fertility also defined as success to mating (h_m^2=0.028 and h_f^2=0.038) or WELLER AND RON (1992), BOICHARD and MANFREDI (1994) and WEIGEL and REKAYA (2000) in dairy cattle, whose estimates of female heritability for no-return rate at 56 days after AI ranged between 2.2% to 3.5%. However, reported estimates of genetic correlation between male and female fertility in pigs and dairy cattle were small or moderate and negative. In rabbits, BLASCO et al., (1979) estimated the repeatability of the trait number of presentations to the buck to get a fertile mating obtaining a null value.

Table 1. Summary statistics of marginal posterior distributions of male and female heritabilities (h_m^2, h_f^2), percentage of environmental variation due to the male and female (p_m, p_f) and genetic correlation (r_g) between male and female fertility.

line		PM[1]	PSD[1]	5%[1]	50%[1]	95%[1]	MCse[1]	Lag-1[1]	ESS[1]	$\sqrt{R}$ [1]
	h_m^2	0.013	0.006	0.004	0.013	0.024	0.00012	0.995	117.25	1.08
C	h_f^2	0.056	0.013	0.035	0.056	0.080	0.00024	0.987	174.45	1.01
	r_g	0.733	0.197	0.359	0.766	0.993	0.00379	0.996	136.50	1.00
	p_m	0.031	0.007	0.019	0.031	0.043	0.00012	0.979	208.45	1.01
	p_f	0.128	0.018	0.099	0.128	0.158	0.00025	0.955	695.96	1.00
	h_m^2	0.010	0.008	0.001	0.009	0.025	0.00016	0.995	165.88	1.03
P	h_f^2	0.062	0.018	0.035	0.061	0.093	0.00029	0.983	1065.90	1.00
	r_g	0.434	0.381	-0.260	0.478	0.962	0.00771	0.997	208.92	1.05
	p_m	0.053	0.010	0.036	0.053	0.069	0.00015	0.959	390.63	1.00
	p_f	0.231	0.024	0.191	0.231	0.271	0.00028	0.928	2937.45	1.01

[1]PM: posterior mean; PSD: posterior standard deviation; 5%, 50%, 95%: percentiles at 5, 50 and 95%, Mcse: Monte Carlo standard error of the mean, Lag-1: correlation between two successive samples; ESS: effective sample size, $\sqrt{R}$: Shrink factor.

CONCLUSIONS

This study demonstrates the existence in rabbit of genetic and environmental variation for female (but negligible for male) fertility, defined as success or failure to natural mating. Genetic correlation between both traits was high and positive suggesting that their genetic control could be close, but this result should be confirmed. Therefore, reproductive performance could be improved by including female fertility in a breeding program but, due to the low values of heritability, efficacy of selection would be very small. An alternative may be indirect selection for other related traits, like semen quality traits, but further research is needed to know their genetic correlation with fertility in order to evaluate possible strategies of selection.

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