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CAN WE SELECT ON WITHIN LITTER HOMOGENEITY FOR RABBIT BIRTH WEIGHT ? A DIVERGENT SELECTION EXPERIMENT

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ABSTRACT

A divergent selection experiment based on homogeneity of birth weight was carried out at the INRA experimental farm of Auzeville. The two lines have been created by selecting breeding does and bucks from the female strain AGP22 bred at the Grimaud Frères Sélection company. This involved a new model incorporating a genotypic value for the mean and a genotypic value for the residual variance. There was a favourable selection response with a difference in residual variance and in within-litter standard deviation of birth weight between the lines in the first two generations of selection. The mortality of kits at birth was significantly lower in the "homogeneous" line (low variability of birth weight), but total number born was lower in this line. The number born alive in the homogeneous line was higher in the first generation but lower in the second one. The selection on the homogeneity of birth weight had no significant influence on other traits.

Key words: rabbit, canalisation, birth weight, divergent selection.

INTRODUCTION

There is high within-litter variability for rabbit birth weight (BOLET *et al.*, 1996). This heterogeneity of weight is strongly linked with pre-weaning mortality: The weakest animals of the litter cannot compete with the stronger ones and often die of starvation (POIGNIER *et al.*, 2000). In heterogeneous litters the weakest animals are also more sensitive to disease and can contaminate the whole litter. Homogeneous weight at weaning should contribute to a better start of the rearing period. Grading birth weight and fostering methods have been shown to improve pre-weaning survival (PERRIER *et al.*, 2003) but these methods are time consuming, stressful and can contribute to the spread of diseases. Canalisation is a new concept in quantitative genetics, which aims to reduce environmental sensitivity by selection. Several studies have indeed provided evidence for genetic control of environmental sensitivity (WADDINGTON, 1960; SCHEINER and LYMAN, 1991; HILL, 2002). Based on this hypothesis, a statistical model has been proposed to allow the statistical treatment of canalising selection for population under selection (SAN CRISTOBAL *et al.*, 1998). This model incorporates classical genetic effects acting on the mean production level and other genetic

effects acting on the residual variance. Using this new model we have carried out a divergent selection experiment on homogeneity of birth weight. The aim of this study was to estimate the efficiency of canalising selection on birth weight, to estimate the correlated response on other traits and to provide new issues susceptible to validate this innovative statistical method.

MATERIAL AND METHODS

Animals

Does of generation 0 (G0) were selected from the maternal line AGP22 owned by the breeding company Grimaud Frères Sélection (GFS) and introduced in the experimental farm of the Station d'Amélioration Génétique des Animaux in Auzeville (SAGA, INRA centre of Toulouse). Bucks also originated from the line AGP22. They stayed at the GFS facilities and fresh semen was sent to Auzeville in order to inseminate the does.

Method of genetic analysis

We used a heteroscedastic model incorporating a genotypic value for the mean and a genotypic value for the environmental variance, associated with a single phenotypic value (San Cristobal-Gaudy *et al.*, 1998). Birth weights, measured since 1997 in the base population, were analysed as a trait of the doe. We have first estimated the genetic parameters of birth weight, using a classical mixed linear model introducing fixed effects β , the genetic effect u and a residual value e .

$$Y = X \beta + Z u + e \quad (1)$$

We have then estimated the genetic parameters of the log squared residual, as a function describing the environmental variance of birth weight, using a second mixed linear model introducing fixed effects δ and the genetic effect v of the residual variance.

$$\begin{aligned} \text{Log}(\sigma_e^2) &= H \delta + K v + \varepsilon \\ \text{With } e &= Y - X \beta - Z u \end{aligned} \quad (2)$$

The variance components of both mean and residual variance were estimated by a REML procedure applied to an animal model with the VCE software (NEUMAIER et GROENEVELD, 1998). These genetic parameters were used to calculate the breeding value of the birth weight variability (EBVV) of each animal of the base population with the PEST software (GROENEVELD et KOVAC, 1990).

Selection, creation and management of the lines

Fifteen does and 4 bucks with the highest EBVV (heterogeneity of birth weights) and fifteen does and 5 bucks with the lowest EBVV (homogeneity of birth weights), were respectively chosen among 193 does and 108 bucks of the GFS selection nucleus in order to set up the G0. Each generation was inseminated 3 times with a 6 weeks interval. The females selected as breeders for G1 and G2 were chosen in the experimental line while the selected bucks were chosen in the GFS nucleus. The

EBVV of the variability of birth weight were calculated by introducing the own performances of the does and their relatives, recorded in the GFS farm. The G1 consisted of 68 homogeneous does and 96 heterogeneous does from the 3 parities progeny while the G2 consisted of 55 does in each line originated from the last parity progeny. The kits were identified and weighed at birth and at weaning. The prolificacy traits were recorded in all litters.

Statistical analyses of traits

The studied traits were the log squared residual (LSR)(2), the total number born (NB), the number born alive (NBA), and the number weaned (NW) per litter, the mortality at birth (MB), the mortality between birth and weaning (MW), individual body weight at birth (WB) and at weaning (WW), within litter standard deviation of birth weight (STDB) and of weaning weight (STDW). The analyses were performed using the SAS software. The GLM procedure was applied for NB, NBA, NW, STB and STDW while the MIXED procedure was applied for LSR, WB and WW. The GENMOD procedure was applied for MB and MW because of the non normal distribution of these traits. The effects kept in the model are given in Table 1.

Table 1. Effects used to describe the traits analysed

Trait	LSR	NT	NBA	MB	NW	MW	WB	WW	STDB	STDW
Fixed effects										
Generation	X	X	X	X	X	X	X	X	X	X
Line within generation	X	X	X	X	X	X	X	X	X	X
Batch within generation	X						X	X		
Parity		X	X	X	X	X	X	X	X	
Total born in the litter	X						X		X	
Born alive in the litter										X
Number weaned in the litter								X		
Random effect										
Dam within line within generation	X						X	X		

RESULTS AND DISCUSSION

The log-squared residual was higher in the heterogeneous line, suggesting a favourable response to selection but the difference between the lines was not significant. However the log transformation of the residual value lead to a particularly unbalanced distribution of the variable, which could affect the results of a least-square analysis. The most remarkable result was the significantly lower mortality at birth in the homogeneous line (9.94 % vs. 19.36 % in G1 and 5.24 % vs. 7.92% in G2). However the total number born was significantly higher in the heterogeneous line, and more particularly in G2 (9.60 vs. 8.40). The significant difference in the number born alive between the lines was actually associated with contradictory results: The number alive in the homogeneous line was higher in G1 (8.15 vs. 7.33) but lower in G2 (7.96 vs. 8.84). The number weaned and the mortality between birth and weaning were not significantly different between the lines. In G1, the poor level of performances, and more particularly the high mortalities recorded in both lines,

was partly explained by the very high summer heat, which occurred during the experiment. This unfavourable environmental effect may have reduced the benefit of homogeneity of birth weight on survival between birth and weaning.

Table 2. Significance of generation and line within generation fixed effects; Least-square means of prolificacy traits, individual body weights and within litter standard deviation (STD) of weight in the homogeneous line (h) and in the heterogeneous line (H).

	N ^A	σ_p ^B	Generation ^C	Line ^C	G1		G2	
					h ^D	H ^D	h ^D	H ^D
Selection criterion								
Log squared residual	3931	2.24	***	NS	2.58	2.69	2.87	3.07
Prolificacy traits								
Total number born	515	3.28	NS	*	9.05	9.09	8.40	9.60
Number born alive	515	3.49	*	*	8.15	7.33	7.96	8.84
Mortality at birth (%)	515	—	***	***	9.94	19.3 6	5.24	7.92
Number weaned	487	3.20	NS	NS	6.82	6.23	7.31	7.51
Mortality birth-weaning(%)	487	—	NS	NS	16.3	15.0	8.17	15.04
Individual body weight								
Birth weight (g)	3931	13.2	*	NS	60.0	62.1	63.6	65.2
Weaning weight (g)	3154	181	**	NS	632	624	800	813
Within litter STD of weight								
Birth weight (g)	462	3.13	NS	**	6.63	7.31	6.93	8.07
Weaning weight (g)	434	37.8	*	NS	67.3	71.6	77.2	84.3

A: Number; B: Phenotypic standard deviation; C: NS: non significant, * P< 0,05, ** P<0,01, *** P<0,001; D: Least-square means

Individual birth and weaning weights were not significantly different between the lines, but the global trend showed lower birth weights in the homogeneous line, suggesting a possible negative correlation between the mean and the variability of the trait. The significant difference in within litter standard deviation of birth weight (6.63 vs 7.31 in G1 and 6.93 vs 8.07 in G2) demonstrated a favourable correlated response to selection. This difference is partly due to the difference in birth weight and to the link between the standard deviation and the mean of the trait; A decrease of the mean of birth weight lead to a proportional decrease of the standard deviation of the trait. However, giving a constant coefficient of variation of 23.5 %, the average difference of 2 grams in birth weight between lines lead to a difference of 0.47 in standard deviation. The observed difference in standard deviation between lines (0.68 in G1 and 1.14 in G2) is higher the one due only to the difference in the mean

birth weight. The standard deviation of weaning weight was lower in the homogeneous line, but line effect was not significant.

Some authors have studied the genetic relationship between the variation of piglet's birth weight and their survival. DAMGAARD *et al.* (2001) and HÖGBERG *et al.* (1999) have estimated the genetic parameters of within litter standard deviation of birth and weaning weights. Estimates of heritability ranged from 0.06 to 0.10, suggesting a possible genetic improvement of the trait. Heritability of piglet survival was lower (from 0.04 to 0.05). The genetic correlations between survival and within litter standard deviation were favourable. BODIN *et al.* (2002) remind that a genetic analysis of phenotypic standard deviation could be biased by the omission of environmental and genetic factors acting on the mean of the trait. The model developed by SAN CRISTOBAL *et al.* (1998) seems to be more relevant for selection on homogeneity. We just have to keep in mind the possible unfavourable genetic correlation between the mean and the residual variance which could lead to a negative genetic trend of individual birth weight, as suggested by our results. This undesirable response could affect the young survival as some studies have shown the favourable correlation between the average birth weight and the survival of piglets.

We expect that further generations of selection will confirm the efficiency of selection on homogeneity of weight and will provide more accurate results about the link between the homogeneity of birth weight and litter size traits and kits survival. Except for recent studies in snail weight (Ros *et al.*, 2004) and in pig litter size (SORENSEN and WAAGPETERSEN, 2003), there is few convincing experimental evidence for a genetic control of environmental variability.

CONCLUSION

This divergent selection experiment on homogeneity of birth weight showed a favourable selection response with a difference in residual variance and in within litter standard deviation of birth weight between the lines. The mortality at birth was significantly lower in the homogeneous line but further generations of selection are requested to provide a more accurate estimation of the correlated response.

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