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Fatty acid composition and adipogenic enzyme activity of muscle and adipose tissue, as affected by Iberian × Duroc pig genotype

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Abstract

The adipogenic potential of subcutaneous fat (SCF) and muscles *Longissimus dorsi* (LD) and *Biceps femoris* (BF) were evaluated in three different Iberian × Duroc pig genotypes: GEN1: ♂ Iberian × ♀ Duroc1; GEN2: ♂ Duroc1 × ♀ Iberian; GEN3: ♂ Duroc2 × ♀ Iberian. Reciprocal crosses (GEN1 vs. GEN2) showed similar traits, while the genotype of the Duroc sire line (GEN2 vs. GEN3) significantly influenced the adipogenic character. GEN3 had lower fat depths and a more unsaturated SCF than GEN2. The intramuscular fat (IMF) content of the LD was higher in GEN2 than in GEN3, while BF showed a similar trend. The fatty acid compositions of IMF and neutral lipid fraction (NL) in LD and BF were more unsaturated in GEN3 than in GEN2. Glucose-6-phosphate dehydrogenase (G6PDH) and malic enzyme (ME) activities in SCF and in both muscles analysed were higher in GEN2 than in GEN3. The higher fat depths and IMF of GEN1 and GEN2 correspond to higher G6PDH and ME activities, which indicated that the lipid synthesis and deposition in muscles and in SCF were higher in GEN1 and GEN2 than in GEN3; these differences were associated with the Duroc sire line. Therefore, the use of Duroc selected genotypes reduced the adipogenic character of Iberian × Duroc crosses, which could have important repercussions on the quality of meat and dry-cured products.

Keywords: Lipogenic enzymes; Glucose-6-phosphate dehydrogenase; Malic enzyme; Intramuscular fat; Fatty acid; Duroc line; Iberian pig

1. Introduction

Nowadays, the Iberian pig breed has increased its popularity, because the meat and meat products traditionally obtained from this breed are highly appreciated by consumers for their excellent quality. Different studies have shown that meat from Iberian pigs has better quality (colour, fatty acid profile and sensory characteristics) than that obtained from industrial genotype pigs (Estévez, Morcuende, & Cava, 2003). As a result, the population of Iberian pigs has increased in the last years, which has led to an improvement of the feeding and production systems. As Iberian is a rustic breed with a slow growth rate and low prolificity (Dobao, García, De Pedro, Rodrigáñez, & Silió, 1986), to improve productive parameters, it is often crossed with Duroc at 50%. This increases the prolificity by 2–3 piglets, improves the growth rate, the feed efficiency and the lean content (Dobao et al., 1986) without a significant reduction in the quality of the meat and meat products (López-Bote, 1998). These crosses are so frequent that it is estimated that less than 25% of the animals slaughtered as "Iberian", are pure Iberian (Sierra Alfranca, 1992).

Despite the fact that consumption of fresh Iberian pig meat has increased in recent years, the production of Iberian pigs is mainly focused on obtaining raw meat to manufacture dry-cured meat products. For this purpose, the industry requires fat carcasses from castrated heavy pigs slaughtered at around 160 kg live weight. A high intramuscular fat content is important to aid a slow dehydratation during the curing process (Gandemer, 2002). Fat content and fatty acid composition are determinant factors for the quality of Iberian dry-cured meat products (Ruíz-Car-

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rascal, Ventanas, Cava, Andrés, & García, 2000). Cava, Ruíz, Ventanas, and Antequera (1999) observed a marked influence of intramuscular fatty acid composition of fresh meat on the flavour of Iberian dry-cured meat products. Also intramuscular fat with high levels of linoleic acid can affect water migration, as very unsaturated fat retards water migration within the meat and, hence lengthens the drying process (Girard, Bucharles, Berdague, & Ramihone, 1989; López-Bote, 1998).

In Spain, a specific law for Iberian products was passed in 2001, to regulate the market (Quality regulation of Iberian products – Norma de Calidad sobre productos del cerdo Ibérico, B.O.E., 2001). One of the most important aspects that this law regulates is the genotype used for the manufacture of dry-cured meat products (hams, forelegs and loins) labelled as "Iberian". The law allows the use of pure Iberian pigs as well as Iberian × Duroc crosses, but the mother of the crossbreed must be Iberian, to preserve the genetic patrimony and biodiversity of the Iberian breed. Selection of the Duroc paternal line is crucial; because the Duroc breed is so widespread, it cannot be considered as an homogeneous breed, since important differences in its production and carcass parameters and in the quality of its meat and meat products have been reported (Cilla et al., 2006; Lonergan, Huff-Lonergan, Rowe, Kuhlers, & Jungst, 2001). However, Morcuende, Estévez, Ramírez, de Alba, and Cava (2003) did not find important differences between Iberian × Duroc reciprocal crosses.

In contrast to other species, in which the lipogenesis of fatty acids takes place in the liver, in pigs it mainly takes place *in situ*, in the adipose tissues (O'Hea & Leveille, 1969). The synthesis of triglycerides of the adipose tissue comes from fatty acids derived from existing triglycerides, as a result of adipose lipoprotein lipase activity (Steffen, Brown, & Mersmann, 1978) and from fatty acid synthesised *de novo* (mainly from dietary starch) in that tissue (O'Hea & Leveille, 1969). The NADPH for synthesis of *de novo* fatty acids is supplied by malic enzyme (ME) and by glucose-6-phosphate dehydrogenase (G6PDH) (Young, Sharago, & Lardy, 1964; Wise & Ball, 1964). G6PDH takes part in the pentose phosphate pathway, while ME transforms malic acid to pyruvic acid. Endogenous synthesis of fatty acids comes from acetyl CoA and malonyl CoA molecules, to produce palmitic acid (C16:0), from which can be synthesised stearic acid (C18:0) by elongation. These fatty acids are unsaturated, by means of desaturase enzymes, to palmitoleic acid (C16:1 $n-7$) and oleic acid (C18:1 $n-9$). Differences in the lipogenic enzyme activity are mostly caused by animal genotype and to a lesser extent by diet (Morales, Pérez, Baucells, Mourot, & Gasa, 2002). In this respect, higher lipogenic activity has been found in rustic breeds with high intramuscular fat levels than in industrial ones (Mourot & Kouba, 1998; Morales et al., 2002). Moreover, we have found important differences among genotypes in a previous study (Ramírez & Cava, 2006) on meat quality. The objectives of this study were to assess the consequences of the use of different Duroc paternal lines in Iberian × Duroc crosses, as well as the differences between Iberian × Duroc reciprocal crosses on the adipogenic character and fatty acid composition of subcutaneous and intramuscular fat.

2. Materials and methods

2.1. Animals

In order to develop this work, 3 groups of 10 pigs were studied (five males and five females) from different genotypes: GEN1: ♂ Iberian × ♀ Duroc 1; GEN2: ♂ Duroc 1 × ♀ Iberian; GEN3: ♂ Duroc 2 × ♀ Iberian. GEN1 and GEN2 are reciprocal crosses, while the difference between GEN2 and GEN3 is the Duroc sire line. The genotype Duroc 1 (DU1) were pigs selected for the production of dry-cured meat products (hams, loins and forelegs), with a high level of fattening. The genotype Duroc 2 (DU2) were animals selected for meat production, with high percentages of muscle and with low carcass fattening. Pigs were raised all together in an intensive system and were fed ad libitum with the concentrate feeds shown in Table 1. Pigs were randomly slaughtered after 316 days of rearing, at 150–165 kg live weight.

2.2. Back fat and ham thickness

The backfat thickness (BFT) and ham fat thickness (HFT) were measured at the 5th rib and in the *Biceps femoris* muscle in the carcass and ham, respectively. *Biceps femoris* (BF) and *Longissimus dorsi* (LD) muscles were removed from the carcasses and stored at −80 °C until analysis. For the analyses, the central part of the muscles was taken. Subcutaneous fat (SCF) was taken from the inner layer of the backfat at the 7th and 8th thoracic rib and also was stored at −80 °C until analysis.

Table 1
Proximate composition (%) and fatty acid composition (% total fatty acids) of the pig diets

	Mixed Diet I from 60 to 100 kg l.w.	Mixed Diet II from 100 to 165 kg l.w.
Proximate composition (%)		
Crude protein	16.0	13.5
Crude fat	3.3	5.0
Crude fibre	4.8	3.7
Ash	6.9	6.2
Lysine	0.9	0.5
Metabolisable energy (kcal/kg)	3072	3184
Fatty acid composition (% total fatty acids)		
C14:0	0.1	0.1
C16:0	14.6	21.0
C18:0	4.4	5.6
C18:1 $n-9$	23.3	31.3
C18:2 $n-6$	34.7	35.1
C18:3 $n-6$	2.0	2.3

2.3. Fat extraction, lipid fractionation and fatty acid analysis

Intramuscular lipids were extracted from 5 g of meat with chloroform:methanol (1:2), according to the method of Bligh and Dyer (1959) and quantified by weighing after solvent evaporation. Moisture content was determined by drying samples at 102 °C until constant weight, according to the AOAC method (AOAC, 2000). Total lipid extracts from intramuscular fat were fractionated by solid phase extraction on 100 mg aminopropyl minicolumns (Varian, CA), following the procedure described by Monin, Hortós, Díaz, Rock, and Garcia-Regueiro (2003). Fatty acid methyl esters (FAMEs) from neutral lipids (NL), total IMF and SCF were prepared by acidic esterification (5% sulfuric acid in methanol). FAMEs were analysed in a Hewlett-Packard HP 5890A gas chromatograph equipped with a flame ionisation detector. The FAMEs were separated on a wide-bore capillary column (Hewlett-Packard FFAP-TPA fused silica column, 30 m length, 0.53 mm i.d., and 1.0 μm film thickness). The injector and detector temperatures were held at 230 °C. The column oven temperature was maintained at 220 °C. The flow rate of the carrier gas (N_2) was set at 1.8 ml/min. Identification of FAMEs was based on the retention times of reference compounds (Sigma). Fatty acid composition was expressed as a percentage of FAMEs analysed.

2.4. Tissue enzyme activity of lipogenesis enzymes

SCF (1 g) or muscle (LD and BF, 2 g) was homogenised in 10 ml of ice-cold 25 mM Tris–HCl buffer containing 9% glycerol, 5 mM $MgCl_2$ and 7 mM β-mercaptoethanol (pH 7.6). The homogenate was centrifuged at 3000*g* at 4 °C for 10 min and the supernatant was recentrifuged at 25,000*g* for 20 min at 4 °C. The resulting supernatants were analysed for glucose-6-phosphate dehydrogenase (G6PDH) (EC 1.1.1.49) and malic enzyme (ME) (EC 1.1.1.40) activities.

Enzyme activities were measured at 340 nm at 30 °C for 3 min with a spectrophotometer (Helios α Thermo Electron Corp. Waltham, MA) and expressed on the basis of nmol $NADP^+$ reduced to NADPH per min per mg protein, using the extinction coefficient of NADPH at 340 nm of $6.22 \times 10^6\ M^{-1}\ cm^{-1}$. Glucose-6-phosphate dehydrogenase (G6PDH) was determined by the method of Bautista, Garrido-Pertierra, and Soler (1988). The enzymatic extract (400 μL) was mixed with 540 μl of buffer at pH 8 (10 ml of 1 M Tris, 2 ml of 10 mM $NADP^+$, 10 ml of 0.1 M $MgCl_2$ and 63 ml of Milli-Q water). The reaction was initiated by the addition of 60 μl of 20 mM glucose-6-phosphate. The rate of reduction of $NADP^+$ was monitored at 340 nm. Malic enzyme (ME) determination was measured according to the method of Spina, Bright, and Rosenbloom (1970). The reaction mixture contained 25 μl of 40 mM $NADP^+$, 252 μl of Milli-Q water and 323 μl of a buffer with pH 7.4 (200 μl of 0.5 M Tris, 10 μl of 0.1 M $MgCl_2$, 12.5 μl of 80 mM NH_4, 50 μl of 2 M KCl, 50 μl of 200 mM malic acid). The reaction was initiated by the addition of 400 μl of the enzyme extract to a final volume of 1 ml and monitored at 340 nm. Protein determination was measured spectrophotometrically at 595 nm, according to the method of Bradford (1976). All enzyme determinations were carried out in triplicate.

2.5. Statistical analysis

The effects of genotype and sex were analysed by analysis of variance (SPSS, 2003, version 12.0). A two-way analysis of variance (genotype and sex) with interaction (genotype × sex) was applied. Means were used to compare differences. When means were significantly different, Tukey's test was applied to compare the mean values of the genotypes. Mean values and standard errors of the means (SEM) were reported. The relationships between traits were analysed by the calculation of Pearson's coefficient. Principal component analysis (PCA) was applied to determine relationships between variables and samples.

3. Results and discussion

3.1. Fat depths and fatty acid composition of subcutaneous fat

Fat depths and fatty acid composition were significantly influenced by genotype, while they were not affected by animal sex (Table 2). Backfat thickness (BFT) and ham fat thickness (HFT) were significantly higher in GEN2 than in GEN3, while GEN1 carcasses had an intermediate degree of fattening. There was no effect of animal sex on the fatty acid composition of SCF, whereas differences were found between genotypes. SCF of GEN3 was the most unsaturated, showing the highest percentages of C18:2 $n-6$, C20:4 $n-6$ and PUFA, and the lowest percentage of C18:0.

Results indicate a higher fattening in GEN2 carcasses than in those from the other two genotypes, while no significant differences were found between the reciprocal crosses (GEN1 vs. GEN2). However, the differences found between the genotypes from the two paternal lines of Duroc (GEN2 vs. GEN3) indicate that the use of the DU2 Duroc genotype for crossing with the Iberian breed reduced carcass fat and increased the degree of unsaturation of the SCF. Differences in fatty acid composition are explained by differences in carcass fattening, due to genotype. As the backfat in the carcass develops, the proportion of fatty acids stored in the adipose tissue arising from *de novo* fatty acid synthesis increases, specifically SFA and MUFA, and the PUFA content decreases, since the proportion of PUFA provided by dietary lipids is lower (Gandemer, 2002). In terms of meat and technological quality, fatty acid composition has an important effect on the softness and oxidative stability of fat and meat, as high PUFA levels result in a softer fat and an increase in rancidity (Wood et al., 2003).

Table 2
Fat depths (mm) and fatty acid composition (g/100 g FA) of subcutaneous fat from 3 different Iberian × Duroc genotypes

	Genotype			Sex		Probability		
	GEN1	GEN2	GEN3	♂	♀	Genotype	Sex	Interaction
Fat depths (mm)								
BFT	$63^{ab} \pm 7.7$	$64^{a} \pm 8.8$	$53^{b} \pm 9.1$	59 ± 9.9	61 ± 9.6	*	ns	ns
HFT	$31^{ab} \pm 4.2$	$34^{a} \pm 5.2$	$27^{b} \pm 5.8$	32 ± 5.1	29 ± 6.3	**	ns	ns
Fatty acid composition								
C12:0	0.05 ± 0.00	0.05 ± 0.01	0.13 ± 0.25	0.11 ± 0.21	0.05 ± 0.00	ns	ns	ns
C14:0	0.04 ± 0.01	0.04 ± 0.00	0.05 ± 0.01	0.05 ± 0.01	0.05 ± 0.01	ns	ns	ns
C16:0	24.1 ± 0.47	24.7 ± 0.59	24.6 ± 0.37	24.4 ± 0.52	24.5 ± 0.57	ns	ns	ns
C16:1 $n-7$	$2.14^{b} \pm 0.19$	$2.24^{b} \pm 0.21$	$2.68^{a} \pm 0.26$	2.30 ± 0.27	2.42 ± 0.36	***	ns	ns
C17:0	0.31 ± 0.03	0.30 ± 0.04	0.32 ± 0.05	0.31 ± 0.04	0.31 ± 0.04	ns	ns	ns
C17:1 $n-7$	0.31 ± 0.02	0.30 ± 0.04	0.36 ± 0.08	0.32 ± 0.04	0.33 ± 0.07	ns	ns	ns
C18:0	$13.4^{ab} \pm 0.56$	$13.7^{a} \pm 0.83$	$12.4^{b} \pm 1.02$	13.2 ± 0.94	13.0 ± 1.07	*	ns	ns
C18:1 $n-9$	47.0 ± 0.87	45.7 ± 0.94	46.1 ± 1.29	46.2 ± 1.38	46.3 ± 0.92	ns	ns	ns
C18:2 $n-6$	$9.70^{b} \pm 0.69$	$10.1^{ab} \pm 0.41$	$10.7^{a} \pm 0.77$	10.1 ± 0.86	10.2 ± 0.64	*	ns	ns
C18:3 $n-6$	0.47 ± 0.11	0.49 ± 0.11	0.57 ± 0.04	0.48 ± 0.14	0.53 ± 0.04	ns	ns	ns
C20:0	0.21 ± 0.02	0.22 ± 0.02	0.21 ± 0.02	0.22 ± 0.02	0.21 ± 0.02	ns	ns	ns
C20:1 $n-9$	$1.49^{a} \pm 0.17$	$1.40^{ab} \pm 0.17$	$1.20^{b} \pm 0.20$	1.44 ± 0.22	1.28 ± 0.18	**	ns	ns
C20:2 $n-6$	0.67 ± 0.06	0.63 ± 0.08	0.54 ± 0.16	0.62 ± 0.15	0.61 ± 0.07	ns	ns	ns
C20:4 $n-6$	$0.15^{b} \pm 0.02$	$0.15^{b} \pm 0.01$	$0.17^{a} \pm 0.01$	0.16 ± 0.02	0.15 ± 0.01	**	ns	ns
C22:4 $n-6$	0.07 ± 0.04	0.01 ± 0.03	0.06 ± 0.04	0.06 ± 0.04	0.03 ± 0.04	ns	ns	ns
SFA	38.1 ± 0.76	39.0 ± 1.08	37.7 ± 1.31	38.3 ± 1.06	38.2 ± 1.34	ns	ns	ns
MUFA	50.9 ± 0.98	49.7 ± 1.10	50.3 ± 1.61	50.2 ± 1.55	50.3 ± 1.14	ns	ns	ns
PUFA	$11.1^{b} \pm 0.74$	$11.3^{ab} \pm 0.47$	$12.0^{a} \pm 0.78$	11.4 ± 0.88	11.5 ± 0.68	*	ns	ns

GEN: genotype; GEN1: IB × DU1; GEN2: DU1 × IB; GEN3: DU2 × IB. BFT: backfat thickness. HFT: ham fat thickness. SFA, saturated fatty acids; MUFA, monounsaturated fatty acids; PUFA, polyunsaturated fatty acids.
Different letters in the same row indicate significant statistical differences within the same day of analysis (Tukey's test, $p < 0.05$).
* $p < 0.05$.
** $p < 0.01$.
*** $p < 0.001$.

3.2. Intramuscular fat content and fatty acid composition

In general, the genotype was the main factor for the differences in IMF content and fatty acid composition of total IMF and NL of LD (Table 3) and BF (Table 4), while animal gender had no effect.

The IMF content of the LD muscle was significantly affected by the genotype, as GEN2 had significantly higher IMF content than GEN1 and GEN3. BF showed a similar trend, GEN3 contained less IMF than the other two genotypes, although the differences were not significant. IMF content is a highly variable parameter and its variability is dependent on the genetics of the pig breed (McLaren, Buchanan, & Johnson, 1987). Intensive pig production and selection based on lean growth rate have led to a significant decrease in the IMF content of commercial breeds (Karlsson et al., 1993). Important differences have been reported by Cilla et al. (2006) in the IMF and BFT of crosses with different Duroc sire lines. Increased IMF levels reduce the force for chewing and promote saliva secretion, helping chewing and increasing juiciness and tenderness perception (Wood et al., 2003). Moreover, an adequate level of IMF is a determinant factor for the preparation of dry-cured meat products (Gandemer, 2002; López-Bote, 1998). Therefore, the high IMF content of GEN2 could improve the sensory quality of the meat and meat products.

In general, the fatty acid composition of LD was more affected by the genotype than BF, although fatty acid composition of the latter showed a trend similar to the former.

In LD, IMF from GEN3 was more unsaturated than that from GEN2, with higher contents of C18:1 $n-9$, MUFA, C18:2 $n-6$, C20:4 $n-6$ and PUFA, and lower contents of C16:0, C18:0 and SFA. These differences between GEN2 and GEN3 were associated with the Duroc sire line. The fatty acid profile of GEN1 was more unsaturated than GEN2, as a result of higher percentages of C18:2 $n-6$, C18:3 $n-6$, C20:4 $n-6$ and PUFA, and lower percentages of C16:0 and SFA. Similarly, NL of the LD muscle showed important differences, depending on the genotype of the Duroc paternal line, with higher levels of C16:0, C18:0 and SFA in GEN2 and higher levels of C18:3 $n-6$, C20:2 $n-6$, C20:4 $n-6$, C20:3 $n-3$ and PUFA in GEN3. However, reciprocal crosses GEN1 and GEN2 showed similar percentages of SFA, MUFA and PUFA. In addition, significant differences in some fatty acid percentages were due to the sex of the animals. Females showed higher percentages of C18:0 and SFA, while males showed higher percentages of some PUFA, such as C20:4 $n-6$ and C22:4 $n-6$.

In BF, neither the genotype nor the sex of the pigs affected the levels of any major fatty acids of the IMF.

Table 3
Intramuscular fat content (g/100 g) and fatty acid composition (g/100 g FA) of intramuscular fat and neutral lipid of m. *Longissimus dorsi* from three different Iberian × Duroc genotypes

	Genotype			Sex		Probabilities		
	GEN1	GEN2	GEN3	♂	♀	Genotype	Sex	Interaction
IMF	$3.84^{b} \pm 0.72$	$5.87^{a} \pm 1.42$	$3.32^{b} \pm 1.03$	4.39 ± 1.63	4.33 ± 1.47	***	ns	ns
IMF (dm)	$13.4^{b} \pm 2.30$	$19.6^{a} \pm 3.80$	$11.7^{b} \pm 3.67$	15.0 ± 5.14	14.9 ± 4.33	***	ns	ns
Intramuscular fat fatty acid composition								
C12:0	$0.04^{b} \pm 0.00$	$0.06^{a} \pm 0.01$	$0.05^{ab} \pm 0.01$	0.05 ± 0.01	0.05 ± 0.01	***	ns	*
C14:0	$1.16^{b} \pm 0.10$	$1.36^{a} \pm 0.10$	$1.18^{b} \pm 0.10$	1.24 ± 0.17	1.23 ± 0.09	***	ns	*
C16:0	$23.8^{b} \pm 0.77$	$25.2^{a} \pm 0.54$	$23.6^{b} \pm 1.13$	24.1 ± 1.39	24.3 ± 0.76	***	ns	*
C16:1 $n-7$	$3.65^{b} \pm 0.32$	$3.94^{ab} \pm 0.33$	$4.16^{a} \pm 0.39$	4.00 ± 0.42	3.86 ± 0.38	**	ns	ns
C17:0	$0.17^{ab} \pm 0.03$	$0.14^{b} \pm 0.02$	$0.18^{a} \pm 0.03$	0.17 ± 0.04	0.16 ± 0.02	**	ns	ns
C17:1 $n-7$	$0.21^{ab} \pm 0.02$	$0.18^{b} \pm 0.02$	$0.21^{a} \pm 0.04$	0.20 ± 0.03	0.20 ± 0.04	*	ns	ns
C18:0	$12.9^{a} \pm 0.66$	$13.6^{a} \pm 0.69$	$11.8^{b} \pm 1.05$	12.5 ± 1.29	13.0 ± 0.94	***	ns	ns
C18:1 $n-9$	$48.8^{ab} \pm 0.93$	$48.0^{b} \pm 0.99$	$49.2^{a} \pm 1.12$	48.7 ± 1.09	48.6 ± 1.14	*	ns	ns
C18:2 $n-6$	$6.15^{a} \pm 0.47$	$4.95^{b} \pm 0.60$	$6.38^{a} \pm 1.12$	5.90 ± 1.21	5.73 ± 0.79	***	ns	ns
C18:3 $n-6$	$0.29^{a} \pm 0.05$	$0.23^{b} \pm 0.03$	$0.34^{a} \pm 0.06$	0.29 ± 0.08	0.28 ± 0.04	***	ns	ns
C20:0	$0.26^{a} \pm 0.01$	$0.25^{ab} \pm 0.02$	$0.23^{b} \pm 0.05$	0.23 ± 0.04	0.26 ± 0.02	*	*	**
C20:1 $n-9$	0.97 ± 0.10	0.88 ± 0.09	0.87 ± 0.09	0.92 ± 0.11	0.88 ± 0.09	ns	ns	ns
C20:2 $n-6$	$0.35^{a} \pm 0.19$	$0.23^{b} \pm 0.02$	$0.26^{ab} \pm 0.04$	0.31 ± 0.17	0.25 ± 0.03	*	ns	ns
C20:4 $n-6$	$1.05^{b} \pm 0.25$	$0.76^{c} \pm 0.17$	$1.35^{a} \pm 0.35$	1.09 ± 0.43	1.02 ± 0.28	***	ns	ns
C20:5 $n-3$	$0.04^{ab} \pm 0.03$	$0.02^{b} \pm 0.01$	$0.05^{a} \pm 0.02$	0.04 ± 0.03	0.03 ± 0.01	**	ns	ns
C22:2 $n-6$	0.03 ± 0.01	0.02 ± 0.01	0.02 ± 0.00	0.02 ± 0.01	0.02 ± 0.00	ns	ns	ns
C22:4 $n-6$	$0.19^{ab} \pm 0.07$	$0.15^{b} \pm 0.03$	$0.23^{a} \pm 0.07$	0.19 ± 0.09	0.19 ± 0.04	**	ns	**
SFA	$38.3^{b} \pm 1.28$	$40.6^{a} \pm 1.00$	$37.0^{b} \pm 2.06$	38.3 ± 2.68	38.9 ± 1.52	***	ns	**
MUFA	$53.6^{ab} \pm 0.90$	$53.0^{b} \pm 1.05$	$54.4^{a} \pm 1.37$	53.8 ± 1.25	53.6 ± 1.25	*	ns	ns
PUFA	$8.09^{a} \pm 0.74$	$6.37^{b} \pm 0.81$	$8.63^{a} \pm 1.58$	7.85 ± 1.78	7.52 ± 1.15	***	ns	ns
Neutral lipids								
C12:0	0.07 ± 0.02	0.07 ± 0.00	0.08 ± 0.02	0.08 ± 0.02	0.07 ± 0.01	**	ns	ns
C14:0	$1.35^{b} \pm 0.08$	$1.51^{a} \pm 0.10$	$1.30^{b} \pm 0.12$	1.40 ± 0.15	1.37 ± 0.09	***	ns	*
C16:0	$25.3^{ab} \pm 0.57$	$26.1^{a} \pm 0.47$	$24.6^{b} \pm 0.81$	25.2 ± 1.05	25.5 ± 0.56	***	ns	*
C16:1 $n-7$	$3.88^{b} \pm 0.39$	$4.08^{ab} \pm 0.33$	$4.40^{a} \pm 0.44$	4.22 ± 0.48	4.04 ± 0.39	*	ns	ns
C17:0	0.17 ± 0.02	0.15 ± 0.02	0.18 ± 0.03	0.17 ± 0.03	0.16 ± 0.02	ns	ns	ns
C17:1 $n-7$	0.20 ± 0.06	0.17 ± 0.05	0.23 ± 0.05	0.20 ± 0.05	0.20 ± 0.05	ns	ns	ns
C18:0	$13.0^{ba} \pm 0.72$	$13.5^{a} \pm 0.70$	$11.6^{b} \pm 1.14$	12.3 ± 1.29	13.0 ± 0.94	***	*	ns
C18:1 $n-9$	$49.6^{a} \pm 0.63$	$48.5^{b} \pm 0.93$	$50.5^{a} \pm 1.28$	49.6 ± 1.62	49.3 ± 0.94	***	ns	**
C18:2 $n-6$	4.33 ± 0.45	3.98 ± 0.47	4.71 ± 0.51	4.48 ± 0.56	4.21 ± 0.49	ns	ns	ns
C18:3 $n-6$	$0.25^{ab} \pm 0.02$	$0.22^{b} \pm 0.02$	$0.29^{a} \pm 0.04$	0.26 ± 0.04	0.25 ± 0.03	***	ns	ns
C20:0	0.27 ± 0.02	0.29 ± 0.03	0.28 ± 0.03	0.28 ± 0.03	0.28 ± 0.03	ns	ns	*
C20:1$n-9$	$0.95^{a} \pm 0.08$	$0.87^{b} \pm 0.08$	$0.89^{ab} \pm 0.08$	0.93 ± 0.09	0.88 ± 0.07	*	ns	ns
C20:2 $n-6$	$0.26^{ab} \pm 0.03$	$0.24^{b} \pm 0.02$	$0.29^{a} \pm 0.03$	0.27 ± 0.04	0.25 ± 0.03	*	ns	ns
C20:4 $n-6$	$0.23^{b} \pm 0.04$	$0.28^{ab} \pm 0.07$	$0.42^{a} \pm 0.09$	0.37 ± 0.12	0.26 ± 0.05	**	*	ns
C20:5 $n-3$	$0.05^{b} \pm 0.01$	$0.03^{c} \pm 0.01$	$0.07^{a} \pm 0.02$	0.05 ± 0.02	0.05 ± 0.01	***	ns	*
C22:2 $n-6$	0.04 ± 0.02	0.05 ± 0.01	0.05 ± 0.02	0.05 ± 0.01	0.05 ± 0.02	ns	ns	ns
C22:4 $n-6$	0.08 ± 0.01	0.10 ± 0.02	0.10 ± 0.02	0.11 ± 0.02	0.08 ± 0.02	ns	*	ns
SFA	$40.2^{a} \pm 1.07$	$41.5^{a} \pm 0.98$	$38.1^{b} \pm 1.86$	39.4 ± 2.33	40.4 ± 1.34	***	*	*
MUFA	$54.6^{b} \pm 0.82$	$53.6^{b} \pm 0.96$	$56.0^{a} \pm 1.53$	55.0 ± 1.89	54.5 ± 1.14	***	ns	*
PUFA	$5.25^{ab} \pm 0.53$	$4.89^{b} \pm 0.57$	$5.93^{a} \pm 0.63$	5.60 ± 0.68	5.13 ± 0.60	*	ns	ns

GEN: genotype; GEN1: IB × DU1; GEN2: DU1 × IB; GEN3: DU2 × IB. IMF, intramuscular fat; IMF(dm), intramuscular fat (dry matter); SFA, saturated fatty acids; MUFA, monounsaturated fatty acids; PUFA, polyunsaturated fatty acids.
Different letters in the same row indicate significant statistical differences within the same day of analysis (Tukey's test, $p < 0.05$).
* $p < 0.05$.
** $p < 0.01$.
*** $p < 0.001$.

Nevertheless, the fatty acid composition of BF showed similar a trend to LD, with the highest percentages of unsaturated fatty acids in GEN3. Moreover, the fatty acid composition of NL of this muscle was significantly affected by the genotype. So, the highest levels of unsaturated fatty acids, such as C18:2 $n-6$, C22:2 $n-6$ and PUFA were found in GEN3, while GEN1 and GEN2 contained the highest percentages of SFA, C18:0 being highest in GEN1 and C20:0 in GEN2.

Higher PUFA in BF could be due to the different metabolic pattern of LD (glycolytic) and BF (intermediate oxidative) muscles (Leseigneur-Meynier & Gandemer, 1991). Higher PUFA content in more oxidative muscles than in glycolytic ones is a consequence of their abundance of

Table 4
Intramuscular fat content (g/100 g) and fatty acid composition (g/100 g FA) of intramuscular fat and neutral lipid of m. *Biceps femoris* from three different Iberian × Duroc genotypes

	Genotype			Sex		Probabilities		
	GEN1	GEN2	GEN3	♂	♀	Genotype	Sex	Interaction
IMF	3.40 ± 1.19	3.66 ± 0.92	3.02 ± 0.72	3.36 ± 1.10	3.35 ± 0.80	ns	ns	ns
IMF(dm)	13.07 ± 4.34	13.66 ± 3.15	11.21 ± 3.33	12.67 ± 3.93	12.60 ± 2.78	ns	ns	ns
Intramuscular fat fatty acid composition								
C12:0	0.06 ± 0.01	0.06 ± 0.01	0.05 ± 0.01	0.06 ± 0.01	0.06 ± 0.01	ns	ns	ns
C14:0	1.16^{ab} ± 0.08	1.24^{a} ± 0.11	1.12^{b} ± 0.07	1.19 ± 0.12	1.16 ± 0.07	*	ns	ns
C16:0	22.7 ± 1.06	22.6 ± 0.73	22.0 ± 0.71	22.4 ± 1.02	22.4 ± 0.74	ns	ns	ns
C16:1 $n-7$	3.70 ± 0.23	4.12 ± 0.30	3.95 ± 0.42	3.95 ± 0.36	3.92 ± 0.37	ns	ns	ns
C17:0	0.22 ± 0.07	0.23 ± 0.06	0.24 ± 0.05	0.24 ± 0.05	0.23 ± 0.06	ns	ns	ns
C17:1 $n-7$	0.26 ± 0.08	0.27 ± 0.08	0.26 ± 0.05	0.27 ± 0.07	0.26 ± 0.06	ns	ns	ns
C18:0	11.8 ± 1.04	11.4 ± 0.47	10.8 ± 0.80	11.3 ± 0.98	11.4 ± 0.80	ns	ns	ns
C18:1 $n-9$	49.0 ± 1.26	48.9 ± 1.50	49.1 ± 1.17	48.9 ± 1.33	49.1 ± 1.26	ns	ns	ns
C18:2 $n-6$	7.27 ± 1.31	7.32 ± 1.09	8.21 ± 1.07	7.64 ± 1.27	7.58 ± 1.16	ns	ns	ns
C18:3 $n-6$	0.42 ± 0.13	0.46 ± 0.11	0.48 ± 0.08	0.45 ± 0.12	0.45 ± 0.10	ns	ns	ns
C20:0	0.24 ± 0.10	0.26 ± 0.06	0.24 ± 0.07	0.25 ± 0.07	0.24 ± 0.08	ns	ns	ns
C20:1$n-9$	0.86 ± 0.32	0.85 ± 0.08	0.83 ± 0.12	0.90 ± 0.08	0.79 ± 0.25	ns	ns	ns
C20:2 $n-6$	0.35 ± 0.06	0.34 ± 0.06	0.35 ± 0.05	0.35 ± 0.06	0.33 ± 0.05	ns	ns	ns
C20:4 $n-6$	1.58 ± 0.51	1.51 ± 0.42	1.85 ± 0.41	1.65 ± 0.48	1.64 ± 0.44	ns	ns	ns
C20:5 $n-3$	0.07 ± 0.04	0.07 ± 0.04	0.08 ± 0.03	0.08 ± 0.04	0.07 ± 0.03	ns	ns	ns
C22:2 $n-6$	0.04 ± 0.04	0.02 ± 0.01	0.03 ± 0.01	0.02 ± 0.01	0.03 ± 0.03	ns	ns	ns
C22:4 $n-6$	0.31 ± 0.07	0.32 ± 0.10	0.38 ± 0.09	0.36 ± 0.11	0.32 ± 0.07	ns	ns	ns
SFA	36.2 ± 2.07	35.8 ± 1.00	34.5 ± 1.33	35.4 ± 1.89	35.5 ± 1.43	ns	ns	ns
MUFA	53.8 ± 1.36	54.2 ± 1.58	54.2 ± 1.54	54.0 ± 1.53	54.1 ± 1.43	ns	ns	ns
PUFA	10.0 ± 2.07	10.0 ± 1.74	11.4 ± 1.59	10.6 ± 1.96	10.4 ± 1.80	ns	ns	ns
Neutral lipids								
C12:0	0.05^{b} ± 0.01	0.07^{ab} ± 0.02	0.08^{a} ± 0.02	0.07 ± 0.02	0.06 ± 0.01	**	*	ns
C14:0	1.13 ± 0.09	1.23 ± 0.13	1.15 ± 0.14	1.16 ± 0.14	1.18 ± 0.12	ns	ns	ns
C16:0	23.5 ± 0.74	23.4 ± 0.56	22.9 ± 0.73	23.2 ± 0.83	23.3 ± 0.59	ns	ns	ns
C16:1 $n-7$	3.93 ± 0.23	4.23 ± 0.33	4.15 ± 0.41	4.12 ± 0.35	4.11 ± 0.35	ns	ns	ns
C17:0	0.19 ± 0.05	0.21 ± 0.04	0.21 ± 0.04	0.21 ± 0.05	0.20 ± 0.04	ns	ns	ns
C17:1 $n-7$	0.19 ± 0.05	0.19 ± 0.06	0.22 ± 0.06	0.20 ± 0.06	0.20 ± 0.07	ns	ns	ns
C18:0	11.5^{a} ± 0.90	11.3^{ab} ± 0.52	10.6^{b} ± 0.87	11.1 ± 1.14	11.2 ± 0.54	*	ns	ns
C18:1 $n-9$	51.8 ± 1.16	50.8 ± 1.07	51.6 ± 1.28	51.2 ± 1.42	51.56 ± 1.03	ns	ns	ns
C18:2 $n-6$	5.24^{b} ± 0.56	5.94^{ab} ± 0.77	6.29^{a} ± 0.91	5.99 ± 0.85	5.70 ± 0.88	*	ns	ns
C18:3 $n-6$	0.30 ± 0.05	0.31 ± 0.05	0.34 ± 0.05	0.33 ± 0.05	0.31 ± 0.05	ns	ns	ns
C20:0	0.25^{b} ± 0.05	0.42^{a} ± 0.19	0.39^{ab} ± 0.07	0.38 ± 0.17	0.34 ± 0.10	*	ns	ns
C20:1$n-9$	0.97 ± 0.09	0.87 ± 0.09	0.92 ± 0.09	0.94 ± 0.11	0.90 ± 0.08	ns	ns	ns
C20:2 $n-6$	0.28 ± 0.07	0.31 ± 0.04	0.31 ± 0.09	0.33 ± 0.05	0.28 ± 0.08	ns	ns	ns
C20:4 $n-6$	0.39^{b} ± 0.15	0.60^{a} ± 0.17	0.60^{a} ± 0.10	0.58 ± 0.18	0.50 ± 0.15	**	ns	ns
C20:5 $n-3$	0.06 ± 0.01	0.04 ± 0.03	0.06 ± 0.02	0.05 ± 0.03	0.06 ± 0.02	ns	ns	ns
C22:2 $n-6$	0.06^{ab} ± 0.02	0.04^{b} ± 0.03	0.08^{a} ± 0.01	0.06 ± 0.03	0.06 ± 0.02	**	ns	ns
C22:4 $n-6$	0.10 ± 0.02	0.14 ± 0.05	0.11 ± 0.04	0.12 ± 0.05	0.12 ± 0.03	*	ns	ns
SFA	36.7^{a} ± 1.51	36.6^{a} ± 0.88	35.3^{b} ± 1.45	36.2 ± 1.81	36.2 ± 0.98	**	ns	ns
MUFA	56.9 ± 1.14	56.1 ± 1.03	56.9 ± 1.56	56.5 ± 1.55	56.8 ± 1.01	ns	ns	ns
PUFA	6.45^{b} ± 0.74	7.38^{ab} ± 0.99	7.79^{a} ± 1.11	7.45 ± 1.08	7.03 ± 1.09	*	ns	ns

GEN: genotype; GEN1: IB × DU1; GEN2: DU1 × IB; GEN3: DU2 × IB. IMF, intramuscular fat; IMF(dm), intramuscular fat (dry matter); SFA, saturated fatty acids; MUFA: monounsaturated fatty acids, PUFA: polyunsaturated fatty acids.
a,b: Different letters in the same row indicate significant statistical differences within the same day of analysis (Tukey's test, $p < 0.05$).
* $p < 0.05$.
** $p < 0.01$.
*** $p < 0.001$.

membranes rich in polyunsaturated phospholipids. Fatty acid profiles high in oleic acid and low in linoleic acid have been associated with better flavour in Iberian dry-cured meat products as an excess of oxidation development increases rancid flavours (Cava et al., 1999). Also, meat with abundant PUFA levels can cause undesirable technological and sensory consequences, since PUFA are more sensitive to oxidation, leading to meat texture, flavour and colour alterations (Morrissey, Sheehy, Galvin, Kerry, & Buckley, 1998). Although the meat from GEN3 contained the highest MUFA level, which is desirable in Iberian products (Ruíz-Carrascal et al., 2000), it also contained the highest percentage of PUFA, such as C18:2 $n-6$ and C18:3 $n-6$ and the lowest IMF content. There-

fore, the IMF content and the fatty acid profile of GEN3, although better from a nutritional point of view (Simopoulos, 2003), could also reduce the oxidative stability of chilled fresh meat and dry-cured meat products.

3.3. Lipogenic enzyme activity of subcutaneous fat and muscles

There was neither an effect ($p > 0.05$) of the sex nor significant interaction between the sex and the genotype on the lipogenic enzyme activity of SCF (Table 5). However, the genotype caused important differences in the activity of both enzymes.

G6PDH and ME activities were higher in SCF than in muscle (Table 5), which is in agreement with the literature (Gondret et al., 2005; Kouba & Mourot, 1999; Martinez-Puig et al., 2006; Morales et al., 2002; Morcuende, Estévez, Ramírez, & Cava, in press). G6PDH activity was higher than ME activity in SCF, whereas an opposite behaviour was found in muscles. Higher activity of ME than G6PDH in LD and BF could be due to the fact that NADPH in the muscle is mostly provided by ME activity and not by the pentose phosphate pathway, in which G6PDH is involved (Mourot & Kouba, 1998). Some authors (Martinez-Puig et al., 2006) have suggested that this fact would make muscle less sensitive than adipose tissue to variations of peripheral glucose, since the regulation of lipogenic enzymes is very different in both tissues, as numerous regulating factors are involved in these processes (Azain, 2004).

In SCF, GEN3 had the lowest G6PDH activity and ME activity. Similar results were found in LD muscle, as lower G6PDH activity and ME activity were found in GEN3 than in GEN1 and GEN2, despite the fact that these differences were not significant in the latter. BF muscle showed the same trend: GEN1 and GEN2 showed the highest G6PDH activity and ME activity.

Results revealed no differences in the lipogenic potential in SCF, LD and BF between reciprocal crosses (GEN1 vs. GEN2), agreeing with the findings of Morcuende et al. (in press). These authors reported no differences in G6PDH and ME activities in muscle and SCF of pigs from the reciprocal cross-Iberian × Duroc. However, the activities of both enzymes in the different tissues were strongly influenced by the Duroc sire genotype (GEN2 vs. GEN3). G6PDH and ME activities in SCF were 1.3-fold and 1.5-fold higher in GEN2 than in GEN3, respectively; G6PDH and ME activities in BF and LD were 3-fold and 1.5-fold higher in GEN2 than in GEN3, respectively. The influence of genetics on lipogenic activity has been reported by different authors (Morales et al., 2002; Mourot & Kouba, 1998; Mourot, Kouba, & Bonneau, 1996) who stated a higher enzyme lipogenic activity in rustic pig breeds, such as Iberian or Meishan, than in industrial pig genotypes, such as Landrace or Large White. However, as far as we know, no studies have previously reported differences in the lipogenic activity, due to the genotype of pigs within the same breed. Nonetheless, different authors (Cilla et al., 2006; Lonergan et al., 2001) previously described important differences between lines of Duroc in the IMF content, carcass composition and meat quality parameters, which can support the differences in the adipogenic character and fatty acid composition found between the genotypes in the present study.

The higher activity in both lipogenic enzymes (ME and G6PDH) is consistent with the higher BFT, HFT and IMF content of the muscles. The highest fat thicknesses and IMF content of GEN1 and GEN2 agree with the highest G6PDH and ME activities, which indicate that the net production of NADPH, and as a consequence, lipid synthesis and storage in muscle and in subcutaneous fat were higher in GEN1 and GEN2 than in GEN3. Different studies have related the lipogenic enzyme activity with the number or

Table 5
Glucose-6-phosphate dehydrogenase (G6PDH) and malic enzyme (ME) activity in subcutaneous fat, *L. dorsi* and *B. femoris* muscles (expressed as nmol of NADPH formed min^{-1} mg of $protein^{-1}$) from three different Iberian × Duroc genotypes

	Genotype			Sex		Probabilities		
	GEN1	GEN2	GEN3	♂	♀	Genotype	Sex	Interaction
SCF								
G6PDH	$1282^{a} \pm 133$	$1333^{a} \pm 269$	$1005^{b} \pm 165$	1156 ± 277	1249 ± 206	***	ns	ns
ME	$838^{a} \pm 154$	$708^{ab} \pm 229$	$561^{b} \pm 200$	633 ± 215	758 ± 218	*	ns	ns
LD								
G6PDH	$1.7^{a} \pm 0.6$	$1.7^{a} \pm 0.6$	$0.5^{b} \pm 0.5$	1.3 ± 0.8	1.2 ± 0.8	***	ns	ns
ME	7.5 ± 1.5	6.6 ± 1.3	5.5 ± 1.9	6.2 ± 1.2	6.7 ± 1.3	ns	ns	ns
BF								
G6PDH	$2.1^{a} \pm 1.5$	$2.9^{a} \pm 0.8$	$0.8^{b} \pm 0.8$	1.8 ± 1.6	2.0 ± 1.9	***	ns	ns
ME	$7.3^{a} \pm 1.5$	$7.7^{a} \pm 1.3$	$5.5^{b} \pm 1.0$	6.5 ± 1.7	7.2 ± 1.4	***	ns	ns

GEN: genotype; GEN1: IB × DU1; GEN2: DU1 × IB; GEN3: DU2 × IB. ME, malic enzyme; G6PDH, glucose 6 phosphate dehydrogenase.
a,b: Different letters in the same row indicate significant statistical differences within the same day of analysis (Tukey's test, $p < 0.05$).
* $p < 0.05$.
*** $p < 0.001$.

volume of adipocytes from different adipose tissues in cattle (Eguinoa et al., 2003) and also in pigs (Mourot et al., 1996), as the increase of adipocyte size was associated with a higher lipogenic enzyme activity and backfat thickness.

3.4. Correlations and multivariate analysis

Correlations between lipogenic enzyme activity and fatty acid composition of SCF and IMF of LD and BF are shown in Table 6.

Significant correlations were found between BFT and G6PDH ($r = 0.564$, $p < 0.001$) and ME activities ($r = 0.411$, $p < 0.05$) in SCF. However, no correlations were found between HFT and the enzyme lipogenic activity in SCF, may be because SCF to evaluate enzyme lipogenic activity was taken from the backfat and not from the ham fat. In this respect, some authors (Mourot et al., 1996) found significant differences between the enzyme activities of SCF from different tissues, such as neckfat and backfat. These authors also suggested that pigs have certain adipose tissues in which fat is deposed preferentially and other adipose tissues where lipogenesis is higher and which deliver triacylglycerides to the bloodstream. IMF dry matter content positively correlated with G6PDH in LD ($r = 0.416$, $p < 0.05$) and with EM in BF ($r = 0.388$, $p < 0.05$). The positive relationship between G6PDH and ME, and BFT, HFT and IMF indicate that these traits are closely related to the different adipogenic potential of the genotypes which is consistent with differences in the BFT, HFT and IMF content of the studied genotypes.

In SCF and LD, G6PDH activity correlated positively with those fatty acids related with *de novo* synthesis of fat, C16:0, C18:0 and SFA, while the correlations were negative in fatty acids more influenced by the diet, such as polyunsaturated fatty acids, C18:2 $n-6$ and PUFA. In LD, relations between G6PDH and saturated fatty acids were clearer due to the fact that NL are less rich in PUFA than total fat. In BF, ME activity correlated positively with the percentage of C16:0, C18:0, and SFA of IMF. In NL, ME activity correlated positively with C16:0, C18:0 and SFA, and negatively with C18:2$n-6$ and PUFA. As endogenous synthesis of FA produces C16:0 and C18:0, positive correlations between enzyme activities and SFA, and negative correlations with unsaturated fatty acids are expected, as the relative level of PUFA and MUFA decrease, when SFA percentage and lipogenic activity increase.

PCA of the variables resulted in 5 significant factors that accounted for 76.0% of the variability. Principal components PC1 and PC2 explained 34.8% and 15.1% of the variation of the data, respectively. The loadings of this PCA are shown in Fig. 1. In this plot, it is possible to differentiate two groups of variables. On the positive x-axis of the PC1 are located MUFA and PUFA from SCF, LD and BF muscles (both muscle IMF and NL fractions) while on the negative x-axis are placed SFA, fat depths, IMF

Table 6
Correlations between lipogenic enzyme activity and fatty acid composition of subcutaneous and intramuscular fat of m. *L. dorsi* and m. *B. femoris* from three different genotypes Iberian × Duroc

SCF			LD			BF		
	G6PDH	ME		G6PDH	ME		G6PDH	ME
BFT	0.564***	0.411*	IMF	0.405*	0.046	IMF	0.224	0.361
HFT	0.320	0.267	IMF (dm)	0.416*	0.022	IMF (dm)	0.239	0.388*
IMF								
C16:0	−0.035	−0.156	C16:0	0.27	0.02	C16:0	0.12	0.458*
C18:0	0.414*	0.400*	C18:0	0.491**	0.328	C18:0	0.098	0.414*
C18: 1 $n-9$	0.117	0.081	C18: 1 $n-9$	−0.329	−0.385*	C18: 1 $n-9$	0.172	−0.195
C18:2 $n-6$	−0.492**	−0.297	C18:2 $n-6$	−0.248	0.173	C18:2 $n-6$	−0.335	−0.351
SFA	0.364*	0.266	SFA	0.406*	0.184	SFA	0.156	0.504**
MUFA	−0.003	−0.037	MUFA	−0.384*	−0.441*	MUFA	0.228	−0.14
PUFA	−0.537+	−0.338	PUFA	−0.267	0.103	PUFA	−0.317	−0.337
NL								
			C16:0	0.411*	0.039	C16:0	0.108	0.509**
			C18:0	0.513**	0.344	C18:0	0.105	0.451*
			C18: 1 $n-9$	−0.406*	−0.353*	C18: 1 $n-9$	0.101	−0.254
			C18:2 $n-6$	−0.356	0.201	C18:2 $n-6$	−0.325	−0.403**
			SFA	0.503**	0.212	SFA	0.13	0.504**
			MUFA	−0.437*	−0.383*	MUFA	0.12	−0.23
			PUFA	−0.391*	0.152	PUFA	−0.286	−0.397*

GEN: genotype; GEN1: IB × DU1; GEN2: DU1 × IB; GEN3: DU2 × IB. BFT, backfat thickness; HFT, ham fat thickness; IMF, intramuscular fat; NL, neutral lipids; ME, malic enzyme; G6PDH, glucose 6 phosphate dehydrogenase; SFA, saturated fatty acids; MUFA, monounsaturated fatty acids; PUFA, polyunsaturated fatty acids.

* $p < 0.05$.
** $p < 0.01$.
*** $p < 0.001$.

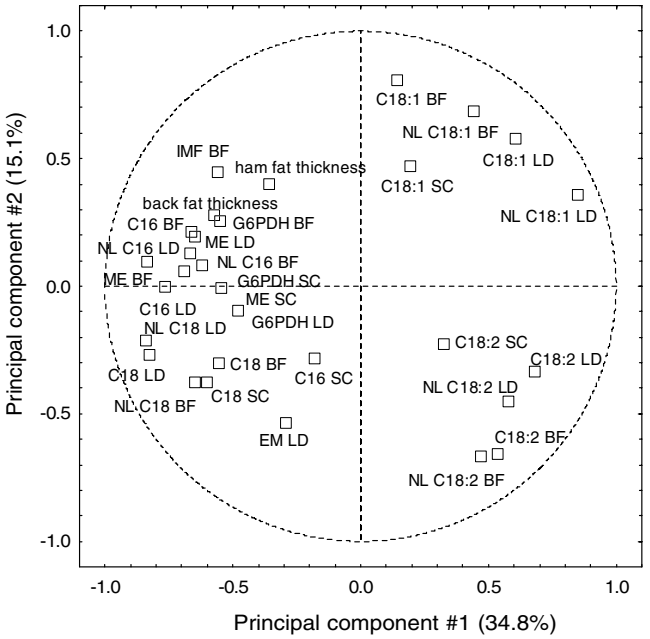

Fig. 1. Loadings plot after principal component analysis of the variables in the plane defined by the two first principal components (PC1 and PC2).

content and the activity of the lipogenic enzymes. PC2 differentiates MUFA from PUFA. The distribution of data on PC1 and PC2 (Fig. 2) shows two separate groups, one corresponding to the reciprocal crosses (GEN1 and GEN2), and the other to GEN3. Results show a close connection between high lipogenic enzyme activity, which generates SFA, and, as a consequence, increased adipose tissues in SCF and IMF, and GEN1 and GEN2. The lowest lipogenic potential of GEN3 decreased the fatness of the pigs, which increased the relative levels of PUFA and MUFA, the main variables associated with this genotype.

4. Conclusion

Iberian × Duroc reciprocal crosses had a similar lipogenic character. Nonetheless, the differences between paternal lines of Duroc crossed with Iberian pigs had a marked influence on the adipogenic potential. The use of Duroc sires with selected genotypes (DU2) reduces G6PDH and ME enzyme activities and the IMF content, which has negative consequences for the manufacture of dry-cured meat products. Moreover, it also modifies the fatty acid profile, increasing unsaturated fatty acids, which have positive nutritional effects, although they can also cause a decrease in the shelf life of the meat, making it more prone to oxidation during refrigerated storage and during the preparation of dry-cured meat products.

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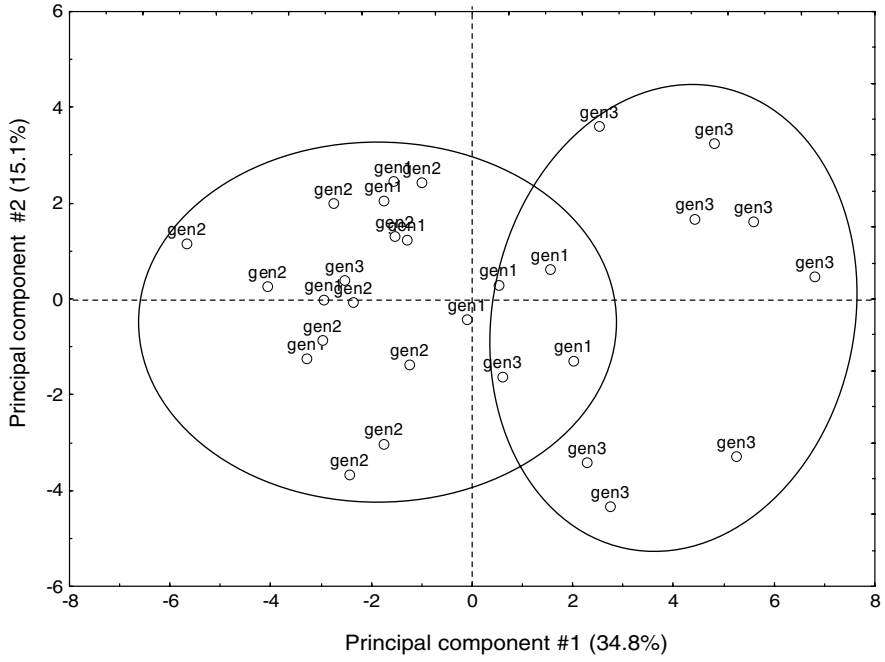

Fig. 2. Scores plot after principal component analysis of the individuals in the plane defined by the two first principal components (PC1 and PC2).

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