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Chemical Composition and Fatty Acid Profile in Crossbred (*Bos taurus vs. Bos indicus*) Young Bulls Finished in a Feedlot

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ABSTRACT : This study was conducted to determine the effect of breed on the chemical composition of first (PUR1) and second (PUR2) generations of Purunã young bulls, and to compare both generations with different genetic groups: CAN vs. ANG; CAR; and CHA vs. CAR. Thirty bulls were used. The animals from the PUR2 and CHA vs. CAR genetic groups featured higher ($p<0.05$) moisture percentage in comparison to the PUR1, CAR and CAN vs. ANG groups. The moisture percentage was similar ($p>0.05$) between PUR2 and CHA vs. CAR animals. The same was observed among the PUR1, CAR, CAN vs. ANG and CHA vs. CAR animals. There was no difference ($p>0.05$) among genetic groups for ash, total lipids and total cholesterol. The PUR1, CAR and CAN vs. ANG specimens had higher ($p<0.05$) crude protein percentages as compared to PUR2 and CAN vs. CAR animals. The fatty acid profile was different ($p<0.05$) among genetic groups. However, the percentages of SFA, MUFA, PUFA, *n*-6, *n*-3, PUFA:SFA, and *n*-6:*n*-3 were similar ($p>0.05$) among genetic groups. (**Key Words :** Cholesterol, CLA, PUFA, Purunã)

INTRODUCTION

The employment of techniques such as industrial crossbreeding allows for the search of genotypes that can adequately meet market demand and improve meat quality (Perotto et al., 2000; Arboitte et al., 2004; Prado et al., 2008a; b). Changes in the concept of production in which quality, yield and carcass meat characteristics are essential would create the conditions for beef to become competitive in a growing and ever more demanding market. These changes include the adoption of well-oriented crossbreeding systems, which would simultaneously enable the optimization of non-additive effects (heterosis) and the additive effects of genes on carcass characteristics, by choosing breeds that complement one another.

Beef has an excellent nutritional quality because it has proteins of high biological value, is rich in vitamin content (especially B-complex), and is associated with high mineral content (especially iron), in high bioavailability form (Saucier, 1999). Beef contains all the amino acids in nearly ideal levels as required by humans (Pensel, 1998).

Several factors in beef production affect fatty acid composition, including breed and diet (Aricetti et al., 2008; Macedo et al., 2008; Prado et al., 2008a; b; c; d). Breed affects meat fat content, and fat content itself is a factor for determining fatty acid composition (Aricetti et al., 2008; Macedo et al., 2008; Prado et al., 2008a; b; c; d). Ruminants naturally consume a diet low in fat but high in PUFA whether as fresh grass, conserved grass or the concentrate portion of the diet (Moreira et al., 2003; Prado et al., 2008b; c; d). However, a large proportion of PUFA undergoes microbial biohydrogenation in the rumen, leading to predominantly SFA being absorbed in the intestine and deposited in tissues.

The State of Paraná, located in southern 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 bulls (Moreira et al., 2003; Padre et al., 2006; Padre et al., 2007; Prado et al., 2008a; b; c; d). After several stages of crossbreeding, an ideal crossbreeding ratio was found as the best adapted for the region. Initially, Nellore specimens

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were crossbred with Charolais, Angus, Caracu and Canchim cattle (Perotto et al., 1998), giving rise to a breed denominated Purunã.

Feedlot has been a cost-effective alternative for raising beef cattle in regions where either the grassland price or dietary components are inflating operating costs (Prado and Moreira, 2002). Consequently, both conditions require the use of intensive systems to produce high-quality meat. Presently, the use of cereal grains (such as corn) has been the main source of energy in finishing diets, but oils and fats can also be used as alternative components (Prado et al., 2008a; b; c; d).

This work was conducted in order to evaluate the chemical composition and fatty acid profile in the LM of crossbred first- and second-generation Purunã, as well as Caracu, Canchin vs. Angus, Charolais vs. Caracu.

MATERIAL AND METHODS

Animals and management

The Committee of Animal Production at the State University of Maringá approved this experiment, which was carried out at the Experimental Farm of the Agronomic Institute of Paraná, Brazil, and followed the guiding principles of biomedical research with animals (CIOMS, 1985).

Feed samples were analyzed at the Laboratory of Feed Analyses and Animal Nutrition at the State University of Maringá, northwestern Paraná, Brazil. Thirty bulls (PUR1 n = 6; PUR2 n = 6; CAR n = 6; CAN vs. CAR n = 6 and CHA vs. CAR n = 6) were selected, all belonging to the experimental herd of the Agronomic Institute of Paraná. The mating plan established by the Agronomic Institute of Paraná was to avoid consanguinity of the genetic groups by continuous maintenance of heterozygosis, using purebred bulls from the four starter breeds (Angus, Canchin, Caracu and Charolais).

Diets

The animals were set for intensive finished and were confined at an average age of 12 months, with an initial live weight of 245 kg.

From birth to the age of 90 days, the calves followed their mothers in the annual winter pastures. After precocious weaning (at 90 days of age), the calves were kept in pastures of *Hemarthria altissima* with concentrate supplementation (1.5 kg/animal/d of a mixture made up of 25% soybean meal+73% cracked corn).

The animals were kept separate in individual pens (5 m^2 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 animals were fed corn silage *ad libitum* along with a concentrate made up of 25% soybean meal, 73% cracked corn, and 2% salt, calculated as 1.2% of animal live weight/d. The young bulls were weighed at the beginning of the experiment. Thereafter, they were weighed every 28 days, observing a 16-h fast of solids, accomplished by removing all feed at 4 p.m. on the day prior to weighing. Silage was provided *ad libitum*, with adjustments made according to the previous day's intake. Around 5% to 10% refusals, in order not to limit intake. The experimental lasted for 180 days, during which the animals reached an average final live weight of 464 kg. The development of the thickness fat cover was monitored every 28 days after a period of adaptation for the animals, using an ultrasound device (Aloka 500 with a Ust-5049-3.5 transducer). After reaching 4 mm cover fat thickness and an average age of 16 months, the animals were slaughtered.

Slaughter protocol, sampling and analysis

The animals were slaughtered at a commercial slaughterhouse 100 km away from the Research Farm, following the usual practices of the Brazilian beef industry. Thereafter, the carcasses were identified and weighted and chilling at 4°C for 24 h. After chilling, the right half carcass was used to determine the quantitative characteristics. Twenty-four hours later, LM samples were taken by a complete cross-section between the 12^{th} and 13^{th} ribs. The fat thickness was discarded and the muscle portion was frozen at -20°C for further analyses.

Laboratory beef analyses were carried out four months after sampling. The samples were unfrozen at 0°C, grounded, homogenized, and analyzed in triplicate.

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 by the Bligh and Dyer method (1959) with a chloroform/methanol mixture. Fatty acids 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).

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 μm Ohio Valley-30). Injector, column, and detector temperatures

Table 1. Chemical composition of the *Longissimus* muscle of young bulls of different breeds finished in feedlot

Parameters	PUR1[1]	PUR2[2]	CAR[3]	CAN vs. ANG[4]	CHA vs. CAR[5]	SE[6]
Moisture (%)	73.0[b]	75.2[a]	72.1[b]	72.7[b]	73.7[ab]	0.66
Ashes (%)	0.94	0.98	0.96	1.03	0.96	0.04
Crude protein (%)	22.3[ab]	21.1[b]	23.1[ab]	24.4[a]	21.7[b]	0.62
Total lipids (%)	2.21	3.81	2.45	2.33	2.37	0.53
Total cholesterol[7]	43.8	39.9	44.7	44.8	36.8	2.86

[1] First-generation Purunã. [2] Second-generation Purunã. [3] Caracu. [4] Canchim vs. Aberdeen Angus. [5] Charolais vs. Caracu. [6] Standart Errors.
* Means in the same line followed by different letters differ by the Tukey test, $p<0.05$. [7] (mg/100 g muscle)

were 260, 280, and 280°C, respectively. Ultra-pure gas fluxes (White Martins) of 1.5 ml/min H_2 as carrier gas, 30 ml/min N_2 as make-up gas, 300 ml/min synthetic gas, and 30 ml/min N_2 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 5α-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 µl. The curve obtained was used for cholesterol analysis in mg 100 g^{-1}.

Fatty acids methyl esters (FAMEs) 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 was: 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 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). Standard FAME solutions were prepared in concentrations of 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 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 (Rowe et al., 1999; Milinsk et al., 2005).

Experimental design and statistical analysis

The experimental design with 5 treatments (PUR1; PUR2; CAR; CAN vs. ANG and CHA vs. CAR) and 30 replications (animals) was completely randomized. 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, … 5;
e_{ij} = random error associated with each observation.

RESULTS AND DISCUSSION

Chemical composition

Table 1 shows the chemical composition of the *Longissimus* muscle of the different genetic groups finished in feedlot.

There was no difference ($p>0.05$) among the genetic groups for ash, total lipids and total cholesterol. The average levels of ash (0.97%), total lipids (2.63%) and total cholesterol (42.00 mg/100 g of muscle) were similar to those found by other authors (Moreira et al., 2003; Padre et al., 2006; Padre et al., 2007; Aricetti et al., 2008).

Animals from the PUR2 and CHA vs. CAR genetic groups featured similar levels ($p>0.05$) of moisture, which were greater than those found in specimens from the PUR1, CAR and CAN vs. ANG groups. The latter three featured similar moisture levels. The moisture levels were similar to those found by other authors under similar conditions as this experiment (Padre et al., 2007; Aricetti et al., 2008; Kazama et al., 2008).

Higher values were observed by Silva et al. (2002) in crossbred heifers (Limousin vs. Nellore and Simmental vs. Nellore) with an approximate age of 18 months, featuring average moisture levels of 74.65%.

The obtained average crude protein levels (22.52%) are similar to those observed by other authors (Padre et al., 2006; Padre et al., 2007). Animals from the CAN vs. ANG genetic group featured higher ($p<0.05$) percentages of crude

Table 2. Treatment effects on the fatty acid profile of the *Longissimus* muscle of young bulls finished in feedlot

Parameters	PUR1[1]	PUR2[2]	CAR[3]	CAN vs. ANG[4]	CHA vs. CAR[5]	SE[6]
14:00	2.65[a]	2.31[a]	1.36[b]	1.12[b]	1.41[b]	0.26
14:1 *n*-7	0.19	0.18	0.11	0.07	0.18	0.06
16:00	28.9[b]	31.9[a]	23.5[c]	25.7[c]	26.5[c]	0.75
16:1 *n*-7	2.78[ab]	3.41[a]	1.66[b]	1.73[b]	1.91[b]	0.32
17:00	0.65[a]	0.53[ab]	0.55[a]	0.31[b]	0.58[a]	0.06
18:1 *t*-11	0.64	0.79	0.89	1.27	0.57	0.03
17:1 *n*-9	0.48	0.42	0.55	0.36	0.43	0.12
18:00	17.2	16.2	20.7	19.6	18.2	2.57
18:1 *n*-9	41.1[ab]	39.1[b]	44.1[a]	41.4[ab]	44.0[a]	3.57
18:2 *n*-6	3.41	3.21	3.94	5.34	4.16	0.05
18:3 *n*-6	0.11	0.17	0.16	0.17	0.11	0.03
18:3 *n*-3	0.15	0.11	0.15	0.12	0.18	0.03
CLA	0.24	0.19	0.21	0.11	0.16	0.02
20:4 *n*-6	0.81	0.77	1.26	1.27	0.98	0.24
22:00	0.21	0.16	0.41	0.28	0.39	0.05
20:5 *n*-3	0.14	0.11	0.17	0.26	0.14	0.04
22:5 *n*-3	0.12	0.16	0.12	0.25	0.15	0.02
22:6 *n*-3	0.21	0.15	0.24	0.15	0.13	0.05

[1] First-generation Purunã. [2] Second-generation Purunã. [3] Caracu. [4] Canchim vs. Aberdeen Angus. [5] Charolais vs. Caracu. [6] Stardart Errors.
* Means in the same line followed by different letters differ by the Tukey test, $p<0.05$.

protein (24.4%) when compared to specimens from the PUR2 (21.1%) and CHA vs. CAR (21.7%) genetic groups. Furthermore, no difference was observed ($p>0.05$) among animals from the PUR1 (22.3%), CAR (23.1%) and CAN vs. ANG (24.4%) genetic groups.

The average of intramuscular fat was 2.63 per cent. Higher results were observed by Padre et al. (2007), who found an average of 3.14%. Lower values were found by Abularach et al. (1998) in Nellore young bulls between 23 and 29 months of age, finished in feedlot, with an average percentage of 1.71%. Low levels of intramuscular fat can compromise the juiciness and tenderness of striploin, which is a meat for fast grilling in dry heat. There is evidence that the lowest lipid content required for a tender and juicy steak is 3.0%. There was a difference of 58% in total lipid levels in PUR2 (3.81%) as compared to the lowest value found, which was in PUR1 (2.21%).

Total cholesterol levels were similar ($p>0.05$) among the different genetic groups. The average observed in this experiment was 42.0 mg/100 g of muscle. Similar results to this experiment were obtained by Costa et al. (2002), who observed average levels of 43.1 mg/100 g of muscle in animals intensively finished. However, higher values were obtained by Prado et al. (2008a) while evaluating *in natura* cholesterol concentration in the *Longissimus* muscle of 1/2 Nelore vs. 1/2 Simmenthal crossbreds, when a concentration of 54.4 mg/100 g of muscle cholesterol was observed. Terrel et al. (1969) also obtained higher values while researching the influence of slaughter weight of Aberdeen Angus young bulls and heifers in that study, it was observed that cholesterol contents were highest in animals slaughtered at 455 kg (82.4 mg/100 g of muscle).

Cholesterol is an essential compound for the body; it takes part in the synthesis of hormones and bile salts, with half of total cholesterol produced endogenously and the remainder derived from the diet (Nelson and Cox, 2002). Until recently, the solution for reducing blood cholesterol levels seemed simple: the recommendation was to eat foods low in cholesterol, such as replacing butter with vegetable margarine and eating less meat and eggs. However, after advances in the knowledge of the functions of the human body, it is now known that the amount of cholesterol in food does not necessarily determine blood cholesterol levels. The liver synthesizes and stores cholesterol, and these processes are regulated by bodily needs and cholesterol availability in the diet. Currently, the recommendations are to keep cholesterol levels under control, and not necessarily eliminate them from the diet altogether. Nevertheless, saturated fat intake must be kept under strict control, as it can raise blood cholesterol levels. The American Heart Association has recommended an intake of 300 mg of cholesterol a day for humans, meaning up to 600 g of beef a day.

Fatty acid profile

Table 2 presents the fatty acid profile of the *Longissimus* muscle of the different genetic groups finished in feedlot.

The levels of C14:1 *n*-7; C18:1 *t*-11 (vaccenic acid); C17:1 *n*-9 (8-heptadecenoic acid); C18:0 (stearic acid); C18:2 *n*-6 (linoleic acid); 18:3 *n*-6 (γ-linolenic acid); C18:3 *n*-3 (α-linolenic acid); C18:2 cis-9 trans-11 (conjugated linoleic acid-CLA); C20:4 *n*-6 (arachidonic acid); C22:0 (behenic acid); C20:5 *n*-3 (timnodonic acid-EPA); C22:5 *n*-

Table 3. Proportion (%) of saturated fatty acids (SFA), monounsaturated fatty acids (MUFA), polyunsaturated fatty acids (PUFA), fatty acids *n*-6, fatty acids *n*-3, PUFA:SFA and *n*-6:*n*-3 ratio in the *Longissimus* muscle of young bulls finished in feedlot

Parameters	PUR1[1]	PUR2[2]	CAR[3]	CAN vs. ANG[4]	CHA vs. CAR[5]	SE[6]
SFA	49.6	51.4	46.5	47.0	47.0	1.68
MUFA	45.2	43.9	47.3	44.8	47.0	1.26
PUFA	6.38	6.17	6.9	8.31	7.12	0.75
n-6	4.33	4.13	5.36	7.28	5.23	0.94
n-3	0.63	0.38	0.58	0.78	0.6	0.15
PUFA:SFA	0.13	0.13	0.15	0.18	0.15	0.02
n-6:*n*-3	6.97	11.07	9.12	7.32	8.92	1.33

[1] First-generation Purunã. [2] Second-generation Purunã. [3] Caracu. [4] Canchim vs. Aberdeen Angus. [5] Charolais vs. Caracu. [6] Stardart error.
* Means in the same line followed by different letters differ by the Tukey test, p<0.05.

3 (clupanodonic acid - DPA) and C22:6 *n*-3 (cervonic acid-DHA) were similar (p>0.05) among animals from the different genetic groups.

The levels of C14:0 (myristic acid) were higher (p<0.05) in PUR1 (2.65%) and PUR2 (2.31%) animals. Specimens from the CAR (1.36%), CAN vs. ANG (1.12%) and CHA vs. CAR (1.41%) genetic groups featured lower levels (p<0.05) of this fatty acid. The mean percentage of C14:0 was 1.77%. Higher values (2.34%) were observed by Padre et al. (2007), who used crossbred animals, although finished in pasture systems. This demonstrates that animals finished in feedlot featured higher levels of these fatty acids, which are classified as saturated due to their structure, and are therefore considered harmful to human health.

Of the five fatty acids found in the *Longissimus* muscle, C16:0 (palmitic acid) was observed in higher levels as compared to the others. The mean percentage of C16:0 was 27.9%. Padre et al. (2007) observed lower levels (24.7%) for animals from different genetic groups. The percentage of C16:0 was higher (p<0.05) in animals from the PUR2 genetic group (31.9%). PUR1 animals displayed intermediate levels (28.9%). Animals from the CAR (23.5%), CAN vs. ANG (25.7%) and CHA vs. CAR (26.5%) genetic groups featured lower levels than animals from the other groups.

The percentage of C16:1 *n*-7 (palmitoleic acid) was higher (p<0.05) in animals from the PUR2 genetic group (3.41%). The percentage of this acid in PUR1 (2.78%) was similar in PUR2 and in animals from the other genetic groups. The animals from the CAR (1.66%), CAN vs. ANG (1.73%) and CHA vs. CAR (1.91%) groups featured the lowest percentages, which were similar amongst themselves.

C17:0 (margaric acid) featured greater (p<0.05) percentage in animals from the PUR1 (0.65%), CAR (0.55%) and CHA vs. CAR (0.58%) genetic groups. Prado et al. (2003) observed higher percentages in crossbred animals finished in pasture systems (2.37%).

The highest (p<0.05) levels of C18:1 *n*-9 (oleic acid) was found in animals from the CAR (44.11%) and CHA vs. CAR (44.0%) genetic groups. PUR2 animals (39.1%) obtained a lower percentage (p<0.05) of C18:1 *n*-9. However, animals from the PUR1 (41.1%) and CAN vs. ANG (41.4%) genetic groups featured similar percentages among them and the other treatments.

When the diet of ruminants features low fat concentrations, the majority of adipose tissue is formed from the synthesis of fatty acids through animal metabolism. Fatty acids are elongated up to C18:0 and, through desaturation, are converted into C18:1 (Rule et al., 1997). Thus, as the formation of adipose tissue is increased, a greater deposition of oleic acid takes place.

However, oleic acid increases the concentration of HDL-cholesterol and lowers the concentration of LDL (Katan et al., 1994). Given that only LDL is related with cardiovascular conditions, in this case a higher concentration of oleic acid does not bring any negative effects to human health.

Table 3 presents the percentages of saturated fatty acids (SFA), monounsaturated fatty acids (MUFA), polyunsaturated fatty acids (PUFA), *n*-6 and *n*-3 fatty acids, as well as PUFA:SFA and *n*-6:*n*-3 ratios, in the *Longissimus* muscle of animals from different genetic groups finished in feedlot.

The levels of SFA, MUFA, PUFA, *n*-6 and *n*-3, as well as the PUFA:SFA and *n*-6:*n*-3 ratios were similar (p>0.05) among animals from the different genetic groups.

The mean percentage found for SFA was 48.32%. Padre et al. (2006) observed higher percentages of SFA in animals finished in pasture, 54.2%. However, Holo et al. (2001a;b), Ruiz et al. (2005) and Kazama et al. (2008) obtained results close to those found in this study.

The mean percentage of MUFA was 45.6%. Kazama et al. (2008) observed a similar level (43.1%) as this study. In this study, MUFA content was higher than that found by Greghi et al. (2003), 37.4%.

The average PUFA among animals from the different genetic groups was 6.98%. Moreno et al. (2008) obtained 4.1% for crossbred animals (Belgian Blue vs. Holstein-Friesian) finished in feedlot. However, Kazama et al. (2008) observed an average of 8.46% in crossbred heifers (Nellore vs. Angus) finished in feedlot. Therefore, animal breed influences PUFA in the *Longissimus* muscle of bovines.

The mean percentage of fatty acids from the *n*-6 group was 5.27%. This value is higher than that obtained by Moreno et al. (2008) (2.59%) and similar to what Kazama et al. (2008) observed (7.34%).

The mean percentage of fatty acids from the *n*-3 group was 0.60%. Kazama et al. (2008) and Moreno et al. (2008) observed higher values for *n*-3 fatty acids (1.27 and 1.23%, respectively).

The mean PUFA:MUFA ratio was 0.15, lower than what is recommended (0.45) by the English Health Department (HSMO, 1994).

The ratio *n*-6:*n*-3 fatty acid was 8.68. *N*-6 and *n*-3 fatty acids have 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).

CONCLUSION

In bovines, genetic groups have a certain influence in the chemical composition and fatty acid profile of the *Longissimus* muscle of animals intensively finished in feedlot. This difference is related to the origin of the various genetic groups. Animals with Zebu features have the highest levels of unsaturated fatty acids, due to characteristics in fiber composition and a higher percentage of muscle collagen. However, genetic manipulation has shown only small variations in beef composition.

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