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Intramuscular fat and fatty acid profile of muscle of lambs finished in irrigated pasture

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The aim of this research was to study the differences between breeds through the analyses of the intramuscular fat content and fatty acid profile of the main local hair sheep breeds of Brazil, Morada Nova (MO), Brazilian Somali (SO) and Santa Inês (SI) and the crossbred ½ Dorper × ½ Morada Nova (F1). Genetic group was a significant source of variation for intramuscular fat content, individual fatty acids, polyunsaturated fatty acid (PUFA)/saturated fatty acid (SFA) ratio, total PUFA, essential fatty acids (EFA), total n-3 and n-6 PUFA and Δ9 desaturase and atherogenic index. MO breed presented the highest values of conjugated linoleic acid, PUFA (similar to F1) and PUFA/SFA (similar to F1). MO meat had the highest proportion of EFA, despite the value was similar to F1. SO breed showed highest proportion of myristc, pentadecanoic, palmitic and palmitoleic acids in muscle, and highest Δ9 desaturase indices. In conclusion, there are differences between genetic group for the profile of fatty acids and intramuscular fat. The meat from MO lambs had better attributes of fatty acid composition with higher PUFA, PUFA/SFA ratio, EFA and total n-3 PUFA.

Keywords: CLA; desaturase; hair sheep; lipids; meat quality

1. Introduction

Sheep meat is an important source of protein in the diet of the population of all states of Brazil, mainly for local populations in the north-east and midwest regions. However, meat from ruminants has high content of saturated fatty acids (SFAs), which has been implicated in diseases (Wood et al. 2003). However, researches carried out during the last few years have revealed that not only the amount of fat but also its profile should be taken account, as other nutritional benefits of the consumption of ruminant meat which has good levels of conjugated linoleic acid (CLA). CLA participates in various metabolic processes and is beneficial to human health.

In Brazil, in general, the researches on meat quality (intramuscular fat content and fatty acid composition) of sheep have been performed with animals finished under feedlot, considering mainly the nutrition as a source of variation affecting these traits (Madruga et al. 2006, 2008; Costa et al. 2009; Landim et al. 2011). However, the base system for the sheep industry in the north-east of Brazil is the pasture, either native or cultivated, and the great diversity of animal genotypes available in the region also indicates the possibility of differences of these traits in these genotypes.

The north-eastern region of Brazil has around 54% of the population of sheep of the country (14 million, IBGE 2006), and these are almost entirely of hair sheep. The main genotypes available in this region are the local breeds of hair sheep: Morada Nova (MO), Santa Inês (SI) and Brazilian Somali (SO). These breeds show differences in size at birth, as well different patterns of development and muscle growth. The SI breed is commonly used in cross-breeding as maternal breed in all regions of Brazil. SO and MO are important genetic resources and are characterised by small body size and slow growth when compared with SI. Currently, the breeders have used these local breeds with Dorper breed (introduced into Brazil from South Africa) in terminal crossings with the objective to obtain lambs with rapid growth and better carcass conformation.

Considering the importance of the local breeds and the extreme conditions that the sheep breeding activity finds to develop in semi-arid regions (Costa et al. 2009) and the demand for a quality product by consumers, it is important to improve the aspects of production, industrialisation and commercialisation of these animals, to meet consumers' needs in terms of health and presentation (Landim et al. 2011).

The aim of this study was investigate the differences in fatty acid profile and intramuscular fat content of the main genotypes of sheep raised in semi-arid of Brazil to identify the best options for the finishing of lambs on pasture.

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2. Materials and methods

The experiment was carried out using the experimental flock of Embrapa Caprinos e Ovinos, Sobral, CE – Brazil. Thirty-four unrelated males lambs of MO ($n = 6$), SO ($n = 7$) and SI ($n = 13$) breeds and ½ Dorper × ½ Morada Nova (F1, $n = 8$) crossbred, born in the same season, with the same birth type (single) and weaned at an average of 84 days of age were used in this study. After the weaning, the lambs were raised on irrigated pasture of Tanzania grass (*Panicum maximum* Jacq cv. Tanzania) with free access to water and mineral salt. The lambs were free to graze and were supplemented once a day with a concentrate (corn – 48%, cotton cake – 35%, soybean meal – 15%, limestone –1%, mineral salt –1%) at a rate of 1.5% of body weight. The pasture and concentrate chemical compositions are presented in Table 1. All animals were managed in the same flock in the same pasture, following the principle of rotational grazing, allowing appropriate conditions of grass surface. The trial followed a completely randomised design with four treatments (genotype), respecting the principles of randomisation, repetition and uniformity of animals and management. The lambs were slaughtered at Embrapa Caprinos e Ovinos facilities with the same ages with averages of 200.18 ± 7.54 days of age (a minimum of 191 and a maximum of 208 days) and 20.62 ± 3.46 kg of body weight. The averages of age were similar according to breeds (F1 = 196.71 days; MO = 198.17 days; SI = 199.15 days; SO = 198.28 days), however, there were some differences in slaughter weight according to genetic differences of the breeds (F1 = 20.82 kg; MO = 14.38 kg; SI = 23.98 kg; SO = 19.54 kg). The conditions analysed here seek to simulate the present conditions of diet/management and production system for lambs in Brazil. The purpose of this was to compare the breeds under practical conditions imposed by the market and production systems in Brazil. A 5-cm length of the *Longissimus dorsi* muscle, between 12th and 13th ribs, was removed from one side of the carcass. All samples were vacuum-packed, frozen rapidly and stored at −20°C for further analysis.

Table 1. Chemical composition of Tanzania grass (*Panicum maximum* Jacq cv. Tanzania) and concentrate (corn – 48%, cotton cake – 35%, soybean meal – 15%, limestone –1%, mineral salt – 1%).

	Tanzania grass	Concentrate
Dry matter (DM)%	28.46	86.92
Organic matter (% DM)	87.34	92.74
Crude Protein (% DM)	11.29	25.26
Ashes (% DM)	12.65	4.06
Ether extract (% DM)	2.61	2.78
Neutral detergent fibre (% DM)	69.93	20.83
Acid detergent fibre (% DM)	38.5	11.49
Lignin (% DM)	4.47	2.14
In vitro digestibility of DM (% DM)	54.4	75.37
Total digestible nutrient (% DM)	49.08	76.13

The lipids from samples were extracted using the methodology presented by Bligh and Dyer (1959). The fatty acids were transmethylated according to method described by Precht and Molkentin (2000). The fat extracted was dissolved in 1 mL of hexane and mixed with 20 μL sodium methylated solution (2 N in methanol) in a sample vial. The solution was shaken vigorously for 3 min (vortex mixer) and centrifuged for 1 min (35 × g). After addition of 10 mg sodium sulphate monohydrate, the vial was recapped, mixed again for 2 min and centrifuged at same speed for 1 min. The clear supernatant was used for gas chromatography analysis.

The fatty acid profile was determined by gas chromatography according to model modified from Chilliard et al. (2006), under the following conditions: Column: SP 2560 (100 m × 0.25 mm × 0.25 μm) – Supelco; Patterns: Supelco 37 – Component FAME Mix (10,000 μg in CH_2Cl_2) – Supelco cat. 47885-U, linoleic conjugated acid methyl ester – SIGMA Cat. O5632; flow of gas, injection in the split mode (1:100), 1 μL of sample, carrier gas – hydrogen (30 mL/min), make up – 30 mL/min, synthetic air – 300 mL/min; temperature of injector and detector (FID) – 250°C; programming temperature of oven: initial temperature 50°C hold 3 min, rate 4°C/min to 150°C hold 1 min, rate 1°C/min to 170°C hold 1 min, rate 8°C/min to 220°C hold 30 min, total run 86.25 min. The analyses were performed in the Animal Nutrition Laboratory of Embrapa Caprinos e Ovinos. The fatty acid composition of intramuscular fat is expressed as amount of each individual fatty acid per total fatty acids present. The atherogenic index was calculated as (C12:0 + (4*C14:0) + C16:0)/total unsaturated fatty acids (Chilliard et al. 2003). The indices used to predict the activity of desaturase enzyme (C18:1n9c/(C18:0 + C18:1n9c)), (C16:1/(C16:0 + C16:1)) and (C18:1n9c + C16:1)/(C18:0 + C18:1n9c + C16:0 + C16:1)) were also evaluated. Desaturase index is based on the relationship between substrate and product for Δ9 desaturase.

Data were analysed as a completely randomised design with a model that included genotype effects and experimental error by least-squares method using the GLM procedure of SAS Institute Inc (1996).

When the effect of genotype was significant, the means were compared by Tukey-Kramer test.

3. Results

The genetic group was a significant source of variation for the percentage of individual fatty acid (FA; Table 2) and the intramuscular fat content (IMF; Figure 1). The IMF varied from 28.84 mg/g to 58.88 mg/g among the four genetic groups, and only two groups differed statistically to each other, SI and SO ($P < 0.05$; Figure 1).

The main fatty acids present in the *Longissimus dorsi* of lambs of the four genetic groups were C18:1n9c (oleic acid – 28%), C18:0 (estearic acid – 25%) and C16:0 (palmitic – 24%) which represented approximately 78% of the total fatty acids (Table 2). Differences among the genetic groups were observed only for capric, myristc, pentadecanoic, palmitic, palmitoleic, stearic, oleic, linoleic, conjugated linoleic, arachidonic and lignoceric acids. The highest proportion of oleic acid was observed in SO (32.15), however, this value did not differ from averages for F1 (29.14) and MO (26.01). Stearic acid proportion was the lowest in SO meat (19.8) and the highest in SI (27.3) and F1 (27.6) meats. SO breed showed highest proportion of myristc, pentadecanoic, palmitic and palmitoleic acids ($P < 0.05$). Proportion of the CLA was higher in MO meat than in the other breeds.

Genotype also was a significant source of variation for polyunsaturated fatty acid (PUFA)/SFA ratio, total PUFA, essential fatty acids (EFA), total n-3 and n-6 PUFA, Δ9 desaturase and atherogenic index (Table 3). The meat of MO lambs had greater proportion of PUFA and EFA than that of SI and SO lambs (Table 3). F1 lambs had similar proportion of PUFA to lambs MO and SI. The SO meat showed lowest proportion of PUFA, similar to SI. MO lambs also had a greater relation of PUFA/SFA (0.30) than SI and SO but similar to F1 lambs. The highest value of total n-3 PUFA was observed in MO (0.80) despite that it did not differ from F1 (0.69) and SI (0.61) values. The lowest value for n-6 PUFA was observed in SO (4.07) that this did not differ from SI (5.89).

The atherogenic index was similar in F1, MO and SI lambs and superior in SO. There was no difference between genetic groups for the total of SFA, monounsaturated fatty acid (MUFA) and UFA. The unsaturated and SFAs represented around 43% and 58%, respectively, of the total fatty acid of lambs' meat (Table 3).

In C18:1n9c/(C18:0 + C18:1n9c) and C16:1/(C16:0 + C16:1) desaturase indices, the highest value was observed in SO meat. For the index (C18:1n9c + C16:1)/(C18:0 + C18:1n9c + C16:0 + C16:1), the highest value was observed in SO meat (0.41), despite that it did not differ from the F1 (0.37) and MO (0.35) meats.

4. Discussion

The present study demonstrated significant difference between breed to IMF content of muscle tissue of the four genetic groups. The total amount of fat is the major factor affecting the fatty acid composition in the muscle of several species (Wood et al. 2008), and the amount of IMF in the *Longissimus* muscle has high phenotypic correlation with marbling and with subcutaneous fat thickness (Sainz & Paganini 2004; McPhee et al. 2006). Genetically, each breed has its own pattern of development and muscle growth and maturing rate according to the process of evolution and selection (natural and artificial) that it was submitted. So the total amount of fat in the muscle is intrinsically dependent of this rate of growth and

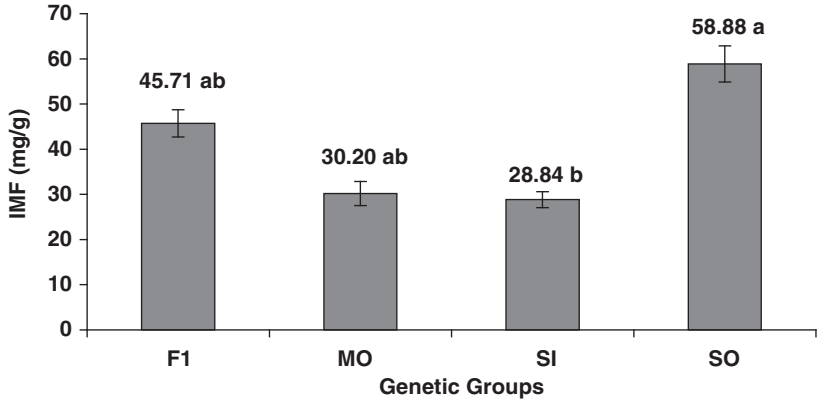

Figure 1. Total intramuscular fat content (mg/g) according to genetics groups (F1 = ½ Dorper × ½ Morada Nova, MO, Morada Nova; SI, Santa Inês; SO, Brazilian Somali).

Table 2. Least square means ± standard error on the fatty acid profile (% of total) in *Longissimus* muscle of ½ Dorper × ½ Morada Nova (F1), Morada Nova (MO), Santa Inês (SI) and Brazilian Somali (SO) lambs.

	Genetic groups			
	F1 ($n = 8$)	MO ($n = 6$)	SI ($n = 13$)	SO ($n = 7$)
Fatty acids				
Capric acid (C10:0)	0.03 ± 0.01 ab	0.00 ± 0.00 b	0.04 ± 0.01 ab	0.09 ± 0.03 a
Lauric acid (C12:0)	0.26 ± 0.06	0.33 ± 0.07	0.26 ± 0.04	0.34 ± 0.06
Myristc acid (C14:0)	0.30 ± 0.03 b	0.30 ± 0.03 b	0.32 ± 0.02 b	0.58 ± 0.03 a
Pentadecanoic acid (C15:0)	0.46 ± 0.03 b	0.49 ± 0.04 b	0.50 ± 0.03 b	0.86 ± 0.06 a
Palmitic acid (C16:0)	23.71 ± 3.08 b	24.01 ± 3.48 b	23.68 ± 2.42 b	28.11 ± 2.46 a
Palmitoleic acid (C16:1)	0.60 ± 0.04 b	0.61 ± 0.05 b	0.65 ± 0.04 b	1.28 ± 0.07 a
Palmitoleate (C16:1n7)	–	–	0.10 ± 0.04	–
Heptadecanoic acid (C17:0)	1.51 ± 0.15	1.58 ± 0.18	1.50 ± 0.12	1.70 ± 0.17
cis-10Heptadecanoic acid (C17:1)	0.05 ± 0.01	0.03 ± 0.001	0.12 ± 0.01	0.09 ± 0.01
Stearic acid (C18:0)	27.58 ± 2.63 a	25.47 ± 3.16 ab	27.25 ± 2.07 a	19.77 ± 3.32 b
Elaidic acid (C18:1n9t)	1.60 ± 0.13	1.87 ± 0.19	2.43 ± 0.18	1.23 ± 0.11
Oleic acid (C18:1n9c)	29.14 ± 3.40 ab	26.01 ± 4.27 ab	25.54 ± 2.94 b	32.15 ± 3.38 a
Linolelaidic acid (C18:2n6t)	–	–	0.03 ± 0.01	0.02 ± 0.01
Linoleic acid (C18:2n6c)	6.60 ± 0.16 ab	9.50 ± 0.22 a	4.79 ± 0.08 bc	3.49 ± 0.09 c
CLA – Conjugated linoleic acid (C18:2c9T11)	0.53 ± 0.01 b	1.24 ± 0.03 a	0.42 ± 0.00 b	0.53 ± 0.01 b
α-Linolenic acid (C18:3n3)	0.60 ± 0.06	0.47 ± 0.06	0.50 ± 0.04	0.23 ± 0.03
Gamma-linolenic acid (C18:3n6)	0.04 ± 0.01	0.06 ± 0.01	0.05 ± 0.01	0.02 ± 0.00
Eicosenoic acid (C20:1)	–	–	0.02 ± 0.01	–
cis-11. 14. 17 Eicosatrienoic acid (C20:3n3)	–	–	0.04 ± 0.01	–
cis-8. 11. 14 Eicosatrienoic acid (C20:3n6)	–	–	0.01 ± 0.01	–
Arachidonic acid (C20:4n6)	2.35 ± 0.12 a	1.76 ± 0.08 ab	1.24 ± 0.04 ab	0.75 ± 0.03 b
Eicosapentaenoic acid (C20:5n3)	0.01 ± 0.001	0.03 ± 0.01	0.02 ± 0.001	–
Adrenic acid (C22:4n6)	–	–	0.01 ± 0.01	0.03 ± 0.01
Lignoceric acid (C24:0)	0.02 ± 0.0001 b	0.08 ± 0.0001 ab	0.00 ± 0.001 b	0.31 ± 0.001 a

[a,b,c]Least square means in the same row with different letters are different by Tukey-Kramer Test ($P < 0.05$).

maturing. These aspects are controlled by many physiological aspects such the hormones biosynthesis. Lobo et al. (2009) determined the polymorphism C242T of the aromatase gene (*Cyp19*) in some of the breeds of this study that can help explain the differences in the growth and maturing rate of them.

Table 3. Least square means ± standard error on the fatty acid profile (% of total) according to classification of saturation and indices of Δ9 desaturase activity in *Longissimus* muscle of ½ Dorper × ½ Morada Nova (F1), Morada Nova (MO), Santa Inês (SI) and Brazilian Somali (SO) lambs.

	Genetic groups			
	F1	MO	SI	SO
TOTAL SFA	57.85 ± 9.02	56.82 ± 10.96	58.33 ± 6.92	59.40 ± 8.96
TOTAL MUFA	33.33 ± 2.88	28.47 ± 3.32	31.90 ± 2.26	34.98 ± 3.07
TOTAL PUFA	9.75 ± 0.77 ab	14.19 ± 1.11 a	6.93 ± 0.49 bc	4.85 ± 0.59 c
TOTAL UFA	42.55 ± 2.94	44.18 ± 3.39	39.85 ± 2.30	40.11 ± 3.14
UFA/SFA	0.72 ± 0.07	0.76 ± 0.09	0.65 ± 0.05	0.67 ± 0.07
PUFA/SFA	0.21 ± 0.01 ab	0.30 ± 0.01a	0.14 ± 0.01 bc	0.08 ± 0.01 c
EFA	7.29 ± 0.56 ab	10.02 ± 0.75 a	5.20 ± 0.36 bc	3.58 ± 0.40 c
TOTAL *n*-3 PUFA	0.69 ± 0.07 ab	0.80 ± 0.09 a	0.61 ± 0.05 ab	0.23 ± 0.04 b
TOTAL *n*-6 PUFA	8.51 ± 0.73 ab	12.02 ± 1.11 a	5.89 ± 0.46 bc	4.07 ± 0.60 c
n-6/*n*-3	11.22 ± 0.85	11.48 ± 1.08	6.76 ± 0.57	6.03 ± 0.93
Atherogenic index	0.82 ± 0.10 b	0.83 ± 0.11 b	0.92 ± 0.08 b	1.28 ± 0.10 a
Δ9 desaturase				
C18:1n9c/(C18:0 + C18:1n9c)	0.52 ± 0.06 b	0.51 ± 0.07 b	0.47 ± 0.06 b	0.62 ± 0.05 a
C16:1/(C16:0 + C16:1)	0.02 ± 0.001 b	0.02 ± 0.001 b	0.03 ± 0.001 b	0.04 ± 0.001 a
(C18:1n9c + C16:1)/(C18:0 + C18:1n9c + C16:0 + C16:1)	0.37 ± 0.01 ab	0.35 ± 0.01 ab	0.31 ± 0.01 b	0.41 ± 0.01 a

[a,b,c]Least square means in the same row with different letters are different by Tukey-Kramer Test ($P < 0.05$); SFA, saturated fatty acids; MUFA, monounsaturated fatty acids; PUFA, polyunsaturated fatty acids; UFA, unsaturated fatty acids; EFA, essential fatty acids; n-6: (C18:2n6t + C18:2n6c + C18:3n6 + C20:3n6 + C20:4n6 + C22:4n6); n-3: C18:3n3 + C20:3n3 + C20:5n3 + C22:6n3); atherogenic index: [C12:0 + (4*C14:0) + C16:0)/UFA].

Lobo et al. (2012) also reported that transcripts involved in skeletal muscle development (MyoD1 and IGFBP4), lipogenesis and adipogenesis (C/EBPδ, PPARγ and PGDS) were differentially expressed in some comparisons between the genetic groups studied here. The proliferative activity of satellite cells, which is the source of new nuclei embedded the muscle fibres, is greater in SO than in MO. The results of that study suggest that the SO lambs are more efficient with respect to tissue growth than the MO lambs during postnatal growth. The results of these studies point out that the sequence of growth rate is F1 = SI > SO > MO and the sequence of mature rate is SO = F1 > SI > MO. The study of the differences in these aspects among breeds is important to choose breeds more appropriated to attend the market since these characteristics are related to meat quality and preference of consumers.

The percentages of the main fatty acids predominant in the meat of ruminants (oleic, estearic and palmitic) observed in this study were similar to those reported in meat of culled woollen ewes raised in south of the Brazil (Pelegrini et al. 2007) and lambs grazed on pasture (Enser et al. 1998). Except for the SI breed, the meat of the lambs had higher proportion of oleic acid than other fatty acids. Oleic acid is a fatty acid typically found in ruminant feed and in the rumen is largely hydrogenated to estearic acid by rumen microorganisms. In tissues, the concentration of oleic acid is dependent upon the activity of Δ^9 desaturase (Smith et al. 2006) that is the major lipogenic enzyme that catalyses the conversion of palmitic (C16:0) to palmitoleic (C16:1) and estearic (C18:0) to oleic (C18:1). Dinh et al. (2010) explain that the significant presence of oleic acid is explained by Δ^9 desaturase, which may convert as much as 10% of estearic to oleic acid in the enterocyte (Byers & Schelling 1993). Oleic acid is considered hypolipidaemic, as it reduces cholesterol and triglycerides in plasma (EFSA 2010; Díaz et al. 2011). The trend of higher oleic acid (C18:1) and lower estearic acid (C18:0) in SO animals was confirmed by the highest activity of the Δ^9 desaturase in these animals (Lobo et al. 2012). Wood et al. (2008) highlighted that oleic acid increases with fatness. In fact, the SO breed is originated from Black-Head Persian breed, which was brought to Brazil in recent years (1939). It is a breed of the fat-tail group which has the ability to accumulate fat in the tail as a reserve to critical periods of food shortages. Among the studied breeds, SO has the highest index of maturing and fatness.

Estearic acid concentrations were significantly smaller in the meat of SO lambs than in all others groups. This may be the result of lower biohydrogenation of oleic acid in the rumen or increased enzyme stearoyl-CoA desaturase (SCD) activity in muscle tissue of animals of this breed. However, no study has suggested breed-related differences in biohydrogenation in the rumen (Dinh et al. 2010). Bauman et al. (1999) and Dinh et al. (2010) suggested that the increase in MUFA concentration, especially regarding the increased concentration of oleic acid, might be an indicator of desaturase activity. Although SO lambs have presented the highest average for the concentration of MUFA, they did not differ from the other genetics groups. Despite the fact that SO lambs had the highest proportion of oleic acid, they differed only from F1. On the other hand, the Δ9 desaturase indices used as an estimator of SCD enzyme activity were significantly highest in SO muscle. Dervish et al. (2010) suggested that the highest content of oleic acid in the muscle could be related to highest enzyme activity.

Higher proportion (9.5%) of the linoleic acid (C18:2n6c; omega 6) was observed in the meat of MO lambs than those of SI and SO lambs, being similar to proportion in F1. According to Wood et al. (2008) linoleic is the main PUFA in sheep tissues and only a small proportion of it, around 10%, is available for incorporation into tissue lipids. Our results for MO lambs were similar to those found in Kivircik and Sakiz lambs fed with concentrates (Demirel et al. 2006) and those found in intramuscular depots by Cañeque et al. (2005). The proportion of α-linolenic (C18:3n3; omega 3), which according to Wood et al. (2008) is the second most important PUFA in sheep and cattle and did not differ among the genotypes, and its proportion represented only around of 0.45% of the fatty acids total proportion. Wood et al. (2008) presented values of 1.2% and 4.6% for the fatty acid composition of *longissimus* muscle triacylglycerol (neutral lipid) and phospholipid, respectively, in sheep. Fisher et al. (2000) reported values of 0.7% and 2.3% for the linolenic acid in the semimembranosus muscle of Suffolk animals fed with concentrates and grass, respectively. The values observed in this study are below that expected for animals fed in pasture. It is possible that the concentrate used for supplementation of animals in this study, with the participation of cotton cake (35%) and soybean meal (15%) have influenced this result. Actually, animals fed with concentrates which are rich in cereals that have high proportion of linoleic acid present a meat with an undesirable and high n-6:n-3 ratio. However, the meat of animals that eat grass (ruminant) which contains high levels of linolenic has beneficial n-6:n-3 ratio (Wood et al. 2003). Therefore, some authors claim that lambs raised at pasture produce meat with quality more

favourable for consumer health than those raised indoors (Landim et al. 2011).

Today special attention has been given to the type of PUFA and the appropriate balance in the diet of n-3 and n-6 PUFA (Williams 2000). In this study, the meat of the lambs did not differ and showed values above that recommended (<4.0) for ratio n-6/n-3 PUFA, although meats of others species also have values superior to this limit (Wood et al. 2003). According to Wood et al. (2008), a long rumen transit time for forage diets and the greater biohydrogenation of 18:3n3 limit its amount available for tissue uptake compared with 18:2n6 from concentrate diets. This occurs because concentrates have small particle size and a shorter rumen transit time than fibrous forage diets limiting the opportunities for microbial biohydrogenation (Wood et al. 2008). This can explain the better ratio n-6/n-3 PUFA in the meat of ruminants such as sheep, compared to other species of non-ruminant.

Though the meat of lambs presented an undesirable n-6/n-3 ratio, it showed a considerable percentage of CLA (c18:2c9t11), that is an important nutrient in human nutrition. The CLA proportion of MO meat represented 1.24% of total fatty acids. This value was higher than those reported for cattle (Laborde et al. 2001) and those presented by Dervish et al. (2010) for lambs. These latter authors reported the following values: 1.17, 1.14, 0.55 and 0.43% for lambs grazing alfalfa pasture, grazing alfalfa pasture with supplementation, indoor lambs with grazing ewes and indoors lambs, respectively. Ruminant CLA isomers come from two sources: one from biohydrogenation in the rumen, produced during microbial biohydrogenation of dietary linoleic acid (LA; C18:2c9c12) and in the tissues through Δ^9-desaturation (through of enzyme stearoyl-CoA desaturase; SCD) of the rumen-derived trans-vaccenic acid (Corl et al. 2001). Lobo et al. (2012) reported greater expression of SCD gene transcripts in the muscle of SO lambs in relation to MO lambs, suggesting a higher activity of this enzyme in SO animals. These observation contrast with observed here where the highest value of CLA was observed in the meat of MO compared to the other groups. Lobo et al. (2012) observed that MO lambs had higher expression of transcripts that are activated at the beginning of preadipocyte differentiation process and lower expression of those transcripts expressed at the intermediate period of this process compared to SO lambs. This indicates that differentiation of preadipocytes in MO breed occurs latter than in SO breed. As CLA could also come from microbial biohydrogenation in rumen we have extrinsic and intrinsic factors related to its levels at the animal tissue. So the reason for the differences observed in CLA among the genetic groups studied is not clear. Wood et al. (2008) reported that CLA increases with fatness; however, in this study the fatness was higher in SO, but MO had highest CLA.

Genetic group influenced the concentration of PUFA and EFA with MO meat showing the highest proportions of desirable fatty acids. This breed had the better PUFA:SFA ratio, similar to F1 lambs. No significant difference between genetic groups was observed by Landim et al. (2011) to PUFA/SFA ratio. In general, F1 lambs were more similar to MO lambs, due to the participation of this breed in this crossing (½ Dorper × ½ Morada Nova). Although MO is an important local breed with high adaptation to the region, it is under the risk of extinction and these aspects are relevant for its conservation and improvement. Values found here for PUFA/SFA ratio are below those recommended by Department of Health (1994) in the UK (above 0.4). However, the meat of MO lambs showed value above those reported to some ruminant meats (0.30 *vs* 0.1). Our results were similar to those reported by Cañeque et al. (2005) and slightly higher than those found by Demirel et al. (2006) in lambs fed with grass and concentrate.

The highest atherogenic index observed in the SO is probably due to highest concentration of C12:0, C14:0 and C16:0. The atherogenic index was proposed as a measure of the tendency of the food to influence the incidence of coronary heart disease. Therefore, from the standpoint of human health, meat with fewer short chain SFAs content is desirable.

The present work demonstrated that there is variation in fatty acid composition among the studied genetic groups. This variability offers opportunities to be explored in production systems of lambs. The influence of genotype on fatty acid composition has also been observed in goats (Santos et al. 2007; Peña et al. 2011). Emphasise that the fatty acid composition is influenced not only by genetic factors but also by environmental factors such as diet and supplementation. But, according Soyeurt et al. (2006), the feed supplementation, the most popular way to improve the nutritional quality, presents certain disadvantages. It does not consider the animal genetic effect, and this improvement is not permanent.

In addition, nutritional aspects must be taken into account, although in Brazil the breeders of sheep tend to lead mass selection only for productivity (weight). However, this usually causes problems with intrinsic product quality, such as very low intramuscular fat

content of lean meats, reducing the flavour and juiciness of cooked meats (OECD 2010).

5. Conclusion

This study revealed differences in the intramuscular fat content and fatty acid composition of meat among the studied genetic groups. This variability is important for improvement of meat quality by choice of breeds to be used in different productions systems. In the conditions of the study, the meat from MO lambs had better attributes of fatty acid composition with higher PUFA, PUFA/SFA ratio, EFA and total n-3 PUFA. These aspects are crucial to reinforce among the breeders the importance of conservation and multiplication of this breed. F1 lambs showed fatty acid profile similar to MO, being this crossing an option for the finishing of lambs on pasture. However, it is important highlight the necessity for further studies to confirm the results. Farther, a future goal should be to identify genetic markers for identifying and selecting animals with improved profiles before they express the phenotype.

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