THE EFFECT OF THE GENOTYPE IN THE HAL LOCUS ON ECONOMIC TRAITS IN PIGS

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SUMMARY

Two samples of females the Landrace Breed have been classified in homozygous for the gene Hal (Hal^N/Hal^N) and heterozygous (Hal^N/Hal^n), using a DNA probe. The differences between the two genotypes regarding reproductive traits (total number of piglets born, number of born alive) were not statistically significant (P>0.10) in the two samples of females. The effect of the genotype in the Hal locus on average daily gain and backfat tickness was analyzed using a group of 132 animals. In this case the differences between the genotypes were not statistically significant either (P>0.10). The consequence of these results in selection strategies are discussed.

INTRODUCTION

The Hal gene provokes important economic losses in the porcine sector through deaths in stress situations and due to the production of PSE meat. Nevertheless, there are certain advantages in those characteristics related to carcass quality (Christian 1990). The results obtained about its influence on growth characteristics and reproduction are contradictory (Webb et al.. 1985), and there is also some doubt as to whether there is any advantage in the heterozygote with respect to these characteristics due, fundamentally, to the difficulty in determining the genotype of the animals correctly. The recent appearance of a highly accurate molecular technique (Fujii et al.. 1991) to determine the genotype in the Hal locus makes the study and comparison of genotypes possible. In this context the objective of this study is to compare the Hal^N/Hal^N and Hal^N/Hal^n genotypes with regard to the total number of piglets born (TNB), those born alive (NBA), the average daily gain (ADG) and backfat thickness (BF).

MATERIALS AND METHODS

For the study of the incidence of the genotype in the Hal locus on the TNB and NBA characteristics, two Landrace populations with no genetic connection between them were used. These belonged to two selection companies (C1 and C2). The C1 group was made up of 110 dams, being the total active population of the company. The C2 group consisted of 145 sows, taken as a random sample from a population of approximately 425 females. The effect of the genotype in the Hal locus on ADG and BF was analyzed using a group of 132 animals from the C2 company chosen at random. The ADG and BF control was carried out at the same farm of origin. The ADG variable is defined as the average daily gain (in grammes) from birth to the end of the fattening process (165 days). The BF variable (in mm) was measured at the level of the last rib, and at 4-5 cm from the central line at the end of the fattening process (165 days).

The genotype of the animals in the Hal locus was investigated using the molecular analysis of the cDNA proposed by Fujii et al. (1991), as modified by Sánchez et al. (1993). Briefly, a fragment of 118 base pairs was amplified with appropriate primers using the polymerase chain reaction (PCR). The PCR product was then submitted to Cfo I and Asp HI restriction enzyme digestion and separated by electroforesis in agarose (NuSieve, 3%). The animals were classified as Hal^N/Hal^N (NN),

Hal^N/Hal^n (Nn), and Hal^n/Hal^n (nn). Of the 110 C1 females 78 were NN, 31 Nn and 1 nn. Of the 145 females making up the C2 group, 93 were NN, 45 Nn and 1 nn. And of the 132 animals from C2 whose ADG and BF variable was controlled 94 were NN, 37 Nn a 1 nn. The breakdown of this data is laid down in Table 1. Given the low number of recessive homozygous animals in the three study groups, these have not been included in the analyses focussing rather on the comparison between homozygous Hal^N/Hal^N and heterozygous Hal^N/Hal^n animals.

In all the analyses a univariate animal model was used. For prolificacy (TNB and NBA) was as follows :

$$Y_{ijkl} = \mu + G_i + O_j + H_k + A_{il} + P_{il} + e_{ijkl}$$

Y_{ijkl} is the TNB, or NBA, of the dam ijkl, and μ the general mean. The fixed effects are the halothane genotype G_i, the parity order O_j, and the year-season H_k. The random effects are the additive genetic A_{li}, the permanent environmental effect P_{il}, and the residual effect e_{ijklm}.

The model for the ADG and BF variables was as follows :

$$Y_{ijklm} = \mu + G_i + S_j + L_k + c_l + A_{ijklm} + \beta X_{ijklm} + e_{ijklm}$$

Y_{ijklm} is the value of the trait of the animal ijklm; μ, G_i, A_{ijklm} and e_{ijklm} represent the same effects as previous model; S_j the fixed effect of sex; L_k the fixed effect of the fattening batch, β the regression coefficient of Y on the fattening period X (days); c_l the random effect due to the common environment shared by animals of the same litter l.

All known family relationships have been considered, and it can be assumed that the model's random effects are not correlated. The estimates of heritability and common environment of the TNB, NBA, ADG and BF variables in the C1 and C2, calculated by means of the REML method, have been used only as a reference to establish a scale of values for these parameters, which we successively assume in the different analyses. The TNB and NBA variables we have considered the following pairs of values of h^2 and p^2 respectively: 0.05 and 0.10; 0.10 and 0.05; 0.15 and 0.05. For ADG the h^2 values assumed are: 0.15; 0.20; 0.30; 0.40. For BF the h^2 values assumed are: 0.50; 0.60; 0.70. In these two variables the c^2 has been considered equal to 0.15. It was assumed that ADG and BF were independently distributed. The models were solved by means of the statistical package PEST (Groeneveld et al.. 1990), and the differences between the genotypes were contrasted using an aproximate statistics test F.

RESULTS AND DISCUSSION

The results of the comparison between NN and Nn genotypes for TNB and NBA are shown in Table 2. In all the cases studied the differences obtained in favour of NN dams compared to Nn were not worthless, between 0.2 and 0.3 piglets in TNB and NBA, with the exception of the NBT variable in the C2 group which was lower. However, all differences between the two genotypes are not significant ($p>0.10$) either in the population or in any assumed value of h^2 and p^2. The animal model provides unbiased estimates of the effects of a major gene, provided all records from the selected population are used and heritability is known (Kennedy et al. 1992). In our case, where only records from one generation were avalaible and heritability was not known, estimates could be biased. Nonetheless, inclusion of all relationship may decrease the possible bias (Kennedy, 1991). Results in Table 2 suggest that differences between genotypes were relatively robust within the ranges of h^2

and c^2 considered. No results have been reported comparing the prolificacy of carrier dams with either positive or negative homozygote. There is evidence, however, concerning the differences in some reproductive traits between animals reacting (HP) and non-reacting (HN) to the anaesthesic halothane. Results are heterogeneous. Some authors did not find any significant difference neither in number born nor in number alive at 42 days, whereas other studies reported a significant reduction in number born alive and weaned in HP animals with respect to HN animals (see review of Christian and Mabry, 1990).

No significant differences between genotypes have been found in ADG and BF, irrespective of values assumed for h^2 and c^2 (table 3). In this case differences are very small, less than 5% phenotypic standard deviation in this population. Thus the same considerations made before with reproductive traits apply with growth traits. Here use of an univariate model could be a source of bias. In order to study this effect, a bivariate animal model assuming the parameters in Ducos et al. (1992) were run but no significant differences between genotypes were detected either (Noguera, 1993). Results presented here are in agreement with those of Carden (1982) and Simpson and Webb (1989). However, Jensen and Barton-Gade (1985) reported that NN animals had significantly larger ADG than heterozygotes. The low precision in ascertaining genotypes and the possible utilization of inadequate statistical models might explain, at least in part, these contradictory results.

In the light of our results on production traits, no advantage of heterozygote animals with respect to the homozygote Hal^N/Hal^N have been found in ADG and BF. These two traits are those normally included in selection indices. Thus the heterozygote should not have any selective advantage with these indices. The better conformation (Simpson and Webb, 1989) would provide exclusively its advantage.

Results obtained here, would confirm that a rational use of the Hal^n gene in traditional porcine improvement schemes, would imply its elimination from the maternal lines, which would then become NN and, at least, equally prolific. In turn, these would be crossed with nn animals to obtain Nn, which, as we have seen, would not have any relevant differences with the NN in either ADG or BF, but would have the advantage of having better carcass quality, as the Hal^n gene would act additively for this characteristic (Simpson & Webb, 1989). However, if the additivity of the gene for the quality of the meat were confirmed, the possible increase in PSE meat should be considered in this scheme.

Table 1.- Description of the data set used in the analysis.

POPULATION	C1	C2	
VARIABLES	TNB and NBA	TNB and NBA	ADG and BF
Animals with data	110	145	132
Total nº animals*	396	4456	4456
Hal^N/Hal^N registers	233	334	94
Hal^N/Hal^n registers	122	179	37

* The total number of animals that make up the relationship matrix.

Table 2.- Differences between the NN and Nn genotypes in NBT aNBA assuming different values of h^2 y p^2.

	h^2	p^2	C1		C2	
			NN - Nn*	s.e.	NN - Nn*	s.e.
TNB	0.05	0.10	0.33	0.39	0.02	0.31
	0.10	0.05	0.36	0.39	0.01	0.31
	0.15	0.05	0.38	0.42	0.01	0.33
NBA	0.05	0.10	0.23	0.37	0.27	0.30
	0.10	0.05	0.25	0.37	0.19	0.30
	0.15	0.05	0.27	0.39	0.19	0.32

* No significant differences (P>0.10).

Table 3.- Differences between NN and Nn genotypes in ADG and BF assuming different values of h^2 y c^2 constant (0.15).

Variable	h^2	NN - Nn*	s.e.
ADG	0.20	- 2.05	11.27
	0.30	- 1.97	11.37
	0.40	- 1.91	11.48
BF	0.50	- 0.06	0.46
	0.60	- 0.05	0.47
	0.70	- 0.03	0.47

* No significant differences (P>0.10).

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