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Carcass characteristics and chemical composition of the *Longissimus* muscle of crossbred bulls (*Bos taurus indicus* vs *Bos taurus taurus*) finished in feedlot

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ABSTRACT

This study was carried out to evaluate final weight, carcass characteristics, chemical composition and fatty acid profile in *Longissimus* muscle (LM) of young bulls of the crossbred type: Canchim×Aberdeen Angus (n=7), Nellore×Aberdeen Angus (n=12) and Nellore×Continental breeds (Simmental, Limousin) (n=8), finished in feedlot. Canchim×Aberdeen Angus and Nellore×Aberdeen Angus bulls had similar final body and hot carcass weights, while these were lower for the Nellore×Continental breed crosses. Fat thickness and LM area were inferior in the Nellore×Continental breed group. In contrast, lipid contents were larger in the LM of the Canchim×Aberdeen Angus bulls. Nellore×Aberdeen Angus and Nellore×Continental breed crosses featured a similar percentage of polyunsaturated, *n*-6 and *n*-3 fatty acids, and a larger ratio of polyunsaturated and saturated and *n*-6 and *n*-3 fatty acids in comparison to Canchim×Aberdeen Angus bulls.

KEY WORDS: cattle, meat quality, *Longissimus* muscle, chemical composition, fatty acids

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INTRODUCTION

Brazil has the largest commercial cattle population in the world, with approximately 159 million animals and a production of approximately 8.2 million tons of carcass each year (Anualpec, 2007). From this total, about 30% (2.4 million tons) are exported to several countries around the world. The consumer market for beef has become increasingly demanding as a result of negative factors associated with meat composition and quality (Saucier, 1999). Among these factors is the relation between beef consumption and heart disease, atherosclerosis, intestinal cancer, obesity, among other diseases (Katan et al., 1994; Kwiterovich, 1997).

As such, the use of biotechnologies - among them crossbreeding between Zebu breeds (*Bos taurus indicus*) (which are well adapted to subtropical and tropical regions) and breeds of European origin (*Bos taurus taurus*) (adapted to colder climates and featuring greater weight gain and meat quality potential) - could become an important tool to increase meat production and especially to improve quality factors. Such factors include increased fat thickness and marbling, improved beef tenderness and flavour, with reduced levels of calpastatins in the muscle of crossbred animals. Zebu breeds such as Nellore, a Zebu breed originating from India (Ongole) that represents about 80% of livestock in Brazil, exhibit a tougher meat as a result of higher content of collagen and an unfavourable profile of enzymes related to meat tenderness.

The State of Paraná, located in south Brazil, features a milder climate as compared to the Center-West, North and Northeastern regions of the country. Consequently, researchers have since the 1980s worked on the crossbreeding between Zebu and European breeds, with the objective of increasing production and quality in the meat of the offspring (Perotto et al., 1998, 2000).

The objective of this study was to evaluate the final weight, carcass characteristics, chemical composition, fatty acid profile, and the ratios between polyunsaturated and saturated fatty acids and between *n*-6 and *n*-3 fatty acids in various crossbred type bulls. In the study, a crossbred type (Canchim) was included which had been created already in 1940 in Brazil from Nellore (3/8) and Charolais (5/8). Purebred Nellore and Canchim were crossed with either Aberdeen Angus or large-framed Continental beef breeds and finished in feedlot.

MATERIAL AND METHODS

Animals management and sampling

This study was carried out at the experimental farm of the Agronomic Institute of Paraná situated in south Brazil. Twenty-seven bulls (7-1/2 Canchim × 1/2 Aberdeen Angus, 12-1/4 Nellore × 3/4 Aberdeen Angus and 8-1/2 Nellore × 1/2 Continental breeds being either Simmental or Limousin) were used. From 8 months

of age, i.e. after weaning, the animals had exclusive grazed together on a fenced pasture of Brachiaria grass (*Brachiaria decumbens* Stapf.) until they were 18 months old. Subsequently, they were finished in a feedlot during 4 further months. During the feedlot period, the animals were kept separately in individual pens (5 m^2 for each animal), and fed twice a day. They were given a diet formulated to meet requirements for fattening beef cattle (NRC, 1996). The diet consisted of, %: maize silage 50, cracked maize 20, cotton meal 13, wheat middling 15, urea 1, limestone 0.5 and mineral salt 0.5. Tables 1 and 2 give the analysed nutrients and fatty acid

Table 1. Chemical composition of the concentrate ingredients

Ingredients	DM	% of Dry matter						
		ash[1]	OM[2]	CP[3]	NDF[4]	ADF[5]	LIG[6]	EE[7]
Maize silage	33.50	4.60	95.40	7.50	45.74	29.42	4.44	3.05
Cracked maize	89.11	3.66	96.34	8.00	12.64	3.11	0.50	3.70
Cotton meal	89.25	6.21	93.79	50.34	23.76	10.16	7.76	1.36
Wheat middling	87.39	7.81	92.19	16.64	38.31	10.17	3.06	2.55
Limestone	99.90	99.54	0.46					
Mineral salt	98.71	89.29	10.71					
Urea	98.80			273.63				

[1] total ash, [2]organic matter, [3] crude protein, [4] neutral detergent fibre, [5] acid detergent fibre, [6] lignin, [7] ether extract

Table 2. Fatty acid profile, % of total fatty acids of Brachiaria and concentrate

Fatty acids	Treatments	
	Brachiaria	concentrate
14:0	1.13	-
16:0	18.92	15.79
18:0	5.81	4.57
18:1 *n*-9	16.79	44.40
18:1 *n*-7	4.24	1.95
18:2 *n*-6	34.63	27.64
18:3 *n*-6	1.41	1.91
18:3 *n*-3	9.55	0.86
20:4 *n*-6	1.67	0.89
20:5 *n*-3	1.76	0.37
22:5 *n*-3	2.64	1.37
22:6 *n*-3	1.48	0.26
PUFA	53.13	33.29
MUFA	21.03	46.35
SFA	25.85	20.36
n-6	37.71	30.43
n-3	15.42	2.86
PUFA:MUFA	2.06	1.64
n-6/*n*-3	2.45	10.73

composition of diets and feeds. The animals were weighed at the beginning of the study and every 28 days, and on the day before slaughter, after 12 h fasting. The animals were slaughtered at a commercial slaughterhouse 90 km away from the Ponta Grossa farm, according to industrial practice in Brazil. Carcass measurements were conducted at this slaughterhouse, whereas meat analyses were carried out at the chemical laboratory of the State University of Maringá.

The State University of Maringá Animal Care and Ethics Committee approved the use of animals in this study.

Carcass characteristics

Hot carcass weight (kg) was determined in right half after slaughter before chilling the carcass. At slaughter, the carcasses were identified, weighed and stored during 24 h in a chilling chamber at a temperature of 4ºC. After chilling, the right half of the carcass was used to determine quantitative characteristics. Dressing percentage for an individual animal was defined as hot carcass weight divided by liveweight. Carcass conformation (CC) it was evaluated by Müller's point scale (Müller, 1980) in which the highest value indicates the best conformation; muscle development was considered after the exclusion of cover fat. Carcass length is the distance from the skull board to the pubic bone on the anterior side of the first rib, measured with a ribbon or a tape measure. Leg length (LL) it was evaluated using a wood compass with metallic edges that measures the distance from the anterior border of the pubic bone to a middle point at the tarsus bone. Cushion thickness (CT) was measured by a wood compass with metallic edges that mark the distance between the lateral face and the median at the superior part of the cushion. Fat thickness (FT) was taken by a caliper averaging three points between the 12th and the 13th rib but over the *Longissimus* muscle (LM).

The *Longissimus* muscle area was analysed using the right part of carcass, where a transversal cut is made between the 12ª and 13ª ribs. After this, a compensating planimeter, which is an instrument that measures the area of irregularly shaped objects, was used to determine the area. Texture was determined through the size of the fascicle (muscle "grain" size) and was evaluated subjectively with a point scale from 1-5 (Müller, 1980). Muscle colour after 24-h carcass chilling was estimated by evaluating the colouration according to a point scale from 1-5 using a colour table (Müller, 1980).

Marbling, intramuscular fat content, was assessed in LM between the 12th and 13th ribs on a scale from 1-18 (Müller, 1980).

Chemical composition

After 24 h, LM samples were taken as the complete cross-section between the 12th and the 13th rib, and were immediately taken to the laboratory. Cover fat was

discarded and the muscle portion was frozen at -20ºC for later analysis. Laboratory analyses of beef were carried out two months after sampling. The samples were thawed at room temperature (20ºC), ground, homogenized, and analysed in triplicate.

Beef moisture and ash contents were determined according to AOAC (1998). Crude protein content was measured by the Kjeldahl method (AOAC, 1998), total lipids were extracted by the Bligh and Dyer (1959) method with a chloroform/methanol mixture. Fatty acid methyl esters (FAME) were prepared by triacylglycerol methylation, according to the ISO (1978) method.

Chromatographic analysis and cholesterol quantification

Cholesterol analysis was carried out by the method modified by Rowe et al. (1999) using a 14-A gas chromatograph (Shimadzu, Japan), equipped with a flame ionization detector and a fused silica capillary column (25 m long, 0.25-mm internal diameter, and 0.20 μm Ohio Valley-30). Injector, column, and detector temperatures were 260, 280 and 280ºC, respectively. Ultra-pure gas fluxes (White Martins) of 1.5 ml min^{-1} H_2 as carrier gas, 30 ml min^{-1} N_2 as make-up gas, 300 ml min^{-1} synthetic gas, and 30 ml min^{-1} N_2 for flame were used. The sample injection split mode was: 1:150. Peak integration was carried out with CG-300 computing integrator (CG Instruments, Brazil) and cholesterol was identified by comparison with standards from Sigma (USA). Sample cholesterol quantification was carried out after verification of method linearity. Standard cholesterol solutions (Sigma, USA) were prepared with concentrations 0.0, 0.4, 0.8, 1.6 and 2.0 mg ml^{-1}, all containing 0.20 mg ml^{-1} 5α-cholestane (Sigma, USA), and analysed. The ratio of the areas of cholesterol and 5α-cholestane was plotted against the cholesterol concentration for injected volumes of 0.0, 2.0, 3.0, 4.0 and 5.0 μl. The curve obtained was used for cholesterol analysis in mg 100 g^{-1}.

Analysis of fatty acid methyl esters

The fatty acids methyl esters (FAMEs) were analysed in a gas chromatograph (Varian, USA) equipped with a flame ionization detector and a fused silica capillary column CP-7420 (100 m, 0.25 mm and 0.39 μm o.d., Varian, USA) Select Fame. Column temperature was programmed at 165ºC for 18 min, 180ºC (30ºC min^{-1}) for 22 min, and 240ºC (15ºC min^{-1}) for 30 min, with 45-psi pressure. The injector and detector were kept at 220 and 245ºC, respectively. The gas fluxes (White Martins) used were: 1.4 ml min^{-1} for the carrier gas (H_2), 30 ml min^{-1} for the make-up gas (N_2) and 30 ml min^{-1} and 300 ml min^{-1} for H_2 and the synthetic flame gas, respectively. Sample injection split mode was 1/80. Fatty acids were identified by comparing the relative retention times of FAME peaks of the sam-

ples with fatty acids methyl esters standards from Sigma (USA) by spiking samples with standard. The peak areas were determined by Star software (Varian). The data were expressed as percentages of the normalized area of fatty acids (Rowe et al., 1999; Milinsk et al., 2005).

Statistical analysis

The data was subjected to analysis of variance with crossbred type as an effect. When the crossbred type effect was significant, means were compared by the Tukey test at 10, 5 and 1% significance levels, using SAS statistical software (2000).

RESULTS AND DISCUSSION

Carcass characteristics (Table 3). Final weight and hot carcass weight were similar (P<0.1) for Canchim × Aberdeen Angus and Nellore × Aberdeen Angus animals. However, these two genetic groups had a larger (P<0.1) final weight and hot carcass weight as compared to the Nellore × Continental breed group. This was likely the result of a different heterosis and of differences in the original breeds used for crossbreeding (Nieto Martin, 2004). In this respect, the presence of genes from Aberdeen Angus in general, increased the advantage of these cattle.

Table 3. Effect of different crossbreeding types on carcass characteristics of bulls

Parameters	Genetic groups			Differences
	Can × Ang[1]	Nel × Ang[2]	Nel × Con[3]	
Final weight, kg	546 + 6.86[a]	558 ± 4.00[a]	485 ± 6.00[b]	***
Hot carcass weight , kg	283 ± 6.05[a]	304 ± 3.53[a]	261 ± 5.30[b]	***
Carcass dressing, %	49.5 ± 0.30[b]	52.1 ± 0.17[a]	54.1 ± 0.26[a]	**
Conformation, points	5.29 ± 0.47[c]	9.08 ± 0.27[a]	7.25 ± 0.42[b]	***
Leg length, cm	68.9 ± 0.38[b]	73.2 ± 0.22[a]	75.1 ± 0.34[a]	*
Carcass length, cm	137 ± 0.89[a]	142 ± 0.52[a]	131 ± 0.78[b]	*
Cushion thickness, cm	25.9 ± 0.30[b]	28.4 ± 0.17[a]	26.4 ± 0.26[b]	**
Fat thickness, cm	4.40 ± 0.28[a]	5.10 ± 0.17[a]	2.40 ± 0.25[b]	**
Longissimus muscle area, cm^2	72.3 ± 0.99[a]	72.4 ± 0.58[a]	65.8 ± 0.86[b]	***
Texture, points	3.86 ± 0.08	4.17 ± 0.05	4.25 ± 0.07	NS
Colour, points	3.86 ± 0.09	3.25 ± 0.06	3.75 ± 0.08	NS
Marbling, points	5.71 ± 0.33	5.75 ± 0.19	4.13 ± 0.28	NS
pH, points	5.4 ± 0.02	5.4 ± 0.01	5.6 ± 0.02	NS

[1] 1/2 Canchim × 1/2 Aberdeen Angus, [2] 1/4 Nellore × 3/4 Aberdeen Angus, [3] 1/2 Nellore × 1/2 Continental, [4] coefficient of variation, * P<0.10, **P<0.05, ***P<0.01, NS - non-significant

Hot carcass dressing percentage was similar (P>0.05) between the Nellore × Aberdeen Angus and Nellore × Continental breed groups, while the lowest (P<0.05) in the Canchim × Aberdeen Angus crossbreds. Notwithstanding, it is important to stress that the dressing percentage found in this group was less than 50%. In general, animals as a result of industrial crossbreeding achieve dressing percentages beyond 54% (Moreira et al., 2003, 2005; Abrahão et al., 2005). The very low dressing percentage therefore may have been related to the thorough cleaning methods performed on the carcass of the bovines by the Brazilian slaughterhouse.

Carcass conformation was superior (P<0.10) for the Nellore×Aberdeen Angus genetic group, lesser for the Canchim×Aberdeen Angus group and intermediate for Nellore×Continental breed group. The superior conformation for Nellore×Aberdeen Angus crosses can be explained by the high proportion of British breed genes (3/4), as these animals are known for to express a favourable carcass conformation. The less favourable conformation of the Canchim×Aberdeen Angus genetic group might have been the consequence of a higher Zebu gene proportion (3/8), which was higher than in the other crossbred type despite the use of Canchim having already *Bos taurus taurus* genes.

Carcass length and leg length were not significantly different between animals of the Nellore × Aberdeen Angus and the Nellore × Continental breed groups. A shorter (P<0.05) carcass and leg length was found in animals of the Canchim × Aberdeen Angus group. This cannot be explained simply by the proportion of Zebu genes, as the latter crossbreds had intermediate Zebu gene proportions. Basically Zebu cattle were selected to endure long walks in search of pasture, which might affect leg length.

The greatest (P<0.05) cushion thickness was observed in animals of the Nellore × Aberdeen Angus genetic group. There was no difference (P>0.05) between the Canchim × Aberdeen Angus and the Nellore × Continental breed group. This might have been a result of the inclusion of Aberdeen Angus, a breed with a high inclination for fat accretion, which had the highest gene proportion (3/4) in the crosses with Nellore.

Fat thickness was similar (P>0.05) between the Canchim × Aberdeen Angus and Nellore × Aberdeen Angus genetic groups and smaller (P<0.05) for animals in the Nellore × Continental breed group. This again is explained by differences in fat accretion of Aberdeen Angus vs Continental breeds. The fat thickness noted in the Canchim × Aberdeen Angus and Nellore × Aberdeen Angus meets the guidelines of the Brazilian market, which requires that carcasses have to have between 3 and 6 mm of fat thickness (Luchiari Filho, 2000).

The *Longissimus* muscle area was similar (P>0.01) in animals from the Canchim × Aberdeen Angus and Nellore × Aberdeen Angus and smaller (P<0.01)

in Nellore × Continental animals. The smaller *Longissimus* muscle area observed in Nellore × Continental animals can be explained by the lower carcass weight of these animals at slaughter (Table 3).

The crossbred type had no effect (P>0.05) on texture, colour and marbling of the *Longissimus* muscle. According to Müller's scale (1980), the colour for all genetic ratios can be considered satisfactory, as they were classified as red-coloured; as such, they are within the standards for beef consumption in the Brazilian market. Similarly, texture was classified as fine (Müller, 1980). Such texture is ideal for the commercialization of beef within the Brazilian market. Still, among the different genetic groups, marbling was classified as average. Average or medium marbling is well accepted within the domestic market; however, in order to reach foreign markets, especially in North America, beef should feature more accentuated marbling.

Chemical composition of Longissimus muscle. Moisture and ash contents of the *Longissimus* muscle were similar (P>0.05) among all three genetic groups (Table 4) averaging at 74 and 1%, respectively. Moreira et al. (2003) and Padre et al. (2006) described similar levels of moisture in *Longissimus* muscle to those

Table 4. Effect of different crossbreeding types on nutrient and total cholesterol contents of *Longissimus* muscle of bulls

Parameters	Genetic groups			Differences
	Can × Ang[1]	Nel × Ang[2]	Nel × Con[3]	
Moisture, %	72.8 ± 0.14	73.7 ± 0.08	73.7 ± 0.12	NS
Ash, %	1.13 ± 0.02	1.07 ± 0.01	1.06 ± 0.02	NS
Crude protein, %	24.9 ± 0.24	24.2 ± 0.14	23.1 ± 0.21	NS
Total lipids, %	3.91 ± 0.11[a]	2.01 ± 0.06[b]	2.55 ± 0.10[b]	*
Total cholesterol, mg/100 g of muscle	34.1 ± 1.14[c]	41.1 ± 0.67[b]	52.5 ± 1.00[a]	**

[1] 1/2 Canchim × 1/2 Aberdeen Angus, [2] 1/4 Nellore × 3/4 Aberdeen Angus, [3] 1/2 Nellore × ½ Continental, [4] coefficient of variation, * P<0.10, **P<0.05, NS - non-significant

observed in this experiment. Similarly, genetic groups had no influence (P>0.05) on the content of protein in *Longissimus* muscle; the average level for all three genetic groups was 24%. Padre et al. (2007) found a similar crude protein level in *Longissimus* of animals finished in feedlot. Diet and cross breeding generally have little influence on gross nutrient composition of *Longissimus* muscle (Webb, 2006), except fat content.

Accordingly, total lipid content was higher (P<0.01) in beef of Canchim × Aberdeen Angus animals as compared to the Nellore × Aberdeen Angus and Nellore × Continental breed bulls, with the latter two groups being not different (P>0.05) in that respect. Again, the high Aberdeen Angus gene proportion in the first men-

tioned crossbred type explains this difference as a result of a long-term selection for high intramuscular fat content (Nieto Martin, 2004). Conversely, animals from Zebu breeds (Nellore) feature lower total lipid levels in carcass (Luchiari Filho, 2000) and beef. Nevertheless, the average value observed in all three genetic groups (3%) remained below the maximum level (5%) recommended by Pensel (1998) as to be acceptable for the prevention of corony heart diseases.

Animals from the Nellore × Continental breed type featured the highest ($P<0.05$) total cholesterol levels in *Longissimus* muscle (Table 4). The lowest levels were found in the Canchim × Aberdeen Angus animals. The Nellore × Aberdeen Angus group featured intermediate levels. Thus, the presence of Zebu genes in the makeup of the genetic groups appeared to result in higher total cholesterol levels in *Longissimus* muscle, perhaps as a result of an increase in muscle membranes. Nevertheless, the average total cholesterol level observed is below that regarded as harmful to human health, which is set to ≥50 mg/100 g of muscle (Pensel, 1998; Saucier, 1999).

Fatty acid profile in the Longissimus muscle (Table 5). The percentages of myristic (14:0), palmitic (16:0) and palmitoleic (16:1 *n*-7) fatty acids were similar ($P>0.05$) between animals in the Nellore × Aberdeen Angus and Nellore × Continental breed groups. A higher percentage of these three fatty acids were observed in Canchim × Aberdeen Angus animals. This leads to the conclusion that a higher proportion of Zebu genes would be contributing to a lower percentage of these three fatty acids. On the other hand, the percentages of ai (17:0), i (17:0 iso), margaric (17:0), heptadecenoid (17:1 *n*-7), cis-vaccenic (18:1 *n*-7) fatty acids were higher ($P<0.05$) for animals in the Nellore × Continental breed group, while in this group percentages of linoleic (18:2 *n*-6), linolenic (18:3 *n*-6), α-linolenic (18:3 *n*-3), arachidonic (20:4 *n*-6), behenic (22:0) and clupadonic (22:5 *n*-3 - DPA) fatty acid were lower. The crossbreeding type had no effect ($P>0.05$) on the percentage of stearic (18:0), oleic (18:1 *n*-9), conjugated linolenic (18:2 *c*-9 *t*-11 - CLA) and cervonic (22:6 *n*-3 - DHA) fatty acids.

The percentages of total saturated and monounsaturated fatty acids were similar ($P>0.05$) among all three genetic groups. The percentage of polyunsaturated fatty acids was similar ($P>0.05$) between Nellore × Aberdeen Angus and Nellore × Continental breed type. Animals from the Canchim × Aberdeen Angus genetic group featured a lower ($P<0.05$) percentage of polyunsaturated fatty acids. Thus, a greater contribution of Zebu genes (Nellore × Aberdeen Angus and Nellore × Continental breeds) obviously results in a higher proportion of polyunsaturated fatty acids. This could have resulted from a greater number of muscle membranes, where the polyunsaturated fatty acids are preferentially stored.

Table 5. Effect of different crossbreeding types on the fatty acid profile (% of total fatty acids) and on fatty acid ratios in the *Longissimus* muscle of bulls

Fatty acids	Can × Ang[1]	Nel × Ang[2]	Nel × Con[3]	Differences
14:0	2.73 ± 0.05[a]	2.05 ± 0.03[b]	1.69 ± 0.05[b]	*
14:1 *n*-7	0.44 ± 0.02	0.35 ± 0.01	0.36 ± 0.01	NS
16:0	30.5 ± 0.42[a]	26.9 ± 0.24[b]	24.2 ± 0.36[b]	**
16:1 *n*-7	2.68 ± 0.07[a]	1.92 ± 0.04[b]	1.72 ± 0.06[b]	*
ai 17:0	0.23 ± 0.01[b]	0.22 ± 0.01[b]	0.29 ± 0.01[a]	*
i 17:0 iso	0.45 ± 0.01[b]	0.47 ± 0.01[b]	0.60 ± 0.01[a]	*
17:0	0.81 ± 0.02[ab]	0.72 ± 0.01[b]	0.96 ± 0.02[a]	**
17:1 *n*-7	0.56 ± 0.01[a]	0.47 ± 0.01[b]	0.56 ± 0.01[a]	*
18:0	19.7 ± 0.37	19.0 ± 0.21	21.3 ± 0.32	NS
18:1 *n*-9	36.0 ± 0.43	36.5 ± 0.25	35.6 ± 0.38	NS
18:1*n*-7	2.32 ± 0.06[ab]	2.09 ± 0.04[b]	2.63 ± 0.06[a]	**
18:1 *t*-11 18:2 *n*-6	0.89 ± 0.03[b]	1.08 ± 0.02[ab]	1.21 ± 0.02[a]	**
18 :2 *n*-6	2.36 ± 0.30[b]	7.25 ± 0.18[a]	5.98 ± 0.27[a]	*
18:3 *n*-6	0.11 ± 0.01[b]	0.11 ± 0.01[b]	0.20 ± 0.01[a]	***
18:2 *c*-9 *t*-11	0.25 ± 0.01	0.22 ± 0.01	0.30 ± 0.01	NS
18:3 *n*-3	0.12 ± 0.02[b]	0.34 ± 0.01[a]	0.40 ± 0.01[a]	*
20:4 *n*-6	0.59 ± 0.09[c]	1.49 ± 0.05[b]	2.29 ± 0.08[a]	**
20:5 *n*- 3	0.68 ± 0.01[a]	0.24 ± 0.01[b]	0.31 ± 0.01[b]	*
22:0	0.10 ± 0.02[c]	0.27 ± 0.01[b]	0.45 ± 0.01[a]	**
22:5 *n*- 3	0.38 ± 0.03[c]	0.44 ± 0.02[b]	0.79 ± 0.02[a]	*
22:6 *n*- 3	0.18 ± 0.08	0.22 ± 0.05	0.22 ± 0.07	NS
Saturated fatty acids	52.6 ± 0.48	49.6 ± 0.28	50.0 ± 0.42	NS
Monounsaturated fatty acids	42.3 ± 0.51	40.6 ± 0.30	38.4 ± 0.45	NS
Polyunsaturated fatty acids	4.95 ± 0.42[b]	8.92 ± 0.25[a]	10.9 ± 0.42[a]	**
n-6	4.29 ± 0.36[b]	7.56 ± 0.21[a]	9.23 ± 0.32[a]	**
n-3	0.48 ± 0.06[b]	1.15 ± 0.03[a]	1.38 ± 0.05[a]	*
PUFA/SFA	0.10 ± 0.01[b]	0.18 ± 0.01[a]	0.22 ± 0.01[a]	**
n-6/*n*-3	11.1 ± 0.65[a]	6.70 ± 0.38[b]	7.00 ± 0.56[b]	*

[1] 1/2 Canchim × 1/2 Aberdeen Angus, [2] 1/4 Nellore × 3/4 Aberdeen Angus, [3] 1/2 Nellore × 1/2 Continental, [4] coefficient of variation, * P<0.10, **P<0.05, ***P<0.01, NS - non-significant

The percentages of total *n*-6 and *n*-3 fatty acids were similar (P>0.05) in animals of the Nellore × Aberdeen Angus and Nellore × Continental breed groups. A lower percentage (P<0.05) of total *n*-6 and *n*-3 fatty acids was observed in animals of the Canchim × Aberdeen Angus group.

The ratio of polyunsaturated fatty acids to saturated fatty acids was similar (P<0.05) in animals of the Nellore × Aberdeen Angus and Nellor Nellore × Continental breed types. A lower ratio between these fatty acids was found in animals of the Canchim × Aberdeen Angus group. Despite the differences observed in the ratio of polyunsaturated to saturated fatty acids, in none of the

crossbreeding types the ratios met the standards considered beneficial to human health (0.45, according to English Health Department - HMSO, 1994).

The ratio of *n*-6 to *n*-3 fatty acids was higher ($P<0.10$) in animals of the Canchim × Aberdeen Angus group as compared to animals of the Nellore × Aberdeen Angus and Nellore × Continental breed types, where there was also a difference ($P>0.05$) between the latter two groups. For all genetic groups, the ratio of *n*-6 to *n*-3 fatty acids studied was higher than that considered adequate to human health (4:1, according to English Health Department - HMSO, 1994).

CONCLUSIONS

Crossbreeding can be used as a tool to alter lipid content and fatty acid profile in the *Longissimus* muscle of bulls grazed from weaning and finished in feedlot for 4 months. The use of genes from English breeds (Angus) significantly increases fat deposition. Conversely, the use of Zebu breeds (Nellore) increases the percentages of polyunsaturated fatty acids, *n*-6 and *n*-3 fatty acids. Furthermore, the use of Zebu genes improves the ratios of polyunsaturated to saturated fatty acids and of *n*-6 to *n*-3 fatty acids. Thus, crossbreeding between *Bos taurus taurus* and *Bos taurus indicus* breeds could be applied on bulls for feedlot finishing, aiming at marketing beef that better meet the demands of consumer food safety and health.

REFERENCES

Abrahão J.J.S., Prado I.N., Perotto D., Moletta J.L., 2005. Effects of replacing corn with increasing levels of cassava starch by-products on carcass and meat characteristics of young bulls (in Portoguese). Braz. J. Anim. Sci. 34, 1640-1650

Anualpec, 2007. Annual of Brazilian Livestock (in Portoguese). Sao Paulo, Institute FNP, pp. 368

AOAC, 1998. Association of Official Analytical Chemists, Official Methods of Analysis. 6th Edition. Arlington, VA

Bligh E.G., Dyer W.J., 1959. A rapid method of total lipid extraction and purification. Can. J. Biochem. Physiol. 3, 911-917

HMSO - England, 1994. Department of Health. Nutritional Aspects of Cardiovascular Disease. (Report on Health and Social Subjects, 46). London: HMSO, pp. 37-46

ISO, 1978. Animal and Vegetable Fats and Oils - Preparation of Metyl Esters of Fatty Acids. ISO 5509, pp. 01-06

Katan M.B., Zock P.L., Mensink R.P., 1994. Effects of fats and fatty acids on blood lipids in humans: an overview. Amer. J. Clin. Nutr. 60, 1017-1022

Kwiterovich P.O., 1997. The effect of dietary fat, antioxidants, and pro-oxidants on blood lipids, lipoproteins, and atherosclerosis. J. Amer. Diet. Assn. 97, 31-41

Luchiari Filho A., 2000. Livestock of Meat Cattle (in Portoguese). 1st Edition. Sao Paulo, pp. 134

Milinsk M.C., Padre R.G., Hayashi C., Oliveira C.C., Visentainer J.V., Souza N.E., 2005. Effects of feed protein and lipid contents on fatty acid profile of snail (*Helix aspersa maxima*) meat. J. Food Compos. Anal. 19, 212-216

Moreira F.B., Prado I.N., Souza N.E., Matsushita M., Mizubitu I.Y., Macedo L.M.A., 2005. Animal performance and carcass characteristics of steers finished in black oat pasture with or whitout energetic supplement. Acta Scient. 27, 469-473

Moreira F.B., Souza N.E., Matsushita M., Prado I.N., Nascimento W.G., 2003. Evaluation of carcass characteristics and meat chemical composition of *Bos indicus* x *Bos taurus* crossbred steers finished in pasture systems. Braz. Arch. Biol. Technol. 46, 609-616

Müller L., 1980. Norms for Carcass Avaliation and Carcass Concourse of Cattle (in Portoguese). Federal University of Santa Maria, Santa Maria, pp. 31

Nieto Martin L., 2004. Genetic factors that change the meat and milk quality in ruminants. In: Prado. Conceits about the Production with Quality of Meat and Milk. 1st Edition. Maringá, pp. 35-52

NRC, 1996. Nutrient Requirements of Beef Cattle. 7th Edition. National Academy Press. Washington, DC

Padre R.G., Aricetti J.A., Gomes S.T.M., Goes R.H.T.B., Moreira F.B., Prado I.N., Visentainer J.V., Souza N.E., Matsushita M., 2007. Analysis of fatty acids in *Longissimus* muscle of steers of different genetic breeds finished in pasture systems. Livest. Sci. 110, 57-63

Padre R.G., Aricetti J.A., Moreira F.B., Mizubuti I.Y., Prado I.N., Visentainer J.V., Souza N.E., Matsushita M., 2006. Fatty acids profile, and chemical composition of *Longissimus* muscle of bovine steers and bulls finished in pasture system. Meat Sci. 74, 242-248

Pensel N., 1998. The future for red meat in human diets. Nutr. Abstr. Rev., Ser A 68, 1-4

Perotto D., Cubas A.C., Moletta J.L., Lesskiu C., 1998. Birth weight, weaning weight and weight gain from birth to weaning of Charolais, Caracu and reciprocal crosses. Braz. J. Anim. Sci. 27, 730-737

Perotto D., Moletta J.L., Oliveira J.E.P., Lesskiu C., 2000. Feed intake and feed:gain ratio of Charolais, Caracu and reciprocal crossbred finished males in feedlot. Braz. J. Anim. Sci. 29, 108-116

Rowe A., Macedo F.A.F., Visentainer J.V., Souza N.E., Matsushita M., 1999. Muscle composition and fatty acid profile in lambs fattened in drylot or pasture. Meat Sci. 51, 283-288

SAS, 2000. SAS User´s Guide. Version 8.1. 4th Edition. Cary, NC

Saucier L., 1999. Meat safety: challenges for the future. Nutr. Abstr. Rev., Ser. A 69, 705-708

Webb E.C., 2006. Manipulation beef quality through feedind. S. Afr. J. Food Sci. Nutr. 7, 1-24