Asian-Aust. J. Anim. Sci.
Vol. 21, No. 10 : 1449 - 1457
October 2008

www.ajas.info

Carcass Characteristics, Chemical Composition and Fatty Acid Profile of the *Longissimus* Muscle of Bulls (*Bos taurus indicus* vs. *Bos taurus taurus*) Finished in Pasture Systems

Ivanor Nunes do Prado*, Juliana Aparecida Aricetti[1], Polyana Pizzi Rotta[2], Rodolpho Martin do Prado[2] Daniel Perotto[3], Jesuí Vergílio Visentainer[4] and Makoto Matsushita[4]

Department of Animal Science. State University of Maringá, Paraná, Brazil

ABSTRACT : This experiment was carried out to evaluate the carcass characteristics, chemical composition and fatty acid profile of the *Longissimus* muscle (LM) of three cattle genetic groups (Purunã, PUR, 11; 1/2 Purunã vs. 1/2 British, PUB, 6 and 1/2 Charolais vs. 1/2 Caracu, CHC, 10) finished in pasture systems. The field work took place at the Lapa Research Farm of the Agronomic Institute of Paraná, in the city of Lapa, south Brazil. The animals were fed during the winter with corn silage, cottonseed meal, cracked corn, urea, limestone and mineral salts as sources of protein, as well as an energy supplement, in pasture systems of *Brachiaria decumbens* Stapf. The animal groups were slaughtered at 20 months of age, at 501±22.6 kg live weight. CHC bulls had higher ($p<0.05$) final weight than PUR and PUB bulls. Hot carcass weight was similar ($p>0.10$) between PUR and PUB. Hot carcass dressing percentage was higher ($p<0.05$) for PUB bulls than for PUR and CHC bulls. On the other hand, hot carcass dressing percentage was similar ($p>0.05$) between PUR and CHC bulls. Fat thickness was similar ($p>0.10$) among all genetic groups. However, the *Longissimus* area of CHC bulls was greater ($p<0.05$) than in PUR and PUB genetic groups. The genetic groups did not affect ($p>0.10$) the marbling of *Longissimus*. There was no observed difference ($p>0.10$) in moisture, ash, crude protein and total cholesterol contents among the three genetic groups. On the other hand, the total lipid percentage was higher ($p<0.05$) for the PUB genetic group in comparison with PUR and CHC. CLA percentage was highest for PUR animals. However, total CLA amounts were not altered by the different genetic groups. (**Key Words :** Beef, British, Caracu, Chemical Composition, *Longissimus* Muscle)

INTRODUCTION

Brazil has the largest commercial cattle herd of the world, and has potential to become the greatest producer of cattle meat for export; there are 159 million heads of cattle, able to produce 8.2 million tons/year of carcasses (Anualpec, 2007), which makes the control of meat quality extremely important to maintain a long-term market.

Beef is considered one of the factors that may lead to the development of human cardiovascular diseases, obesity, hypertension and cancer, especially due to the presence of saturated fat and cholesterol. Low presence of fat contents (less than 3% relative to muscle: Moreira et al., 2003; Padre et al., 2006 and 2007) and low cholesterol contents (less than 50 mg/100 g in the muscle) have been observed in beef chemical analyses, ranging from one-third to one-half of the daily recommended cholesterol intake (Greghi et al., 2003; Padre et al., 2006 and 2007).

Cattle breed is one of the most important factors for fat deposition and composition, which needs to be understood because of its genetic transmission. However, the detailed mechanisms of this variation, and whether or how they can be manipulated are not clearly known (Martin Nieto, 2004). British cattle are well known for their highly marbled meat, while the Nellore breed contains less fat and more connective tissue (Silva et al., 2002; Moreira et al., 2003).

In the warm regions of the Brazil, adapted breeds of cattle are primarily limited to the *Bos indicus indicus* (Zebu) cattle, bred from Brazilian Nellore.

* Corresponding Author: Ivanor Nunes do Prado. Tel: +55-44-3261-4348, Fax: +55-44-3261-4378, E-mail: inprado @uem.br

[1] Department of Chemistry, State University of Maringá, Brazil.

[2] Department of Animal Science, State University of Maringá, Science grant, CNPq, Brazil.

[3] IAPAR Agronomic Institute of Paraná, Curitiba, Paraná, Brazil.

[4] Department of Graduate Chemistry, State University of Maringá, Brazil.

Received January 30, 2008; Accepted April 17, 2008

The Caracu is a tropically adopted, criollo beef breed native to Brazil. Few studies have investigated the meat characteristics of Caracu, focusing instead more on reproductive and carcass performance (Perotto et al., 2000 and 2001). Marbling and fatty acid composition of Caracu cattle, especially as compared to other purebreds and crossbreds, remain little studied. Like most animal production traits, meat quality is influenced by both genetic and environmental factors (Martin Nieto, 2004; Webb, 2006). The latter includes management but mainly feeding, explaining why the majority of studies attempting to achieve meat quality that better correspond to current human nutrition guidelines have dealt with animal feeding (Webb, 2006).

Genetic variability consists of differences between species, breeds or lines; differences due to the crossing of breeds; and differences between animals within breeds. The latter source of variation is estimated by heritability and genetic correlations. Breed effects may be influenced by the segregation of major genes, one of which is the double-muscled gene in cattle. It is sometimes difficult to assess the real contribution of genetics to differences in meat quality. Breed comparisons are often confounded by other effects, like fat level, live weight, age at slaughter and production system (Webb, 2006).

The State of Paraná, located in south Brazil, features a milder climate as compared to the Center-West, North and Northeast regions of Brazil. Thus, research has been undertaken in this region since the 1980s regarding the crossbreeding of Zebu and European breeds, aiming to increase production and quality of offspring beef (Perotto et al., 2000 and 2001; Padre et al., 2007). After several stages of crossbreeding, a bloodline was defined as the best-adapted to the region. In the beginning, crossbreeding between Nellore specimens with Charolais, Angus, Caracu and Canchin breeds was undertaken, which resulted in the creation of a breed denominated Pururuã.

Beef normally has a low PUFA/SFA ratio compared to pork, because of the biohydrogenation of unsaturated fatty acids in the rumen (Tamminga and Doreau, 1991). Enser et al. (1996) found that for steaks and chops, the mean P/S ratio is 0.11 for beef and 0.58 for pork, being more favorable to pork. On the other hand, the *n*-6/*n*-3 ratio is more favorable to beef as compared to pork (2.11 and 7.22, respectively). However, these mean values may vary largely, depending on genetic and feeding factors, and thus should not be generalized.

This work was carried out in order to study the carcass characteristics, chemical composition and fatty acid profile in the *Longissimus* muscle (LM) of bulls breeds Pururuã (11), 1/2 Pururuã vs. 1/2 British (6) and 1/2 Charolais vs. 1/2 Caracu (10), finished in pasture system.

MATERIALS AND METHODS

Animal management and sampling

The State University of Maringá animal care and ethics committee approved the use of animals for this study.

This study was carried out at the Experimental Farm of the Agronomic Institute of Paraná, in the city of Lapa, Brazil. Twenty-seven (11, Pururuã, PUR; 6, 1/2 Pururuã vs. 1/2 British, PUB and 10, 1/2 Charolais vs. 1/2 Caracu, CHC) bulls with an initial average age of 20 months were used. The meat analyzes were carried out in the Chemical Laboratory of the State University of Maringá.

After weaning (8 months old), the animals of each breed were kept in a fenced pasture of Brachiaria grass (*Brachiaria decumbens* Stapf) until 20 months old, when they were slaughtered. The animals were kept in separate paddocks. They were given access to a supplement as a source of protein and energy during the winter (NRC, 1996). The diet consisted of corn silage, cracked corn, cottonseed meal, urea, limestone, and mineral salt.

The animals were weighed in the beginning of the study and every 28 days, as well as on the day before slaughtering after 12 h of fasting. The average final live weight for PUR was 493±22.6 kg, 463±21.2 for PUB, and 546±24.3 for CHC.

Carcass characteristics

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

Hot carcass weight (HCW) : It was determined before cooling. The percentage of individual animal dressing was defined by the ratio of hot carcass weight to live weight.

Carcass conformation (CC) : It was evaluated by Muller's point scale (Müller, 1980) in which the highest value indicates the best conformation; muscle development was considered after the exclusion of thickness fat. The carcass conformations were reported as superior, very good, good, regular, poor, and inferior; ratings may also be reported as plus, mean, and minus. The carcass length was evaluated by measurements taken from the border of the pubis bone until the anterior side of the first rib.

Leg length (LL) : It was evaluated using a wood compass with metallic edges that measures the distance from the anterior border of the pubis bone to a middle point at the tarsus bone.

Cushion thickness (CT) : 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.

Longissimus area (LA) : The right part of the carcass was measured after a transversal cut was made between the

Table 1. Scale for marbling evaluation

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

Source: Müller (1980).

12^{th} and 13^{th} ribs, using a compensating planimeter, which measures the areas of objects with irregular shapes.

Fat thickness (FT) : It was taken by a caliper averaging three points between the 12^{th} and 13^{th} ribs, but over the LM.

Marbling (MAR) : It was measured in the *LM* between the 12^{th} and 13^{th} ribs, following the scores in Table 1.

Texture (TEX) : It was determined through the size of the fascicle (muscle "grain" size) and evaluated by a point scale for marbling (Table 2).

Color (COR) : It was the muscle color after 24-h carcass cooling was analyzed. Color was evaluated by a point scale (Table 2) within 30 minutes after a transversal section was made between the 12^{th} and 13^{th} ribs of the *Longissimus* muscle.

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

Chemical composition

Laboratory beef analyses were carried out four months after sampling. The samples were unfrozen at 20°C, grounded, homogenized, and analyzed in triplicate, according to Padre et al. (2007). There were used samplings from *Longissimus* muscle. This muscle was used because represents the medium found in the total cattle carcass.

Beef moisture and ash contents were determined according to AOAC (1998). Crude protein content was obtained through the Kjeldahl method (AOAC, 1998). Forage and beef total lipids were extracted using the Bligh and Dyer method (1959) with a chloroform/methanol mixture. Fatty acid methyl esters (FAME) were prepared by triacylglycerol methylation, according to ISO method 5509 (1978). All reagents and solvents used in the analysis were of analytical reagent quality and were purchased from Merck (Darmstadt, Germany).

Cholesterol analysis was carried out through direct saponification, according to Al-Hasani et al. (1993). A 60% (w/v) solution of potassium hydroxide was added to the samples, in quantities equivalent to 2 ml/g of sample under 1-h reflux. The residue was dissolved again in 2 ml hexane containing 0.2 mg/ml 5-alpha-cholestane internal standard (Sigma Chemical Co., St. Louis, MO, USA).

Table 2. Point scale for meat texture and color evaluation

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

Source: Müller (1980).

Chromatographic analysis and cholesterol quantification

Cholesterol content was analyzed in a 14-A gas chromatograph (Shimadzu, Japan) equipped with flame ionization detector and fused silica capillary column (25 m long, 0.25 mm internal diameter, and 0.25 μm OV-5, Ohio Valley, USA). Injector, column, and detector temperatures were 260, 280, and 280°C, respectively. Ultra-pure gas fluxes (White Martins) of 1.5 ml/min H_2 as a carrier gas, 30 ml/min N_2 as make-up gas, 300 ml/min synthetic gas, and 30 ml/min H_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 (Sigma Chemical Co., St. Louis, MO, USA). Sample cholesterol quantification was carried out after verification of method linearity. Standard cholesterol solutions were prepared in concentrations 0.0; 0.4; 0.8; 1.6, and 2.0 mg/ml, all containing 0.20 mg/ml 5-alpha-cholestane (Sigma, USA), and analyzed. The ratio of the areas of cholesterol and 5-alpha-cholestane were 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.

Analysis of fatty acid methyl esters

Fatty acids methyl esters (FAME) were analyzed in a gas chromatograph (Varian, USA) equipped with flame ionization detector and fused silica capillary column CP-7420 Select FAME (100 m, 0.25 mm, and 0.25 μm film, Varian, USA). 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 20 min. The injector and detector were kept at 220°C and 245°C, respectively. The gas fluxes (White Martins) used were: 1.4 ml/min (45 psi) for the carrier gas (H_2); 30 ml/min for the make-up gas (N_2), and 30 ml/min and 300 ml/min for H_2 and the synthetic flame gas, respectively. Sample injection split mode was 1/80. Fatty acids were identified by comparing sample relative retention times of FAME peaks with those of FAME

Table 3. Effect of different genetic groups on carcass characteristics of bulls finished in pasture system

Parameters	Genetic Groups			
	PUR[1]	PUB[2]	CHC[3]	p>f
Final weight (kg)	494±14.7[b]	463±18.7[b]	546±17.1[a]	0.05
Hot carcass weight (kg)	241±8.36[b]	238±11.2[b]	269±9.78[a]	0.10
Hot carcass dressing (%)	48.8±0.39[b]	51.3±0.57[a]	49.2±0.42[b]	0.05
Conformation (points)	13.3±0.67	12.8±0.87	13.6±0.72	NS
Carcass length (cm)	71.6±0.82	72.1±1.12	72.9±0.88	NS
Leg length (cm)	139±1.01[b]	135±1.32[b]	144±1.09[a]	0.05
Fat thickness (cm)	2.6±0.47	3.8±0.93	2.7±0.51	NS
Longissimus area (cm^2)	61.8±1.62[b]	62.0±2.20[b]	69.0±1.90[a]	0.05
Color (points)	3.6±0.21	4.0±0.32	3.7±0.23	NS
Texture (points)	4.2±0.15[ab]	4.5±0.22[a]	3.9±0.15[b]	0.10
Marbling (points)	4.5±0.71	6.2±1.33	4.9±0.82	NS

[1] Purunã. [2] 1/2 Purunã vs. 1/2 British. [3] 1/2 Charolais vs. 1/2 Caracu. NS: No significant difference.

standard-spiked samples (Sigma Chemical Co., St. Louis, MO, USA). The peak areas were determined by Star software (Varian).

The quantification of the FAME followed the recommendation of the ACS (1980) and methods proposed by Ackman (1972) and Joseph and Ackman (1992). Standard FAME solutions were prepared in concentrations 4.50, 3.60, 2.57, 1.69, 1.13, 0.90, 0.64, 0.45, 0.30, 0.23, 0.16, 0.11, 0.08, 0.06, 0.04, 0.02 mg/ml of n-heptane, all containing 0.25 mg/ml of the Tricosanoic Acid Methyl Ester (Internal Standard). The ratio of the areas of FAME and internal standard were plotted against the FAME concentration, between a 0.02 to 4.50 mg/ml interval.

Quantification of CLA isomers

CLA isomers were identified by comparison of relative retention times (O-5632, CLA mixture, Sigma Chemical Co., St. Louis, MO, USA). CLA content is reported in mg/g of lipid, by using the following formula:

$$\text{CLA (mg/g LT)} = \frac{(A_x)(W_{IS})(CF_x)}{(A_{IS})(W_x)(1.04)} \times 1{,}000$$

where: A_X is the peak area of CLA, A_{IS} the peak area of the internal standard (IS) (tricosanoic acid, 23:0), W_{IS} is the weight (mg) of IS added to the sample (in mg), CF_x is the theoretical correction factor calculated based on IS (equivalent to 1/RRF), RRF is the relative response factor = $(A_x/A_{IS})\cdot(W_{IS}/W_x)$, W_x is the weight of the sample, 1.04 = conversion factor necessary to express results as mg of fatty acids per gram of lipids rather than as methyl esters (Mendoza et al., 2005; Padre et al., 2006). For total CLA calculation were used all CLA found in the fatty acids profile.

Experiment design and statistical analysis

The experiment design consisted of 3 treatments and 11 (PUR), 6 (PUB) and 10 (CHC) repetitions (animals) per treatment. The results were submitted to Analysis of Variance (ANOVA) at significance levels with 10%, 5% and 1% significance levels. The data were submitted to an analysis of variance 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, 2, 3

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

RESULTS AND DISCUSSION

Carcass characteristics

Final live weight was similar ($p>0.05$) between animals of the Purunã (PUR) and 1/2 Purunã vs. 1/2 British (PUB) genetic groups (Table 3). On the other hand, final live weight was greater ($p<0.05$) for animals from the 1/2 Charolais vs. 1/2 Caracu (CHC) group in comparison with PUR and PUB animals. The higher final live weight of CHC animals is due to their greater weight gain along their lifetime as explained by the breeds involved in this genetic group. The CHC group descends from animals from the Charolais and Caracu breeds. They feature high potential for weight gain, as they have undergone specific selection over time. It must be emphasized that the animals were slaughtered at similar ages; therefore, there was no influence of slaughter weight on the results.

Hot carcass weight was similar ($p>0.10$) for PUR and PUB, and was higher ($p<0.10$) for CHC bulls. Hot carcass weight is resultant from the animals' weight at slaughter.

Hot carcass dressing was greater ($p<0.05$) for PUB animals as compared to animals in the other two treatments, PUR and CHC. PUB animals are the result of the crossbreeding among several breeds of beef cattle (British

Table 4. Effects of different genetic groups on chemical composition in the *Longissimus* muscle of bulls finished in pasture systems

Parameters	Genetic groups			
	PUR[1]	PUB[2]	CHC[3]	p>f
Moisture (%)	74.9±0.57	73.9±0.76	73.6±0.58	NS
Ash (%)	1.02±0.02	1.10±0.03	1.05±0.02	NS
Crude protein (%)	23.9±0.44	22.8±0.57	23.3±0.45	NS
Total lipids (%)	1.13±0.11[b]	2.49±0.33[a]	1.45±0.15[b]	0.05
Total cholesterol (mg/100 g LM)	48.4±1.66	48.9±2.28	52.9±1.91	NS

[1] Purunã. [2] 1/2 Purunã vs. 1/2 British. [3] 1/2 Charolais vs. 1/2 Caracu. NS: No significant difference.

breeds and animals resultant from the crossbreeding between British breeds (Angus) and continental animals of large frame size, for example, Charolais and Blonde D'Aquitaine breeds). It must be mentioned that hot carcass dressing is related to the capacity for thickness fat deposition and marbling fat deposition (Restle et al., 1999).

Carcass conformation and length were similar (p>0.10) in all three genetic groups. In general, the conformation of animals finished with similar dressing levels does not feature differences in carcass conformation (Marques et al., 2005). Similarly, carcass length is determined by breed and slaughter weight. The animals in this experiment featured similar genetic patterns, as well similar carcass weight and age. In reviewing literature by Webb (2006), it is possible to conclude that genetic groups with similar age and slaughter weight do not alter carcass length at slaughter.

Leg length was greater (p<0.05) for animals in the CHC genetic groups as compared to specimens from the PUR and PUB groups. Furthermore, leg length was similar for PUR and PUB animals. The longer leg length for animals from the CHC genetic group is due to the selection the animals in this genetic group (Charolais and Caracu) have undergone over time. These animals were submitted to a selection process for traction; this consequently led to greater bone development.

Cover fat thickness was not altered (p>0.10) by the different genetic groups. Yet, cover fat thickness varied between 2.6 and 3.8 mm. Brazilian norms specify that cover fat thickness must be between 3 and 6 mm, in order to satisfy the domestic market (Luchiari Filho, 2000). Therefore, these animals presented the minimum thickness required for favorable marketing. The low cover fat thickness observed could have been determined by the age at which the animals were slaughtered, as well as by the breeds involved in the different genetic groups. The continental bull breeds are regarded as late developers, and in order to reach higher cover fat thickness levels, they should be slaughtered at a later age (Abrahão et al., 2006).

The *Longissimus* muscle area was greater (p<0.05) in CHC animals as compared to the PUR and PUB genetic groups. On the other hand, no difference was observed (p>0.10) between PUR and PUB animals. The larger *Longissimus* muscle in CHC animals is directly related to the characteristics of the two breeds involved in the crossbreeding of CHC animals. Charolais and Caracu animals are considered to have high weight gain potential and greater muscle deposition (Restle et al., 1999).

Animals in the CHC genetic group featured lower (p<0.05) texture of the *Longissimus* muscle in comparison to animals from the PUB genetic group; no difference was observed between PUR and PUB animals. The lower texture value of animals from the CHC genetic group can be explained by the greater muscle deposition in animals form this genetic group.

No difference was observed (p>0.05) in color or marbling of the *Longissimus* of animals from the three genetic groups. In general, different genetic ratios have little influence on coloration and marbling of beef (Martin Nieto, 2004; Webb, 2006).

Chemical composition

The levels of moisture, ash, crude protein and total cholesterol were not influenced (p>0.10) by the different genetic groups (Table 4).

The variation observed for the levels of moisture, ash and crude protein are close to those presented in scientific studies undertaken with animals of different breeds, lineages and diets (Greghi et al., 2003; Moreira et al., 2003; Padre et al., 2006).

Total lipid levels were greater (p<0.05) in animals from the PUB group in comparison to the PUR and CHC groups. Further, no difference was observed (p>0.05) between animals from the PUR and CHC genetic groups. The higher total lipid levels in animals from the PUB genetic group can be attributed to the breeds that make up this crossbreeding (Purunã and British). British animals are well known for higher deposition of fatty tissue as compared to continental animals (Martin Nieto, 2004).

Total cholesterol concentrations varied little among animals from all three genetic groups. The average cholesterol concentration was 50 mg/100 g of muscle. Padre et al. (2007) found total cholesterol concentrations of 47 mg/100 g of muscle. On the other hand, Moreira et al. (2003) found concentration close to 33 mg/100 g of muscle. Eichhorn et al. (1986) found total cholesterol levels in crossbred animals around 62 mg/100 g of muscle. This demonstrates that total cholesterol concentration varied as a result of several factors, among them genetic group and animal age (Webb, 2006). In general, young animals presented cholesterol levels lower than 40 mg/100 g in the

Longissimus muscle; whereas older animals featured total cholesterol levels greater than 50 mg/100 g of muscle. The animals in this experiment were slaughtered at 20 months of age: an intermediate age, when total cholesterol levels would be greater than 50 mg/100 g of muscle.

Fatty acid profile

The levels of the palmitic fatty acid (C16:0) was higher

Table 5. Effect of genetic groups on the fatty acid profile (% of total of fatty acids) of the *Longissimus* muscle of bulls finished in pasture systems

Fatty acids	Genetic groups			
	PUR[1]	PUB[2]	CHC[3]	p>f
14:0	1.35±0.09^{b}	1.95±0.18^{a}	1.57±0.11^{ab}	0.10
ai 15:0	0.22±0.01^{a}	0.17±0.01^{ab}	0.18±0.01^{b}	0.10
i 15:0	0.15±0.02^{b}	0.23±0.04^{a}	0.20±0.03^{ab}	0.10
15:0	0.29±0.02^{a}	0.22±0.02b	0.24±0.02^{ab}	0.05
15:1 *n* 10	0.45±0.02	0.38±0.03	0.40±0.02	NS
i 16:0	0.24±0.01	0.21±0.01	0.21±0.01	0.10
16:0	23.4±0.50^{b}	25.8±0.75^{a}	24.8±0.56^{ab}	0.05
16:1 *n*-10	0.22±0.04^{a}	0.06±0.01^{b}	0.14±0.03^{ab}	0.10
16:1 *n*-9	0.20±0.02	0.16±0.02	0.18±0.01	NS
16:1 *n*-7	2.27±0.13	2.61±0.20	2.47±0.14	NS
ai 17:0	0.67±0.03^{a}	0.62±0.03^{ab}	0.58±0.02^{b}	0.05
i 17:0	0.27±0.03^{a}	0.01±0.01^{c}	0.13±0.02^{b}	0.10
17:0	1.10±0.04^{a}	0.97±0.04^{b}	0.95±0.03^{b}	0.10
17:1 *n*-10	0.59±0.02^{a}	0.51±0.03^{b}	0.55±0.02^{ab}	0.10
18:0	19.4±0.53	19.0±0.71	19.2±0.55	NS
18:1 *t*-11	3.07±0.18^{a}	1.91±0.16^{c}	2.50±0.16^{b}	0.10
18:1 *n*-9	32.4±0.80	35.0±1.17	33.2±0.86	NS
18:1 *n*-7	0.87±0.06^{ab}	0.67±0.06^{b}	1.04±0.07^{a}	0.10
18:1 *n*-4	0.11±0.02	0.11±0.02	0.13±0.02	NS
18:1 *n*-3	0.26±0.02^{a}	0.15±0.01^{b}	0.18±0.01^{b}	0.10
19:0	0.11±0.02	0.08±0.02	0.08±0.01	NS
18:2 *n*-6	5.72±0.57	4.28±0.57	4.83±0.50	NS
18:2 *n*-4	0.15±0.01^{a}	0.11±0.01^{b}	0.11±0.01^{b}	0.10
18:3 *n*-6	0.01±0.01	0.01±0.01	0.01±0.01	NS
18:3 *n*-3	1.14±0.16^{a}	0.38±0.07^{b}	0.73±0.11^{c}	0.05
18:4 *n*-3	0.01±0.01	0.01±0.01	0.01±0.01	0.05
18:2 *c*-9 *t*-11	0.58±0.03^{a}	0.49±0.04^{ab}	0.46±0.03^{b}	0.05
18:2 *c*-11 *t*-13	0.15±0.01^{a}	0.11±0.01^{b}	0.11±0.01^{b}	0.10
18:2 *t*-10 *c*-12	0.16±0.01^{a}	0.16±0.01^{ab}	0.13±0.01^{b}	0.10
18:2 *c*-8 *c*-10	0.02±0.01	0.01±0.01	0.02±0.01	NS
18:2 *c*-9 *c*-11	0.02±0.01	0.01±0.01	0.02±0.01	NS
18:2 *c*-10 *c*-12	0.02±0.01	0.01±0.01	0.02±0.01	NS
18:2 *c*-11 *c*-13	0.02±0.01	0.01±0.01	0.02±0.01	NS
18:2 *t*-8 *t*-10	0.02±0.01	0.03±0.01	0.02±0.01	NS
18:2 *t*-9 *t*-11	0.02±0.01	0.03±0.01	0.02±0.01	NS
18:2 *t*-10 *t*-12	0.02±0.01	0.03±0.01	0.02±0.01	NS
18:2 *t*-11 *t*-13	0.02±0.01	0.03±0.01	0.02±0.01	NS
20:0	0.04±0.01	0.03±0.01	0.04±0.01	NS
20:3 *n*-6	0.17±0.02	0.15±0.02	0.13±0.02	NS
20:2 *n*-3	0.48±0.05	0.35±0.05	0.37±0.04	NS
20:4 *n*-6	2.42±0.26^{a}	1.41±0.21^{b}	1.76±0.20^{ab}	0.05
20:5 *n*-3	0.43±0.04^{a}	0.18±0.02^{c}	0.31±0.03^{b}	0.10
22:1 *n*-7	0.15±0.01^{a}	0.07±0.01^{c}	0.11±0.01^{b}	0.10
22:4 *n*-6	0.20±0.02^{a}	0.12±0.01^{b}	0.16±0.02^{ab}	0.05
22:5 *n*-3	0.83±0.07^{a}	0.46±0.06^{b}	0.81±0.08^{a}	0.10
22:5 *n*-6	0.04±0.01	0.03±0.01	0.02±0.01	NS
22:6 *n*-3	0.06±0.01	0.06±0.01	0.07±0.01	NS

[1] Purunã. [2] 1/2 Purunã vs. 1/2 British. [3] 1/2 Charolais vs. 1/2 Caracu. NS: no significant difference.

($p<0.05$) in animals from the PUB genetic group and lower in PUR animals (Table 5). However, although the levels were higher among animals from the PUB group, the difference was only 2.4%. As such, the higher levels in PUB animals would not carry negative consequences, given that this fatty acid is considered non-beneficial to human health (Pensel, 1998).

On the other hand, the levels of stearic acid (C18:0), considered neutral to human health (Pensel, 1998), did not suffer influence ($p>0.05$) from any of the genetic groups. Similarly, the levels of linoleic (C18:2 *n*-6) and linolenic (C18:3 *n*-3) fatty acids were not altered ($p>0.05$) according to genetic group. Thus, the genetic groups studied influenced the levels of fatty acids considered beneficial to human health. Garcia et al. (2007) observed that different genetic groups alter little in regards to the fatty acid profile, with diet being one of the factors that most influence this alteration.

The levels of saturated, monounsaturated and polyunsaturated fatty acids, did not differ ($p>0.05$) among genetic groups. The level of saturated fatty acids was 47%. This value is similar to that found among bovines (Padre et al., 2006 and 2007). Similarly, the concentration of monounsaturated fatty acids was close to 38%. Among bovines slaughtered at a similar age as this experiment (Moreira et al., 2003; Muramoto et al., 2005) observed nearly similar values for monounsaturated fatty acids. The average percentage of polyunsaturated fatty acids was 9.9%. Similar values were observed by Moreira et al. (2003).

The levels of *n*-3 were higher ($p<0.10$) in the *Longissimus* muscle of PUR as compared to that of PUB animals. Further, no difference was observed ($p>0.10$) between the animals from the PUB and CHC genetic groups. There was no difference ($p>0.10$) among genetic groups for levels of *n*-6. The average percentage of *n*-6 was 6.79. The *n*-6 and *n*-3 fatty acids have a significant role in reducing the risk of coronary heart disease, but that is still a matter of debate (Hu, 2001).

The average PUFA/SFA ratio was 0.22; this value is lower to 0.40, which is recommended by the English Health Department (HMSO, 1994). This PUFA/SFA ratio has been significant for health care, because it reduces the risk of coronary diseases, although the optimal ratio has been a matter of debate (Hu, 2001). Ruiz et al. (2005) observed a higher PUFA/SFA ratio in the muscles of bulls (0.25); this value is higher to that found in the current study, which was close to the results (0.13) found by French et al. (2000) who studied steers finished on pasture conditions, and unlike the higher results reported by Prado et al. (2003), which found 0.28 for Nellore steers finished on pasture conditions.

The different genetic group had no effect ($p>0.10$) on the levels of conjugated linoleic acid (total CLA) (mg/g lipids) (Table 6), which is considered an important fatty acid to human health. In terms of benefits to human health, products containing CLA (considered nutraceutic or functional) have anticarcinogens (especially rumenic acid: Ip et al., 1999) and anti-obesity properties (isomer *t*-10, *c*-12; Evans et al., 2002). These products also help prevent arteriosclerosis, are antioxidants due to the conjugated double bonds, and contribute to prevent non-insulin dependent diabetes mellitus (Sebédio et al., 1999).

The fatty acid 18:2 *c*-9 *t*-11 is one of the essential fatty

Table 6. Effect of genetic groups on saturated fatty acids (SFA), monounsaturated fatty acids (MUFA), polyunsaturated fatty acids (PUFA), ramificated fatty acids (RFA), *n*-6, *n*-3, PUFA/SFA and *n*-6/*n*-3 ratio of the *Longissimus* muscle of bulls finished in pasture systems

Fatty acids	Genetic groups			
	PUR[1]	PUB[2]	CHC[3]	p>f
Saturated fatty acids (%)	46.6±0.65	47.3±0.90	47.1±0.69	NS
Monounsaturated fatty acids (%)	36.9±0.96	40.2±1.41	38.6±1.05	NS
Polyunsaturated fatty acids (%)	11.7±1.27	8.37±1.24	9.73±1.12	NS
Ramificated fatty acids (%)	1.53±0.07^{a}	1.32±0.08^{ab}	1.26±0.06^{b}	0.10
CLA total (%)	1.05±0.06^{a}	0.95±0.07^{ab}	0.86±0.05^{b}	0.10
n-3 (%)	3.19±0.33^{a}	1.58±0.22^{b}	2.56±0.28^{ab}	0.10
n-6 (%)	7.50±0.70	5.96±0.74	6.92±0.67	NS
PUFA/SFA	0.25±0.03	0.18±0.03	0.21±0.03	NS
n-6/*n*-3	2.35±0.17^{b}	3.77±0.37^{a}	2.70±0.20^{b}	0.10
Quantification				
18:2 *c*-9 *t*-11 (mg/g lipids)	2.23±0.28	2.18±0.37	2.26±0.30	NS
18:2 *c*-11 *t*-13 (mg/g lipids)	0.53±0.07	0.52±0.09	0.49±0.07	NS
18:2 *t*-10 *c*-12 (mg/g lipids)	0.48±0.06^{b}	0.80±0.15^{a}	0.69±0.10^{ab}	0.10
cis, cis (mg/g lipids)	0.28±0.03^{a}	0.23±0.04^{ab}	0.18±0.02^{b}	0.10
trans, trans (mg/g lipids)	0.22±0.03	0.22±0.04	0.19±0.03	NS
CLA total (mg/g lipids)	3.40±0.41	3.73±0.61	3.45±0.43	NS

[1] Purunã. [2] 1/2 Purunã vs. 1/2 British. [3] 1/2 Charolais vs. 1/2 Caracu. NS: no significant difference.

acid to human health (Pensel, 1998). Although the percentage of CLA have been altered by genetic group, the same have not been observed ($p<0.10$) about the quantification in relation to total CLA (Table 6). However, the genetic group altered the quantification of fatty acids 18:2 *t*-10 *c*-12 and of the fatty acids cis-cis.

IMPLICATIONS

The different genetic groups can present alterations in physical carcass composition. However, these alterations are not pronounced. Crossbreeding can be used as a tool to alter the percentage of total lipids and some fatty acids in the *Longissimus* muscle of animals finished in pasture systems. However, it does not alter the levels of moisture, ash, crude protein and total cholesterol. A total of 47% of the fatty acids found were not affected by the different genetic groups. CLA percentage was highest for PUR animals. However, total CLA amounts were not altered by the different genetic groups.

REFERENCES

Abrahão, J. J. S., I. N. Prado, J. A. Marques, D. Perotto and S. M. B. Lugão. 2006. Avaliação da substituição do milho pelo resíduo seco da extração da fécula de mandioca sobre o desempenho de novilhas mestiças em confinamento. Rev. Bras. Zootec. 35:512-518.

Ackman, R. G. 1972. The analysis of fatty acids and related materials by gas-liquid chromatography In: Progress in the chemistry of fats and other. Lipids 12:165-284.

ACS (American Chemical Society). 1980. Subcommittee on environmental analytical chemistry, accuracy and precision revisited. Anal. Chem. 52:2241-2248.

Al-Hasani, S. M., J. Hlavac and M. W. Carpenter. 1993. Rapid determination of cholesterol in single and multi-component prepared foods. J. Assoc. Offic. Anal. Chem. Inter. 76:902-906.

Anualpec. 2007. Anuário da Pecuária Brasileira. São Paulo: Instituto FNP, 2007.

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

AOAC. 1998. Official methods of analysis of AOAC International (6th ed.). Association of Official Analytical Chemists, Arlington.

Eichhorn, J. M., E. J. Wakayama, G. J. Blomquist and C. M. Bailey. 1986. Cholesterol content of muscle and adipose tissue from crossbred bulls and steers. Meat Sci. 16:71-78.

Enser, M., K. Hallett, B. Hewitt, G. A. F. Fursey and J. D. Wood. 1996. Fatty acid content and composition of English beef, lamb and pork at retail. Meat Sci. 42:443-456.

Evans, M. E., J. M. Brown and M. K. Mcintosh. 2002. Isomer-specific effects of conjugated linoleic acid (CLA) on adiposity and lipid metabolism. J. Nutr. Bioch. 13:508-516.

Field, R. A. 1971. Effect on castration on meat quality and quantity. J. Anim. Sci. 32:849-857.

French, P., C. Stanton, F. Lawless, E. G. O'Riordan, F. J. Monahan and P. J. Caffrey. 2000. Fatty acid composition, including conjugated linoleic acid, of intramuscular fat from steers offered grass, grass silage, or concentrate-based diets. J. Anim. Sci. 78:2849-2855.

Garcia, P. T., N. A. Pensel, A. M. Sancho, N. J. Latimori, A. M. Kloster, M. A. Amigone and J. J. Casal. 2007. Beef lipids in relation to animal breed and nutrition in Argentina. Meat Sci. Article in Press.

Greghi, M. E., F. C. Vieira, N. Ruiz, J. V. Visentainer, I. N. Prado and N. E. Souza. 2003. Effects of slaughter weight on the muscle fatty acids compositions of subcutaneous and intramuscular lipids of dutch steers. Anais. Assoc. Bras. Quím. 52:129-133.

HMSO (England). 1994. Department of Health. Nutritional aspects of cardiovascular disease: HMSO, pp. 37-46 (Report on Health and Social Subjects, 46).

Hu, F. B. 2001. The balance between ω-6 and ω-3 fatty acids and the risk of coronary heart disease. Nutr. 17:741-742.

Ip, C., S. Banni, E. Angione, G. Carta, J. McGinley, H. J. Thompson, D. Barbano and D. Bauman. 1999. Conjugated linoleic acid-enriched butter fat alters mammary gland morphogenesis and reduces cancer risk in rats. J. Nutr. 129:2135-2142.

ISO (International Organization for Standardization). 1978. Animal and vegetable fats and oils: Preparation of methyl esters of fatty acids. ISO 5509: 01-06.

Joseph, J. D. and Ackman, R. G. 1992. Capillary column gas chromatography method for analysis of encapsulated fish oil and fish oil ethyl esters: collaborative study. J. AOAC Internat. 75:488–506.

Luchiari F. A. 2000. Pecuária da carne bovina. 1ª ed. São Paulo, 134.

Marques, J. A., D. Maggioni and J. J. S. Abrahão. 2005. Comportamento de touros jovens em confinamento alojados isoladamente ou em grupo. Arch. Latin. Prod. Anim. 13:97-102.

Martin Nieto, L. 2004. Fatores genéticos que alteram a qualidade d carne e do leite em ruminantes. p. 35-52. In: Prado. Conceitos sobre a produção com qualidade de carne e leite. Eduem 1ª Ed., Maringá, p. 301.

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

Müller, L. 1980. Normas para avaliação de carcaças e concurso de carcaças de novilhos. Santa Maria: Universidade Federal de Santa Maria, p. 31.

Muramoto, T., M. Higashiyama and T. Kondo. 2005. Effect of pasture finishing on beef quality of Japanese shorthorn steers. Asian-Aust. J. Anim. Sci. 18:420-426.

NRC. 1996. Nutrient requirements of beef cattle. 7th ed. Nat. Acad. Press, Washington, DC.

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

Meat Sci. 74:242-248.

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

Pensel, N. 1998. The future of meat in human diets. Nutr. Abstr. Rev. 68:1-4.

Perotto, D., J. J. S. Abrahão and J. L. Moletta. 2000. Características quantitativas de carcaça de bovinos Zebu e de cruzamentos *Bos taurus*×Zebu. Rev. Bras. Zootec. 29:2019-2029.

Perotto, D., A. C. Cubas, J. J. Abrahão and S. C. Mella. 2001. Ganho de peso da desmama aos 12 meses e peso aos 12 meses de bovinos Nelore e cruzas com Nelore. Rev. Bras. Zootec. 30:730-735.

Restle, J., F. N. Vaz, A. R. B. Quadros and L. Muller. 1999. Características de carcaça e da carne de novilhos de diferentes genótipos de Hereford×Nelore. Rev. Bras. Zoot. 28:1245-1251.

Ruiz, M. R., M. Matsushita, J. V. Visentainer, J. A. Hernandez and E. L. A. Ribeiro. 2005. Proximate chemical composition and fatty acid profiles of *Longissimus thoracis* from pasture-fed LHRH immunocastred and intact *Bos indicus* bulls. J. Anim. Sci. 1:13-18.

SAS. 2000. User's Guide: Statistics, Version 8.1. 4 Edition. SAS Institute, Inc., Cary, NC.

Sebédio, J. L., S. Gnaeding and J. Chardigny. 1999. Recent advances in conjugated linoleic acid research. Current Opinion in Clinical Nutrition and Metabolic Care 2:499-506.

Silva, R. G., I. N. Prado, M. Matsushita and N. E. Souza. 2002. Dietary effect on muscle fatty acid composition of finished heifers. Pesq. Agropec. Bras. 37:95-101.

StatSoft. 2005. Statistica 7.0 Software. Tucksa, USA: StaSoft.

Tamminga, S. and M. Doreau. 1991. Lipids and rumen digestion. Rumen microbial metabolism and digestion (Ed. J. P. Houany). pp. 151-164. Paris: INRA.

Webb, E. C. 2006. Manipulating beef quality through feeding. South Afr. J. Food Sci. Nutr. 7:1-24.