Genetic parameters for intramuscular fatty acid composition and metabolism in pork

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Abstract

The aim of this study was to estimate genetic parameters for pork intramuscular fatty acid composition and indices for desaturase and elongase activities involved in the *n*-3 and *n*-6 polyunsaturated fatty acid (PUFA) metabolism. Fatty acid composition of the *longissimus* muscle of 437 slaughter pigs was analysed and indices for enzyme activities were calculated from product to precursor fatty acid ratio's. Genetic parameters were estimated with single and multi-trait animal models using VCE-software. The total fatty acid content was either or not included in the model as a covariate. Heritabilities for the ratio's C20:4*n*-6/C18:2*n*-6 and C22:6*n*-3/C18:3*n*-3 were 0.29 and 0.35 respectively, and increased to 0.38 and 0.49 respectively if the total fatty acid content was not in the model. Heritabilities for other indices were of the same order. Genetic correlations for PUFA proportions and indices for enzyme activities with average daily gain were generally negative, whereas the correlations with carcass lean meat percentage were generally positive. It is concluded that there is considerable genetic variation for long chain PUFA metabolism, that is partly independent of the carcass and muscle fat content. This may allow selection for improved fatty acid composition of pork.

Introduction

There is for decades already a large interest in the fatty acid (FA) composition of meats because of its implications for meat quality and its contribution to total FA intake and the associated role in human health (Wood et al., 2003). Many efforts have been made to improve the nutritional value and the sensory quality of meat by controlling the intramuscular fat (IMF) deposition and its FA composition. Particularly long chain (LC) polyunsaturated FA (PUFA) are nowadays the focus of much research because they are of particular relevance to human health.

The FA composition of edible animal fats is determined by genetic factors, e.g. breed, sex and genotype, and environmental factors of which diet is by far the most important one (De Smet et al., 2004; Raes et al., 2004). In contrast to nutritional studies, less studies have been performed on the genetic determinism of the long chain PUFA metabolism and deposition. Therefore, the aim of this study was to estimate genetic parameters for the intramuscular FA profile in slaughter pigs with emphasis on the long chain PUFA. Particular attention was paid to differences in the indices for enzyme activities (desaturases and elongases) involved in the *n*-3 and *n*-6 PUFA metabolism.

Material and methods

Longissimus muscle samples used in this study originated from a QTL search experiment described by Harmegnies et al. (2006). The slaughter pigs were progeny from a commercial four-way cross. Hybrid sows were obtained by mating two distinct Landrace · Large White composite lines. Hybrid boars were obtained by mating a Large White and a composite Large White · Piétrain line. Neither the RYR1 R615C mutation nor the PRKAG3 R200Q mutation was present in these families. The pigs were all born on the same farm and were transferred at the age of 2 months to the finishing farm where they were kept until slaughter at the target commercial slaughter weight of 110 kg.

A sub-sample of 437 samples was analyzed for FA composition, originating from five sires (n = 78-100 per sire) and with approximately equal numbers of barrows and gilts (n = 221 and 216 respectively). Live and carcass weight and carcass lean meat percentage (LMP; CGM device) were determined at slaughter on 25 slaughter days. After homogenization of the minced meat samples taken one day after slaughter, the total lipids were extracted using chloroform/methanol (2/1, v/v). FA were methylated and separated on a HP6890 gas chromatograph with a CP-Sil88 column as described by Raes et al. (2001). Peaks were identified on the basis of their respective retention times, corresponding to their FA methyl ester (FAME)

standards. The FA composition data are expressed as g/100g of FAME. Nonadecanoic acid was used as an internal standard allowing quantification of the total FA content (mg/100g meat) as a measure for the IMF content. The indices for the activities of delta-9, delta-6 and delta-5 desaturase, as well as the elongase activity, were estimated by the ratios of product to precursor FA.

Genetic parameters were estimated with single and multi-trait animal models using VCE software (Kovac and Groeneveld, 2003). The models included the fixed effect of sex and the random effects of animal and slaughter day. To examine the effect of variation in fat level, the total intramuscular FA content was either or not included in the models. Three generations of pedigree information was available on the paternal and grand-maternal side.

Results and discussion

The average (SD) age at slaughter, cold carcass weight, whole life average daily gain (ADG) and carcass LMP were respectively 218 (24.6) days, 87.1 (6.9) kg, 511 (60) g/day and 58.4 (4.1) %. The average total FA content was 1214 (547) mg/100g meat. The average heritability estimate for ADG and LMP using the model including sex, animal and slaughter day was 0.551 and 0.514 respectively, and their genetic correlation was -0.135.

Average values and genetic parameters for the most important individual FA proportions and for FA indices reflecting enzyme activities are given in Table 1. Heritabilities for the FA proportions were relatively high and varied between 0.12 and 0.60 using model 1 (without IMF in the model). These values are in line with literature data for heritabilities of C16:0, C18:0, C18:1 and C18:2 proportions in subcutaneous or intramuscular fat of pigs (Sellier, 1998; Fernandez et al., 2005). Heritabilities generally decreased when IMF was included as covariate in the model and varied between 0.03 and 0.47 using model 2. This points to considerable genetic variability that is partly independent of the intramuscular fat content. Indeed, it is well known that the proportion of PUFA varies inversely with the intramuscular fat level because of the decreased ratio of triacylglycerols to phospholipids with decreasing fat content (De Smet et al., 2004). Also in the present study, the PUFA proportions were phenotypically negatively related, whereas the saturated FA (SFA) and monounsaturated FA (MUFA) proportions were positively related to the total FA content (data not shown). Inversely, the PUFA proportions were genetically positively related to the carcass LMP. Because of the weak negative correlation between ADG and LMP, there was a tendency for slight negative genetic correlations between ADG and PUFA proportions.

We were particularly interested in the genetic variability for ratio's of FA that reflect underlying enzyme activities for desaturation and elongation of FA to more unsaturated and/or longer chain metabolites. It should be realized, however, that these indices are only approximations for the absolute activity of these desaturase and elongase enzymes. Estimates for heritabilities of these indices are in the same order as for the FA proportions, e.g. heritabilities for the ratio's C20:4*n*-6/C18:2*n*-6 and C22:6*n*-3/C18:3*n*-3 reflecting the overall conversion of the parent essential FA C18:2*n*-6 and C18:3*n*-3 to their long chain metabolites were 0.29 and 0.35 respectively, and increased to 0.38 and 0.49 respectively if the total FA content was not in the model. Heritabilities for other more specific indices were of the same order.

The genetic correlation between the two indices for delta-9 desaturase was high (r = 0.59 and 0.51 in model 1 and 2 respectively). The genetic correlation between the ratio's C20:4*n*-6/C18:2*n*-6 and C22:6*n*-3/C18:3*n*-3 was also high (r = 0.71 and 0.34 in model 1 and 2 respectively), pointing to the use of the same enzymes. On the other hand, the formation of C20:5*n*-3 and C22:6*n*-3 from C18:3*n*-3 was not interrelated.

Table 1. Average values (standard deviation), heritabilities and genetic correlations with average daily gain and carcass lean meat percentage for specific FA proportions and FA indices for enzyme activities

	Average (SD)	Model	Heritability	Genetic correlation	
				ADG	LMP
FA (g/100g FAME)					
C16:0	20.97 (1.385)	1	0.234	0.254	-0.779
		2	0.028	0.597	-0.870
C18:0	10.09 (0.873)	1	0.193	-0.129	-0.137
		2	0.198	-0.178	0.049
C16:1	3.248 (0.529)	1	0.549	0.036	-0.350
		2	0.472	-0.009	-0.029
C18:1*cis*-9	35.58 (3.397)	1	0.582	0.199	-0.747
		2	0.180	0.232	-0.588
C18:1*cis-11*	4.587 (0.936)	1	0.116	-0.912	-0.247
		2	0.136	-0.993	-0.020
C18:2*n*-6	10.81 (2.287)	1	0.546	-0.051	0.790
		2	0.237	0.002	0.684
C20:4*n*-6	2.91 (1.068)	1	0.558	-0.277	0.757
		2	0.251	-0.486	0.565
C18:3*n*-3	0.544 (0.135)	1	0.403	0.981	0.203
		2	0.435	0.997	0.116
C20:5*n*-3	0.219 (0.074)	1	0.220	0.001	0.460
		2	0.069	0.149	-0.219
C22:5*n*-3	0.583 (0.202)	1	0.544	-0.275	0.682
		2	0.302	-0.329	0.434
C22:6*n*-3	0.195 (0.108)	1	0.607	-0.336	0.450
		2	0.420	-0.403	0.186
FA indices					
Delta-9 desaturase	0.155 (0.022)	1	0.390	0.023	-0.207
(C16:1/C16:0)		2	0.337	-0.008	0.018
Delta-9 desaturase	3.551 (0.458)	1	0.273	0.296	-0.720
(C18:1*cis*9/C18:0)		2	0.103	0.286	-0.505
Elongase	1.442 (0.352)	1	0.181	-0.977	0.279
(C18:1*cis*11/C16:1)		2	0.115	-0.996	0.176
Delta-6 desaturase	0.013 (0.005)	1	0.431	0.184	-0.443
(C18:3*n*-6/C18:2*n*-6)		2	0.352	0.157	-0.321
Delta-5 desaturase	7.103 (1.168)	1	0.318	-0.535	0.846
(C20:4*n*-6/C20:3*n*-6)		2	0.249	-0.386	0.374
Desaturase + elongase	0.263 (0.053)	1	0.381	-0.551	0.694
(C20:4*n*-6/C18:2*n*-6)		2	0.292	-0.833	0.329
Desaturase + elongase	0.411 (0.137)	1	0.242	-0.432	0.105
(C20:5*n*-3/C18:3*n*-3)		2	0.170	-0.441	-0.475
Desaturase + elongase	1.104 (0.398)	1	0.485	-0.494	0.309
(C22:6*n*-3/C18:3*n*-3)		2	0.347	-0.550	0.034

Model 1: Y = sex + animal + slaughter day
Model 2: Y = sex + animal + slaughter day + IMF

Conclusions

It is concluded that there is considerable genetic variation for long chain PUFA metabolism in pigs, that is partly independent of the carcass and muscle fat content. This may allow selection for improved fatty acid composition of pork.

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