Microrabbits : a factorial design to evaluate genetic and maternal effects on growth and feed efficiency in a line selected for residual feed intake

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Evaluation of genetic and maternal effects on growth and feed efficiency in a rabbit line selected for residual feed intake

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Introduction

Performances of growing rabbits are determined by their genotype and their environment. The effect of maternal environment is particularly important in this species. Improvement of feed efficiency is essential to increase the competitiveness of the rabbit industry but also to reduce the animal excretion, and consequently decrease the environmental impact of the production. It can be achieved in rabbit by selection on residual feed intake (RFI) or on growth under restricted feeding (Drouilhet et al., 2013, 2015). However, these selection strategies do not take into account the contribution of gut microbiota to improved feed efficiency, although some previous results have demonstrated its relation with digestive efficiency in chicken (Mignon-Grasteau et al., 2015). To further investigate the effects of the animal genotype and maternal environment on feed efficiency, an experiment based on cross fostering between a line selected on RFI and a non-selected control line was performed. Ultimately, it should allow disentangling the effect of animal genetic and dam microbiota transmission on the traits. The objective of this preliminary study was to estimate both host genotype effect and maternal environment effect on growth and feed efficiency in rabbit.

Material and methods

Animal management

The experimental rabbit populations were issued from the INRA 1001 line (Larzul and De Rochambeau, 2005) and bred in the experimental INRA farm Pôle d'Expérimentation Cunicole Toulousain (Castanet-Tolosan, France), in accordance with the national regulations for human care and use of animals in agriculture. Two lines were used in this study: the G10 line, selected for 10 generations on RFI and the G0 line produced from frozen embryos of the ancestor population of the selected line. The 490 G10 and 410 G0 rabbits were produced in 3 batches with a 42 days interval. Within 48 hours following birth, every kit was fostered. In each batch, half of kits was fostered by G0 does and the second half of kits was fostered by G10 does. Does adopted alternatively kits from one line and from the other line in successive batches. Litters of 5 to 7 kits were made up, mixing sires families of kits within fostered litters.

At weaning (32 days), in each batch, 152 kits were placed in individual cages, 48 in digestibility cages and the rest in collective cages of 4 to 5 animals. All animals were fed *ad libitum* the same commercial pelleted diet until the end of the fattening period (63 days).

Traits

Animals were weighed at weaning (BW32) and at 63 days of age (BW63). Individual feed intake (FI) was recorded in individual and digestibility cages, and estimated in collective cages by dividing total feed consumption by the number of animals in the cage, taking into account death of animals when occurring prior to the end of the test. Average daily gain (ADG) was obtained by dividing the body weight gain during the test by the number of days of the growing period. Feed conversion ratio (FCR) was calculated as total feed intake divided by the body weight gain.

Statistical analyses

The RFI was computed as the residual of the multiple linear regression of total feed intake on average metabolic body weight (average body weight between weaning and end of the test to the power 0.75) to account for maintenance requirements and ADG to account for production requirements (REG procedure; SAS software).

Fixed effects to be accounted for in the statistical analyses were tested using a linear model (GLM procedure, SAS, 2008):

$$y_{ijklm} = \mu + kit\ line_i + doe\ line_j + batch_k + housing_l + batch_k \times housing_l + e_{ijkml}\ , \quad (1)$$

with y_{ijklm} the trait value for animal *k*, $kit\ line_i$ the line of the animal (2 levels), $doe\ line_j$ the line of the foster doe (2 levels), $batch_k$ the batch of the animal (3 levels), $housing_l$, the type of cage in which the animal was raised (3 levels). The only significant interaction between all fixed effects was $batch_k \times housing_l$ ($P < 0.05$), therefore no other interaction was retained in the models.

Results and discussion

Levels of significance of fixed effects are presented in Table 1. The *batch* effect and the *batch* × *housing* interaction, being significant for all traits, are not mentioned in this table.

Table 1: Level of significance of fixed effects

	P		
Trait	Kit line	Foster doe line	Type of housing
Body weight at 32 days	***	ns	/
Body weight at 63 days	***	ns	***
Average Daily Gain	***	ns	***
Feed Conversion Ratio	***	*	***
Residual Feed Intake	***	ns	***
Feed Intake	***	ns	***

ns = non significant ; *: $P < 0.05$; **: $P < 0.01$; ***: $P < 0.001$.

The kit line effect and the type of housing effect were significant for all traits ($P < 0.001$). The foster doe effect was significant only for FCR, G10 foster does showing an unfavourable effect (-0.06 ± 0.02). Least square means of the kit line and of the type of housing effects are presented in Table 2. The G10 animals were lighter than G0 rabbits at 32 days (-82.9 g) and at 63 days (-161 g). They also had a lower ADG (-2.36 g/day), FCR (-0.36),

RFI (-548 g) and a lower FI (-839 g), illustrating a better feed efficiency. These results demonstrate that selection on RFI was efficient, as already reported (Drouilhet *et al.*, 2013, 2015). Nguyen *et al.* (2005) have also reported a successful selection experiment on RFI in pig.

Table 2: Least square means for kit line and type of housing

	Kit line		Type of housing		
Trait	G0	G10	collective	digestibility	individual
BW32 (g)	916 ± 6	833 ± 6			
BW63 (g)	2,624 ± 13	2,463 ± 12	2,436 ± 14[a]	2,596 ± 20[b]	2,599 ± 11[b]
ADG (g/day)	51.76 ± 0.28	49.40 ± 0.26	47.77 ± 0.32[a]	52.08 ± 0.46[b]	51.88 ± 0.25[b]
FCR	3.02 ± 0.02	2.66 ± 0.02	3.14 ± 0.02[a]	2.69 ± 0.03[b]	2.69 ± 0.01[b]
RFI (g)	298 ± 18	-250 ± 17	333 ± 20[a]	-117 ± 29[b]	-144 ± 16[b]
FI (g)	5,127 ± 23	4,288 ± 21	4,850 ± 26	4,645 ± 38	4,628 ± 21

[a, b] means with different letters are significantly different ($P < 0.05$).

Concerning the type of housing, performances of rabbits raised in individual cages were similar to those raised in digestibility cages. However rabbits raised in collective cages were lighter at 63 days (- 162 g approx.) and presented a lower ADG (- 4.21 g/day approx.) than rabbits raised individually. They had also higher FCR, RFI and FI (around +0.45, +464 g and +205 g, respectively). Coulmin *et al*. (1982) obtained similar results by decreasing the number of rabbit per cage: heavier animals with a higher ADG associated to smaller number of animals per cage, probably due to decreased loss of energy in relation with activity, but they reported no modification of FCR.

Kit and foster doe lines effects are shown in Figure 1. Compared to G0, G10 foster does had an unfavourable effect on FCR, irrespective of the kit line (-0.06). The maternal effect included the permanent environmental effect offered by the doe to the kits, its own genetic effect and its microbiota transmitted to kits. Our results reflect a negative maternal effect of the selected line G10 on feed efficiency. At this stage of the study, it is not possible to identify which component of maternal effect (milk, maternal behaviour, microbiota...) was degraded by the selection (Combes *et al.*, 2013). This can be related to negative correlations previously estimated in some studies between direct and maternal effects on production traits in rabbits (David *et al.*, 2015). In conclusion, FCR was strongly influenced by the genotype of the kit ($\Delta = 0.36$, $P < 0.001$) and to a lesser extent by the maternal environment ($\Delta = 0.06$, $P < 0.05$).

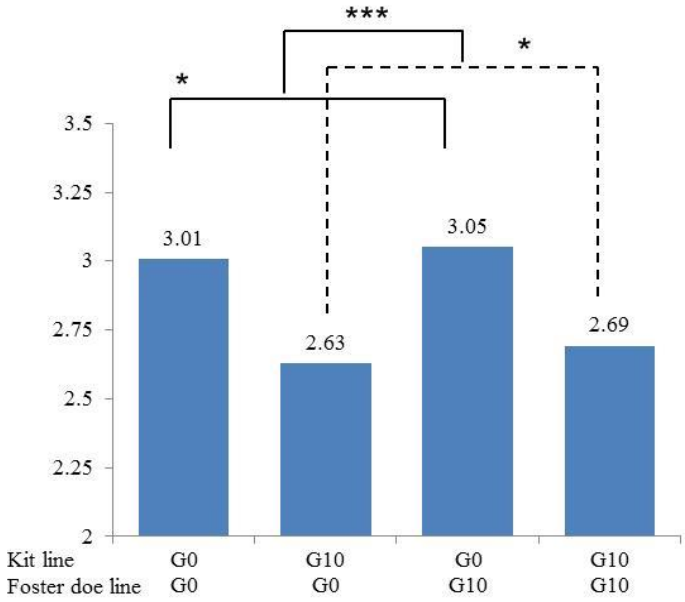

*Figure 1: Kit line and foster doe line effects on feed conversion ratio. *: P < 0.05; ***: P < 0.001.*

Conclusion

Our results demonstrate that selection on feed efficiency was successful. However, maternal effects were degraded by the selection. Further investigations are undergoing to better understand the effect of selection on direct and maternal effects. These investigations include host genotyping and microbiota sequencing.

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