Candidate genes for fatty acid composition assessed with FT-NIR spectroscopy in heavy pigs

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Introduction

The fatty acid contents of the subcutaneous fat and muscle composition affect the economic value of carcass and meat quality. The fatty acid content influences the firmness of fat and the oxidative stability of muscle, affecting flavor and color and represents one the main targets of the Italian pig breeding industry. This paper evaluates putative associations of candidate genes for the fatty acid content of adipose tissue and muscle composition in a Italian population of heavy pigs for the production of the San Daniele ham DOP.

Materials & Metods

A population of 800 pigs, crosses of Italian Duroc X Large White (400 pigs) and Commercial hybrid X Large White (400 pigs) was analyzed. Pigs were reared in commercial farms, with similar feeding and environmental conditions. Fat and muscle samples were collected from tights at slaughterhouse and analyzed with Fourier transform near infrared (FT-NIR) spectroscopy. A total of 159 fat samples and 157 muscle samples were analyzed for fatty acid content and chemical composition, respectively. Chemical data were used as a calibration set with a principal components regression model, applying partial least square regression algorithm with full cross validation as internal validation. External validation was performed using 42 and 36 samples of known chemical data for fatty acid and muscle, respectively. A muscle sample was collected for DNA analyses for each animal. The polymorphism of 103 SNPs in the promoter regions of 52 candidate genes already known for association with fat traits were selected by in silico analysis.

Property	R^2_{cal}	SEC	R^2_{val}	SEP_{val}	RPD
	CALIBRATION		*EXTERNAL VALIDATION*		
FAT					
C16:0	0.95	0.267	0.68	0.68	1.78
C18:0	0.99	0.044	0.18	0.97	1.06
C18:1-c9	0.97	0.286	0.54	0.95	1.4
C18:2-c9-c12	0.99	0.062	0.71	1.17	1.81
SFA	0.99	0.182	0.5	1.02	1.69
MUFA	0.99	0.318	0.66	1.73	1.41
PUFA	0.99	0.244	0.68	1.24	1.77
MUSCLE					
Lipids %	0.59	0.77	—	—	—
Gross protein %	0.29	0.43	—	—	—

Tab. 2 Calibration and validation data
R^2=coefficient of determination; SEC=Standard Error of Calibration
SEP=Standard Error of Prediction; RPD=Ratio Prediction Derivation

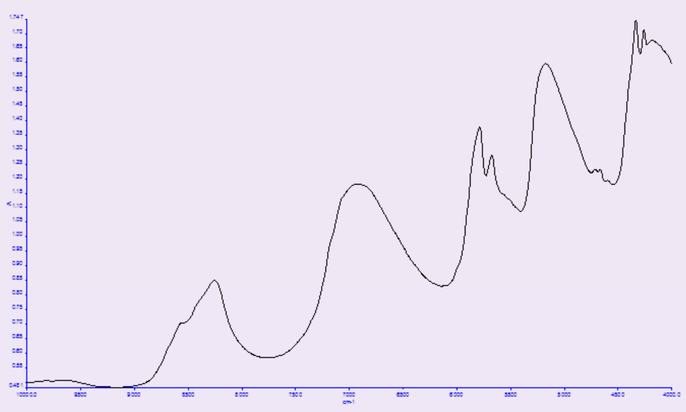

Fig. 1 Fat sample on Perkin Elmer Spectrum One FT-NIR Spectrometer
Fig. 2 FT-NIR spectrum

Results

Property	Mean	sd	Min	Max
FAT				
C16:0	21.29	1.36	15.47	24.49
C18:0	12.69	1.32	10.30	16.32
C18:1-c9	41.60	1.76	36.45	45.68
C18:2-c9-c12	13.31	2.05	8.86	20.54
SFA	36.41	2.11	30.96	42.19
MUFA	47.44	2.90	40.16	53.37
PUFA	15.59	2.27	10.83	23.39
MUSCLE				
Lipids %	2.66	1.07	1.21	6.55
Gross protein %	23.70	2.08	15.34	36.62
Cinder %	1.24	0.10	0.88	1.91
Humidity content %	71.44	2.09	58.23	78.08

Tab. 1 Subcutaneous fat and Muscle compositions

High R^2 values were obtained in calibration analysis of fatty acids composition of fat (Tab. 2), while lower calibration fit was obtained for muscle samples. For fat, external validation evidenced R^2 values between 0.18 and 0.71, therefore a low predicting ability.
On the basis of allele frequencies, 67 SNPs resulted segregating in both hybrids, while 6 SNPs segregated only in Duroc x Large White. Association analysis was carried out with Pearson correlation test and Bonferroni correction and evidenced significant correlations ($P<0.05$) between fat traits and analyzed polymorphisms (Tab. 3).

Property	Genes
C16:0	*Somatotropin, Cholecystokinin A Receptor, ATPase, Na+/K+ transporting , Calpain, Perilipin 2*
C18:0	*Stearoyl-CoA desaturase, Cholecystokinin A Receptor*
C18:1-c9	—
C18:2-c9-c12	*Somatotropin, Osteopontin*
SFA	*Somatotropin, Cholecystokinin A Receptor, ATPase, Na+/K+ transporting*
MUFA	*Stearoyl-CoA desaturase, Cholecystokinin A Receptor, Osteopontin, Calpain*
PUFA	*Somatotropin*

Tab. 3 Genes where SNPs associated with fatty acids of pig adipose tissue were found and analyzed in this study.

Conclusions

NIR spectroscopy was able to predict fatty acid composition of pig fat. However the accuracy of prediction was not satisfactory. This evidence could be imputed to the heterogeneity of samples used, to the presence in the samples of several structural components of fat not considered in the prediction model and to a deterioration of samples due to freezing conditions.