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Correlation between carcass conformation and fat cover degree, and muscle fatty acid profile of yearling bulls depending on breed and *mh*-genotype

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Abstract

The objective was to study the relationships between the actual European beef carcass classification scale, which classifies carcasses with regard to conformation and degree of fat cover scores, and muscle fat quality, depending on breed and *mh*-genotype. For this purpose samples from 100 yearling bulls from "Asturiana de los Valles" (24 AV(*mh/mh*), 26 AV(*mh/+*), 25 AV (+/+)) and "Asturiana de la Montaña" (25 AM) were analysed. The results of the study showed that breed or genotype affect carcass measurement scores and muscle fatty acid profile through its important effect on animal overall fatness. Homozygous double-muscled animals produced carcasses with high conformation and low intramuscular (IM) fat content. While early-maturing and rustic AM animals produced low carcass yield and high IM fat content. The other genotypes (*mh/+*, +/+) showed, in general, intermediate characteristics. Referring to correlations, carcass conformation was negatively related to saturated (SFA) ($r=-0.69$, $P<0.001$) and monounsaturated fatty acid (MUFA) ($r=-0.69$, $P<0.001$) groups, and positively to polyunsaturated (PUFA) ($r=0.72$), n-6 ($r=0.72$), n-3 ($r=0.71$) and unsaturated fatty acid (UFA) ($r=0.69$) groups, being all of them significant ($P<0.001$). However, carcass degree of fat cover was positively related to SFA ($r=0.53$, $P<0.001$) and MUFA ($r=0.62$, $P<0.001$), and negatively to PUFA ($r=-0.61$), n-6 ($r=-0.60$), n-3 ($r=-0.62$) and UFA ($r=-0.53$) groups, being all of them significant. Moreover, simple and low-cost prediction equations were calculated for a rapid and sufficiently accurate fatty acid group (SFA, MUFA, PUFA, n-6, n-3, UFA) estimation ($R^2>0.46$, $P<0.001$). In general, meat obtained from double-muscled animals display a more appropriate IM fatty acid profile from the nutritional point of view according to actual recommendations, but it could happen the disability of these lean animals to deposit sufficient IM fat to ensure consumer overall liking or acceptability.

Keywords: Beef; Genotype; Muscular hypertrophy; Carcass quality; Meat quality; Fatty acids

1. Introduction

In Europe, the Regulations No 1208/81 (OJEC, 1981a) and 2930/81 (OJEC, 1981b) and their amending Regulations No 1026/91 (OJEC, 1991a) and 2237/91

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(OJEC, 1991b) determine the "Community Scale for the Classification of Carcasses of Adult Bovine Animals" as the rule which standardises and gives transparency on carcass grading. This system classifies carcasses with regard to two parameters: carcass conformation and degree of fat cover. In Spain, the law (BOE, 2003) complements carcass grade described by the European Regulation establishing selling categories of beef meat regarding age and sex (veal, yearling bull, young bull or heifer, fattened bull, bullock, cow and bull). Also, retail meat cuts are officially classified in five different categories depending on the muscles involved in each cut. In other words, beef quality criteria for trades are mainly focused on those parameters directly related to carcass characteristics, and these parameters determine the economic value of beef (Horcada, 2001). That is why producers and butchers are usually more interested in carcass quality defined by a good carcass conformation, low fat level, and high proportion of desirable retail cuts. Therefore, meat price in the market is positively related to carcass conformation, but not necessarily with a good sensorial quality (Osoro et al., 2003). Nevertheless, actual consumer tends to be more concerned about meat quality and its consistency in terms of sensorial attributes (i.e., tenderness, flavour, colour), healthiness (i.e., fat quantity and quality), and safety (i.e., *Escherichia coli* O157:H7, Bovine Spongiform Encephalopathy). As a result of this, beef quality should be a combination of carcass quality plus meat quality.

If it is not the case of the European carcass grading system, the degree of marbling (visible intramuscular (IM) fat) has been corroborated to be a good criteria to evaluate meat quality in some other countries' grading systems (i.e. USDA Quality Grades in USA, MSA System in Australia). In particular, Japanese grading standards (for beef and pork) include also the quality of the fat of carcasses as an important aspect to evaluate.

Intramuscular fat, composed by marbling cells (fat cells located between bundles of muscle fibres) and fat within muscle cells (largely comprised by the lipid in cell membrane components, together with that present in vesicles as a lipid droplet) (Gandemer, 1999), firstly, influences several sensorial attributes like flavour, as lubrication effect may improve juiciness and indeed its flavour through a complex interaction between components of fat and lean, and tenderness, by reducing bulk density and decreasing the strength of the connective tissue (Wood et al., 1997). Moreover, it protects meat from drying out during cooking. Secondly, IM fat cannot be considered in isolation from its health effects and related consumer concerns and its fatty acid (FA) profile has to be taken into consideration (Mazier and Jones, 1991; Simopoulos, 1991, 2002; Ulbricht and Southgate, 1991). Many studies have shown that fat partitioning (in the sense of amount and distribution) among the depots is influenced by several factors such as breed or genotype (Callow, 1962; Wright and Russel, 1984; Huerta-Leidenz et al., 1993), sex or physiological status (Kazala et al., 1999; Malau-Aduli et al., 2000), age or live weight (Truscott et al., 1983; Rule et al., 1995), feeding (Mandell et al., 1997; Bas and Morand-Fehr, 2000) and anatomical location (Hood and Allen, 1975; Truscott et al., 1983), and that FA composition could be also influenced by the aforementioned factors and their interactions mainly related to animal's fat content (Nürnberg et al., 1998, 1999; De Smet et al., 2004).

All-in-all, and taking into account the lack of relation between the actual European beef carcass classification scale and meat quality attributes, and especially with fat quality, the aim of this study was to evaluate the reliability of carcass measurement scores taken at abattoir level (conformation and fat cover degree) to predict the FA profile of meat through several genotypes characterised with a wide range of carcass measurement scores. For this purpose FA profile of two Asturian local breeds (Asturiana de los Valles (AV) and Asturiana de la Montaña (AM)) and three genotypes of the first one depending on the presence or absence of muscular hypertrophy gene (AV(*mh/mh*), AV(*mh/+*), AV(+/+)) considered as four biological types or genotypes, were, firstly, compared.

2. Materials and methods

2.1. Animals, management and diet composition

One hundred yearling bulls from "Asturiana de los Valles" (AV, $n=75$), a beef breed adapted to extensive production systems, and "Asturiana de la Montaña" (AM, $n=25$), a beef breed characterised by small to medium-sized rustic animals adapted to less favoured mountain areas, were studied during three consecutive years (2001/03) with similar animal repartition per year. Blood sample from AV animals was analysed to determine the presence of the 11-bp deletion in the coding sequence of the myostatin gene causing double-muscling in cattle (Grobet et al., 1998) and classify animals into three groups: AV double-muscled (*mh/mh*, $n=24$), AV heterozygous (*mh/+*, $n=26$) and AV normal (+/+, $n=25$). AM animals lack the mutation responsible for double-muscling ($n=25$).

Calves were suckled by their mothers from birth (winter) to weaning (early autumn). After a postweaning adjustment period of about 15 days, they were fattened

by feeding concentrate meal (84% barley meal, 10% soya meal, 3% vegetable fat (soya oil), 3% minerals, vitamins and oligoelements) and barley straw, both *ad libitum* (typical Spanish fattening diet), in the housing facilities of the research Institute (SERIDA). Table 1 shows the chemical composition and the FA profile of the experimental concentrate meal. Determination of final dry matter and crude ashes were conducted by drying out and incineration (Van Es and Van Der Meer, 1980; Van Der Meer, 1983), crude protein was conducted by Kjeldahl method (TECATOR, 1995, 2001), crude fat was conducted by Soxhlet extraction (TECATOR, 1991), acid detergent fibre determination was conducted according to Goering and Van Soest (1970) and neutral detergent fibre was conducted according to Robertson and Van Soest (1981) and Van Soest et al. (1991). The FA profile was determined by gas–liquid chromatography based on a modification of the Elmore et al. (1999) method as outlined in Aldai et al. (2005) and validated in Aldai et al. (2006b).

2.2. Carcass measurements and sampling

Animals were slaughtered on reaching an average live weight of 542±4 kg for the AV breed and 491±6 kg for the AM breed. Slaughtering was performed in a commercial abattoir according to standard procedures. Yearling bulls were weighed twice (on the day prior to slaughter and on the day of slaughter) to get the final average live weight. After slaughtering and dressing, hot carcass weight was recorded and carcasses chilled at 3 °C. Cold carcass weight was calculated subtracting 2% to the hot carcass weight and carcass yield proportion was calculated as the relation between live weight at slaughter and cold carcass weight.

Table 1
Chemical and major fatty acid composition of the concentrate meal

	Concentrate
Chemical composition (%)[a]	
Crude protein	14.62
Crude fat	5.69
Crude ash	4.50
Acid detergent fibre	5.18
Neutral detergent fibre	16.73
Fatty acid composition (%)[b]	
C16:0	16.28
C18:0	1.75
C18:1*cis*9	13.02
C18:2n-6	60.38
C18:3n-3	6.25

[a]Values are expressed on dry matter basis.
[b]Percentage of total fatty acids quantified.

Twenty-four hours *post-mortem,* carcasses were classified by visual assessment on conformation and fat cover degree by the same trained and experienced evaluator. For conformation, development of carcass profiles, in particular the essential parts (round, back, shoulder) was taken into consideration according to EUROP classification (E: excellent, U: very good, R: good, O: fair, P: poor), and for fat cover degree the amount of fat on the outside of the carcass and in the thoracic cavity was taken into account using a classification range from 1 to 5 (1: low, 2: slight, 3: average, 4: high, 5: very high). Each level of both scales (conformation and degree of fat cover) was subdivided in 3 sub-classes (i.e. conformation: R^+, R, R^- and fat cover: 3^+, 3, 3^-) to a transformed scale ranging from 1 to 15, being 15 the best conformation and the thickest fat cover (OJEC, 1981a,b, 1991a,b).

The part of the rib joint comprised between the 6th and 8th ribs of the left half carcass was extracted by cutting the length of the bone at the limit of the *serratus dorsalis* muscle (Robelin and Geay, 1975) and transported to the laboratory. Then, the 6th rib was excised, total weight recorded, and the *longissimus thoracis* (LT) muscle separated and weighed while the rest of the rib was frozen at −20 °C until dissection. It was thawed overnight at 4 °C and dissected into lean, subcutaneous (SC) fat, intermuscular (IT) fat, and bone. Other tissues (blood vessels, ligaments, etc.) were recorded as bone. The 6th rib dissection was used as a predictor of the carcass composition (Oliván et al., 1999).

The LT steak of the 8th rib was dissected, vacuum packed and frozen at −80 °C at 24 h *post-mortem* for subsequent fat content and FA analysis.

2.3. Muscle fat content and fatty acid profile

Muscle or IM fat percentage was determined by NIRS (Oliván et al., 2002) calibrated (Pretreatment: SNV-DT, Standard error of calibration: 0.344, R^2=0.958) by reference to a Soxhlet fat extraction method (ISO 1443-1973).

For FA profile determination, duplicate 1 g muscle tissue was saponified in 6 mL 5 M KOH in methanol/water (50:50, v/v) at 60 °C for 1 h, and the extracted FAs were methylated using trimethylsilyl-diazomethane in methanol:toluene (2:1, v/v) at 40 °C for 10 min based on a modification of the method by Elmore et al. (1999) as outlined in Aldai et al. (2005) and validated in Aldai et al. (2006b).

Obtained FA methyl esters were identified according to similar peak retention times using standards (Sigma-Aldrich), and quantified using the chromatographic

peak area according to the internal standard method (free C21:0) with its addition prior to saponification. The response factors of the individual FAs were previously calculated.

Selected abbreviations: FA: fatty acid; saturated FA: SFA=C10:0+C12:0+C13:0+C14:0+C15:0+C16:0+C17:0+C18:0+C19:0+C20:0+C22:0; branched FA: BFA=*iso*C15:0+*anteiso*C15:0+*iso*C16:0+*iso*C17:0+*iso*C18:0; monounsaturated FA: MUFA=C14:1*cis*9+C16:1*cis*9+C17:1*cis*10+C18:1*trans*+C18:1*cis*9+C18:1*cis*11+C18:1*cis*12+C18:1*cis*13; polyunsaturated FA: PUFA=C18:2n-6+C18:3n-6+C20:2n-6+C20:3n-6+C20:4n-6+C22:4n-6+C18:3n-3+C20:3n-3+C20:5n-3+C22:5n-3+C22:6n-3+*cis*9,*trans*11-CLA+*trans*10,*cis*12-CLA; n-6 type of FA: n-6=C18:2n-6+C18:3n-6+C20:2n-6+C20:3n-6+C20:4n-6+C22:4n-6; n-3 type of FA: n-3=C18:3n-3+C20:3n-3+C20:5n-3+C22:5n-3+C22:6n-3; conjugated linoleic acid: CLA=*cis*9,*trans*11-CLA+*trans*10,*cis*12-CLA; unsaturated FA: UFA=MUFA+PUFA; M/S=MUFA/SFA; P/S=PUFA/SFA; U/S=UFA/SFA.

2.4. Statistical analysis

The statistical analysis was conducted using SPSS 11.5 (SPSS, Inc., 2002). ANOVA analysis was applied to study the differences on animal growth rates, carcass quality traits, rib composition, IM fat content and FA composition of muscle tissue between all animal groups as four independent genotypes or biological types: AV (*mh/mh*), AV(*mh*/+), AV(+/+) and AM. Year and genotype x year interaction were also included in the model. When analysis of variance gave significant differences between genotypes the LSD Post-Hoc test was applied (multiple comparison of means).

Correlation and multiple linear regression analysis, using stepwise as a variable adding method, were performed between carcass rapid and inexpensive measurements (conformation and degree of fat cover) and FA composition of IM fat.

Factor analysis, using principal components as an extraction method (eigenvalues over 1), was done including carcass measurements (conformation and degree of fat cover) and FA groups and ratios in the test.

3. Results

3.1. Animal growth rates, carcass measurements, rib dissection and muscle fat content

Animal fattening period, age and live weight at slaughter, carcass traits (weight, yield, conformation, fat cover degree, rib composition) and IM fat content are summarised in Table 2. Animals from AM breed showed a significantly ($P<0.001$) longer fattening period than AV animals (251.9 days *vs*. mean value of 209.4 days) with significantly ($P<0.001$) lower daily live weight gains in comparison to AV animals (1.1 kg/day *vs*. mean value of 1.4 kg/day). Moreover, AM animals were significantly ($P<0.001$) older at slaughter (519.1 days *vs*. mean value of 460.2 days) and they also recorded significantly ($P<0.001$) lighter slaughter and cold carcass weights, and consequently lower carcass yields (54.7% for AM and 63.2% for *mh/mh*). On the other hand, the other three genotypes (AV breed) did not show significant differences between them, except for carcass weight and yield as double-muscled (*mh/mh*) animals showed significantly higher values than the others. According to carcass classification measurements, AM animals obtained the lowest conformation (7.5) and the highest fat cover scores (5.4) while double-muscled animals obtained the best conformation (14.1) and the lowest fat cover score (2.3). Intermediate values were obtained by the other two genotypes.

Table 2
Least square means of growth rates, carcass quality traits, rib composition and muscle fat content for each genotype

	AV (*mh/mh*)	AV (*mh*/+)	AV (+/+)	AM	s.e.m.	Sign.
Fattening period (days)	207.58^{a}	205.58^{a}	215.19^{a}	251.86^{b}	1.866	***
Daily gain (kg/day)	1.46^{b}	1.39^{b}	1.42^{b}	1.11^{a}	0.019	***
Age at slaughter (days)	464.29^{a}	458.52^{a}	457.95^{a}	519.12^{b}	3.145	***
LWS (kg)	547.42^{b}	547.05^{b}	532.76^{b}	491.32^{a}	3.154	***
CCW (kg)	345.79^{d}	315.45^{c}	302.30^{b}	268.67^{a}	2.077	***
Carcass yield (%)	63.18^{c}	57.67^{b}	56.73^{b}	54.69^{a}	0.173	***
Conformation	14.12^{d}	10.71^{c}	9.95^{b}	7.51^{a}	0.106	***
Degree of fat cover	2.25^{a}	4.86^{b}	4.64^{b}	5.39^{c}	0.127	***
Rib composition:						
% Lean	84.36^{c}	77.29^{b}	75.56^{a}	75.31^{a}	0.280	***
% IT fat	4.89^{a}	8.71^{b}	10.12^{c}	9.84^{c}	0.185	***
% SC fat	1.10^{a}	2.24^{b}	2.36^{b}	3.18^{c}	0.073	***
% Total fat	6.00^{a}	10.95^{b}	12.48^{c}	13.01^{c}	0.233	***
% Bone	9.64^{a}	11.76^{b}	11.96^{b}	11.68^{b}	0.165	***
% IM fat	0.81^{a}	1.77^{b}	1.85^{b}	2.39^{c}	0.068	***

s.e.m.: standard error of the mean. ***: $P<0.001$; ^{a,b,c,d}Means with different superscripts are significantly different at $P<0.05$.
LWS: live weight at slaughter; CCW: cold carcass weight; IT: intermuscular; SC: subcutaneous; total fat (%)=IT fat (%)+SC fat (%); IM: intramuscular; AV: Asturiana de los Valles breed; AM: Asturiana de la Montaña breed; *mh/mh*: double-muscled; *mh*/+: heterozygous; +/+: normal.

The dissection of the 6th rib as an estimation of the carcass composition of yearling bulls, showed that *mh*/*mh* animals produced a significantly ($P<0.001$) higher lean percentage (84.4%) and lower total fat (6.0%), due to lower IT (4.9%) and SC (1.1%) fat percentages. However, AM and +/+ animals showed the lowest lean (mean value of 75.4%) and the highest total fat percentages (mean value of 12.7%), whilst *mh*/+ animals showed, in general, intermediate values (77.3% and 11.0% for lean and total fat, respectively). In all genotypes, IT fat was the greatest contributor to total fat at the dissection level. Double-muscled animals, having the highest muscular mass, showed the lowest bone percentage representing only 9.6% in comparison to the other genotypes (mean value of 11.8%). According to linear regressions, total fat (SC%+IT%) percentage of the rib dissection was negatively related to the carcass conformation score ($r=-0.68$, $P<0.001$) and positively related to the fat cover degree ($r=0.60$, $P<0.001$).

Table 3
Intramuscular individual fatty acid percentages (% of total fatty acids quantified) of *longissimus thoracis* muscle for each genotype

Σ FA (mg/100 g meat)	AV(*mh*/*mh*)	AV(*mh*/+)	AV(+/+)	AM	s.e.m.	Sign.	C	FC
	859.08[a]	1790.65[b]	1825.99[b]	2355.00[c]	68.222	***	−0.67***	0.59***
FA (%)								
C10:0	1.64E-02[a]	2.58E-02[b]	2.78E-02[b]	3.82E-02[c]	0.001	***	−0.55***	0.34***
C12:0	4.39E-02[a]	6.03E-02[b]	6.56E-02[b]	8.18E-02[c]	0.002	***	−0.56***	0.37***
C13:0	9.56E-03[a]	1.11E-02[a,b]	1.24E-02[b,c]	1.30E-02[c]	0.000	*	−0.24*	NS
C14:0	1.54[a]	2.71[b]	2.88[b]	3.46[c]	0.056	***	−0.71***	0.64***
C15:0	0.30[a]	0.42[b]	0.43[b]	0.47[c]	0.007	***	−0.59***	0.52***
C16:0	24.25[a]	28.62[b]	28.89[b]	30.85[c]	0.206	***	−0.72***	0.54***
C17:0	0.85[a]	1.12[b]	1.12[b]	1.09[b]	0.014	***	−0.43***	0.46***
C18:0	13.58	14.17	13.74	13.56	0.153	NS	NS	NS
C19:0	0.08[a]	0.12[b]	0.12[b]	0.11[b]	0.003	***	−0.21*	0.37***
C20:0	9.68E-02[b]	8.42E-02[a,b]	8.31E-02[a]	8.15E-02[a]	0.002	NS	0.23*	−0.27**
C22:0	1.85E-02[b]	1.65E-02[b]	1.50E-02[a,b]	1.05E-02[a]	0.001	*	0.29**	−0.22*
*iso*C15:0	5.71E-02[a]	7.59E-02[b]	6.28E-02[a,b]	6.83E-02[b]	0.002	**	NS	NS
*anteiso*C15:0	0.11[a]	0.14[b]	0.12[a]	0.12[a]	0.003	***	NS	NS
*iso*C16:0	0.14[b]	0.15[b]	0.13[a,b]	0.13[a]	0.003	**	0.24*	NS
*iso*C17:0	0.30[c]	0.24[b]	0.21[a]	0.19[a]	0.004	***	0.58***	−0.56***
*iso*C18:0	5.92E-02[b]	5.88E-02[b]	6.00E-02[b]	4.98E-02[a]	0.001	*	0.20*	NS
C14:1*cis*9	0.18[a]	0.32[b]	0.41[c]	0.45[c]	0.013	***	−0.55***	0.44***
C16:1*cis*9†	1.51[a]	2.47[b]	2.38[b]	2.81[c]	0.045	***	−0.71***	0.57***
C17:1*cis*10	0.39[a]	0.56[b]	0.64[c]	0.65[c]	0.011	***	−0.60***	0.46***
C18:1*trans*‡	5.74[b]	5.33[a,b]	5.66[b]	4.18[a]	0.207	*	0.25*	NS
C18:1*cis*9	14.56[a]	21.89[b]	22.36[b,c]	23.90[c]	0.305	***	−0.74***	0.58***
C18:1*cis*11	2.93[a,b]	3.08[b]	2.97[a,b]	2.79[a]	0.036	*	NS	NS
C18:1*cis*12	0.85[a]	1.03[b]	0.96[b]	1.00[b]	0.022	*	NS	0.28**
C18:1*cis*13	0.23[a]	0.30[b]	0.33[b]	0.31[b]	0.006	***	−0.41***	0.46***
C18:2n-6	23.70[c]	12.40[b]	11.72[a,b]	9.86[a]	0.440	***	0.72***	−0.60***
C18:3n-6	0.38[b]	0.14[a]	0.19[a]	0.14[a]	0.010	***	0.48***	−0.47***
C20:2n-6	0.19[c]	0.10[a,b]	0.12[b]	0.08[a]	0.004	***	0.66***	−0.53***
C20:3n-6	1.16[b]	0.52[a]	0.52[a]	0.40[a]	0.024	***	0.70***	−0.61***
C20:4n-6	3.53[b]	1.80[a]	1.81[a]	1.46[a]	0.076	***	0.67***	−0.58***
C22:4n-6	0.49[b]	0.27[a]	0.26[a]	0.24[a]	0.011	***	0.62***	−0.56***
C18:3n-3	0.96[c]	0.79[b]	0.75[b]	0.66[a]	0.011	***	0.61***	−0.57***
C20:3n-3	8.02E-03[b]	7.55E-03[a,b]	5.91E-03[a,b]	5.48E-03[a]	0.000	NS	NS	NS
C20:5n-3	0.47[c]	0.23[b]	0.22[b]	0.14[a]	0.011	***	0.68***	−0.57***
C22:5n-3	0.99[c]	0.47[b]	0.48[b]	0.35[a]	0.020	***	0.70***	−0.60***
C22:6n-3	8.36E-02[c]	3.60E-02[b]	4.05E-02[b]	2.15E-02[a]	0.002	***	0.71***	−0.55***
*cis*9,*trans*11-CLA	0.16[a]	0.23[b]	0.19[a,b]	0.20[a,b]	0.008	*	−0.20*	0.22*
*trans*10,*cis*12-CLA	3.06E-02[b]	1.95E-02[a]	2.33E-02[a,b]	2.12E-02[a]	0.001	*	0.22*	NS

Correlation coefficients (r) between carcass measurements (conformation and degree of fat cover) and fatty acids.
s.e.m.: standard error of the mean. *:$P<0.05$; **: $P<0.01$; ***:$P<0.001$; NS:$P>0.05$. [a,b,c]Means within a row with different superscripts are significantly different at $P<0.05$.
AV: Asturiana de los Valles breed; AM: Asturiana de la Montaña breed; *mh*/*mh*: double-muscled; *mh*/+: heterozygous; +/+: normal; C: conformation; FC: degree of fat cover; †: coelution with *anteiso*C17:0; ‡: coelution of several *trans* isomers; CLA=conjugated linoleic acid.

The genotype or biological type affected significantly ($P<0.001$) the IM fat content (%) of LT muscle where AM animals showed the highest fat content (2.40%) and double-muscled animals the lowest (0.81%), while the other genotypes (*mh*/+ and +/+) showed intermediate contents (mean value of 1.81%).

3.2. Muscle fatty acid profile

Meat FA profile, expressed as % of total FAs quantified (g/100 g of total FAs) and organised as individuals in Table 3, and groups and ratios in Table 4, is presented for each genotype. In general, and for all genotypes, only four were the FAs which showed larger proportions than 10% (C16:0, C18:0, C18:1*cis*9, C18:2n-6) which represented around 77% of the total FAs. Another six were the FAs which showed proportions between 1% and 10% (C14:0, C17:0, C16:1*cis*9, C18:1*trans*, C18:1*cis*11, C20:4n-6) and represented 16% of the total FAs. The rest of the FAs were considered minor FAs as they represented individually lower proportions than 1% of the total FAs.

Significant ($P<0.05$) differences due to the genotype were observed in 89% of the individual (major and minor) FAs (Table 3). Considered FA groups (SFA, BFA, MUFA, PUFA, n-6, n-3, UFA) and ratios (M/S, P/S, U/S, n-6/n-3) showed significant ($P<0.001$) differences due to the genotype effect, except for CLA group (Table 4). Generally, double-muscled animals showed the lowest individual and total SFA percentages (40.8%), while AM animals had the highest values (49.8%). The other two genotypes (*mh*/+, +/+) showed intermediate levels (mean value of 47.4%). However, no significant differences between biological types were found for C18:0, being this one of the major FA.

Significant differences were found between genotypes for BFA individuals and group, where they seemed to be higher in leaner animals, except for *iso*C15:0, showing an opposite trend, and *anteiso*C15:0, not showing any clear trend.

In double-muscled animals, total MUFA percentage was significantly ($P<0.001$) lower (26.4%) than in the other genotypes (mean value of 35.6%). When comparing MUFAs individually, double-muscled animals showed, in general, lower percentages in FAs with less than 18 carbon atoms. Normal and AM animals presented the highest percentages, while *mh*/+ animals showed intermediate values. The C16:1*cis*9 and *anteiso*C17:0 were reported together as we could not separate them probably because of the higher proportion of C16:1*cis*9 in comparison to *anteiso*C17:0 in beef muscle fat. Similar trend was observed for FAs composed by 18 carbon atoms where double muscled animals showed the lowest percentages in comparison to other biological types which had similar values. However, opposite effect was found for C18:1*trans* (*trans* group value was reported as this column incompletely resolved them, and we could not exclude some minor contamination

Table 4
Intramuscular fatty acid group percentages (% of total fatty acids quantified) and ratios of longissimus thoracis muscle for each genotype

	AV(*mh*/*mh*)	AV(*mh*/+)	AV(+/+)	AM	s.e.m.	Sign.	C	FC
SFA	40.79^{a}	47.35^{b}	47.38^{b}	49.76^{c}	0.310	***	−0.69***	0.53***
BFA	0.67^{b}	0.66^{b}	0.58^{a}	0.56^{a}	0.009	***	0.33***	−0.28**
MUFA	26.39^{a}	34.98^{b}	35.71^{b}	36.10^{b}	0.339	***	−0.69***	0.62***
PUFA	32.16^{c}	17.01^{b}	16.33^{ab}	13.58^{a}	0.579	***	0.72***	−0.61***
n-6	29.45^{b}	15.24^{a}	14.62^{a}	12.18^{a}	0.549	***	0.72***	−0.60***
n-3	2.51^{c}	1.53^{b}	1.49^{b}	1.18^{a}	0.040	***	0.71***	−0.62***
UFA	58.54^{c}	51.99^{b}	52.04^{b}	49.68^{a}	0.310	***	0.69***	−0.53***
CLA	0.20	0.25	0.21	0.22	0.008	NS	NS	NS
M/S	0.65^{a}	0.74^{b}	0.75^{b}	0.72^{b}	0.006	***	−0.44***	0.48***
P/S	0.81^{b}	0.36^{a}	0.35^{a}	0.28^{a}	0.018	***	0.70***	−0.58***
U/S	1.46^{c}	1.10^{b}	1.11^{b}	1.00^{a}	0.017	***	0.67***	−0.52***
n-6/n-3	11.79^{b}	10.05^{a}	9.68^{a}	10.17^{a}	0.190	***	0.34***	−0.30**

Correlation coefficients (r) between carcass measurements (conformation and degree of fat cover) and FAs groups and ratios.
s.e.m.: standard error of the mean. **:$P<0.01$; ***:$P<0.001$; NS:$P>0.05$. ^{a,b,c}Means within a row with different superscripts are significantly different at $P<0.05$.
SFA=C10:0+C12:0+C13:0+C14:0+C15:0+C16:0+C17:0+C18:0+C19:0+C20:0+C22:0; BFA=*iso*C15:0+*anteiso*C15:0+*iso*C16:0+*iso*C17:0+*iso*C18:0; MUFA=C14:1*cis*9+C16:1*cis*9+C17:1*cis*10+C18:1*trans*+C18:1*cis*9+C18:1*cis*11+C18:1*cis*12+C18:1*cis*13; PUFA=C18:2n-6+C18:3n-6+C20:2n-6+C20:3n-6+C20:4n-6+C22:4n-6+C18:3n-3+C20:3n-3+C20:5n-3+C22:5n-3+C22:6n-3+*cis*9,*trans*11-CLA+*trans*10,*cis*12-CLA; n-6=C18:2n-6+C18:3n-6+C20:2n-6+C20:3n-6+C20:4n-6+C22:4n-6; n-3=C18:3n-3+C20:3n-3+C20:5n-3+C22:5n-3+C22:6n-3; UFA=MUFA+PUFA; CLA=*cis*9,*trans*11-CLA+*trans*10,*cis*12-CLA; CLA=conjugated linoleic acid; M/S=MUFA/SFA; P/S=PUFA/SFA; U/S=UFA/SFA; AV: Asturiana de los Valles breed; AM: Asturiana de la Montaña breed; *mh*/*mh*: double-muscled; *mh*/+: heterozygous; +/+: normal; C: conformation; FC: degree of fat cover.

with other C18:1*trans* isomers) where its content in meat of AM animals was significantly lower than in other genotypes except for *mh*/+ group.

Concerning total PUFA, n-3 and UFA percentages similar trend was observed. Double-muscled animals presented the highest values (32.2%, 2.5%, 58.5%) and AM animals the lowest (13.6%, 1.2%, 49.7%), while the other genotypes (*mh*/+, +/+) showed intermediate contents (mean values of 16.7%, 1.5% and 52% for PUFA, n-3 and UFA, respectively). When the n-6 group was analysed, the highest percentage was observed in double-muscled animals (29.4%) while lower values were found in the other genotypes (mean value of 14.0%). Individually, n-3 and n-6 type of FAs, showed similar tendency to their main groups, but have been observed some exceptions.

The *cis*9,*trans*11 and *trans*10,*cis*12 were the reported CLA isomers. Significant ($P<0.05$) differences were found between genotypes and double-muscled animals presented the lowest *cis*9,*trans*11-CLA and the highest *trans*10,*cis*12-CLA percentages in comparison to the other three genotypes (Table 3).

Referring to FA group ratios, similar and high M/S values (mean value of 0.74) were observed in *mh*/+, +/+ and AM animals while double-muscled animals had lower values (0.65). Opposite effect was found for P/S and n-6/n-3 ratios where double-muscled animals showed the highest values (0.81 and 11.8 for P/S and n-6/n-3, respectively) while in the other three genotypes lower values (mean values of 0.33 and 10.0 for P/S and n-6/n-3, respectively) were observed. For U/S ratio, the highest ratio happened in double-muscled animals (1.5) and the lowest in AM animals (1.0), while intermediate values were found in the other two genotypes (mean value of 1.1) (Table 4).

3.2.1. Relationship between carcass measurements and muscle fatty acid profile

Since independent genotypes did not show any significant relationship between carcass measurements and FAs (individuals, groups, ratios), all genotypes were grouped and analysed together. Correlation analysis between carcass rapid measurements (conformation and degree of fat cover) and meat FA profile are summarised in Tables 3 and 4.

IM fat content (%) (Table 2) was negatively related to the carcass conformation ($r=-0.65$, $P<0.001$) while positively to the degree of fat cover ($r=0.60$, $P<0.001$). Between carcass conformation score and SFA ($r=-0.69$) and MUFA ($r=-0.69$) groups negative ($P<0.001$) correlations were found. And, in general, the same trend was observed for individual FAs of these groups with some exceptions. C18:0 was one the major FA which showed no correlation with conformation score. On the other hand, positive correlations ($P<0.001$) were found between carcass conformation scores and PUFA ($r=0.72$), n-6 ($r=0.72$), n-3 ($r=0.71$) and UFA ($r=0.69$) groups. In general, similar trend was observed for individual FAs of the same groups, except for C20:3n-3 which had no correlation with conformation score. Moreover, CLA isomers showed low correlations (negative for *cis*9,*trans*11-CLA and positive for *trans*10,*cis*12-CLA isomer). According to FA group ratios, positive ($P<0.001$) correlations were found between conformation scores and P/S ($r=0.70$) and U/S ($r=0.67$).

Referring to carcass degree of fat cover, positive correlations ($P<0.001$) were observed between this score and SFA ($r=0.53$) and MUFA ($r=0.62$) groups. In general, the same tendency was observed for individual SFA with some exceptions. Again, C18:0 was one of the

Table 5
Estimated linear regression equations

Equation	R^2	Sign.	s.e.
$SFA(\%) = -1.19_{(0.13)}C + 58.88_{(1.36)}$	0.479	***	3.23
$BFA(\%) = 0.01_{(0.004)}C + 0.47_{(0.05)}$	0.107	***	0.11
$MUFA(\%) = -0.97_{(0.18)}C + 0.90_{(0.26)}FC + 39.76_{(2.70)}$	0.535	***	3.53
$PUFA(\%) = 1.98_{(0.30)}C - 1.30_{(0.44)}FC + 4.43_{(4.64)}$	0.564	***	6.06
$n-6(\%) = 1.85_{(0.28)}C - 1.21_{(0.42)}FC + 3.50_{(4.40)}$	0.556	***	5.75
$n-3(\%) = 0.13_{(0.02)}C - 0.10_{(0.03)}FC + 0.72_{(0.33)}$	0.552	***	0.43
$UFA(\%) = 1.17_{(0.13)}C + 40.66_{(1.36)}$	0.470	***	3.25

R^2: coefficient of determination; s.e.: standard error of the estimate; values in parentheses are standard errors of the coefficients; ***:$P<0.001$. SFA=C10:0+C12:0+C13:0+C14:0+C15:0+C16:0+C17:0+C18:0+C19:0+C20:0+C22:0; BFA=*iso*C15:0+*anteiso*C15:0+*iso*C16:0+*iso*C17:0 + *iso*C18:0; MUFA=C14:1*cis*9+C16:1*cis*9+C17:1*cis*10+C18:1*trans*+C18:1*cis*9+C18:1*cis*11+C18:1*cis*12+C18:1*cis*13; PUFA=C18:2n-6+C18:3n-6+C20:2n-6+C20:3n-6+C20:4n-6+C22:4n-6+C18:3n-3+C20:3n-3+C20:5n-3+C22:5n-3+C22:6n-3+*cis*9,*trans*11-CLA+*trans*10,*cis*12-CLA; n-6=C18:2n-6+C18:3n-6+C20:2n-6+C20:3n-6+C20:4n-6+C22:4n-6; n-3=C18:3n-3+C20:3n-3+C20:5n-3+C22:5n-3+C22:6n-3; UFA=MUFA+PUFA; C: conformation; FC: degree of fat cover.

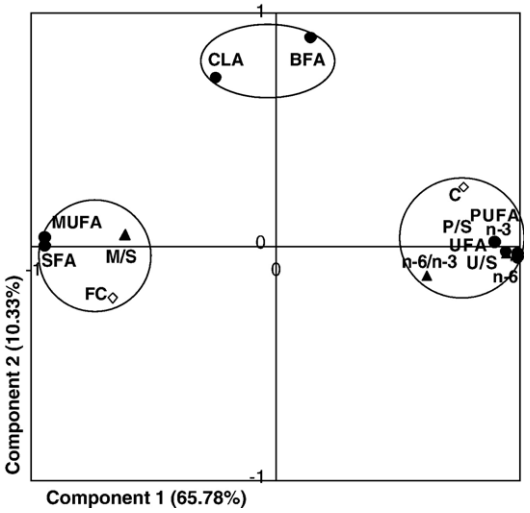

Fig. 1. Loading plot of the variables (fatty acid groups and ratios, and carcass measurement scores) included in the Principal Component Analysis. SFA = C10:0 + C12:0 + C13:0 + C14:0 + C15:0 + C16:0 + C17:0 + C18:0 + C19:0 + C20:0 + C22:0; BFA = *iso*C15:0 + *antei-so*C15:0 + *iso*C16:0 + *iso*C17:0 + *iso*C18:0; MUFA = C14:1*cis*9 + C16:1*cis*9 + C17:1*cis*10 + C18:1*trans* + C18:1*cis*9 + C18:1*cis*11 + C18:1*cis*12 + C18:1*cis*13; PUFA = C18:2n-6 + C18:3n-6 + C20:2n-6 + C20:3n-6 + C20:4n-6 + C22:4n-6 + C18:3n-3 + C20:3n-3 + C20:5n-3 + C22:5n-3 + C22:6n-3 + *cis*9,*trans*11-CLA + *trans*10,*cis*12-CLA; n-6 = C18:2n-6 + C18:3n-6 + C20:2n-6 + C20:3n-6 + C20:4n-6 + C22:4n-6; n-3 = C18:3n-3 + C20:3n-3 + C20:5n-3 + C22:5n-3 + C22:6n-3; UFA = MUFA + PUFA; CLA = *cis*9,*trans*11-CLA + *trans*10,*cis*12-CLA; CLA = conjugated linoleic acid; M/S = MUFA/SFA; P/S = PUFA/SFA; U/S = UFA/SFA; C: conformation; FC: degree of fat cover.

major FA which showed no correlation, while C16:0 and C14:0 were the FAs which mainly followed the observed correlation. In MUFA group, on the other hand, C16:1*cis*9 and C18:1*cis*9 were the FAs which mainly influenced the observed correlation. However, negative correlations ($P<0.001$) were found between fat cover score and PUFA ($r=-0.61$), n-6 ($r=-0.60$), n-3 ($r=-0.62$) and UFA ($r=-0.53$) groups. In general, the same trend was observed for individual FAs except for C20:3n-3, which again did not show any correlation, and CLA isomers where *cis*9,*trans*11 isomer showed a low but positive correlation while *trans*10,*cis*12 had no correlation. According to FA group ratios, negative ($P<0.001$) correlation was found between fat cover degree score and P/S ($r=-0.58$) and U/S ($r=-0.52$). Neither carcass conformation nor fat cover degree scores showed strong correlations with BFA (individuals or group) except for *iso*C17:0 ($r=0.58$ for conformation and $r=-0.56$ for fat cover degree scores, $P<0.001$).

Trying to predict muscle FA group proportions, linear equations were estimated from carcass conformation and fat cover degree scores (predictor variables) (Table 5). Simple regression equations ($P<0.001$), with conformation score as an independent variable, were obtained to predict SFA ($R^2=0.48$) and UFA ($R^2=0.69$) proportions. While multiple regression equations ($P<0.001$), with carcass conformation and fat cover degree scores as independent variables, were obtained to predict MUFA ($R^2=0.54$), PUFA ($R^2=0.56$), n-6 ($R^2=0.56$) and n-3 ($R^2=0.55$) contents. In this sense, although conformation and fat cover degree scores were significantly correlated, multiple regressions, including both variables, improved the prediction of MUFA, PUFA, n-6 and n-3 groups. In contrast, equation with very poor coefficient of determination was obtained for BFA, and no significant regression was found for CLA proportion. To ensure the prediction capacity of the estimated equations (Table 5) cross validation of them was carried out. From the total amount of samples in this study ($N=100$), a sub-sample ($n=80$) was taken at random and new prediction equations were calculated for each FA group (SFA, BFA, MUFA, PUFA, n-6, n-3, UFA). Then, with the rest of the samples not included in the prediction step ($n=20$) obtained equations were checked. The outlined procedure was repeated twice and, in general, the percentage of accuracy obtained was of 75% or higher for all FA groups in both repetitions. According to this verification, the estimated equations from carcass conformation and fat cover degree scores could be useful to predict main muscle FA group contents (%).

3.3. Principal component analysis

Principal Component Analysis (PCA) was carried out including carcass measurements (conformation and fat

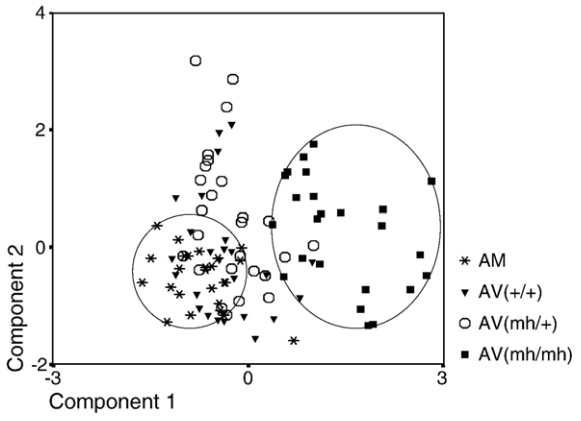

Fig. 2. Plot of the samples analysed in function of the obtained data from Principal Component Analysis. AV: Asturiana de los Valles; AM: Asturiana de la Montaña; mh/mh: double-muscled; mh/+: heterozygous; +/+: normal.

cover degree scores) and FA groups and ratios as study variables. There were obtained three principal components which explained the 84.16% of the variability found among samples. Fig. 1 shows the loading plot, using the first two components, where aforementioned variables are represented. Component 1 explained the 65.78% of the variability and it was positively defined by polyunsaturated groups and ratios (PUFA, UFA, n-6, n-3, P/S, U/S, n-6/n-3) and carcass conformation score, but negatively defined by more saturated groups and ratios (SFA, MUFA, M/S) and carcass fat cover degree score. Component 2 explained the 10.33% of the variance, showing high values for minor and rumenic FAs (CLA, BFA). In Fig. 2, sample representation on the first two components obtained in the PCA is shown, and thus, the reliability of using muscle FA profile and carcass measurement scores to allocate genotypes (or different samples). Double-muscled animals were quite well separated from the rest of the genotypes and thus related to highly unsaturated FAs (groups and ratios) and to conformation score. However, high dispersion was observed for this group. In contrary, AM animals appeared forming an homogeneous group and they were mainly related to SFA, MUFA, M/S and fat cover degree score as it was previously seen in correlation data. Normal animals tended to locate near AM, having a quite similar FA profile, while *mh*/+ or heterozygous animals were characterised by high dispersion due to the high heterogeneity within this group, and they were located in the intermediate area between AM and *mh/mh* genotypes.

4. Discussion

Animal growth performance, according to a lower live weight gains, was inferior in AM animals in comparison to the other genotypes studied, probably due to the rusticity of these animals, and this was also reflected in lower live and carcass weights. Moreover, AM animals obtained the lowest conformation and the highest fat cover degree scores in agreement with earlier studies comparing AV and AM breeds (Martínez et al., 2003) and with other Spanish and European breeds (Piedrafita et al., 2003). Double-muscled cattle are, in general, characterised by a better feed conversion and higher energetic efficiency of protein deposition and less efficient fat deposition compared to other animal groups as was found by Demeyer et al. (1995). Consequently, double muscling character produced a significant increase in carcass conformation, and a significant decrease in fat cover scores and fineness of bones as widely reported in Belgian Blue (Bouton et al., 1982; Uytterhaegen et al., 1994; Arthur, 1995; Nürnberg et al., 1999), Piedmontese (Wheeler et al., 2001; Biagini and Lazzaroni, 2005) and AV breeds (Martínez et al., 2003; Oliván et al., 2004). As reported in earlier studies (Martínez et al., 2003; Aldai et al., 2006a), the lower fat cover degree of *mh/mh* animals was also reflected in the dissection of the 6th rib which showed significantly higher lean and lower total, IT and SC fat proportions. Moreover, they presented the lowest IM fat proportion in comparison to the other genotypes (*mh*/+, +/+, AM) probably caused by the reduced production of adipocytes and the reduced fat cell diameter as found by Nürnberg et al. (1999) in Belgian Blue animals. Whilst a completely opposite pattern was followed by AM breed, being these the fattiest animals.

According to previous works (Eichhorn et al., 1985; Nürnberg et al., 1999), breed affects the composition of fat tissue mainly through its effect on total fat content. In this sense, the lowest percentages of SFA and MUFA, and the highest proportions of PUFA and UFA were observed in meat from the leanest animals (*mh/mh*), and the opposite effect was found in the fattest animals (AM) corresponding with previous works with animals fed on just concentrate (Nürnberg et al., 1999; Raes et al., 2001; Aldai et al., 2006a) or a high concentrate ration (Purchas et al., 2005). On the other hand, *mh*/+ and +/+ animals, having an intermediate IM fat content, showed medium SFA, PUFA and UFA percentages but high proportion of MUFA as happened in the fattiest animals (AM). The higher IM fat content of yearling bulls of AM breed compared to *mh/mh* was mainly due to a higher absolute contents of SFA and MUFA, while the absolute PUFA content was constant through all the genotypes (mean value of 273 mg/100 g muscle, $P>0.05$). These variations on the major FA groups could be related to the heterogeneous composition of IM fat, containing mainly triglycerides in adipocytes (between bundles of fibres) and muscular cells (as lipid droplets), and polar lipids, mainly phospholipids, in the membrane structures of both cell types where lower fat content reflects fewer and smaller adipocytes, containing fewer triglycerides, accompanied by a relative increase in the proportion of phospholipids and an increased PUFA content (Nürnberg et al., 1999; Laborde et al., 2001; Raes et al., 2003). Differences observed in FA groups of lean and fatty animals were fairly well reflected in the correlations carried out with carcass measurement scores (Tables 3 and 4). In general, the conformation score obtained better correlations with muscle FAs than the fat cover degree score did. Carcass measurements are related to animal muscle development, and in general, muscle development is negatively related to animal fatness and thus, to

fat cover degree score (Piedrafita et al., 2003). In this sense, the better muscle development and carcass conformation were, the lower fat content was, being also reflected in the muscle FA composition (Raes et al., 2003; De Smet et al., 2004). Animal carcass conformation was positively correlated with unsaturated groups (PUFA, n-6, n-3, UFA), and negatively with SFA and MUFA as reported by Clinquart et al. (1991, 1994). While degree of fat cover showed positive correlations with SFA and MUFA, and negative correlations with unsaturated groups (PUFA, n-6, n-3, UFA), also found by Lo Fiego et al. (2005) in pigs from different genotypes and Kosulwat et al. (2003) in lambs from different carcass classification scores.

For many years, reducing carcass fatness has been one of the major breeding goals in beef cattle. Fat deposition is highly heritable and, depending on the emphasis that is put on this trait relative to other selection traits, breeds and animals within breeds may strongly differ in their mean carcass and meat fat content (Marschall, 1999). In AV breed, double-muscled gene is an heritable major gene which correlates negatively with carcass fatness and IM fat content, and positively with meat yield. In contrast, differences in maturity, age and/or live weight at slaughter contribute to differences in fatness, whereas AM breed being an early-maturing and rustic biological type have low meat yield but high IM fat content. Due to the high phenotypical heterogeneity, *mh*/+ animals were distributed between lean and fatty genotypes.

Concerning n-6 and n-3 FAs, these appeared in significantly higher proportions in double-muscled animal tissue than in the other genotypes, and they were positively correlated with carcass conformation and negatively with fat cover degree scores as was observed by Kosulwat et al. (2003) between fatness score and FA profile in lamb, and by Lo Fiego et al. (2005) between backfat thickness and FA profile in pork.

The major FA of n-6 group, C18:2n-6 percentage, was significantly ($P<0.001$) higher in double-muscled animals (23.7%) than in AM animals (9.9%), while the other two genotypes (*mh*/+, +/+) showed intermediate percentages (mean value of 12.1%). On the other hand, no significant differences between genotypes were found when comparing absolute contents (mean value of 198.3 mg/100 g muscle, $P>0.05$). In this sense, the high percentage of C18:2n-6 found in animals with double muscling character in comparison to the other genotypes seemed to be related to the lower total IM fat content. The low proportions of this FA were also found in other studies carried out with intensively fed Belgian Blue (Raes et al., 2001) and German Simmental (Nürnberg et al., 2005) bulls of 600–650 kg live weight at slaughter.

Referring to minor FA groups of muscle tissue, BFAs, which are of microbial origin (predominantly bacterial), made up an average value of 0.62% in IM fat. Similar values were obtained by Rule et al. (2002) in concentrate fed beef cattle and Wolff (1995) and Leth et al. (1998) in different retail cuts. Nevertheless, Duncan and Garton (1978) and Bas and Morand-Fehr (2000) found that BFAs of bacterial origin could make up from 1 to 3% of carcass lipids in ruminants. Odd-chain and BFA in meat and milk have been considered tools for characterising rumen bacterial populations while these are influenced by feeding strategies (Dewhurst et al., 2002; Vlaeminck et al., 2002). In this study, concentrate meal was equal for all animals within the experimental design, what makes probable that differences in BFA percentages between animal groups could be related to the genotype and, consequently, to the total muscle fat content. However, poor relationships were found between carcass measurements and these FAs (BFA) decreasing their predictability using carcass scores measured at abattoir level.

The average value of total CLA percentage found in muscle fat was 0.22%. The reported isomers were *cis*9, *trans*11 and *trans*10,*cis*12 as these are considered the major isomers in ruminant products (Dehority, 2003). Content of *trans*10,*cis*12-CLA was much lower than *cis*9,*trans*11-CLA in muscle tissue examined as found in other studies (Chin et al., 1992; Mossoba et al., 1999). Double-muscled animals showed the lowest *cis*9, *trans*11-CLA percentage in comparison to the other genotypes, probably because its content was positively related to the fat content, and hence with variation in the neutral lipid fraction (Kazala et al., 1999; Raes et al., 2001). Moreover, in animal tissues, it is known that *cis*9,*trans*11-CLA isomer can be also synthesised endogenously from C18:1*trans*11. The enzyme responsible for the conversion of C18:1*trans*11 into *cis*9, *trans*11-CLA is Δ9-desaturase (Chang et al., 1992; Palmquist and Santora, 1999; Griinari et al., 2000; Corl et al., 2001) and its activity can be enhanced or inhibited depending on breed or genotype. The higher fat content and the possible higher desaturase activity in fatty animals, as found by Siebert et al. (2003), could help to explain the higher *cis*9,*trans*11-CLA content in these animals in comparison to lean animals. However, the general low content of *cis*9,tran11-CLA in muscle tissue (half of that observed by other authors (Nürnberg et al., 2002; Rule et al., 2002)) with the employment of concentrate fairly rich in linoleic acid (C18:2n-6) in the current study (Table 1) could have been due to the low

production of C18:1*trans*11 in the rumen and/or decreased activity of Δ9-desaturase (Hristov et al., 2005). In contrast with our previous work with a lower number of animals (Aldai et al., 2006a), in the present work we have found a linear correlation between C18:1*trans* and *cis*9,*trans*11-CLA in absolute basis (mg/100 g of muscle) ($r=0.46$, $P<0.001$) as seen in some other studies (Enser et al., 1999; Lawless et al., 1999). Probably the influence of *trans* isomers other than C18:1*trans*11 could have interfered in the low correlation value (but significant) obtained since the C18:1*trans* isomers could not be separated. Hristov et al. (2005) found greater deposition of C18:1*trans*10 than C18:1*trans*11 in muscle tissue when employing linoleic acid-rich oil in concentrate meal of cattle. Furthermore, the content of C18:1*trans* obtained (percentage or absolute basis) in our study, was much higher than values obtained in some other studies with animals fed on concentrate (Raes et al., 2001; Nürnberg et al., 2002, 2005; Rule et al., 2002). The reason for the high content of C18:1*trans* was not clear. It seemed that a considerable amount of PUFA (mainly C18:2n-6 as major FA) could have been converted to *cis*9,*trans*11-CLA as first intermediate, and to C18:1*trans*11 as next intermediate in rumen environment (Harfoot and Hazlewood, 1997; Demeyer and Doreau, 1999), or to *trans*10,*cis*12-CLA as first and to C18:1*trans*10 as next intermediate also found in animals fed on high-concentrate diets (Piperova et al., 2002) or vegetable oil-rich concentrate diets (Griinari et al., 1998). And that intestinal absorption of C18:1*trans* could have been high reflecting the high C18:1*trans* content of muscle fat (Table 3).

On the other hand, *trans*10,*cis*12-CLA isomer appeared in lower content, and it was significantly ($P<0.05$) higher in double-muscled animals than in the other animal groups. Low correlations were found between CLA individual isomers and carcass measurements. CLA and BFA, both considered minor groups as they represented individually less than 1% of total FAs, were positively related to the component 2 of the PCA (Fig. 1). Therefore, this component seemed to be related to the origin of muscle FAs as BFA and CLA are of rumen origin (biosynthesis).

Concerning ratios of nutritional interest, M/S, P/S, U/S and n-6/n-3 were calculated (Table 4). The influence of genotype on the nutritional value of muscle lipid fraction was evidenced in the results. In general, double-muscled animals, being very lean, nearly approached the current recommendations for P/S initially established on 0.45 or higher, and actually, in 1 (reviewed in Simopoulos, 2002), while the other genotypes did not reach the recommendations. The values obtained in AV genotypes (*mh/mh*, *mh/+*, *+/+*) were similar to values obtained in some other studies with Belgian Blue breed and its genotypes (Raes et al., 2001; De Smet et al., 2004). Referring to M/S and U/S ratios, our animals showed, in general, similar values to other studies (Raes et al., 2001). However, higher M/S values are obtained in works carried out with highly fatty breeds (Kazala et al., 1999; Yang et al., 1999; Elías Calles et al., 2000).

The obtained n-6/n-3 ratios were quite high for every biological type, particularly double-muscled animals, showed ratios around 2.5-fold the current recommendation set closed to 4 (Department of Health, 1994; reviewed in Simopoulos, 2002). However, similar high values were obtained in some other studies carried out with German Simmental bulls and German Holstein steers fed on concentrate (Nürnberg et al., 2002). N-6/n-3 ratio of the total lipid fraction of muscle may vary depending on the n-6/n-3 ratio of the phospholipid and triacylglycerol fractions though this ratio is much more affected by feeding regimes of animals than by genetics (Enser et al., 1996; Itoh et al., 1999), and thus, it could be related to the high n-6 content of the concentrate meal given to these animals (60.4% C18:2n-6). In this sense, the n-6/n-3 ratio obtained in our animals (grain fed domestic beef) is another evidence of the increase of n-6/n-3 ratio in the food supply of industrialised societies occurred over the last years (reviewed in Simopoulos, 2002).

The obtained prediction equations offer an inexpensive and useful method to assess the FA profile in muscle tissue using carcass conformation and fat cover degree scores as independent variables, and with an acceptable accuracy level for main FA groups. In this sense, we could not find any other studies where these type of equations was examined.

5. Conclusion

The results of the study show that breed or genotype affect carcass measurement scores and muscle fatty acid profile through its important effect on animal overall fatness. Homozygous double-muscled animals produce carcasses with high conformation and low IM fat content, with high PUFA proportion. While early-maturing and rustic AM animals produce low yield and high IM fat content, with high SFA and MUFA proportions. Mostly explained by the genotype, it is noteworthy the relationship between carcass measurements and fat quantity and quality, and its practical application using simple and low-cost prediction equations for a rapid and sufficiently accurate main FA group estimation at abattoir level in yearling bulls of Asturian local biological types.

In general, meat obtained from double-muscled animals display a more appropriate IM fatty acid profile from the nutritional point of view according to actual recommendations, but it could happen the disability of these lean animals to deposit sufficient IM fat to ensure consumer acceptability regarding to other sensorial attributes as flavour and tenderness.

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