Genetic Evaluation Of The French Piétrain Purebred Population Including The Halothane Genotype

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Introduction

The halothane sensitivity allele (n) is segregating in the French Piétrain breed. Currently, the halothane genotype (NN, Nn, nn) is used for the selection among the young candidates though it is not included in the genetic evaluation. This study was conducted to determine whether the addition of the halothane genotype in statistical models used for the genetic evaluation of the French Piétrain purebred population could improve the accuracy of the estimates of breeding values.

Material and methods

Animals and data recording. Data considered in this study were recorded between 2002 and 2008. Average daily gain (**ADG**), daily feed intake (**DFI**) and feed conversion ratio (**FCR**) from 35 to 105 kg body weight, lean meat content (**LMC**), carcass dressing percentage (**DRESS**) and meat quality index (**MQI**) were recorded on females in the French central test stations. Age (**A100**), average ultrasonic backfat thickness (**BT**) and loin depth (**LD**) adjusted at 100 kg body weight were recorded on entire males and females in French pig breeding farms.

Genotype imputation. The halothane genotype (NN, Nn, nn) was determined using a DNA test (Fujii, Otsu, Zorzato *et al.* (1991)) for 90 % of the pigs controlled in test stations and 23 % of the animals controlled in breeding farms. The missing halothane genotype of the remaining animals (175 females controlled in test stations and 28,698 on-farm tested pigs) was deduced from the genotypes of their parents and/or their offspring using a program developed by Druet, Fritz, Boussaha *et al.* (2008), assuming that all the ungenotyped founders were homozygous nn. A total of 47,804 pigs (6,211 NN, 8,151 Nn and 33,442 nn) were considered in the data set: 2,147 females with phenotypes for the traits recorded on-station (ADG, DFI, FCR, LMC, DRESS and MQI) and 45,657 pigs with on-farm performance traits (A100, BT and LD).

Statistical analyses. (Co)variance components and breeding values were estimated using two statistical models, including (M2) or not (M1) the halothane genotype as fixed effect. For each trait, models M1 and M2 included the fixed effect of animal contemporary group

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(year x herd x batch x sex for on-farm test traits, year x station x batch for station test traits, except for MQI, adjusted for the slaughter date) and the random effects of birth litter and individual additive genetic effect. Models also included initial weight (for ADG, DFI and FCR) or slaughter weight (for LMC, DRESS and MQI) as covariates.

Variance components were estimated by restricted maximum likelihood (REML) applied to a multiple-trait animal model (Patterson and Thompson (1971)). Breeding values were estimated for the nine traits with the PEST software (Groeneveld and Kovac (1990)) using models M1 or M2. Genetic groups were defined for animals with unknown parents depending on their birth year and geographical origin. Pearson linear correlation coefficients and Kendall rank correlation coefficients were calculated between M1 and M2 estimates of breeding values for each halothane genotype.

Results and discussion

Heritabilities. Heritability estimates for each trait using the models M1 and M2 are presented in Table 1. The values obtained with M1 and M2 were similar, except for LMC (0.42 for M1 versus 0.52 for M2). The growth related traits (ADG and DFI) had the highest heritabilities whereas MQI had the lowest values (0.33 for M1 and 0.34 for M2). Heritabilitiy estimates were higher than those used in the current genetic evaluation, estimated in 2001, especially for ADG (0.47), FCR (0.23), DRESS (0.28), MQI (0.23) and LD (0.30).

Table 1 : Estimates of heritability for nine production traits in the French Piétrain breed$^{\alpha}$

Traits	ADG	DFI	FCR	LMC	DRESS	MQI	A100	BT	LD
M1	0.57	0.51	0.46	0.42	0.42	0.33	0.39	0.46	0.41
M2	0.59	0.57	0.44	0.52	0.42	0.34	0.39	0.45	0.41

$^{\alpha}$Standard errors of estimates ranged from 0.02 to 0.07

Breeding values. Correlations between the breeding values estimated with M1 and M2 are shown in Table 2. Linear correlations were very high for all the traits, except for DRESS (0.65 to 0.92), whatever the halothane genotype. No significant difference was observed between the results of the two models for BT and LD, despite carcass traits were strongly affected by the halothane genotype as shown in previous studies (Guéblez, Paboeuf, Sellier *et al.* (1995) ; Larzul, Le Roy, Guéblez *et al.* (1997) ; Mérour, Hermesch, Schwob *et al.* (2009)). According to Kendall correlation coefficients, the inclusion of the halothane genotype in the genetic evaluation had an impact on the ranking of animals, particularly for heterozygous individuals. As we can observe in the Figure 1 for LMC, ranks of breeding values of animals carrying the N-allele are lower in the model M2 than in the model M1. Since lower ranks indicate better breeding values, animals carrying the N-allele are more penalized in the model M1.

Table 2 : Pearson linear correlation coefficients and Kendall rank correlation coefficients between M1 and M2 estimates of breeding values for each halothane genotype

		ADG	DFI	FCR	LMC	DRESS	MQI	A100	BT	LD
NN	Pearson	0.98	0.97	0.98	0.96	0.85	0.93	1.00	0.98	1.00
	Kendall	0.89	0.84	0.88	0.82	0.67	0.76	0.97	0.90	0.96
Nn	Pearson	0.99	0.97	0.95	0.88	0.65	0.92	0.99	0.94	0.99
	Kendall	0.89	0.84	0.78	0.67	0.43	0.74	0.94	0.77	0.91
nn	Pearson	0.99	0.98	0.99	0.97	0.92	0.98	1.00	0.99	1.00
	Kendall	0.89	0.88	0.91	0.85	0.76	0.89	0.96	0.93	0.97

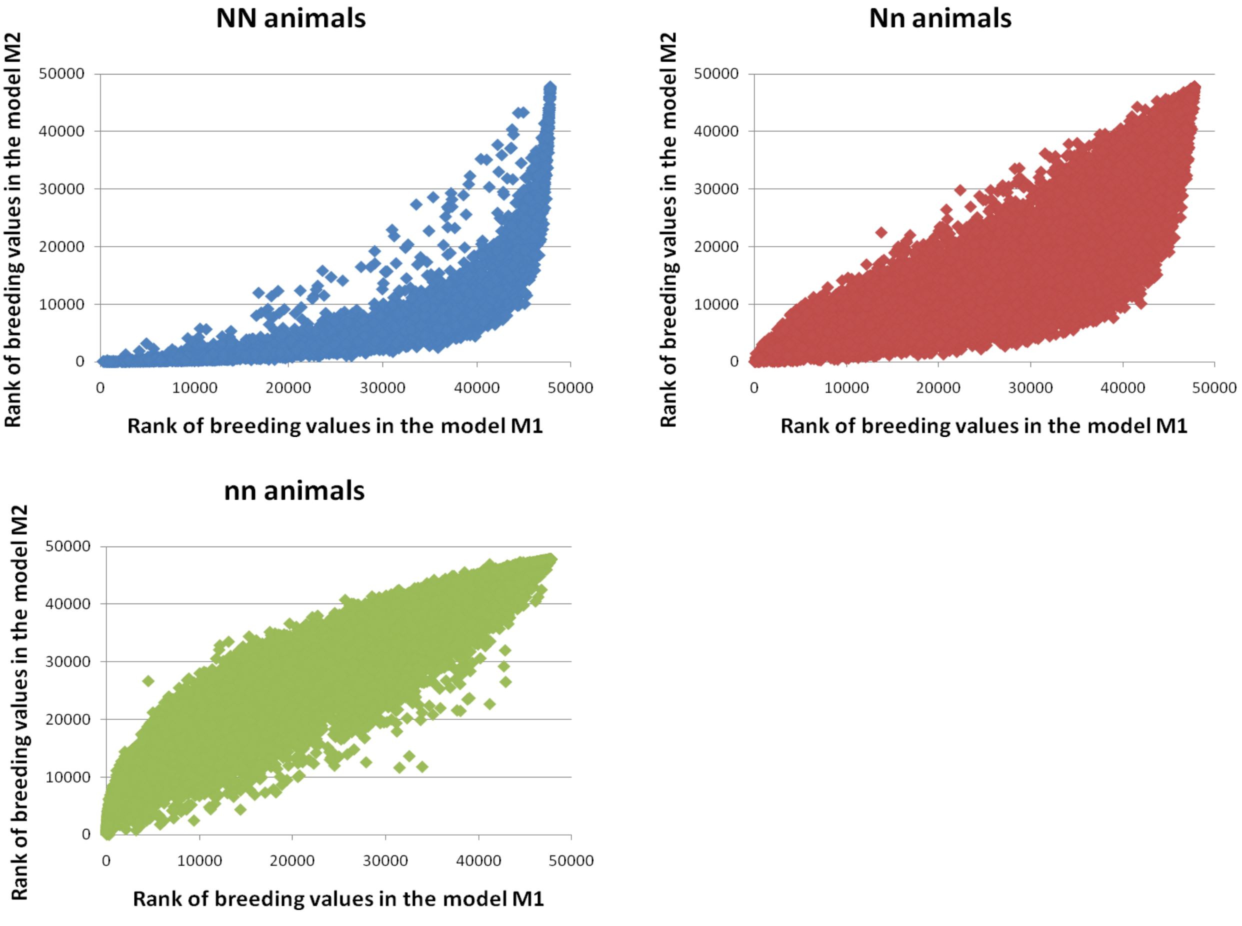

Figure 1 : Rank of breeding values estimated for LMC using models M1 and M2

Conclusion

Genetic parameters used in the current genetic evaluation of the French Piétrain purebred population were estimated in 2001. Updating of genetic parameters considering halothane genotype as fixed effect should improve the accuracy of the estimates of breeding values in this population. However, availability of molecular data is necessary to implement genetic evaluation including the halothane genotype. This implies to develop a reliable and rapid system for collecting and storing genotypes. Moreover, an optimal strategy has to be considered to manage missing genotypes. This study is included in a largest scale project about the use of molecular data in the French pig breeding programs, which should lead to the implementation of a marker/gene assisted selection in pig breeding populations.

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