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Fatty acid composition of heavy pig back fat in relationship to some animal factors

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ABSTRACT - The influence of genetic type, lean meat percentage and sex on fatty acids (FA) composition of back fat of heavy pigs, reared for the production of San Daniele dry cured ham, was studied. One-hundred pigs of four genetic types - Large White or Duroc x (Landrace x Large White), GOLAND and DANBRED - were considered. They were randomly chosen during the slaughtering of 21 lots of heavy animals, in groups of four to eight subjects, balanced by sex, female and castrated males, and carcass leanness, U and R classes following the European grading system. Principal components (PCs) analysis showed that 94.3% of lot-diets' FA variability was accounted for a five PCs model. The diet effect on the lard composition was weighted using the PCs scores as covariates in a tri-factorial (genotype, carcass leanness, sex) covariance design. Diet had a great effect on lard composition, indeed every examined back fat FA co-varied with the extracted PCs. On the other hand, sex effect never reached a significance threshold, as well as the interactions between factors. Genetic type influenced stearic acid and MUFA content and n6-PUFA to n3-PUFA ratio of back fat while leanness mainly influenced PUFA, the fatter class showing a significantly lower content of linoleic acid (13.2 *vs.* 11.9% total lipids in U *vs.* R class respectively).

Key words: Back fat fatty acids, Heavy pig, Animal factors, Diet.

Introduction - The increasing consumers demand of lean meat oriented pig selection towards genetic types with a strong muscular growth and reduced fat deposits (Bosi & Russo, 2004), these changes led to important modifications in lipid characteristics too, which gradually became richer in unsaturated fatty acids and therefore more subjected to oxidative phenomena (Lo Fiego *et al*., 2005). Moreover, lipid composition is known to be influenced by other several factors, including diet, sex, weight and age at slaughter and carcass fatness (Wood *et al*., 2008). The aim of the research was to evaluate the effects of genotype, fatness and sex on back fat composition of heavy pig. The experiment is a part of a larger project that is going to lead to the characterization of the San Daniele dry-cured ham, the second PDO in Italy producing more than 2,5 milions of hams/year.

Material and methods - One-hundred pigs of four genetic types, randomly chosen during the slaughtering of 21 lots of heavy animals from different northern Italian farms were used. Every farm comprised only one of the following genotypes: two "traditionals" obtained from Italian selection by using Italian Duroc (ID) or Large White (LW) boars, and two industrial hybrids produced with Goland C21 (GOLAND) or Danline HD (DANBRED) boars. The sows used for the traditional genetic type were Landrace x Large White (LxLW) crossbreeds, while for GOLAND and DANBRED their own selected lines were used. From each slaughtering lot was selected a group of four to eight subjects, balanced by sex, female and castrated males, and carcass leanness, U and R classes following the European grading system. Table 1 summarizes the distribution in the experimental theses of pigs, together with their average carcass weight. During breeding, the pig farms, belonging to the San Daniele dry-cured ham PDO chain, were visited for diet sampling.

Table 1. Pigs distribution in the experimental theses and hot carcass weight (CW, kg).

	Genetic type				Leanness		Sex	
	IDx(LxLW)	LWx(LxLW)	GOLAND	DANBRED	U	R	Castrated	Female
Pigs (lots), no	24 (5)	24 (5)	28 (6)	24 (5)	50 (21)	50 (21)	50 (21)	50 (21)
CW (mean±SD)	136±9.7	136±13.5	139±11.2	140±10.9	135±9.4	141±12.0	139±11.5	137±10.9

After carcass preparation and evaluation, a 10x10 cm back fat sample (comprising all layers) was collected from the right side of each subject, taking as referee points for the area the line between the third and fourth last rib and the splitting line of the carcass. The fatty acid (FA) composition of diets and adipose tissue was determined following ASPA procedure (2007). In particular, lipids were extracted with Chloroform:Methanol (2:1,v/v) and converted to methyl esters (FAME) with methanolic HCl prior to analysis on a gas chromatography (Carlo Erba 5300 megaseries) equipped with a flame ionization detector. The concentration of individual fatty acids was determined in two extracts from all samples. Principal component analysis (PCA) was used to explore and understand the variability of diet composition by studying the correlation among the various FA and summarizing them in few meaningful components (PCs). A score for each component was then compute and used as a covariate variable for testing the diet effect on the back fat FA composition. With this aim a tri-way covariance design was examined, considering the four-level genotype factor and the two-level carcass leanness and sex fixed factors. The statistical analysis was performed by SPSS v.17 software package (SPSS Inc., Chicago, IL).

Table 2. Descriptive statistics of main diets FA (total lipids %, if not otherwise specified) and their contribution (coefficients >0.40) to the PCA factors describing diet composition variability.

	Mean	SD	PCA factors matrix				
			1	2	3	4	5
Total lipids (diet %)	3.70	0.814		-0.81	-0.42		
Linoleic a. (DM %)	1.76	0.319		-0.60			0.69
Short chain SFA	1.40	2.485				-0.93	
Odd chain SFA	0.13	0.064	0.94				
C16	17.84	2.300			-0.83		
C18	3.50	1.276	0.44				0.79
Long chain SFA	0.58	0.061		0.87			
SFA	23.48	3.692	0.42		-0.50	-0.73	
C16:1	0.61	0.383	0.92				
C18:1	25.79	3.370	0.72		-0.49		
Long chain MUFA	0.40	0.114	0.74				0.43
MUFA	26.80	3.718	0.77		-0.46		
MUFA / SFA	1.16	0.166				0.90	
C18:2n6	46.75	5.722	-0.73		0.54		
C20:2n6	0.28	0.053		0.84			
n6-PUFA	47.03	5.753	-0.73		0.54		
C18:3n3	2.50	0.570		0.41	0.77		
Long chain n3-PUFA	0.19	0.072		0.94			
n3-PUFA	2.69	0.609		0.49	0.74		
n6-PUFA / n3-PUFA	17.97	2.256		-0.50	-0.79		
PUFA	49.72	6.258	-0.70		0.57		
PUFA /SFA	2.21	0.619	-0.57		0.55	0.53	
Eigenvalues			6.24	4.84	4.82	3.05	1.80
Explained variance (%)			28.4	22.0	21.9	13.8	8.2

Results and conclusions

- Diets presented relatively high variability in terms of composition (Table 2), determined by the high variety of ingredients (up to 13) and fat sources included. PCA showed that 94.3% of farm-diets' FA variability was accounted for a model of five PCs relatively balanced on their contribution

to the total variance (Table 2). These PCs are interpretable by the presence of specifics FA or relations between FA categories as shown in Table 2 (e.g. the first PC was positively correlated with MUFA and odd chain SFA and negatively correlated with n6-PUFA). As expected in a monogastric species, diet had a great effect on lard composition, indeed every examined back fat FA co-varied with almost one of the five extracted PCs. Sex effect never reached a significance threshold, as well as the interactions between factors (results not tabulated). Genetic type influenced stearic acid and MUFA content and n6-PUFA to n3-PUFA ratio of back fat (Table 3), the main differences being found between the industrial genetic types, which cannot be simply considered as an undifferentiated homogeneous group. An inverse relationship between the proportion of linoleic acid in subcutaneous fat and the back fat thickness was confirmed (Wood *et al*., 2008), together with other significant effects of carcass leanness on UFA composition.

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Table 3. Fatty acid composition of heavy pig back fat (total lipids %, if not otherwise specified).

	Genetic type				Leanness		RSE	Significance	
	IDx(LxLW)	LWx(LxLW)	GOLAND	DANBRED	U	R		Genetic t.	Leanness
Total lipids (%)	89.9	89.4	89.5	86.2	88.4	89.1	5.18	0.34	0.51
Short SFA	1.60	1.65	1.68	1.69	1.63	1.68	0.151	0.54	0.15
Odd SFA	0.39	0.50	0.43	0.45	0.46	0.42	0.144	0.31	0.20
C16	24.9	25.4	25.2	24.9	24.9	25.3	1.20	0.54	0.18
C18	13.7^{ab}	14.2^{a}	12.8^{b}	14.1^{a}	13.8	13.6	1.36	0.01	0.40
SFA	40.7	41.9	40.3	41.3	41.0	41.1	2.35	0.29	0.83
C16:1n9	1.87^{b}	1.89^{b}	2.16^{a}	1.80^{b}	1.88	1.98	0.258	0.00	0.10
C18:1	42.1	41.5	42.0	40.4	40.9	42.1	1.78	0.12	0.00
MUFA	44.8^{a}	44.2^{ab}	44.9^{a}	42.8^{b}	43.5	44.9	1.92	0.04	0.00
C18:2n6	12.2	11.6	12.5	13.7	13.2	11.9	2.39	0.25	0.01
long n6-PUFA	0.77	0.70	0.72	0.69	0.76	0.68	0.145	0.52	0.02
n6-PUFA	13.0	12.3	13.2	14.4	13.9	12.5	2.51	0.29	0.01
C18:3n3	0.55	0.60	0.59	0.63	0.63	0.56	0.137	0.70	0.02
long n3-PUFA	0.24^{a}	0.17^{b}	0.19^{b}	0.11^{c}	0.19	0.17	0.065	0.00	0.26
n3-PUFA	0.88	0.86	0.86	0.85	0.91	0.81	0.171	0.97	0.01
n6-PUFA/n3-PUFA	15.0^{b}	14.6^{b}	15.6^{b}	16.9^{a}	15.5	15.5	1.68	0.02	0.97
PUFA	13.8	13.0	14.0	15.2	14.7	13.3	2.64	0.33	0.01

a,b,c within genetic type means different (P≤0.05).

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