

Results of 10 generations of canalising selection for rabbit birth weight

L. Bodin *, M. Garcia *, G. Saleil †, G. Bolet *, and H. Garreau*

Introduction

In natural selection, stabilisation of the phenotypes around a dominant expression has been well-known for a long time to be decisive for the evolution of the species. Several authors have proposed genetic models to explain this natural stabilisation (Falconer, 1952; Rendel, 1979) and experiments on laboratory animals have been made to understand the underlying mechanisms. Those experiments showed selection response and comforted the theory of a genetic control of environmental variability. Genetic parameters for the variability of production traits have been estimated in livestock species according to the model proposed by SanCristobal-Gaudy et al. (1998) which assumes that a set of genes controls the mean expression of a trait while another set controls its environmental variability. The additive genetic part of the environmental variance was generally low, but it would allow a genetic response to selection. In order to study the possibility of selection and to measure its effectiveness, a divergent selection for the within litter homogeneity of rabbit birth weight was initiated. This present study reports genetic parameters estimated during this selection experiment and the direct response obtained after ten selection generations.

Selection process

A divergent selection for rabbit birth weight variability, already described in Garreau et al. (2008), has been carried out since 2003 in an INRA experimental farm. The two lines were created from a strain bred by the Grimaud Frères Sélection (GFS) company. Males and females of the G0 generation were selected from this nucleus according to their breeding value for within litter variability of birth weight (BWSTD) irrespective of the individual birth weight (BW). During all the selection experiment, females of each generation, had opportunity to have 3 litters with males of the corresponding line. Weights of resulting young rabbits were recorded at birth and were considered as a trait of the doe. These weights were analysed using the model for canalisation proposed by SanCristobal-Gaudy et al. (1998). Computing for breeding values (EBV) was done in two steps as described in Garreau et al. (2008).

Methods

In line with previous works, SanCristobal et al. (1998) proposed the first estimation of breeding values for a residual component or the environmental variance, considering a logarithm

*INRA, UR631 Station d'amélioration génétique des animaux, F-31320 Castanet-Tolosan, France

†INRA, IE631 Unité expérimentale SAGA, F-31320 Castanet-Tolosan, France

link between the variance and the predictive parameters. Mulder et al. (2007) developed a different model, which assumes that effects are additive on the variance rather than on the log parameters. A third model, presented recently by Garcia et al. (2009) considered a linear link function between the predictive parameters and the environmental standard deviation of each individual. In the present study genetic parameters was assessed by the last mentioned model implemented in a new version of the GSEVM software (Garcia and Ibañez-Escriche, 2009). Systematic effects considered for the mean and the variability of birth weight were the number of kits in the litter, the gestation duration, the parity of the dam and the generation within line. The model also included genetic effects for the mean (u) and the variability (v) and a dam random permanent effect for the mean (p). Flat priors were used for all parameters and estimations were obtained after running 500 000 iterations with a burn in of 100 000 iterations of the McMC algorithm.

The direct response to selection was assessed by comparing breeding values \hat{v} of the two lines obtained with the same two step method used during the selection process, using the ASREML package. The correlated responses on BWSTD and BW were studied by comparing the phenotypic value of these traits between the divergent lines using GLM procedure (SAS, 1999). The significant effects included in the model for each trait were the same as for breeding evaluation.

Results and discussion

Variance components and genetic parameters for the mean and the within litter variability of birth weight are given in table 1. After 500 000 iterations the model seemed to converge and all posterior distributions were Gaussian like and presented a low standard deviation.

Table 1: Variance components of birth weight traits (mean and within litter variability)

Components	Bayesian estimates			VCE estimates
	Present study		Garcia et al.	Garreau et al.
	Mean of posterior distribution	Std	Mean of posterior distribution	Estimates
σ_u^2	23.90	2.92	19.88	8.50
σ_p^2	35.23	1.70	22.76	38.40
σ_v^2	3.28	0.31	1.20	0.06
$\sigma_{\hat{p}}^2$	–	–	2.11	0.16
ρ	0.085	0.066	-0.024	–

The additive genetic component of birth weight variance was similar to the recent parameters observed in the GFS nucleus (Garcia et al., 2009), but higher than that observed in the first selection generations (Garreau et al., 2008). This discrepancy might come from the larger number of data and the increasing variability due to the divergence selection. In contrast, the maternal permanent environment effect on the mean birth weight was similar to that observed at the beginning of the selection experiment. As a usual trend genetic component for

the environmental variability was much lower than for the mean, however posterior distribution showed that this value was actually different from zero (figure 1 - left). This genetic component of birth weight variability was higher than the value obtained in the GFS nucleus, but similar to the sum of random effects (genetic and permanent) included in the model for variability (i.e. 3.23) in this study (Garcia et al., 2009). The genetic correlation between the mean birth weight and its environmental variability (σ_v^2) was low and not different from zero (figure 1 - right). That agrees with results obtained during the first selection generations and with those of the GFS nucleus. However this correlation was very different from estimations obtained in mice ($\rho = 0.97$; Gutierrez et al. (2006)) or in pig ($\rho = 0.60$; Damgaard et al. (2003)).

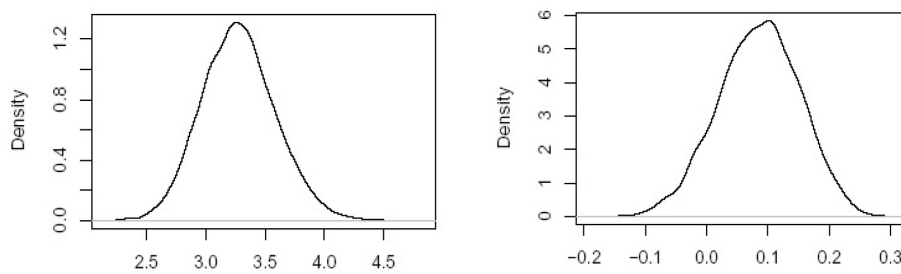


Figure 1: Posterior density of genetic variance for the within birth weight variability (left) and of the genetic correlation between mean and variability (right)

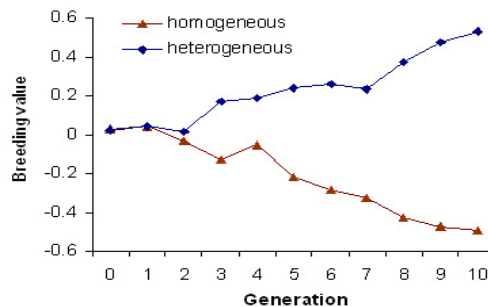


Figure 2: Change of breeding values of environmental variability (\hat{v}) over the 10 generations of selection

A significant difference ($P < 0.001$) of EBV for environmental variability between lines appeared at generation 3 and increased regularly until generation 10 (figure 2). The global symmetry of this divergence was noticeable and indicated that genetic values of both lines changed in a similar way. On the whole data, mean BWSTD was 7.85g and line difference induced by selection reached 3.9g at the last generation (figure 3). On average, the decrease of standard deviation of the homogeneous line from the generation G1 was 0.09g by generation (i.e. 1.1% of the mean). In contrast at each generation there was no difference between lines of EBV for BW and there was no line effect on weight at birth.

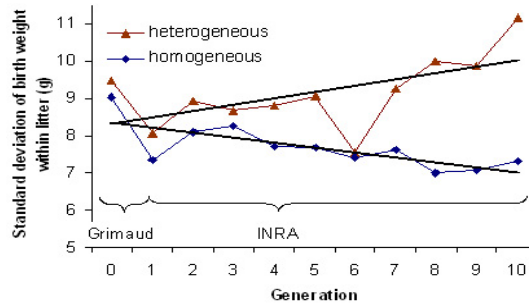


Figure 3: Phenotypic least square means of BWSTD in the two divergent lines over the 10 generations of selection

Conclusion

This analysis confirms previous estimations of genetic variances for the mean (σ_u^2) and the variability (σ_v^2) of rabbit birth weight as well as correlation between these characteristics, made by different methods on similar data set. The selection induced a significant decrease of the variability without any influence on mean. Significant favourable correlated responses, like kits survival and some characteristics of the female genital tract, have also been observed (Bolet et al., 2007). This experiment showed that canalising selection could be efficient and included in genetic improvement programs as did Grimaud Frères Sélection company.

References

- Bolet, G., Garreau, H., Joly, T., Theau-Clement, M., Falières, J., Hurtaud, J., and Bodin, L. (2007). *Lives. Sci.*, 111(1-2):28–32.
- Damgaard, L., Rydhmer, L., Lovendahl, P., , and Grandinson, K. (2003). *J. Anim. Sci.*, 81(3):604–610.
- Falconer, D. (1952). *Am. Natur.*, 86:293–298.
- Garcia, M., David, I., Garreau, H., Ibañez-Escriche, N., Mallard, J., Masson, J., Pommeret, D., Robert-Granié, C., and Bodin, L. (2009). In *Proc. 60th EAAP meeting*.
- Garcia, M. and Ibañez-Escriche, N. (2009). In *Proc. 60th EAAP meeting*.
- Garreau, H., Bolet, G., Larzul, C., Robert-Granie, C., Saleil, G., SanCristobal, M., and Bodin, L. (2008). *Livest. Sci.*, 119:55–62.
- Gutierrez, J., Nieto, B., Piqueras, P., Ibañez, N., and Salgado, C. (2006). *Genet. Sel. Evol.*, 38:445–462.
- Mulder, H., Bijma, P., and Hill, W. (2007). *Genetics*, 175(4):1895–1910.
- Rendel, J. M. (1979). In Thompson, J. N. and Thoday, J. M., editors, *Quantitative genetic variation*. Academic Press, New York.
- SanCristobal-Gaudy, M., Elsen, J., Bodin, L., and Chevalet, C. (1998). *Genet. Sel. Evol.*, 30(5):423–451.