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EFFECT OF THE HALOTHANE GENOTYPE ON GROWTH PERFORMANCES, CARCASE AND MEAT QUALITY TRAITS IN THE PIETRAIN BREED OF THE FRENCH NATIONAL PIG BREEDING PROGRAM

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SUMMARY

The halothane allele (n) is segregating in the French national Pietrain breed. Records from the three French central test stations were available for 1,557 Pietrain pigs of known halothane gene status (128 NN, 334 Nn and 1,095 nn). Production traits, carcase composition and meat quality measurements were studied to compare the three genotypes and assess the allele effects. Water holding capacity was the trait most affected by the halothane allele (-0.76 phenotypic standard deviations, sd) followed by the length of the carcase (-0.62 sd) and by carcase traits related to leanness and fatness: dressing percentage, fat and muscle depth and weights of back leg, loin, and fat and rind above loin. The magnitude of the effect of the halothane allele varied from 0.21 to 0.47 phenotypic standard deviations for these carcase traits. In addition, performance of the heterozygous genotype was more similar to the homozygous (NN) genotype. Significant differences between the three genotypes were found for ultimate pH but not for colour. Colour (L*-value) was the only trait for which the heterozygous genotype was more similar to the superior homozygous genotype. In comparison to carcase and meat quality traits, the halothane allele effect was lower for production traits (from -0.12 to 0.02 sd).

INTRODUCTION

Following the new grading criteria and payment scheme in France implemented in 2006, the use of Pietrain pigs as terminal boars has increased at the expense of terminal hybrid boars. In 2007, 69% of semen doses sold to production farms were from the Pietrain breed. The halothane positive allele (n) is segregating in this breed at a high frequency. The effect of the halothane allele in pigs has been studied for nearly thirty years and it is well established that this allele influences carcase and meat quality traits (Aalhus *et al.* 1991; Guéblez *et al.* 1995; Hanset *et al.* 1995 and Larzul *et al.* 1997). However, these past studies were based on data from crossbred populations and the magnitude of the effect of the halothane allele may have been affected by selection. The accuracy of genetic evaluation can be improved if genetic evaluation models are adapted to account for major gene effects explicitly (Tier and Bunter 2003). Thus, the aim of this study was to investigate and quantify the effect of the halothane allele on growth, carcase and meat quality traits in the French national Pietrain breed.

MATERIALS AND METHODS

Data were recorded on female pigs between 2002 and 2008 in three French test stations located in Argentré, Le Rheu and Mauron. The purebred Pietrain animals were sourced from seven herdbook farms participating in the French national breeding scheme. Each herd had at least two halothane genotypes represented. Pigs from each herd were tested in no less than two stations. Pigs arriving at each station at the same time formed a batch, which consisted of a minimum of two herds. Animals from the same herd were housed in groups of 12 animals. The halothane genotype

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(NN, homozygous halothane-negative; Nn, heterozygous halothane-negative; nn, halothane-positive) was deduced from the genotypes of their parents or, if this was not possible, was determined using a DNA test (Fujii *et al.* 1991). A total of 1,557 pigs (128 NN, 334 Nn and 1,095 nn) descending from 399 sires were tested within stations. No data recorded on farm were used in this study.

Pigs arrived at stations at the maximum age of five weeks and given *ad libitum* access to feed. However, performance testing was from 35 to 105 kg body weight. Daily feed intake (**DFI**), feed conversion ratio (**FCR)** and average daily gain (**ADG**) were recorded for this test period. Empty body weight was recorded after a fasting period of 16 hours to derive dressing percentage in the abattoir. Pre-slaughter management of pigs and transport time (around 35 minutes) were similar for the three stations. Pigs were slaughtered in two commercial abattoirs. Fat and muscle depth (**FD** and **MD**) between the third and fourth last ribs were recorded using a fat and lean sensor (Sydel CGM – reflectance measurements). Carcases were allowed to chill for approximately 24 hours at 4ºC. Dressing percentage was defined as the ratio of cold carcase weight to empty body weight. Carcase length was measured from the atlas to the anterior edge of the pubic symphysis. The right half of each carcase was submitted to a normalised cutting procedure (Métayer and Daumas 1998) and weights of the back leg, the loin with the skin and fat trimmed, the shoulder, the belly and the fat and rind above the loin (**backfat**) were recorded. Meat quality measurements were taken 24 h *post mortem*. Ultimate pH (**pHu**) was recorded on the *semimembranosus* muscle using a Sydel or Knick pH meter. Meat colour (**L***) was assessed on the *gluteus medius* (GM) using a Minolta CR-300 photocolorimeter (a lower value of L* is associated with darker meat). Water holding capacity (**WHC**) scores, measured at the freshly cut surface of the GM muscle, were determined by the time (in tenths of seconds) required to wet completely one cm^2 of filter paper; a larger value is associated with better WHC.

Contemporary group (61 levels) defined as a concatenation of year, batch and station along with genotype (three levels) were fitted as class effects for all traits. Cold carcase weight was included as a linear covariable in the model used for all carcase traits except for dressing percentage. A Log Likelihood ratio test was used to evaluate the significance of random effects. Effect of the herd in which a piglet was born proved to be significant for all traits except feed conversion ratio, weight of shoulder and meat quality traits. So, herd was included as a random effect. As there were few animals per genotype and per slaughter day nested within batch, slaughter day was included as a random effect in the model for the three meat quality traits. An animal model did not converge and sire linked with pedigree information was fitted as a random effect to account for additive genetic effects. On average, there were 1.2 animals per litter tested in station and litter effect was not included in the model. The ASReml program (Gilmour *et al*. 2006) was used to predict significant differences between genotypes and to estimate the additive (a) and the dominance (d) effects of the n allele along with the estimates of their standard errors, which were used to derive the 95% confidence limits for each estimate. A number of alternative models were evaluated but showed minimal differences between estimates.

RESULTS AND DISCUSSION

Production traits. Heterozygous pigs grew faster than homozygous NN pigs, whereas homozygous nn pigs had significantly better feed conversion ratio than the other two genotypes (Table 1). Hanset *et al.* (1995) also found that heterozygous pigs had the highest growth rate. In comparison, other studies reported no significant differences between the three genotypes (Guéblez *et al*. 1995) or a better growth rate for NN pigs (McPhee *et al*. 1994). Similar to results from this study, the nn genotype had the lowest feed intake and feed conversion ratio in the studies by McPhee *et al*. (1994) and Guéblez *et al*. (1995).

Table 1. Phenotypic standard deviations (σ_p), predicted values with standard errors for each halothane genotype, allele effect (a=((nn-NN)/2)/σ_p) and dominance (d=(Nn-5*(nn+NN))/σ_p), both expressed in σ_p units

Traits[1]	σ_p	NN	Nn	nn	a	d
ADG (g/d)	87.0	822.1 ± 15.7[a]	843.0 ± 13.38 [b]	834.6± 12.83 [b]	0.07	0.17*
FCR (kg/kg)	0.17	2.53 ± 0.02[a]	2.52± 0.01[a]	2.49± 0.008 [b]	-0.12*	0.06
DFI (kg/d)	0.20	2.08± 0.04[ab]	2.12 ± 0.03 [a]	2.07± 0.03 [b]	-0.02	0.22*
Dressing %	1.13	81.4 ± 0.15 [a]	81.7 ± 0.11 [b]	82.4 ± 0.10 [c]	0.47*	-0.13
Length (mm)	25.3	971.0 ± 3.67 [a]	962.3 ± 2.71 [b]	939.6 ± 2.44 [c]	-0.62*	0.27*
Back leg wt (kg)[2]	0.44	11.12 ± 0.06 [a]	11.21 ± 0.04 [b]	11.43 ± 0.04 [c]	0.36*	-0.14
Belly wt (kg) [2]	0.37	4.52 ± 0.05 [ab]	4.58 ± 0.04 [a]	4.47 ± 0.03 [b]	-0.06	0.21*
Shoulder wt(kg)[2]	0.36	9.11 ± 0.04	9.09 ± 0.02	9.13 ± 0.02	0.03	-0.07
Loin wt (kg) [2]	0.54	11.78 ± 0.07 [a]	11.83 ± 0.05 [a]	12.00 ± 0.04 [b]	0.21*	-0.10
Backfat wt (kg) [2]	0.33	2.29 ± 0.05 [a]	2.20 ± 0.04 [b]	1.98 ± 0.04 [c]	-0.46*	0.20*
FD (mm)	1.70	11.88 ± 0.26 [a]	11.31 ± 0.19 [b]	10.44 ± 0.18 [c]	-0.42*	0.10
MD (mm)	4.93	64.38 ± 0.63 [a]	65.87 ± 0.40 [b]	67.76 ± 0.34 [c]	0.35*	-0.05
pHu	0.14	5.59 ± 0.01 [a]	5.62 ± 0.009 [b]	5.64 ± 0.007 [c]	0.18*	0.06
WHC (scores)	3.22	6.73 ± 0.32 [a]	3.44± 0.19 [b]	1.85± 0.12[c]	-0.76*	-0.26*
L* value	3.46	51.04 ± 0.39 [a]	51.50 ± 0.24 [a]	53.47 ± 0.19 [b]	0.36*	-0.21*

Within row, predictions with different superscript letters were significantly different ($P < 0.05$). *Additive and dominance effects of n allele were significant ($P < 0.05$). [1]Abbreviations for traits: ADG: Average Daily Gain; FCR: Feed Conversion Ratio; DFI: Daily Feed Intake; FD: Fat Depth; MD: Muscle Depth; WHC: Water Holding Capacity; pHu: ultimate pH. [2]Weight based on right half of carcase only.

Carcase traits. The three halothane genotypes differed significantly for dressing percentage, length, weight of back leg and backfat, fat depth and muscle depth. The magnitude of the allele effect varied from 0.35 to 0.62 phenotypic standard deviations for these traits which correspond well with the effects reported by Larzul *et al*. (1997) for dressing percentage, carcase length and fat depth measurements. In contrast, larger differences were found between NN and nn pigs for ham and loin weight in the studies by Guéblez *et al*. (1995) and Hanset *et al*. (1995). Shoulder weight was not affected by the halothane allele (Table 1). For all carcase traits affected by the halothane allele, heterozygotes were closer to the inferior NN than to the superior nn genotype, which was also observed by Larzul *et al.* (1997) for comparable traits.

Meat quality traits. As expected, halothane sensitivity was accompanied by worse overall meat quality. Relative to other traits in this study, the largest effect of the n allele was on water holding capacity (-0.76 sd). In comparison, the magnitude of the allele effect on water holding capacity was substantially lower (-0.37 sd) in the study by Larzul *et al*. (1997). A scoring system was used for WHC in this study which superseded the paper wetting time method used in Larzul et al. (1997). The heterozygous genotype was closer to nn carcases for water holding capacity, which was also reported by Larzul *et al*. (1997) and Guéblez *et al*. (1995). Significant differences between the three genotypes for ultimate pH were found in this study confirming results from a recent meta-analysis (Salmi *et al*. 2009). In contrast, other studies (Fàbrega *et al*. 2004; Larzul *et al*. 1997) reported that the n allele had no significant effect on ultimate pH. With respect to the L*-values, nn carcases had paler meat colour in the *gluteus medius* than both Nn and NN carcases, which did not differ significantly from each other. Among all the traits investigated, this meat colour measurement was the only trait for which the heterozygous carcases were closer to the superior homozygous genotype.

CONCLUSIONS

The halothane allele affected significantly most of the traits considered in this study. The magnitude of the allele was highest for water holding capacity and carcase traits related to leanness and fatness measurements. Performance in these carcase traits of the heterozygous genotype was more similar to the inferior homogeneous (NN) genotype for these carcase traits. The current study presents results based on purebred data for a wider range of traits, improving knowledge from historical analyses conducted more than ten years ago on crossbred data. The estimates from this study should be used in genetic evaluations that incorporate the halothane allele effect explicitly (Tier and Bunter 2003).

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