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Rosario Ramírez
Universidad de Extremadura, Cáceres

Ramon Cava
Universidad de Extremadura, Cáceres

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Carcass composition and meat quality of three different Iberian × Duroc genotype pigs

R. Ramírez, R. Cava *

Tecnología de los Alimentos, Facultad de Veterinaria, Universidad de Extremadura, Cáceres 10071, Spain

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Abstract

Carcass composition and meat quality of *Longissimus dorsi* (LD) and *Biceps femoris* (BF) muscles from three different Iberian × Duroc genotype pigs were studied: GEN1: ♂ Iberian × ♀ Duroc1; GEN2: ♂ Duroc1 × ♀ Iberian; GEN3: ♂ Duroc2 × ♀ Iberian. Duroc1 (DU1) were selected for the manufacture of dry-cured meat products while Duroc2 (DU2) were pigs selected for meat production, with high percentages of meat cuts and low carcass fat. Genotype had a significant effect on the differences found while sex had not. GEN2 showed the highest weights at days 180 and 238 of weaning and the highest slaughter weights (day 316) followed by GEN3, while the lowest weights were found in GEN1. GEN3 had well conformed carcasses in comparison with GEN1 and GEN2, since GEN3 showed the highest percentages of ham and loin and the highest weight of loin as well as the lowest back and ham fat thickness. However, the use of DU2 pigs in the cross with Iberian had negative effects on meat quality, as GEN3 gave the worst meat quality in both muscles, postmortem pH, cook and drip loss, and colour and the lowest percentages of intramuscular fat (IMF). In subcutaneous fat (SCF), GEN3 had higher percentages of polyunsaturated fatty acids (PUFA) than GEN2, while GEN2 had higher saturated fatty acids (SFA) levels. In LD, IMF from GEN3 showed the highest percentage of MUFA and PUFA; while the fatty acid profile of GEN2 was more saturated. BF muscle showed similar trends, but not significantly so. On the other hand, few differences were found between reciprocal crosses (GEN1 vs. GEN2). GEN2 showed higher IMF in LD than GEN1, agreeing with their carcass weight. As a result, GEN1 had a fatty acid profile of IMF in the LD that was more unsaturated.

Keywords: Meat quality; Carcass; Iberian; Duroc; Crossbreeding; pH

1. Introduction

The number of Iberian pigs (pure and crossed) has increased in recent years, mainly as a consequence of the increase in consumption of dry-cured meat products and fresh meat, which has improved the productive and feeding systems of the Iberian pig. Nowadays, one of the alternatives applied to improve productive parameters is to cross with the Duroc breed at 50%. These crosses increase the number of piglets per sow and the weight at weaning and at the end of fattening (Aparicio, 1987), without changes on the adaptation capacity of the Iberian pig to the environment and without reducing the quality of the cured meat products (Antequera et al., 1994; López-Bote, 1998; Tejeda, Gandemer, Antequera, Viau, & García, 2002).

Iberian × Duroc crosses are so popular that it is estimated that among the pigs slaughtered as "Iberian", less than the 25% are pure (Sierra Alfranca, 1992). This makes it really important to assess the selection of the Duroc lines to cross with Iberian, because the Duroc breed cannot be considered a homogeneous breed as a consequence of its vast distribution (Jonnes, 1998), which has favoured genetic selection according to the different criteria of production and meat quality.

Some authors (Castellanos, Barragán, Rodríguez, Toro, & Silió, 1997) have warned that the high frequency of Iberian × Duroc crosses could be a danger for the genetic purity of the Iberian breed. As a consequence, a specific law for

* Corresponding author. Tel.: +34 927 257169; fax: +34 927 257110.
E-mail address: rcava@unex.es (R. Cava).

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Iberian products was passed in 2001 in Spain (B.O.E., 15th October 2001). One of the most important aspects of this law is the genotypes that can be used in the manufacture of dry-cured meat products (hams, shoulders and loins) labelled as "Iberian". The law allows the use of pure Iberian pigs as well as Iberian × Duroc crosses. However, in the crosses it is necessary to use Iberian females to preserve the genetic purity and the biodiversity of the Iberian breed. In this sense, Morcuende, Estévez, Ramírez, and Cava (in press) have reported on the existence of productive improvements such as higher slaughter weight and meat yields in the crosses that use Duroc sows rather than Iberian ones.

Previous research (Lonergan, Huff-Lonergan, Rowe, Kuhlers, & Jungst, 2001; Morcuende, Estévez, Ramírez, & Cava, 2004) has assessed the differences between Duroc genetic lines. Cilla et al. (2006) and Soriano et al. (2005) found significant differences between sire Duroc lines in crossbreedings which affected carcass composition and meat quality for the manufacture of dry-cured meat products. The selection carried out in some Duroc lines was to improve lean growth efficiency yielding leaner fat pigs and higher growth rates. Different authors have reported that when emphasis is placed on high lean conversion efficiency, unfavourable changes in pork quality can occur (Cameron, Nute, Brown, Enser, & Wood, 1999; Lonergan et al., 2001; McPhee & Trout, 1995 & Oksbjerg et al., 2000). Therefore, the cross of Iberian with the Duroc lines could affect productive parameters and meat quality. The limited amount of research on the consequences of the use of different Duroc lines in crosses with Iberian pigs, as well as the consequences of using the Iberian line as maternal or paternal line shows the need for studies to clarify these aspects.

2. Materials and methods

2.1. Animals

Three groups of 10 pigs were studied (5 males and 5 females) from different genotypes: GEN1: ♂ Iberian × ♀ Duroc1, GEN2: ♂ Duroc1 × ♀ Iberian; GEN3: ♂ Duroc2 × ♀ Iberian. The genotype Duroc1 (DU1) corresponded to pigs selected for the production of dry-cured meat products (hams, loins, shoulders), with a high level of fattening. The genotype Duroc2 (DU2) corresponded to animals selected for meat production, with high percentages of meat cuts and low carcass fat. Pigs were castrated, as is traditionally done and were raised together in a semi-intensive system and were fed *ad libitum* with the diet shown in Table 1. Pigs were randomly slaughtered after 316 days of rearing at 150–165 kg live weight.

2.2. Growth performance and carcass composition

The weights of hams, shoulders and loins were taken 5 h postmortem. The backfat thickness (BFT) and ham fat thickness (HFT) were measured in the 5th rib and in the m. *Gluteo-biceps* in the carcass and ham, respectively. Samples of subcutaneous fat (taken from backfat at 5th–6th rib) and *Biceps femoris* (BF) and *Longissimus dorsi* (LD) muscles were dissected from the carcasses and 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 fiber	4.8	3.7
Ash	6.9	6.2
Lysine	0.9	0.5
Metabolizable energy (kcal/kg)	3071.5	3183.7
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. Muscles composition

pH values 45 min (pH_{45}) and 24 h (pH_U) after slaughter in the BF and LD were measured with a puncture pHmeter Crisol mod. 507. Lipids were extracted from 5 g of meat with chloroform/methanol (1:2), according to Bligh and Dyer (1959). Protein content was determined by the Kjieldalh method (AOAC, 2000), moisture was determined by drying the samples (~5 g) at 102 °C (AOAC, 2000) and haem pigments were assessed following the method of Hornsey (1956).

2.4. Fatty acid profile determination

Fatty acid methyl esters (FAMEs) were prepared by transesterification using methanol in the presence of sulphuric acid (5% sulphuric acid in methanol). FAMEs were analyzed using a Hewlett–Packard model HP-5890A gas chromatograph, equipped with a flame ionization detector (FID). They were separated on a semicapillary column (Hewlett-Packard FFAP-TPA fused-silica column, 30 m length, 0.53 mm i.d., and 1.0 mm film thickness). The injector and detector temperatures were held at 230 °C and the oven temperature 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 retention times of reference compounds (Sigma). Fatty acid composition was expressed as percent of major FAMEs.

2.5. Instrumental colour

Colour measurements were made following the recommendations on colour determination of the American Meat

Science Association (Hunt et al., 1991). The following colour coordinates were determined: lightness (L^*), redness (a^*, red ± green) and yellowness (b^*, yellow ± blue). Colour parameters were determined using a Minolta CR-300 colorimeter (Minolta Camera, Osaka, Japan) with illuminant D65, a 0° standard observer and a 2.5 cm port/viewing area. The colorimeter was standardized before use with a white tile. In addition, hue angle, which describes the hue or colour was calculated ($H^\circ = \text{arctg}\, b^*/a^* \cdot 360/2\pi$) as well as the saturation index or chroma (C^*) ($C = (a^{*2} + b^{*2})^{0.5}$), which describes the brightness or vividness of colour. The measurements were repeated at 5 randomly selected places on each slice and averaged.

2.6. Drip and cook loss

Drip loss was measured following the method of Honikel (1998). The samples were weighed and suspended in two plastic bags, the inner bag perforated, and the exudates was collected in the outer bag. Meat was stored for 10 days at 4 °C. Drip loss (%) was calculated by difference in weight between day 0 and 10 of storage. For cook loss (%), each chop was placed in a plastic bag and cooked by immersion at 80 °C for 60 min. The difference of weight before and after cooking was used to calculate cook loss percentage.

2.7. Statistical analysis

The effects of genotype and sex were analyzed by the analysis of variance (ANOVA) procedure of SPSS, version 12.0 (SPSS, 2003). A two-way analysis of the variance (genotype and sex) with interaction (genotype × sex) was carried out. Means were used to compare differences. HSD Tukey's test was applied to compare the mean values of the genotypes. Mean values and standard errors of the means (SEM) are reported. The relationships between traits were analyzed by calculation of Pearson's coefficient.

3. Results and discussion

3.1. Growth performance and carcass composition

Genotype significantly affected live weight and average daily gain (ADG) during the whole rearing period while sex had no effect on growth and ADG (Table 2). Pigs from GEN2 showed the highest live weights at day 180 and 238 and at the end of rearing (day 316), in contrast animals from GEN1 had the lowest weights. Animals from GEN3 showed intermediate weights. Animals from GEN2 and GEN3 had a significant higher ADG than GEN1 from day 180 to 238 (GEN1: 674g/d, GEN2: 753g/d, GEN3: 782g/d), however, between days 238 and 316 ADG was similar in the three genotypes (GEN1: 390g/d, GEN2: 397g/d, GEN3: 396g/d).

Carcass composition was significantly affected by genotype whereas sex only affected the loin and shoulder weights; these were significantly higher in males than in females (Table 3). Carcass weight was significantly higher in GEN2 than in GEN1, while GEN3 presented an intermediate weight, agreeing with the results for slaughter weight (day 316). In contrast, killing out percentage (KOP) was significantly lower in GEN3 than in GEN1 and GEN2. Genotype had a major effect on the weight and percentage of loin and ham, being higher in carcasses from GEN3 than in the other two genotypes. The level of carcass fattening, measured as BFT and HFT, was significantly higher in GEN2 than in GEN3, while the fattening of GEN1 was intermediate.

Results show an important effect of the Duroc sire line on carcass composition. Therefore, the use of Duroc lines selected on the basis of their productive parameters (DU2) produce hybrids (GEN3) with high weights and percentages of the main cuts and low levels of carcass fat. Nevertheless, for the manufacture of high quality dry-cured meat products (hams, shoulders, loins, etc) a high level of fattening is required to provide correct ripening during maturation for the development of their sensory characteristics (Gandemer, 2002).

As regards the differences between reciprocal crosses (GEN1 vs. GEN2), only small differences were found, which suggests that maternal effects did not play an important role on productive and carcass parameters. These results contrast with those reported by Morcuende et al. (in press) in a study with Iberian × Duroc reciprocal crosses, who found better productive parameters in animals from Duroc sows than in animals from Iberian sows.

3.2. Meat quality parameters

In general, differences found in meat quality were mainly due to pig genotype, sex did not affect them (Table 4).

Table 2
The weight of the different genotypes and the males and females during the growth

Day of rearing	Genotype			Sex		SEM	Significance		
	GEN1	GEN2	GEN3	♂	♀		Genotype	Sex	Interaction
180	80.1b	91.2a	84.0ab	86.6	84.0	1.7	*	ns	ns
238	119.2b	134.9a	129.4ab	131.1	125.4	2.3	*	ns	ns
316	149.7b	165.9a	160.3ab	162.3	155.8	2.4	*	ns	ns

ns: non significant; *: $p < 0.05$; **: $p < 0.01$; ***: $p < 0.001$.
GEN1: IB × DU1; GEN2: DU1 × IB; GEN3: DU2 × IB.
a,b: Different letters in the same row indicate significant statistical differences (Tukey's test, $p < 0.05$).

Table 3
Production parameters of the genotypes and sexes

	Genotype			Sex		SEM	Significance		
	GEN1	GEN2	GEN3	♂	♀		Genotype	Sex	Interaction
Carcass (kg)	124.6b	135.8a	125.9ab	132.0	125.5	2.04	*	ns	ns
KOP (%)	82.8a	81.9a	78.6b	81.5	80.7	0.62	**	ns	ns
Backfat thickness (cm)	6.3ab	6.4a	5.3b	5.9	6.1	0.18	*	ns	ns
Ham fat thickness (cm)	3.1ab	3.4a	2.7b	3.2	2.9	0.11	**	ns	ns
Meat pieces weight									
Ham (kg)[A]	13.9b	15.3a	15.1ab	15.2	14.3	0.23	ns	ns	ns
Shoulder (kg)[A]	9.6	10.4	9.9	10.3	9.6	0.16	ns	**	ns
Loin (kg)	2.5b	2.7b	3.2a	2.9	2.7	0.09	***	*	**
Percentages (%)									
Ham percentage (%)	11.2b	11.3b	11.9a	11.5	11.4	0.10	**	ns	ns
Shoulder percentage (%)	7.7	7.6	7.9	7.8	7.7	0.05	ns	ns	ns
Loin percentage (%)	2.0b	2.0b	2.5a	2.2	2.1	0.07	***	ns	*

GEN1: IB × DU1; GEN2: DU1 × IB; GEN3: DU2 × IB.
ns: non significant; *: $p < 0.05$; **: $p < 0.01$; ***: $p < 0.001$.
a,b: Different letters in the same row indicate significant statistical differences (Tukey's test, $p < 0.05$).
KOP: killing out percentage.
[A] Weight without shaping.

Regarding differences between muscles, the effect of the genotype on the parameters analyzed was more marked in LD than in BF.

The rate of pH decline was significantly higher in GEN3 than in GEN1 and GEN2. In this respect, the pH value at 45 min postmortem (pH_{45min}) was significantly lower in BF from GEN3 than in the other two genotypes, and the ultimate pH values (pH_U) were the lowest in LD and BF from GEN3.

Muscles from GEN3 tended to have a higher loss of water during cooking and storage than those from GEN1 and GEN2. Thus, drip loss during refrigerated storage was the highest in the LD from GEN3 and significantly higher than GEN1 in the BF. Similarly, water loss during cooking was higher in muscles from GEN3 than in the other two genotypes, although differences were only significant in the LD.

Regarding instrumental colour, lightness (CIE L^*-value) was highest in LD and BF from GEN3, which indicates that meat from GEN3 was paler compared with the other genotypes. No significant differences were found in CIE a^*-value and CIE b^*-value due to genotype. The effect of sex on instrumental colour was small and only redness (CIE a^*-value) of the BF muscle was significantly higher in females than in males. The content of haem pigments was highest in GEN1 in both muscles, although the differences were only significant in LD.

The incidence of PSE meat is one of the main quality problems in pork (Oliver, Gisperr, & Diesdre, 1993). The appearance of this type of meat can be monitored by measurements of pH, instrumental colour and exudate loss (Kauffman et al., 1993) as PSE meat is characterized by its intense paleness, low pH, low consistency and intense exudation (Briscke y, 1964). The LD and BF from GEN3 showed the characteristics of PSE meat since they were paler (CIE-L^*), had high acidification postmortem (pH_{45} and pH_U) and were associated with high drip and cook losses. Postmortem pH is important since it is normally associated with muscle paleness. In this respect, significant negative correlations ($p < 0.01$) were found ($r = -0.624$) between pH_U and L^*. IMF content is one muscle parameter that influences meat and meat product quality. GEN2 had higher IMF contents than GEN3 in both muscles, whereas in the reciprocal crosses (GEN1 vs. GEN2) the IMF of the LD muscle was higher in GEN2 than in GEN1, according to the higher fat and carcass weights of GEN2. Differences due to genotype were only significant in LD, although BF showed the same trend. Therefore, meat from GEN2 because of the higher content of IMF has the best characteristics for the manufacture of high quality meat products, in which an increase in IMF supposes a marked enhancement of quality (Gandemer, 2002). However, the lower IMF content in LD and BF of the GEN3 could be negative for the sensorial characteristics of meat and meat products, such as taste, aroma, tenderness and juiciness (Essén-Gustavson, Karlsson, Lundström, & Enfalt, 1994; Ruiz-Carrascal, Ventanas, Cava, Andrés, & García, 2000).

Sex had no effect on the fatty acid composition of SCF and IMF of the LD and BF muscles, however, genotype significantly affected fatty acid profiles of both locations (Table 5).

SCF from GEN3 had a higher content of unsaturated fatty acids than GEN1, mainly due to a higher content of C18:2$n-6$ and polyunsaturated fatty acids (PUFA), and a lower content of C18:0 than GEN2. The differences between genotypes GEN2 and GEN3 are due to the different paternal lines of Duroc (DU1 and DU2); whereas no significant differences were found between reciprocal crosses (GEN1 vs. GEN2).

Table 4
Moisture, intramuscular fat (IMF) and protein contents (g/100 g), haem pigments (mg/kg) pH, drip loss (% DL) cook loss (% CL) and instrumental colour of the LD and BF muscles

	Genotype			Sex		SEM	Significance		
	GEN1	GEN2	GEN3	♂	♀		Genotype	Sex	Interaction
$pH_{45}LD$	5.7	5.8	5.8	5.7	5.8	0.05	ns	ns	ns
$pH_{45}BF$	5.8a	5.9a	5.6b	5.7	5.7	0.05	**	ns	ns
$pH_{U}LD$	5.7a	5.5ab	5.1b	5.4	5.4	0.07	*	ns	ns
$pH_{U}BF$	5.8a	5.7a	5.2b	5.5	5.6	0.06	***	ns	ns
Drip and cook loss									
DL LD (%)	4.0b	4.3b	6.0a	4.8	4.8	0.30	**	ns	ns
DL BF (%)	3.4b	4.0ab	5.1a	3.9	4.4	0.28	*	ns	ns
CL LD (%)	6.0b	6.5b	10.4a	8.1	7.3	0.54	***	ns	ns
CL BF (%)	9.7	11.0	11.6	10.9	10.7	0.35	ns	ns	ns
Instrumental colour									
Cie L^* LD	48.9b	53.1a	52.8a	51.8	51.6	0.52	***	ns	ns
Cie L^* BF	41.9b	42.4b	46.8a	44.7	42.9	0.74	*	ns	ns
Cie a^* LD	10.2	10.0	9.9	9.9	10.2	0.26	ns	ns	ns
Cie a^* BF	18.3	17.4	17.9	17.2	18.5	0.31	ns	*	ns
Cie b^* LD	4.3	4.9	5.0	4.7	48	0.17	ns	ns	ns
Cie b^* BF	6.2	6.2	7.2	6.7	6.4	0.23	ns	ns	ns
Haem pigments									
Hematine LD (mg/kg)	48.7a	38.3b	37.9b	41.0	41.7	1.42	**	ns	ns
Hematine BF (mg/kg)	93.1	86.8	82.4	80.6	93.4	2.26	ns	***	**
Chemical composition									
Moisture LD (g/100 g)	71.4ab	70.3b	71.7a	71.0	71.2	0.24	*	ns	ns
Moisture BF (g/100 g)	74.1a	73.3 b	73.6b	73.6	73.5	0.16	*	ns	ns
Protein LD (g/100 g)	23.4a	21.3b	21.3b	22.2	21.7	0.34	*	ns	ns
Protein BF (g/100 g)	19.2b	19.3b	20.5a	19.9	19.5	0.23	*	ns	ns
IMF LD (g/100 g)	3.8b	5.9a	3.5b	4.4	4.4	0.28	***	ns	ns
IMF BF (g/100 g)	3.4	3.7	3.0	3.4	3.4	0.17	ns	ns	ns

GEN1: IB × DU1; GEN2: DU1 × IB; GEN3: DU2 × IB.
LD: *Longissimus dorsi*; BF: *Biceps femoris*.
DL drip loss, CL cook loss.
ns: non significant; *: $p < 0.05$; **: $p < 0.01$; ***: $p < 0.001$.
a,b: Different letters in the same row indicate significant statistical differences (Tukey's test, $p < 0.05$).

Genotype significantly affected fatty acid composition of IMF from the LD muscle, while the BF muscle did not show significant differences among genotypes, although the trend was similar to LD (Table 5). PUFA content was significantly higher in LD from GEN1 and GEN3 than from GEN2, which showed the highest percentages of C16:0, C18:0 and saturated fatty acids (SFA). In LD, the Duroc sire line (DU1, DU2) caused significant differences in the fatty acid composition of the IMF, since IMF from GEN3 was more unsaturated with high contents of C18:1$n-9$, monounsaturated fatty acids (MUFA), C18:2$n-6$, C20:4$n-6$, PUFA and a low content of C16:0, C18:0 and SFA. Similarly, some differences in the fatty acid profile of IMF were found between LD from reciprocal crosses (GEN1 vs. GEN2). IMF from GEN1 was more unsaturated than GEN2 as a consequence of a higher content of C18:2$n-6$, C18:3$n-6$, C20:4$n-6$, PUFA, and a lower content of C16:0 and SFA, which agrees with the higher IMF in GEN2 than in GEN1 (5.9 vs. 3.8 g/100 g, respectively).

Morcuende et al. (in press) did not find significant differences in quality parameters from LD and BF muscles of Iberian × Duroc reciprocal crosses. Nevertheless, reciprocal crosses in this study (GEN1 and GEN2) showed some differences, principally, in the chemical composition of the muscles and in the fatty acid composition of the LD. Probably, some of the differences found could be reduced with more homogeneous slaughter weights between these 2 groups (149.6 vs. 165.8 kg.).

Differences in fatty acid profiles between genotypes could be attributed to different causes: (i) a different content of IMF; (ii) a different potential for endogenous synthesis of fatty acids. On the one hand, the lowest content of PUFA in GEN2 could be caused by the dilution effect of phospholipids and/or PUFA due to a high content of IMF. Similar results have been found in breeds or genotypes with high IMF contents (Cameron & Enser, 1991; Morcuende et al., in press; Suzuki, Shibata, Kadowaki, Abe, & Toyoshima, 2003). On the other hand, differences in the thickness of back and ham fat and the different fatty acid compositions, especially of SFA, suggest a different adipogenic potential for the genotypes, as a result of a different capacity for the synthesis and storage of fat related to genetic characteristics. This was supported

Table 5
Major fatty acids composition (% total fatty acids) in subcutaneous and intramuscular fat in *Longissimus dorsi* and in *Biceps femoris* muscles as related genotype and sex

	Genotype			Sex		SEM	Significance		
	GEN1	GEN2	GEN3	♂	♀		Genotype	Sex	Interaction
Subcutaneous fat									
C16:0	24.1	24.7	24.6	24.4	24.5	0.10	ns	ns	ns
C18:0	13.3ab	13.7a	12.3b	13.2	13.0	0.19	*	ns	ns
C18:1$n-9$	46.9	45.7	46.1	46.1	46.2	0.21	ns	ns	ns
C18:2$n-6$	9.7b	10.1ab	10.7a	10.1	10.2	0.14	*	ns	ns
C18:3$n-6$	0.5	0.5	0.5	0.5	0.5	0.02	ns	ns	ns
C20:4$n-6$	0.1b	0.1b	0.2a	0.1	0.1	0.00	**	ns	ns
SFA	38.0	39.0	37.7	38.3	38.2	0.22	ns	ns	ns
MUFA	50.9	49.7	50.3	50.2	50.3	0.25	ns	ns	ns
PUFA	11.0b	11.3ab	12.0a	11.4	11.5	0.14	*	ns	ns
Longissimus dorsi									
C16:0	23.8b	25.2a	23.6b	24.1	24.2	0.20	***	ns	*
C18:0	12.8a	13.6a	11.7b	12.5	12.9	0.21	***	ns	ns
C18:1$n-9$	48.8ab	48.0b	49.1a	48.7	48.6	0.20	*	ns	ns
C18:2$n-6$	6.1a	4.9b	6.4a	5.9	5.7	0.19	***	ns	ns
C18:3$n-6$	0.3a	0.2b	0.3a	0.3	0.3	0.01	***	ns	ns
C20:4$n-6$	1.0b	0.8c	1.3a	1.1	1.0	0.07	***	ns	ns
SFA	38.3b	40.6a	36.9b	38.3	38.9	0.40	***	ns	**
MUFA	53.6ab	53.0b	54.4a	53.8	53.6	0.23	*	ns	ns
PUFA	8.1a	6.4b	8.6a	7.8	7.5	0.27	***	ns	ns
Biceps femoris									
C16:0	22.7	22.6	22.0	22.4	22.4	0.17	ns	ns	ns
C18:0	11.8	11.4	10.8	11.3	11.4	0.16	ns	ns	ns
C18:1$n-9$	49.0	48.9	49.1	48.9	49.1	0.24	ns	ns	ns
C18:2$n-6$	7.3	7.3	8.2	7.6	7.6	0.22	ns	ns	ns
C18:3$n-6$	0.4	0.5	0.5	0.5	0.5	0.02	ns	ns	ns
C20:4$n-6$	1.6	1.5	1.9	1.7	1.6	0.08	ns	ns	ns
SFA	36.2	35.8	34.5	35.4	35.5	0.32	ns	ns	ns
MUFA	53.8	54.2	54.2	54.0	54.1	0.27	ns	ns	ns
PUFA	10.0	10.0	11.4	10.6	10.4	0.34	ns	ns	ns

GEN1: IB × DU1; GEN2: DU1 × IB; GEN3: DU2 × IB.
ns: non significant; *: $p < 0.05$; **: $p < 0.01$; ***: $p < 0.001$.
a,b,c: Different letters in the same row indicate significant statistical differences (Tukey's test, $p < 0.05$). SFA: saturated fatty acids (C12:0, C14:0, C16:0, C17:0, C18:0, C20:0), MUFA: monounsaturated fatty acids (C16:1$n-7$, C17:1$n-7$, C18:1$n-9$, C20:1$n-9$), PUFA: polyunsaturated fatty acids (C18:2$n-6$, C18:3$n-6$, C20:2 $n-6$, C20:4$n-6$, C22:2$n-6$, C22:4$n-6$).

by the significant correlations between BFT and HFT and the percentages of the major fatty acids found (Table 6). BFT and HFT correlated positively with C16:0, C18:0 and SFA, whereas they correlated negatively with C18:1$n-9$, C18:2$n-6$, PUFA and MUFA. It could indicate a higher adipogenic character of GEN2 than GEN3, while GEN1 would show an intermediate adipogenic potential. In pigs, endogenous synthesis of fatty acids takes place from acetyl CoA and malonil CoA molecules to produce palmitic acid (C16:0), from which stearic acid (C18:0) is synthesized. The highest proportion of SFA in GEN2 suggests a high endogenous synthesis capacity of this genotype, as a consequence of the increase of the activity of the metabolic routes in which the enzymes involved in the synthesis of "de novo" fatty acids take part (Mourot & Kouba, 1998). Ramírez, Morcuende, and Cava (Submitted) determined the activity of lipogenic enzymes in LD and BF muscles and in SCF, found a higher activity of both enzymes in GEN1 and GEN2 than in GEN3.

The differences in the fatty acid profile of SCF and IMF due to genotype could have important consequences. Firstly, the fatty acid profile of the SCF determines Iberian pig carcass value (De Pedro, Casillas, & Miranda, 1997; García-Olmo et al., 2002), so differences in the fatty acid profile between genotypes can modify carcass classifications with regard to quality, which can change its economic value. In addition, high proportions of PUFA reduce the oxidative stability of lipids, which could have negative effects on the sensory characteristics of fresh meat and meat products (Nawar, 1996). The implication of fatty acid profile on the quality of chilled meat and dry-cured meat products, suggests meat from GEN3, due to its higher PUFA content, could be more susceptible to lipid oxidation, and therefore, to the development of rancidity.

3.3. Pearson's correlation coefficient

Table 7 shows Pearson's correlation coefficients between carcass composition and meat quality parameters. Significant

Table 6
Pearson's coefficient correlation (r) between fatty acid composition of the subcutaneous and intramuscular fat of the *L. dorsi* and *B. femoris* and back and ham fat thickness (BFT, HFT)

Subcutaneous fat	BFT	HFT
C16:0	0.120	−0.140
C18:0	0.286	0.374*
C18:1$n-9$	0.194	−0.05
C18:2$n-6$	−0.631**	−0.189
SFA	0.347	0.318
MUFA	0.076	−0.149
PUFA	−0.636**	−0.237
Longissimus dorsi		
C16:0	0.467*	0.279
C18:0	0.433	0.042
C18:1$n-9$	−0.255*	0.126
C18:2$n-6$	−0.462*	−0.374*
SFA	0.491**	0.187
MUFA	−0.260	0.155
PUFA	−0.497**	−0.403*
Biceps femoris		
C16:0	0.362	0.249
C18:0	0.147	0.111
C18:1$n-9$	0.047	0.195
C18:2$n-6$	−0.322	−0.398*
SFA	0.300	0.227
MUFA	0.096	0.223
PUFA	−0.342	−0.377*

SFA: saturated fatty acids (C12:0, C14:0, C16:0, C17:0, C18:0, C20:0), MUFA: monounsaturated fatty acids (C16:1$n-7$, C17:1$n-7$, C18:1$n-9$, C20:1$n-9$), PUFA: polyunsaturated fatty acids (C18:2$n-6$, C18:3$n-6$, C20:2$n-6$, C20:4$n-6$, C22:2$n-6$, C22:4$n-6$).
* Bilateral significant Pearson's correlation at level $p < 0.05$.
** Bilateral significant Pearson's correlation at level $p < 0.01$.

positive correlations ($p < 0.01$) were found between carcass weight and ham ($r = 0.857$) and shoulder weight ($r = 0.907$), ham fat thickness ($r = 0.482$) and IMF content of the LD ($r = 0.423$). In contrast, killing out percentage was negatively correlated ($p < 0.05$) with loin ($r = -0.440$), ham ($r = -0.489$) and shoulder ($r = -0.382$) percentage and positively ($p < 0.05$) with the thickness of back ($r = 0.370$) and ham fat ($r = 0.473$). Loin weight correlated positively with loin ($r = 0.880$, $p < 0.01$) and ham percentage ($r = 0.488$, $p < 0.01$) and ham weight ($r = 0.469$, $p < 0.01$), whereas it correlated negatively with BFT ($r = -0.514$, $p < 0.01$). Similar correlations were observed in ham and shoulder weights, since they showed significant positive correlations with percentages of other meat cuts and negative correlations with fat measurements, such as back and ham fat depths and IMF content. These correlations are evidence that high percentages of lean cuts in pork are associated with increases of lean growth efficiency and with decreases in fat depots such as the IMF content. IMF is a determinant factor for the manufacture of dry-cured meat products (Gandemer, 2002; Ruiz-Carrascal et al., 2000). Lonergan et al. (2001), in a study of different lines of Duroc pigs, found that selection of Duroc in terms of lean growth efficiency caused important reductions in pork quality. Finally, significant positive correlations ($p < 0.05$) were found between BFT and IMF content of LD ($r = 0.416$) and BF ($r = 0.457$) as previously reported by Hovenier, Brascamp, Kanis, Van Der Werf, and Wassenber (1993) and Suzuki et al. (2003), who showed the importance of BFT measurements because of their close correlation with IMF levels.

4. Conclusion

Iberian × Duroc reciprocal crosses did not show important differences in carcass composition and meat quality parameters. However, the different paternal lines of Duroc crossed with Iberian had marked influences on production characteristics and meat quality. The use of Duroc males with selected genotypes (DU2) increases the lean meat con-

Table 7
Pearson's correlation coefficient (r) between some production parameters and the chemical composition of *L. dorsi* and *B. femoris* of the pigs

	KOP	Loin (wt.)	% Loin	ham (wt.)	% ham	Shoulder (wt.)	% Shoulder	BFT	HFT	% IMF LD	% IMF BF
Carcass (wt.)	0.345	0.214	−0.268	0.857**	−0.233	0.907**	−0.131	0.227	0.482**	0.423*	0.031
KOP		−0.283	−0.440*	0.087	−0.489**	0.181	−0.382*	0.370*	0.473*	0.269	−0.007
Loin (wt.)			0.880**	0.469**	0.488**	0.247	0.109	−0.514**	−0.220	−0.264	−0.180
% Loin				0.052	0.595**	−0.185	0.183	−0.620**	−0.465*	−0.448*	−0.201
Ham (wt.)					0.301	0.885**	0.142	−0.086	0.342	0.161	−0.007
% Ham						−0.012	0.502**	−0.586**	−0.256	−0.449*	−0.081
Shoulder (wt.)							0.298	0.082	0.393*	0.237	−0.026
% Shoulder								−0.309	−0.183	−0.377*	−0.142
BFT									0.269	0.416*	0.457*
HFT										0.354	0.324
% IMF LD											0.277

KOP: killing out percentage.
BFT: backfat thickness.
HFT: ham fat thickness.
IMF: intramuscular fat.
* Bilateral significant Pearson's correlation at level $p < 0.05$.
** Bilateral significant Pearson's correlation at level $p < 0.01$.
*** Bilateral significant Pearson's correlation at level $p < 0.001$.

tent, although it reduces meat quality, since low postmortem pH, intense paleness, low fatness and high cook and drip losses were found in the meat from this cross (GEN3), which could reduce the acceptability and shelf-life of the meat as well as its suitability for the manufacture of cured meat products. By contrast, the cross of Iberian females with Duroc males selected for the production of meat products (DU1) increases the carcass weight, though it reduces the lean meat content. Moreover, it produces high percentages of intramuscular fat and better quality characteristics in the meat, making it suitable for both cured meat production and fresh consumption.

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