S.14 “Free communications in genetics of meat animals”
Abstract number: 4739
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GENETIC ANALYSIS OF FERTILITY AND AVERAGE DAILY GAIN IN RABBIT

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ABSTRACT

A Bayesian bivariate Linear-Threshold Animal Model was implemented to determine the genetic correlation between doe fertility (F), defined as success or failure to conception, and average daily gain (ADG) in a rabbit line selected for growth rate during the fattening period. A total of 27,234 data of fertility from 7,895 females and 114,135 data of ADG, which included all the information of the selection process, were used for the analysis. The pedigree included 114,485 animals. The model used for ADG included the systematic effects of year-season, parity order and number of kids born alive, the animal additive effect, the maternal genetic plus permanent environmental effects, the environmental permanent effect of litter, and the random residual effect. The model for the liability for the binary trait (F) included the systematic effects of year-season and physiological status of the female, the female additive genetic effects, the female non additive genetic plus permanent environmental effects and the residual, which was divided in an environmental permanent effect related with the common litter environmental effect for ADG, and a random residual term. The obtained heritabilities were 0.04 and 0.14 for F and ADG, respectively. The genetic correlation was low and negative (-0.12) with a probability of 88% of being lower than 0. Thus, it is not expected that female reproductive performance is affected by selection for growth traits in rabbit lines.

Keywords**:** *Fertility, Growth, Correlation, Rabbit*

INTRODUCTION

In paternal rabbit lines where growth traits are objective of selection, it is of special interest to determine which kind of relationship have those traits with reproductive traits in order to avoid a possible deterioration of the reproductive efficiency.

The aim of this study was to analyse the genetic relationship between average daily gain during the fattening period and female fertility.

MATERIAL AND METHODS

Animals and data

Animals belonged to the Caldes line selected for ADG during the fattening period. They were bred and reared on an experimental farm from IRTA in Caldes de Montbui (Barcelona) with a photoperiod of 16 h light/d. This farm has system for avoiding extreme temperatures. Males and females started the reproductive period at 5mo and 4.5mo of age, respectively, under a photoperiod of 16h light per day. Females followed a semi-intensive rhythm, leading 42d between consecutive parturitions. At 28d of age, bugs were weaned and allocated in groups of 8 and fed *ad libitum* during 32d. Data belongs to the period from November 1,983 to October 2,008. Until June 2,003 natural mating was adopted for reproduction, after that, artificial insemination with hormonal treatment to induce female ovulation and receptivity was used until the end of the study.

Traits analysed were: female fertility (**F**), defined as success or failure to conception (27,234 data from 7,895 females) and average daily gain during the fattening period (**ADG**) (114,135 data, which included all the information of the selection process). The pedigree had 114,485 animals.

Model and statistical analysis

Both traits were analysed jointly with a threshold-gaussian mixed model. The following model was adopted for ADG:

$$\mathbf{y}_{adg} = \mathbf{X}_{adg}\boldsymbol{\beta}_{adg} + \mathbf{Z}_{1,adg}\mathbf{u}_{adg} + \mathbf{Z}_{2,adg}\mathbf{p}_{adg} + \mathbf{Z}_{3,adg}\mathbf{c}_{adg} + \mathbf{e}_{adg}$$

Where $\boldsymbol{\beta}_{adg}$ is the vector of systematic effects, $\mathbf{u}_{adg}$ is the vector of additive genetic effects, $\mathbf{p}_{adg}$ and $\mathbf{c}_{adg}$ are the vectors of maternal and common litter environmental effects, respectively, and $\mathbf{e}_{adg}$ is the random residual vector. Incidence matrices $\mathbf{X}_{adg}$, $\mathbf{Z}_{1,adg}$, $\mathbf{Z}_{2,adg}$ y $\mathbf{Z}_{3,adg}$ relate data with the systematic, genetic and permanent environmental effects, respectively. The systematic effects included in the model were: year-season, parity order and number of kids born alive in the litter where the individual was born.

For the underlying variable (*l*) of female fertility a mixed model was used. The random residual vector was decomposed in two terms $\mathbf{c}_f$ y $\mathbf{e}_f$, being the first one an environmental effect related with the common litter effect for ADG. This residual decomposition increases the data connectivity and allows estimating a possible environmental correlation between both traits. Then the model assumed for the underlying variable was:

$$\mathbf{l}_f = \mathbf{X}_f\boldsymbol{\beta}_f + \mathbf{Z}_{1,f}\mathbf{u}_f + \mathbf{Z}_{2,f}\mathbf{p}_f + \mathbf{Z}_{3,f}\mathbf{c}_f + \mathbf{e}_f$$

Where $\boldsymbol{\beta}_f$ is the vector of systematic effects, $\mathbf{u}_f$ is the vector of female additive genetic effects, $\mathbf{p}_f$ is the vector of female non-additive genetic plus permanent environmental effects and $\mathbf{c}_f$ and $\mathbf{e}_f$ are the vectors resulting from the residual decomposition described above. $\mathbf{X}_{adg}$, $\mathbf{Z}_{1,adg}$, $\mathbf{Z}_{2,adg}$ y $\mathbf{Z}_{3,adg}$ are incidence matrices that relate the underlying variable with the systematic, genetic and permanent environmental effects, respectively. The systematic effects included in the model were: physiological status of the female (nulliparous does, multiparous does in lactation and multiparous does not in lactation at the pregnancy moment) and year-season.

Data conditioned to the model parameters was distributed as follows:

$$\mathrm{p}(\mathbf{y}\,|\,\boldsymbol{\beta},\mathbf{u},\mathbf{p},\mathbf{c},\mathbf{R}) \sim \mathrm{N}(\mathbf{X}\boldsymbol{\beta}+\mathbf{Z}_1\mathbf{u}+\mathbf{Z}_2\mathbf{p}+\mathbf{Z}_3\mathbf{c},\ \mathbf{I}\otimes\mathbf{R})$$

where $\mathbf{y}'=\left(\mathbf{l}',\mathbf{y}'_{\mathrm{adg}}\right)$; $\boldsymbol{\beta}'=\left(\boldsymbol{\beta}'_{\mathrm{f}},\boldsymbol{\beta}'_{\mathrm{adg}}\right)$; $\mathbf{u}'=\left(\mathbf{u}'_{f},\mathbf{u}'_{adg}\right)$; $\mathbf{p}'=\left(\mathbf{p}'_{f},\mathbf{p}'_{adg}\right)$ y $\mathbf{c}'=\left(\mathbf{c}'_{f},\mathbf{c}'_{adg}\right)$ are decomposed in the vectors described above for both traits, $\mathbf{I}$ is an identity matrix and $\mathbf{R}$ is the (co)variances residual matrix with the following structure:

$$\mathbf{R}=\begin{bmatrix}1 & 0\\ 0 & \sigma_e^2\end{bmatrix}$$

The following prior distributions for the parameters were considered:

$$p(\boldsymbol{\beta})\sim k,\ p(\mathbf{u}\,|\,\mathbf{G})\sim N(\mathbf{0},\mathbf{A}\otimes\mathbf{G}),\ p(\mathbf{p}\,|\,\mathbf{P})\sim N(\mathbf{0},\mathbf{I}\otimes\mathbf{P}), p(\mathbf{c}\,|\,\mathbf{C})\sim N(\mathbf{0},\mathbf{I}\otimes\mathbf{C})$$

Where $\mathbf{A}$ is the relationship matrix and $\mathbf{G}=\begin{bmatrix}\sigma^2_{u;f} & \sigma_{u;f,adg}\\ \sigma_{u;f,adg} & \sigma^2_{u;adg}\end{bmatrix}$; $\mathbf{P}=\begin{bmatrix}\sigma^2_{\mathrm{p;f}} & \sigma_{\mathrm{p;f,adg}}\\ \sigma_{\mathrm{p;f,adg}} & \sigma^2_{\mathrm{p;adg}}\end{bmatrix}$ and $\mathbf{C}=\begin{bmatrix}\sigma^2_{\mathrm{c;f}} & \sigma_{\mathrm{c;f,adg}}\\ \sigma_{\mathrm{c;f,adg}} & \sigma^2_{\mathrm{c;adg}}\end{bmatrix}$ are the (co)variances matrix of the genetic and environmental permanent effects described above. Bounded uniform priors were assumed for the elements of $\mathbf{G}$, $\mathbf{P}$ and $\mathbf{C}$.

The marginal posterior distributions of the variables of interest for F and ADG were approximated using the Gibbs sampler algorithm.

A single chain of 500,000 iterations was run. The first 100,000 iterations were discarded, and samples of the parameters of interest were saved for each of 10 iterations. The sampling variance of the chains was obtained by computing Monte Carlo standard errors (Geyer, 1992). Statistical from the marginal posterior distributions were calculated directly from the samples saved.

RESULTS AND DISCUSSION

Table 1 shows the descriptive statistics of the marginal posteriors distributions for the ratios between the variance components and the correlations between both traits.

The obtained h^2 for female fertility was similar than the obtained in the same line in a previous study (Piles *et al*., 2005). The obtained h^2 for ADG is also in accordance with h^2 described in other rabbit lines (Larzul y Gondret, 2005) and in this line in a previous study (Piles *et al*., 2004). Genetic correlation between both traits was low and negative with high probability ($P<0=0.88$). There is no previous published information concerning the relation between fertility and growth traits in prolific species. Nevertheless, the high correlation between male fertility and male litter size (0.97 p.s.d. 0.05) obtained in this line (Tusell *et al*., 2008), allow us to compare the results obtained in this study with the obtained in other studies where correlation between growth and litter size of the female was analysed. In those studies, the observed genetic correlation was negative, null or positive but it always has low magnitude (García y Baselga 2002, Bünger *et al*., 2005).

As a conclusion, whereas F and ADG are negatively correlated, the magnitude of this correlation does not seem to be high enough to expect that female reproductive performance is affected by selection for growth traits in rabbit lines.

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Table 1. *Posterior mean (PM). Highest posterior density interval at 95% (HPD95%). Monte Carlo standard error (MCse).Correlation between two successive samples (Lag) of the model parameters for growth rate (ADG) and fertility (F).*

ADG

Parameter	PM	HPD95%	MCse	Lag
h^2[a]	0.143	0.122 , 0.164	0.001	0.952
p[b]	0.024	0.016 , 0.031	0.000	0.872
c[c]	0.278	0.268 , 0.287	0.000	0.436
σ^2[d]	51.539	50.821 , 52.311	0.021	0.474

F

Parameter	PM	HPD95%	MCse	Lag
h^2[a]	0.041	0.017 , 0.070	0.002	0.994
p[b]	0.140	0.108 , 0.174	0.000	0.941
e[e]	0.819	0.793 , 0.845	0.001	0.902
σ^2[d]	6.898	4.472 , 9.111	0.124	0.988

Parameter	PM	HPD95%	MCse	Lag
rg[f]	-0.121	-0.303 , 0.068	0.011	0.986
rp[g]	0.474	0.283 , 0.667	0.005	0.918
re[h]	0.215	0.100 , 0.334	0.004	0.955
rf[i]	0.111	0.052 , 0.166	0.002	0.957

[a] h^2: heritability; [b] p: ratio of female permanent effect variance; [c] c: ratio litter effect variance; [d] σ^2: phenotypic variance; [e] e: ratio of residual variance; [f] rg: genetic correlation; [g] rp: correlation of female permanent effect; [h] re: residual correlation; [i] rf: phenotypic correlation.

Acknowledgments: Research was supported by INIA-RTA2005-0008-C02 project and an INIA fellowship for LL. Tusell. The authors are grateful to the personal support of the farm for their contribution to the experimental work.