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GENETIC DETERMINISM OF FEED EFFICIENCY IN RABBIT. ANALYSIS OF A SELECTION EXPERIMENT FOR TWO CRITERIA OF FEED EFFICIENCY

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ABSTRACT

Genetic parameters of feed efficiency and growth traits were estimated in two selected rabbit lines after 6 generations of selection. The ConsR line was selected for residual feed intake (RFI) under *ad libitum* feeding. The AlimR line was selected for average daily gain (ADG from 30 to 63 days) under restricted feeding corresponding to 80 % of *ad libitum* feed intake of control animals. Estimates of heritability of ADG and FCR (feed conversion ratio) were higher in the AlimR line than in the ConsR line, while estimates of heritability of weight at 30 and 63 days-old were similar between lines. Heritability of ADG (0.25), the selection criterion of the AlimR line, was higher than RFI (0.15), the selection criterion of the ConsR line. Estimates of heritability and genetic correlations between weaning weight, weight at 63 days, ADG and FCR are also presented for each line.

Key words : Rabbit, genetic selection, feed efficiency, feed conversion ratio, growth rate.

INTRODUCTION

Feed represents around 60% of production costs of rabbit meat and the increase of feedstuff prices highly impacts profitability of rabbit farms. Additionally, improving feed efficiency should reduce the animal effluent release. A way to improve feed efficiency is to limit the intake for two or three weeks after weaning, and then to feed *ad libitum* to obtain a compensatory growth. Such strategies are commonly used by 95% of the French rabbit farms, to limit digestive disorders (Gidenne *et al.*, 2009) and reduce the feed costs. Improvement can also be achieved by selection (Larzul and De Rochambeau, 2005). For this purpose, a selection experiment for feed efficiency in growing rabbits began in 2007 at INRA Toulouse, to create two rabbit lines, AlimR selected for average daily gain (ADG) under restricted feeding and ConsR selected for residual feed intake (RFI) under *ad libitum* feeding. RFI represents the estimated fraction of total feed intake that is unexplained by maintenance requirements and growth needs. The goal of this study is to present the genetic parameters for growth and feed efficiency traits estimated in both lines after 6 generations of selection.

MATERIAL AND METHODS

Animals

The experimental population was from the INRA 1001 line, bred at the experimental INRA farm PECTOUL. This population, originally from a heavy strain of HYPHARM firm, have already been used for two successive experiments of divergent selection (weight at 63 days-old then residual feed consumption). The founders of the present experiment result from a mixing of those two previous divergent lines.

Lines creation and management

The two selected lines were composed each of 54 females, divided in 9 reproduction groups. Those females were raised at the same time within the same breeding units. For each generation, females of the two lines were inseminated three times with an interval of 42 days. At each generation and for each line, 300 animals born from the insemination 2 and 3 were tested in individual cages. Animals selected for the growth rate (AlimR line) received restricted feed. The feed amount delivered to those animals was adjusted each week at 80% of the feed eaten by 20 control animals raised in the same room with *ad libitum* access to feed. Animals selected for RFI were fed *ad libitum* (ConsR line). The analysis included 1716 animals tested in the AlimR line and 1804 animals tested in the ConsR line, including G0 to G6 individuals and up to five generations of ancestors.

Traits analyzed

For the two lines, the measure of the weaning weight at 30 days and the 63 days-old weight led to calculate the average daily gain (ADG). Individual feed consumptions from 30 to 63 days-old allowed calculating the feed conversion ratio (FCR), *i.e.* feed consumption divided by weight gain.

Selection criteria

In the AlimR line, males and females were selected for ADG from 30 to 63 days. In the ConsR line, males and females were selected on the RFI, corresponding to the total feed consumption corrected (by linear regression) for requirements for maintenance, metabolic weight=(mean body weight)$^{0.75}$ and for weight gain between 30 and 63 days. The coefficients of the regression equation were estimated at each generation. For example, the equation of the G2 generation is:

$$\text{Feed intake} = 243.99 + 1.15 * \text{ADG} + 10.85 * (\text{mean body weight})^{0.75} + \text{RFI}$$

In this equation, Feed intake is the dependent variable; ADG, average metabolic body weight and RFI are the independent variables. We focus on the residual of the model which is named RFI (Residual Feed Intake).

Statistical analyses

The RFI was estimated by the REG procedure of the SAS software. In a first time, traits were analyzed individually to estimate the fixed effects. The fixed effects included in the models were sex (2 levels), batch (14 levels), parity (3 levels), litter size at weaning (5 levels) and interaction batch*litter size at weaning (significant only for the body weight at 30 days-old in the AlimR line). Then, to estimate genetic correlations, two- or three –trait analyses were performed, systematically including the trait selected to properly account for the effects of selection for these traits in the two selected lines (Hofer, 1998). Genetic parameters were estimated by the restricted maximum likelihood (REML) methodology applied to an animal model for all traits with adequate selection of fixed effects mentioned above, as well as two random effects: common litter effects and the animal additive effect, using ASReml software (Gilmour *et al.*, 2009).

RESULTS AND DISCUSSION

Descriptive statistics

Descriptive statistics of measured traits in the two lines are given in Table 1. The two lines had a similar weight at 30 days-old (around 871g). As expected, the weight at 63 days-old was lower in the AlimR line than in the ConsR line (2241g *vs.* 2707g) and mainly explained by the restricted feeding in the AlimR line.

Table 1. Descriptive statistics in the AlimR and ConsR lines.

line	AlimR		ConsR	
Trait	Mean	Std. Dev.	Mean	Std. Dev.
Weight at 30 days (g)	871	131	872	130
Weight at 63 days (g)	2241	175	2707	273
ADG (g/day)	40.4	4.0	54.1	5.5
FCR	2.77	0.27	2.86	0.22

AlimR: Selected for ADG (average daily gain) with restricted feeding; ConsR:
Selected for RFI (residual feed intake) with *ad libitum* feeding; FCR: Feed conversion ratio.

Comparison of heritability estimates of the two selected lines

ADG and FCR had a higher heritability in the AlimR line with restricted feeding than in the ConsR line with *ad libitum* feeding (Table 2). Nevertheless, concerning the weight at 30 and 63 days-old, the two lines showed similar heritabilities. The heritability of the selected trait in the AlimR line (ADG) was higher than the one of the selected trait in the ConsR line (RFI) (0.25 vs. 0.15). However, those heritability values had a low precision due to their standard error varying from 0.04 to 0.07.

Table 2. Estimation of heritability (h^2) and common litter effects (c^2) in the AlimR and ConsR lines.

Line	AlimR		ConsR	
Trait	h^2	c^2	h^2	c^2
Weight at 30 days	0.04 (0.05)	0.33 (0.04)	0.06 (0.04)	0.43 (0.03)
Weight at 63 days	0.11 (0.05)	0.22 (0.03)	0.13 (0.05)	0.26 (0.03)
ADG	0.25 (0.07)	0.17 (0.03)	0.19 (0.05)	0.13 (0.03)
FCR	0.23 (0.07)	0.16 (0.03)	0.19 (0.06)	0.06 (0.03)
RFI	-	-	0.15 (0.05)	0.05 (0.02)

See footnotes of Table 1

Genetic correlations in AlimR line

The genetic correlations between the different traits measured in the AlimR line were given in Table 3. ADG was fully negatively correlated to the FCR (-1) and was highly positively correlated to the weight at 63 days-old (0.91). In contrast, it was negatively correlated to the weight at 30 days-old (-0.17).

Table 3. Estimation of genetic correlations in the AlimR line.

	Weight at 30 days	Weight at 63 days	ADG
Weight at 63 days	0.26 (0.57)		
ADG	-0.17 (0.43)	0.91 (0.18)	
FCR	0.14 (0.43)	-0.89 (0.19)	-1 (0.003)

See footnotes of Table 1

There was no previous study about genetic selection on growing rabbits with restricted feeding to compare our results with. However, such selection has been realized in pigs (Nguyen *et al.*, 2005). Authors showed an improvement of feed efficiency, with an increase of growth rate and a decrease of spontaneous intake, even if animals were *de novo* fed *ad libitum*. Their heritability estimates of ADG and FCR were lower than those estimated in our study (0.19 vs. 0.25 and 0.16 vs. 0.23). Nevertheless, the authors described the same very high negative genetic correlation between ADG and FCR (-1). Taking into account this strong link, selection for growth rate with restricted feeding allowed efficient improvement of FCR.

Genetic correlations in ConsR line

The Table 4 shows the genetic correlations between the different measured traits in the ConsR line. RFI was highly correlated to FCR (0.96) and to the weight at 30 days-old (0.87), which was unfavorable for selection purposes (the selection objective was not to decrease the weaning weight). RFI was genetically independent of ADG (-0.10) and weakly correlated to weight at 63 days-old (0.17). ADG was highly correlated to the weight at 63 days-old (0.95) but weakly correlated to weight at 30 days-old (0.14).

Table 4. Estimation of genetic correlations in the ConsR line.

	Weight at 30 days	Weight at 63 days	ADG	FCR
Weight at 63 days	0.50 (0.25)			
ADG	0.14 (0.32)	0.95 (0.04)		
FCR	0.73 (0.26)	-0.13 (0.24)	-0.39 (0. 18)	
RFI	0.87 (0.37)	0.17 (0.24)	-0.10 (0. 20)	0.96 (0. 03)

See footnotes of Table 1

The genetic parameters of growth and feed efficiency traits for rabbits with *ad libitum* feeding were quite largely described in the literature. Heritability estimates of the weight at 30 and 63 days-old (0.06 and 0.13, respectively) in our study were in accordance with the values reported by Lukefahr *et al.* (1996). Heritability estimate of ADG in our study (0.19) is moderate. In rabbits, the values reported for ADG heritability during the fattening period range from 0.11 (Piles and Blasco, 2003) to 0.48 (Moura *et al.*, 1997). Heritability estimate of FCR in our study (0.19) was lower than estimates reported in the literature ranging from 0.25 to 0.31 (Piles *et al.*, 2004). The heritability of RFI was quite low compared to the value given by Larzul and De Rochambeau (2005) (0.15 vs. 0.45). Usually, estimates of RFI range from 0.14 to 0.45, depending on the species and the study (Gilbert *et al.*, 2011). Although favorable for selection purposes, the weak correlation between FCR and ADG (-0.39) indicated that a selection on the ADG only moderately improved FCR. By construction, the genetic correlation between RFI and ADG was low (-0.10). This value is similar to the estimate of Larzul and De Rochambeau (2005) in rabbit (-0.09). In pigs, Nguyen *et al.* (2004) reported values of positive correlation between RFI and ADG (0.18), and between RFI and backfat thickness (0.24). Those correlations were explained by a different evaluation of RFI in pigs, estimated as the residual of a model including ADG and backfat thickness as covariates. In rabbit, the low adiposity of growing animals and the lack of precision of in vivo measurement tools did not allow to estimate properly the part of RFI dedicated to fat deposit in the equation of RFI estimation (Larzul and De Rochambeau, 2005). The very high correlation between RFI and FCR (0.96) is in accordance with the value of 1 given by Larzul and De Rochambeau (2005). In pig, genetic correlations between RFI and FCR were also high (0.70 ; Gilbert *et al.*, 2007).

CONCLUSION

This study aimed to test out improvement of feed efficiency by two ways of selection. The genetic parameters of growth rate under restricted feeding have been estimated for the first time in rabbit. This criterion was completely correlated with the feed conversion ratio and its heritability was 0.25. Residual feed intake with *ad libitum* feeding had a lower heritability (0.15) but is still highly correlated with the feed conversion ratio. However, residual feed intake was weakly correlated with average daily gain.

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