Genetic Parameters For Intramuscular Oleic Fatty Acid Content In A Duroc Line

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Introduction

Intramuscular fat (IMF) content and composition, particularly the oleic fatty acid content (OL), are major quality characteristics of pork dry-cured products. They are known to be related to nutritional, manufacturing and organoleptic properties, as well as to human health. The challenge for the meat industry is to improve them without affecting carcass lean growth. However, although it is known that IMF is unfavourably genetically correlated with carcass lean content, little evidence is known about OL. There are very few estimates in the literature regarding genetic parameters for OL (De Smet *et al.*, 2004) and, besides, they are based on small data sets from experiments designed for other purposes. Genetic parameters for IMF and OL are needed for developing selection criteria aimed at capturing the genetic variance associated to IMF content and composition but not to backfat and other fat deposits. The objective of this paper is to estimate the genetic parameters associated to OL in a Duroc line used for high quality dry-cured ham production.

Material and methods

Line and animals. Data from a purebred Duroc line were used for the analyses. The line was completely closed in 1991 and since then it has been selected for an index combining number of piglets born alive, growth rate, backfat thickness (BT) and IMF (Solanes *et al.*, 2009). The data set used for the estimation of the genetic parameters consisted of 91,343 pigs, from which 82,190 had at least one recorded trait. Pigs with records were born from 1996 to 2009. A summary of the population characteristics and number of records used for each analysed trait is given in Table 1. At about 75 days of age piglets were moved to the fattening units, where they were penned by sex. Pigs were performance-tested at an average age of 180 days for body weight (BW) and BT. BT was ultrasonically measured at 5 cm off the midline at the position of the last rib (Piglog 105 ®, Herlev, Denmark). During the test period pigs had *ad libitum* access to commercial diets. At the end of the fattening period, a sample of pigs was slaughtered in a commercial slaughterhouse. Sampled pigs were either chosen at random or selected according to their predicted breeding values for BW and BT. After chilling for about 24 h at 2ºC, a sample of at least 50 g of the *gluteus medius* muscle was taken from the left side ham, immediately vacuum packaged and stored in deep freeze until required.

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Table 1: Description of the data set used in the analyses

Traits	n	Mean	SD	Minimum	Maximum
BW, kg	81,941	104.8	12.6	62.0	180.0
BT, mm	77,640	15.6	3.6	6.5	36.0
IMF, %	947	4.9	1.9	1.5	18.7
OL, % fatty acid	947	44.8	3.1	36.3	55.5
Age at test, days	82131	180.4	10.7	140.0	246.0
Age at slaughter, days	3706	207.9	15.3	170.0	252.0

Laboratory analyses. IMF was determined by gas chromatography as the sum of individual fatty acids expressed as triglyceride equivalents (Bosch *et al.*, 2009). Fatty acid composition analysis was performed in duplicate by quantitative determination of the individual fatty acids by gas chromatography. Fatty acid methyl esters were directly obtained by transesterification using a solution of 20% boron trifluoride in methanol. Methyl esters were determined by gas chromatography using a capillary column SP2330 (30 m × 0.25 mm, Supelco, Bellefonte, PA) and a flame ionization detector with helium as carrier gas. The analytical column was coated with a 0.20-µm film. The oven temperature program was increased from 150 to 225°C (by 7°C per min). The injector and detector temperatures were 250°C. OL quantification was carried out via normalization of the area under appropriate pick after adding 1,2,3-tripentadecanoylglycerol into each sample as an internal standard.

Statistical analyses. Genetic parameters for BW, BT, IMF and OL were estimated using a multiple four-trait animal model. The model for BW and BT included batch (1006 classes) and sex (males, females and castrates) as fixed effects and litter as random effect. IMF and OL were logratio transformed and then analyzed with a model including batch (13 classes) as fixed effect. The isometric logratio transformation of IMF and OL was used to convert the compositional data to samples in real space (Egozcue *et al*., 2003) Age at measurement was included as a covariate in all models. Genetic parameters were estimated in a Bayesian framework using Gibbs sampling with the TM software (Legarra *et al.*, 2008). Flat priors were used for variance components and fixed effects. Statistical inferences were derived from the samples of the marginal posterior distribution using a unique chain of 500,000 iterations, where the first 100,000 were discarded and one sample out of 100 iterations retained. Statistics of marginal posterior distributions and the convergence diagnostics were obtained using the BOA package (Smith, 2005, http://www.public-health.uiowa.edu/boa/). Convergence was assessed using the method described by Geweke and visual inspection of convergence plots.

Results and discussion

Estimates of heritability for BW, BT, IMF and OL are shown in Table 2. Common environmental litter effects accounted for 0.10 (SD<0.01) and 0.07 (SD <0.01) of phenotypic variance for BW and BT, respectively. Estimates of the genetic correlation between IMF and

OL with BW and BT are given in Table 3. The genetic correlation between BW and BT was 0.63 (SD 0.02) and the correlation between the litter effects of BT and BW 0.58 (SD 0.02).

Table 2: Heritability estimates for body weight (BW), backfat thickness (BT), intramuscular fat (IMF) and oleic fatty acid (OL) content

Traits	Heritability	
	Mean (SD)	HPD_{95} [α]
BW	0.31 (0.01)	0.29; 0.33
BT	0.44 (0.01)	0.42; 0.47
IMF	0.56 (0.08)	0.42; 0.71
OL	0.50 (0.08)	0.37; 0.68

[α] HPD95: Highest probability density interval at 95%

Table 3: Genetic correlations (r_g) of intramuscular fat (IMF) and oleic fatty acid (OL) with body weight (BW) and backfat thickness (BT)

Traits	Genetic correlation with IMF			Genetic correlation with OL		
	Mean (SD)	HPD_{95} [α]	$P(r_g>0.2)$ [α]	Mean (SD)	HPD_{95} [α]	$P(r_g>0.2)$ [α]
BW	0.28 (0.11)	0.08; 0.50	0.76	0.13 (0.11)	-0.11; 0.34	0.26
BT	0.40 (0.11)	0.18; 0.60	0.94	0.24 (0.11)	0.04; 0.48	0.66
IMF	-	-		0.50 (0.10)	0.30; 0.68	1.00

[α] HPD95: Highest probability density interval at 95% ; $P(r_g>0.2)$: Probability of r_g being higher than 0.2

The heritability estimate for OL resulted to be high (0.50) and very similar to those obtained for IMF, either in the present or in previous analyses performed in this line (Solanes *et al.*, 2009). Ntawumbizi *et al.* (2010), using data from the *longissimus* muscle of a four-way cross, obtained a similar value. However, estimates reported by Suzuki *et al.* (2006), in *longissimus* in Duroc, and Fernandez *et al.* (2003), in subcutaneous fat of Iberian pigs, were lower (around 0.30). OL showed a favorable and moderately high genetic correlation with IMF, which is in accordance with the expected trend of IMF fatty acid composition with IMF content. Contrarily, Suzuki *et al.* (2006) found that the genetic relationship between OL and IMF was almost negligible. The genetic correlation of OL with BW and BT was positive but lower than that observed between IMF and BW and BT, in the same range as in Suzuki *et al.* (2006). OL was genetically less correlated to BT than IMF (the probability of this genetic correlation being higher than 0.4 was 52%, for IMF, but only 7%, for OL).

Parameter estimates associated to IMF and in particular to OL hardly differed when IMF and OL were isometric logratio transformed. This should not be necessarily the case for other less abundant fatty acids displaying higher variability. Previous estimates obtained in this

line using only the data set from pigs with OL records led to lower genetic correlations of OL and IMF with BW and BT, even suggesting a negative genetic relationship between them. Some of the OL records were collected from experimental pigs selected for BW and BT. Including all the data set in the analysis removed this source of selection bias and put in evidence the risks of estimating genetic parameters using data recorded for other purposes.

Genetic differences between individuals for OL may come from differential ability of pigs (1) to incorporate dietary fat OL to IMF, or (2) to synthesize OL from palmitic and stearic acids via increased enzymatic activity of elongases and delta-9 desaturases, respectively. Cánovas *et al.* (2009) found that selection for decreased backfat thickness at restrained IMF led to changes in acetyl-CoA carboxylase and delta-9 desaturase protein expression.

The results indicate that selection for OL can be effective, provided it can be recorded cost-efficiently. Moreover, favourable response scenarios for OL, IMF, BT and BW can be expected. An experiment has been undertaken to validate whether selection for OL is a good strategy for improving IMF and OL at restrained BT.

Conclusion

These results show that there is scope for commercial pig lines to be successfully selected for OL and IMF without decreasing carcass lean growth.

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