



Carcass Characteristics and Chemical Composition of the *Longissimus* Muscle of Purunã and 1/2 Purunã vs. 1/2 Canchin Bulls Meat Quality of Bulls

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ABSTRACT : This work was conducted to study the performance, carcass characteristics, chemical composition and fatty acid profile of the *Longissimus* muscle (LM) of first-generation Purunã (n = 7, PUR1), second-generation Purunã (n = 9, PUR2), and 1/2 Purunã vs. 1/2 Canchin (n = 13, PUCA) bulls finished in a feedlot. The animals averaged 18 months of age at the beginning of the experiment. The animals were kept in a feedlot from 18 to 22 months of age. They were fed twice a day with corn silage *ad libitum*, along with soybean meal, cracked corn, urea, limestone and mineral salt. PUR1 bulls had greater (p<0.05) final weight (496.0 kg) than PUCA bulls (449.2 kg). However, there was no difference (p>0.05) between PUR1 and PUR2 (472.0 kg), and between PUR2 and PUCA. Hot carcass weight was similar (p>0.05) among the different genetic groups. Hot carcass dressing percentage was similar (p>0.10) between PUR1 (50.4%) and PUCA (53.8%), and higher (p<0.10) than PUR2 (48.6%). Cushion thickness was greater (p<0.05) in PUCA bulls (27.12 cm). The other parameters were similar (p<0.05) among the three genetic groups. Total lipid and cholesterol contents were higher (p<0.01) in PUR2. Moisture, ash and crude protein contents were similar (p>0.05) among the three genetic groups. Saturated fatty acid (SFA) levels were higher (p<0.10) in PUR1 and PUR2 (51.58% and 50.41%, respectively). Polyunsaturated fatty acid levels were higher (p<0.05) in PUR1 and PUCA (6.50% and 8.29%, respectively). N-6, n-3 and PUFA/SFA ratios were higher (p<0.05) in PUCA. MUFA and n-6/n-3 ratios were similar (p>0.05) among the different genetic groups. (**Key Words :** Cattle, Crossbreed, Fatty Acids, *Longissimus* Muscle, Meat Quality)

INTRODUCTION

Brazil has the largest commercial cattle herd in the world, with approximately 159 million animals and a production of approximately 8.2 million tons of carcass each year. From this total, about 30% (2.4 million tons) are exported to several countries around the world (Anualpec, 2007).

The State of Paraná, located in south Brazil, features a milder climate as compared to other regions of the country. Consequently, researchers have been conducting studies since the 1980s on the crossbreeding between Zebu and European breeds, with the objective of increasing production (Perotto et al., 2000) and meat quality of the

bulls (Moreira et al., 2003; Padre et al., 2006; Padre et al., 2007). After several stages of crossbreeding, an ideal crossbreeding ratio was found as the best adapted for the region. Initially, Nellore specimens were crossbred with Charolaise, Angus, Caracu and Canchim cattle (Perotto et al., 1998; Perotto et al., 2000), giving rise to a breed denominated Purunã. Purunã bulls are very well adapted to subtropical and tropical regions, and show good weight gain potential. Their carcass has better conformation and greater fat thickness than Zebu bulls. Cattle breeding is one of the most important factors for fat deposition and composition that needs to be understood because of its genetic transmission. British breeds are well-known for their highly marbled meat, while the Zebu breeds feature less fat and more connective tissue. In the warmer region of Brazil, adapted cattle breeds are primarily limited to *Bos indicus* cattle crossbred with Brazilian Nellore.

Beef has excellent nutritional value because it includes proteins of high biological value, is rich in vitamin content (particularly B-complex), and is associated with high

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Received December 4, 2007; Accepted April 17, 2008

Table 1. Point scale for meat texture and color evaluation

Texture	Points	Coloration	Points
Very fine	5	Cherry red	5
Fine	4	Red	4
Slightly coarse	3	Slightly dark red	3
Coarse	2	Dark red	2
Very coarse	1	Dark	1

Source: Müller (1987).

mineral content, especially iron, in high bioavailability form (Saucier, 1999). It also contains all the amino acids required by humans (Pensel, 1988). However, beef is regarded as one of the factors that may lead to the development of cardiovascular disease in humans, obesity, hypertension and cancer, especially due to the presence of saturated fat and cholesterol. Nevertheless, fat contents lower than 5% of muscle weight and cholesterol contents lower than 50 mg per 100 g of muscle have been reported in literature (Gregghi et al., 2003; Moreira et al., 2003; Padre et al., 2007), which represents a third to a half of the daily intake by humans. However, fat represents between 25 to 30% of the total body weight of an adult, and performs important functions in the body (Hegarty, 1995). Therefore, fat must be present in the diet, especially some polyunsaturated fatty acids, which, if not consumed in the necessary amount, may alter ideal body functioning, as they cannot be synthesized (Ewin, 1997).

The objective of this study was to evaluate animal performance, carcass characteristics, chemical composition, and fatty acid profile of the LM of crossbreed first-generation Purunã, second-generation Purunã, and 1/2 Purunã vs. 1/2 Canchim bulls.

MATERIALS AND METHODS

Animal management and sampling

The State University of Maringá animal care and ethics committee approved the use of bulls in this study (CIOMS/OMS, 1985).

This study was carried out at the Experimental Farm of the Agronomic Institute of Paraná, in south Brazil. Twenty-nine (7 first-generation Purunã, PUR1; 9 second-generation Purunã, PUR2; and 13 1/2 Purunã vs. 1/2 Canchim, PUCA) animals, with an initial average age of 18 months, were used. The meat analyses were carried out at the Chemistry Laboratory of the State University of Maringá.

The animals were kept separate in individual pens (5 m² for each animal), and fed twice a day. They were given access to a diet formulated to meet requirements for fattening beef cattle (NRC, 1996). The diet consisted of 50% silage corn, 20% cracked corn, 13% cotton meal, 15% wheat middling, 1% urea, 0.5% limestone, and 0.5% mineral salt.

The animals were weighed at the beginning of the study

and every 28 days thereafter, as well as on the day before slaughter, after 12-hour fasting. The average final live weight for PUR1 was 496.0±32.5 kg, 472.0±28.8 kg for PUR2, and 449.9±26.7 kg for PUCA.

Carcass characteristics

The animals were slaughtered at a commercial slaughterhouse 90 km away from the farm, in Curitiba, Paraná, according to industrial practice in Brazil. After slaughter, the carcasses were identified and cooled for 24 h at 4°C.

Hot carcass weight : hot carcass weight (kg) was determined right after slaughter, before cooling the carcass. In the slaughter of bulls, the carcasses were identified, weighted and conducted to a cooling chamber at a temperature of 4°C, during 24 h. After cooling, the right part of the carcass was used to determine quantitative characteristics.

Dressing percentage : the dressing percentage for an individual animal is defined as hot carcass weight divided by live weight.

Conformation : it was evaluated by Müller's point scale (Müller, 1987), in which the highest value indicates the best conformation; muscle development was considered after the exclusion of cover fat. The carcass conformation is reported as superior, very good, good, regular, poor, and inferior; ratings may also be reported as plus, average, and minus.

Carcass length : 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 : 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 : it was taken by a wood compass with metallic edges that measures the distance between the lateral face and the median at the superior part of the cushion. After this, the distance was measured with a ribbon or a tape measure.

Fat thickness : it was taken using a caliper, averaging three points between the 12th and the 13th rib, but over the LM.

Longissimus muscle area : the *Longissimus* muscle area was analyzed using the right part of carcass, where a cross-section cut was made between the 12th and 13th ribs, exposing the *Longissimus* muscle. After this, a compensating planimeter, which is an instrument that measures the area of irregularly shaped objects, was used to determine the area.

Color : muscle color after 24-h carcass cooling was analyzed. Coloration was evaluated according to a point scale (Table 1) 30 min after a cross-section was made on the *Longissimus* between the 12th and 13th ribs.

Table 2. Point scale for marbling grade evaluation

Marbling	Plus	Average	Minus	Marbling	Plus	Average	Minus
Abundant	18	17	16	Small	9	8	7
Moderate	15	14	13	Light	6	5	4
Mean	12	11	10	Traces	3	2	1

Source: Müller (1987).

Texture : texture was determined through the size of the fascicle (muscle “grain” size) and evaluated subjectively with a point scale, the same as that of marbling (Table 2).

Marbling : intramuscular fat was measured in the LM between the 12th and 13th ribs, according to the scores on Table 2.

After 24 h, LM samples were taken by complete cross-section between the 12th and 13th ribs, and were immediately taken to the laboratory. Cover fat was discarded, and the muscle portion was frozen at -20°C for later analysis.

Chemical composition

Laboratory analyses of beef were carried out two months after sampling. The samples were unfrozen at room temperature (20°C), grounded, homogenized, and analyzed in triplicate.

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

Cholesterol quantification

Cholesterol analysis was carried out by the method modified by Rowe et al. (1999). A 60% (w/v) solution of potassium hydroxide was added to the samples in quantities equivalent to 2 ml/h of sample under 1-h reflux. The residue was dissolved again in 2 mL hexane containing 0.2 mg/ml 5- α cholestane internal standard (IS) (Sigma, USA).

Cholesterol content was analyzed in 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 μ m Ohio Valley-30). Injector, column, and detector temperatures were 260, 280, and 280°C, respectively. Ultra-pure gas fluxes (White Martins) of 1.5 ml/min H₂ as carrier gas, 30 ml/min N₂ as make-up gas, 300 ml/min synthetic gas, and 30 ml/min N₂ for flame were used. The sample injection split mode was: 1:150. Peak integration was carried out with a 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, all containing 0.20 mg/ml 5 α -cholestane (Sigma, USA), and analyzed. The ratio of the areas of cholesterol and 5- α cholestane was plotted against the cholesterol concentration for injected volumes of 0.0; 2.0; 3.0; 4.0, and 5.0 μ l. 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 analyzed 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 μ m o.d., Varian, USA) Select Fame. Column temperature was programmed at 165°C for 18 min, 180°C (30°C/min) for 22 min, and 240°C (15°C/min) for 30 min, with 45-psi pressure. The injector and detector were kept at 220°C and 245°C, respectively. The gas fluxes (White Martins) used were: 1.4 ml/min for the carrier gas (H₂); 30 ml/min for the make-up gas (N₂) and 30 ml/min and 300 ml/min for H₂ 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 samples 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).

Experimental design and statistical analysis

The experimental design consisted of 3 treatments: 7 first-generation Purunã, 9 second-generation Purunã, and 13 1/2 Purunã vs. 1/2 Canchin genetic groups. The data were submitted to an analysis of variance, and the averages (when different) were compared using the Tukey test at 10, 5 and 1% significance levels, using SAS statistical software (2000), according to the following mathematical model:

$$Y_{ij} = \mu + t_i + e_{ij}$$

In which:

Y_{ij} = observation of animal j, subjected to treatment i;

μ = overall constant;

t_i = treatment effect $i = 1; \dots; 3$;

e_{ij} = random error associated with each observation.

Table 3. Final weight (FW), hot carcass weight (HCW), hot carcass dressing (HCD), conformation (COF), leg length (LL), carcass length (CL), cushion thickness (CT), *Longissimus* muscle area (LMA), fat thickness (FT), color (COL), texture (TEX), and marbling (MAR) of first-generation Purunã bulls, second-generation bulls, and 1/2 Purunã vs. 1/2 Canchim bulls finished in feedlot

Parameters	Genetic groups			p>f
	PUR1 ¹	PUR2 ²	PUCA ³	
FW (kg)	496.00±5.24 ^a	472.00±4.08 ^b	449.92±2.82 ^c	**
HCW (kg)	249.86±2.79 ^a	228.75±2.17 ^b	241.58±1.50 ^a	*
HCD (%)	50.38±0.47 ^b	48.46±0.37 ^c	53.70±0.25 ^a	*
COF (points)	12.43±0.18	12.78±0.14	12.46±0.10	NS
LL (cm)	68.86±0.43	68.22±0.33	70.00±0.23	NS
CL (cm)	133.57±0.76	131.56±0.59	132.46±0.41	NS
CT (cm)	25.4±0.17 ^b	24.72±0.13 ^b	27.12±0.09 ^a	**
FT (cm)	3.71±0.14	3.00±0.11	3.50±0.07	NS
LMA (cm ²)	64.57±0.92	66.67±0.71	64.23±0.49	NS
COL (points)	3.57±0.13	3.56±0.10	3.77±0.07	NS
TEX (points)	4.14±0.08	3.89±0.06	4.38±0.04	NS
MAR (points)	7.14±0.25	7.78±0.19	6.85±0.13	NS

¹ First-generation Purunã, ² Second-generation Purunã, ³ 1/2 Purunã vs. 1/2 Canchim.

** Significant at 5% level by Tukey test. * Significant at 10% level by Tukey test. NS: No significant difference among means.

RESULTS AND DISCUSSION

Final weight and carcass characteristics

Table 3 shows final live weight and hot carcass weight and characteristics of PUR1, PUR2, and PUCA bulls finished in feedlot. PUR1 bulls had greater ($p<0.01$) final weight (496.0 kg) in comparison to PUR2 (472.0 kg), and PUCA bulls (449.9 kg). Further, animals from the PUR2 genetic group had greater ($p<0.01$) final weight in comparison to PUCA animals. The greater final weight observed in PUR1 bulls could be related to greater heterosis in this genetic group (Nieto Martin, 2004), as they belonged to the first generation of the Purunã breed. The lower weight for the PUCA genetic group could be attributed to the use of crossbred animals and the lower weight of Canchim animals in comparison to the breeds that gave rise to the Purunã.

Hot carcass weight was lower ($p<0.05$) for bulls from the PUR2 genetic group (228.7 kg) in comparison to the PUR1 (249.9 kg) and PUCA (241.6 kg) groups. However, there was no observed difference ($p>0.05$) between bulls from the PUR1 and PUCA genetic groups. The lower carcass weight for the PUR2 group was determined by the lower final weight and low carcass dressing in animals from this genetic group. Notwithstanding, the hot carcass weight observed in all three groups meets the guidelines of the Brazilian market for beef commercialization (minimum carcass weight of 225 kg).

Hot carcass dressing was greatest ($p<0.05$) in bulls from the PUCA genetic group (53.7%), intermediate for the PUR1 group (50.4%), and lowest among the PUR2 genetic group (48.5%). However, hot carcass dressing for animals from the Purunã breed is below that of animals from similar categories (Abrahão et al., 2005; Moreira et al., 2005). However, such low carcass dressing may be related to the

thorough cleaning methods performed in the carcass of bovines by slaughterhouses in Brazil. Moreira et al. (2005) observed carcass dressing above 54% in crossbred animals resultant from industrial crossbreeding. The greater carcass dressing in bulls from the PUCA breed could be related to the higher ratio of genes from Zebu cattle, which feature greater cover fat deposition.

Carcass conformation and length, as well as leg length were similar ($p<0.05$) among the three genetic groups studied. According to Müller's scale (1987), the observed conformation can be considered adequate to meet the standards of the Brazilian market.

Cushion thickness was similar ($p<0.05$) for the PUR1 and PUR2 genetic groups. However, bulls from the PUCA group showed greater ($p<0.05$) cushion thickness. The greater cushion thickness for PUCA bulls is explained by the higher ratio of genes from beef cattle breeds, which are characterized by greater muscle development in the posterior of these animals.

There was no observed difference ($p>0.05$) in fat thickness, *Longissimus* muscle area, color, texture and marbling in the *Longissimus* muscle of all three genetic groups. Fat thickness met the guidelines of the Brazilian market, which requires that carcasses have at least 3 mm of fat thickness. Similarly, *Longissimus* muscle area was greater than 64 cm² for all three genetic groups. The *Longissimus* muscle area determines the bull's muscle development. The color, texture and marbling observed in the *Longissimus* muscle indicate that the meat of all three genetic groups meets the standards of beef commercialization in Brazil.

Chemical composition

Table 4 shows the chemical composition results for PUR1, PUR2 and PUCA bulls. Moisture, ash and crude

Table 4. Moisture, ash, crude protein, total lipids and total cholesterol in *Longissimus* muscle of bulls finished in feedlot

Parameters	Genetic groups			p>f
	PUR1 ¹	PUR2 ²	PUCA ³	
Moisture (%)	74.20±0.20	73.02±0.15	73.80±0.11	NS
Ash (%)	1.06±0.01	1.05±0.01	1.01±0.01	NS
Crude protein (%)	23.56±0.19	24.23±0.15	23.47±0.10	NS
Total lipids (%)	1.71±0.07 ^b	3.00±0.05 ^a	1.96±0.04 ^b	*
Total cholesterol (mg/100 g of muscle)	41.65±0.19 ^b	52.73±0.17 ^a	36.54±0.14 ^b	**

¹ First-generation Purunã, ² Second-generation Purunã, ³ 1/2 Purunã vs. 1/2 Canchim.

*** Significant at 1% level by Tukey test. ** Significant at 5% level by Tukey test. * Significant at 10% level by Tukey test.

NS: No significant difference among means.

protein contents were similar ($p>0.05$) among genetic groups. There was no difference in moisture levels in the LM muscle among genetic groups. Average moisture content was 73.5%, which is similar to other studies (Moreira et al., 2006; Lee et al., 2007). Padre et al. (2006) found 73.7% of moisture content in 1/2 Nellore vs. 1/2 Aberdeen Angus. Variations in moisture levels occur when there is a variation in lipid levels in the *Longissimus* muscle.

Similarly, ash content was not affected ($p>0.05$) according to genetic group. The average ash content was 1.0%. Prado et al. (2003), Padre et al. (2006 and 2007), Brown et al. (2007), Lee et al. (2007) observed ash content levels similar to this study. Thus, ash content is little influenced by diet or genetic group.

The average protein level in the *Longissimus* muscle was 23.7%, with no difference ($p>0.05$) among the

different genetic groups. In literature (Prado et al., 2003; Marques et al., 2006; Brown et al., 2007; Padre et al., 2007), there are reports of average crude protein content in *Longissimus* varying between 21 and 23%. Thus, it can be concluded that diet or genetic group would not alter protein levels in the muscles of bovines.

Total lipid content was greater ($p<0.05$) in the *Longissimus* muscle of animals from the PUR2 genetic group in comparison to animals from the PUR1 and PUCA genetic groups. However, there was no observed difference ($p>0.05$) in the *Longissimus* muscle of animals from the PUR1 and PUCA genetic groups. In general, total lipid levels in the *Longissimus* muscle of steers finished in feedlot is close to 3% (Prado et al., 2003; Padre et al., 2006 and 2007). However, total lipid levels observed in all three groups is below the maximum level regarded as acceptable

Table 5. Fatty acid profile (% of total fatty acids) of *Longissimus* muscle of first-generation Purunã, second-generation Purunã, and 1/2 Purunã vs. 1/2 Canchin

Fatty acids	PUR1 ¹	PUR2 ²	PUCA ³	p>f
14:0 Myristic acid	1.77±0.06	1.89±0.05	1.95±0.03	NS
14:1 <i>n</i> -7	0.34±0.02	0.29±0.01	0.40±0.01	NS
16:0 Palmitic acid	29.33±0.43 ^a	29.08±0.33 ^a	25.30±0.23 ^b	***
16:1 <i>n</i> -7 Palmitoleic acid	2.37±0.08	2.94±0.06	2.59±0.04	NS
ai 17:0 anti-iso	0.23±0.01	0.24±0.01	0.26±0.01	NS
i 17:0 iso	0.49±0.01	0.54±0.01	0.51±0.01	NS
17:0 Margaric acid	0.71±0.02 ^{ab}	0.59±0.01 ^b	0.72±0.01 ^a	***
17:1 <i>n</i> -7 Heptadecenoic acid	0.54±0.02	0.50±0.01	0.59±0.01	NS
18:0 Stearic acid	19.15±0.30	19.34±0.23	17.47±0.16	NS
18:1 <i>n</i> -9 Oleic acid	34.57±0.47 ^b	37.99±0.37 ^a	38.68±0.25 ^a	***
18:1 <i>n</i> -7 Cis-Vaccenic acid	2.68±0.06 ^b	3.23±0.05 ^a	3.22±0.03 ^a	**
18:1 <i>n</i> -11 -Octadecenoic acid	0.85±0.03	0.86±0.02	0.92±0.01	NS
18:2 <i>n</i> -6 Linoleic acid	4.31±0.16 ^a	2.26±0.13 ^b	4.99±0.09 ^a	*
18:3 <i>n</i> -6 Linolenic acid	0.11±0.01 ^b	0.11±0.01 ^b	0.14±0.01 ^a	***
18:2 <i>c</i> -9 <i>t</i> -11 Conjugated linoleic acid - CLA	0.18±0.02 ^b	0.17±0.01 ^b	0.34±0.01 ^a	*
18:3 <i>n</i> -3 α -Linolenic acid	0.25±0.01	0.18±0.01	0.26±0.01	NS
20:4 <i>n</i> -6 Arachidonic acid	1.50±0.05 ^a	0.69±0.04 ^b	1.71±0.03 ^a	*
20:5 <i>n</i> -3 Timnodonic acid (EPA)	0.12±0.01 ^b	0.09±0.01 ^b	0.32±0.01 ^a	*
22:0 Behenic acid	0.22±0.01 ^b	0.13±0.01 ^b	0.32±0.01 ^a	***
22: 5 <i>n</i> -3 Clupadonic acid (DPA)	0.15±0.01 ^b	0.07±0.01 ^c	0.22±0.01 ^a	**
22:6 <i>n</i> -3 Cervonic acid (DHA)	0.36±0.02 ^a	0.19±0.01 ^b	0.46±0.01 ^a	**

¹ First-generation Purunã, ² Second-generation Purunã, ³ 1/2 Purunã vs. 1/2 Canchim.

*** Significant at 1% level by Tukey test. ** Significant at 5% level by Tukey test. * Significant at 10% level by Tukey test.

NS: No significant difference among means.

Table 6. Saturated fatty acids (SFA), monounsaturated fatty acids (MUFA), polyunsaturated fatty acids (PUFA), *n*-6, *n*-3, PUFA/SFA and *n*-6/*n*-3 ratio of *Longissimus* muscle of first-generation Purunã, second-generation Purunã, and 1/2 Purunã vs. 1/2 Canchim

Parameters	Genetic groups			p>f
	PUR1 ¹	PUR2 ²	PUCA ³	
SFA	51.58±0.59 ^a	50.41±0.46 ^a	46.38±0.32 ^b	***
MUFA	38.99±0.55	42.48±0.43	39.34±0.30	NS
PUFA	6.50±0.26 ^a	3.99±0.20 ^b	8.29±0.14 ^a	**
<i>n</i> -6	5.19±0.22 ^b	3.44±0.17 ^c	6.78±0.12 ^a	***
<i>n</i> -3	0.72±0.05 ^b	0.53±0.04 ^b	1.13±0.03 ^a	**
PUFA/SFA	0.10±0.01 ^b	0.08±0.01 ^b	0.17±0.01 ^a	**
<i>n</i> -6/ <i>n</i> -3	6.92±0.23	5.60±0.17	7.04±0.12	NS

¹ First-generation Purunã, ² Second-generation Purunã, ³ 1/2 Purunã vs. 1/2 Canchim.

*** Significant at 1% level by Tukey test. ** Significant at 5% level by Tukey test. * Significant at 10% level by Tukey test.

NS: No significant difference among means.

for the prevention of diseases related to fat content in beef, according to recommendations from the English Health Department (HMSO, 1994).

Cholesterol content was higher ($p < 0.05$) in PUR2 bulls (52.73 mg/100 g of muscle). This can be related to the fact that these bulls showed higher total lipid content. LM cholesterol content in PUR1 (41.6 mg/100 g of muscle) was similar ($p > 0.05$) in comparison to that of PUCA (36.5 mg/100 g of muscle). Padre et al. (2006) found that crossbred bulls had 45.8 mg/100 g of muscle of cholesterol content.

Fatty acid profile

The percentage of fatty acid in LM intramuscular fat is shown on Table 5. Fatty acid diversity is partly explained by the biohydrogenation that occurs in the rumen (Tamminga and Doreau, 1991).

Myristic acid (14:0), palmitoleic acid (16:1 *n*-7), anti-iso (ai 17:0), iso (i 17:0), heptadecenoic acid (17:1 *n*-7), stearic acid (18:0), octadecenoic acid (18:1 *n*-11), and α -linolenic acid (18:3 *n*-3) contents were similar ($p > 0.05$) in the different crossbreeds. Palmitic acid (16:0) was higher ($p < 0.10$) in PUR1 bulls and PUR2 bulls. Margaric acid (17:0) was higher ($p < 0.10$) in PUCA and PUR1 bulls. Oleic acid (18:0) and vaccenic acid were higher ($p < 0.10$) in PUR2 and PUCA bulls. Linoleic acid (18:2 *n*-6) and conjugated linoleic acid - CLA were higher ($p < 0.01$) in PUR1 and PUCA bulls. γ -linoleic acid (18:3 *n*-6) was higher ($p < 0.10$) in PUCA bulls. Arachidonic acid (20:4 *n*-6), timnodonic acid (20:5 *n*-3), behenic acid (22:0), and clupadonic acid (22:5 *n*-3) were higher ($p < 0.10$) in PUCA bulls. Cervonic acid (22:6 *n*-3) was higher ($p < 0.05$) in PUR1 and PUCA bulls.

As ruminant diets contain low fat concentration, the majority of the adipose tissue is synthesized from lipogenesis. Fatty acids are elongated up to 18:0 and are converted into 18:1 by desaturation (Rule et al., 1997). As the adipose tissue increases, the deposition of 18:1 content also increases and that of 18:2 is reduced.

Oleic acid increases human HDL-Cholesterol (High Density Lipoprotein) and decreases LDL-cholesterol (Low Density Lipoprotein) concentration in blood (Katan et al., 1994). Studies demonstrated a strong relationship between LDL-cholesterol levels and human cardiovascular diseases, and that HDL-cholesterol has an inverse relation with the risk of cardiovascular diseases (Kwiterovich, 1997).

Saturated fatty acids (SFA) content was higher ($p < 0.10$) in PUR1 (51.58%), and PUR2 (50.41%). Polyunsaturated fatty acids (PUFA) content was higher ($p < 0.05$) in PUR1 (6.50%), and PUCA (8.29%). *N*-6 and *n*-3 contents were higher ($p < 0.10$) in PUCA bulls (6.78 and 1.13% respectively). PUFA/SFA ratio was higher ($p < 0.05$) in PUCA bulls (0.17). Monounsaturated fatty acids and *n*-6/*n*-3 ratios were similar ($p > 0.05$) among the genetic groups.

Although the animal diet contained high levels of PUFA, the meat presented high values of SFA due to biohydrogenation in the rumen (Tamminga and Doreau, 1991). PUFA/SFA fatty acids play important roles in reducing the risk of coronary heart disease; however, the optimal balance between these two classes of fatty acids is still a matter of debate (Hu, 2001).

IMPLICATIONS

Crossbreeding between Zebu cattle (well adapted to tropical and subtropical climates) with European breeds (with greater zootechnical potential) alters the carcass characteristics and chemical composition of the *Longissimus* muscle in bulls finished in feedlot. Similarly, the concentration of fatty acids in the *Longissimus* is altered by crossbreeding between these two subspecies of bovines. Thus, industrial crossbreeding could become a tool for introducing genes that could improve animal performance and carcass characteristics, as well as fatty acid levels.

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