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## Meat quality from four genetic groups of bulls slaughtered at 14 months old

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**ABSTRACT.** Carcass characteristics and chemical composition of *Longissimus* muscle of 32 young bulls from four genetic groups slaughtered at 14 months old were evaluated. Experimental design was completely randomized and distributed into four genetics groups: 1. Caracu (CAR); 2. Canchin (CAN); 3. Charolais *vs.* Caracu (CHC) and 4. Aberdeen Angus *vs.* Canchin (AAC). Carcass dressing and carcass conformation were lower for CAR than CAN, CHC and AAC genetic groups. No difference has been reported with regard to moisture, ash, crude protein, total lipids and total cholesterol among four genetics groups. The genetic groups influence fatty acid profile on *Longissimus* muscle in bulls. Cattle with zebu genes had the highest rates in unsaturated fatty acids, saturated fatty acids represented approximately 50% of total fatty acid composition on *Longissimus* muscle. The genetic groups presented differences in PUFA, SFA, *n*-6 and *n*-3 percentages and *n*-6 and *n*-3 ratios.

**Keywords:** crossbreed, production systems, total cholesterol, total lipids.

## Qualidade da carne de bovinos não castrados de quatro grupos genéticos abatidos aos 14 meses de idade

**RESUMO.** Este trabalho foi realizado para avaliar as características de carcaça e composição química do músculo *Longissimus* de 32 bovinos não castrados de quatro grupos genéticos abatidos aos 14 meses de idade. Foi usado um modelo experimental inteiramente casualizado e distribuídos em quatro grupos genéticos: 1. Caracu (CAR); 2. Canchin (CAN); 3. Charolês *vs.* Caracu (CHC) e 4. Aberdeen Angus *vs.* Canchin (AAC). O rendimento e a conformação de carcaça foram menores para os animais do grupo genético CAR em comparação ao grupo genético CAN, CHC e AAC. Não houve diferença para umidade, cinzas, proteína bruta e colesterol total entre os quatro grupos genéticos. O grupo genético teve influência sobre o perfil de ácidos graxos do músculo *Longissimus* dos bovinos. Os bovinos com genes zebu tiveram maiores níveis de ácidos graxos saturados. Os ácidos graxos saturados representaram aproximadamente 50% da composição dos ácidos graxos do músculo *Longissimus*. O grupo genético teve efeito nas percentagens de ácidos graxos saturados e poliinsaturados, *n*-3 e *n*-6 e sobre a razão entre *n*-6 e *n*-3.

**Palavras-chave:** cruzamento, sistema de produção, colesterol total, lipídeos totais.

### Introduction

Carcass production characterized by adequate weight and subcutaneous fat thickness that guarantees meat quality during the chilling process is essential in beef cattle-production system (SUGUISAWA et al., 2006). According Perotto et al. (2000), weight increase and better quality carcass are the benefits that crossbreeds between *Bos taurus taurus* and *Bos taurus indicus* provide to beef cattle. Since cattle breed is one of the most important factors for fat deposition and composition (MAGGIONI et al., 2009, 2010; PRADO et al., 2008d, 2009b; ROTTA et al., 2009a and b) it should be understood

due to its genetic transmission. However, the variation's detailed mechanisms and whether or how they may be manipulated are still not clearly known. British cattle are known for their highly marbled meat, while the Zebu breeds contain less fat and more connective tissue (PRADO et al., 2009a and c; ROTTA et al., 2009a and b). Genetic variability comprises differences among species, breeds or lines, differences due to breed crossing and to the difference between animals within breeds (ROTTA et al., 2009b). The latter source of variation is estimated by heritability and genetic correlations. Breed effects may be influenced by segregation of

major genes, one of which is the double-muscling gene in cattle. It is rather difficult to assess the real genetic contribution to differences in meat quality. Comparison of breed is often confused with other effects, such as fat level, body weight, age at slaughter and production system (ARICETTI et al., 2008; KAZAMA et al., 2008; PRADO et al., 2008a, b and c; ROTTA et al., 2009a and b; WEBB, 2006).

The fatty acid profile of meat is highly relevant for two main reasons: it determines nutritional value, and it affects various aspects of meat quality, including shelf life and flavor (WOOD et al., 2003). Nutritional value is partially determined by the ratio between polyunsaturated fatty acids (PUFA) and saturated fatty acids (SFA) in the meat, and by the balance between fatty acids of the *n*-6 and *n*-3 series. In general, ratio PUFA:SFA above 0.45 and ratio *n*-6:*n*-3 below 4.0 are required in the diet against several "life style diseases", such as coronary heart diseases and cancers (HMSO, 1994).

Current analysis evaluates the carcass characteristics, chemical and fatty acid composition of Caracu, Canchin (5/8 Charolais *vs.* 3/8 Zebu), Charolais *vs.* Caracu and Aberdeen Angus *vs.* Canchin bulls finished in feedlot and slaughtered at 14 months old.

## Material and methods

### Animal management and sampling

The Animal Production Committee of the State University of Maringá approved this study (CIOMS/OMS, 1985) which was carried out on the Model Farm Experimental Station of the Paraná Agronomic Institute (IAPAR) in Ponta Grossa, Paraná, Brazil. Thirty-two bulls from four different genetic groups were used. The experimental design was randomized and distributed according to the following groups: 1. CAR – Caracu, 2. CAN – Canchin (5/8 Charolais *vs.* 3/8 Zebu), 3. CHC – 1/2 Charolais *vs.* 1/2 Caracu and 4. AAC – 1/2 Aberdeen Angus *vs.* 1/2 Canchin, with eight replications each. The bulls were weaned at 90 days and remained on hermartria (*Hermarthria altissima*) pastures grown with supplementation based on 1.5 kg animal<sup>-1</sup> day<sup>-1</sup> of the mixture 25% soybean meal + 73% corn grain + 2% mineral salt. After this period, the bulls remained on hermartria pastures during 6 months (spring and summer) without supplementation. Bulls were then finished in feedlot during 150 days in individual 8 m<sup>2</sup> covered stalls, provided with concrete floor, feeder for roughage, concentrate, mineral salt and water trough regulated by an automatic ball system. Initial weights were 294, 278, 295 and 285 kg respectively for CAR, CAN, CHC

and AAC genetic groups. The bulls were weighed at the beginning of the experiment, at 8h00 in the morning. Periodic weights were undertaken at every 28 days, with fasting of solid for 16 hours, obtained by total withdrawal of food on the previous day at 16:00h. The bulls received a diet with 12% crude protein and 72% total digestible nutrients. Forage consisted of corn silage and concentrate (25% soybean meal, 73% corn grain and 2% mineral salt). The ratio roughage:concentrate was 52:48, and the formulation was expected to provide a weight gain of 1.4 kg day<sup>-1</sup>, according to NRC recommendations (NRC, 1996). Table 1 shows the composition of fatty acids of the experimental diet. Table 2 shows the chemical composition of the diet.

**Table 1.** Composition of fatty acid of the experimental diet.

Fatty acids	%
14:0	0.55
16:0	14.6
16:1 <i>n</i> -7	0.20
17:0	0.51
18:0	2.23
18:1 <i>n</i> -9	30.6
18:1 <i>n</i> -7	1.31
18:2 <i>n</i> -6	44.6
18:3 <i>n</i> -6	0.48
18:3 <i>n</i> -3	3.98
20:4 <i>n</i> -6	0.22
22:6 <i>n</i> -3	0.81

The animals were slaughtered at a commercial slaughterhouse 90 km from Ponta Grossa Research Farm, according to industrial practices in Brazil. After slaughter, the carcasses were identified and chilled for 24h at 4°C. After chilling, the right part of the carcass was used to determine the quantitative characteristics. Twenty-four hours later, *Longissimus* muscle samples were taken by a complete cross section between the 12<sup>th</sup> and 13<sup>th</sup> ribs. The fat thickness was discarded and the muscle portion was frozen at -20°C for further analyses.

**Table 2.** Chemical composition of experimental diets (%DM).

Composition	Feed (% of DM)	
	Concentrate	Corn Silage
Dry Matter	88.0	92.3
Crude Protein	18.7	6.16
Ether extract	7.04	3.05
Ashes	3.10	4.60
Neutral detergent fiber	19.5	58.6
Acid detergent fiber	6.69	27.6

### Carcass characteristics

Hot carcass weight (HCW): Weight was determined before chilling.

Hot carcass dressing (HCD): The percentage of individual animal dressing was defined by the ratio of hot carcass weight and live weight.

Carcass conformation (CON): CON was evaluated by Müller's point scale (MÜLLER, 1980), in which the highest value indicated the best conformation; muscle development was calculated after the exclusion of thickness fat. Carcass conformation was reported as superior, very good, good, regular, poor, and inferior; ratings were also qualified as plus, average, and minus. The carcass length was evaluated by measurements taken from the skull board to the pubic bone on the anterior side of the first rib.

Fat thickness (FAT): FAT was calculated by a caliper averaging three points between the 12<sup>th</sup> and 13<sup>th</sup> ribs on the *Longissimus* muscle (LM).

Longissimus muscle area (LMA): The right part of the carcass was measured after a cross section cut was made between the 12<sup>th</sup> and 13<sup>th</sup> ribs using a compensating planimeter which measures areas of irregularly-shaped objects.

Color (COL): Muscle color was analyzed after 24-hour carcass chilling. Color was evaluated according to a point scale 30 min after a cross-sectional cut was made on the *Longissimus* muscle between the 12<sup>th</sup> and 13<sup>th</sup> ribs (MÜLLER, 1980).

Marbling (MAR): MAR was measured in the LM between 12<sup>th</sup> and 13<sup>th</sup> ribs, following scores described by MÜLLER (1980).

Percentage of muscle (MUS), fat (FAT) and bone (BON): Muscle, fat and bone were physically separated from the *Longissimus* section, which corresponded to the 10<sup>th</sup>, 11<sup>th</sup> and 12<sup>th</sup> ribs, and individually weighed according to Hankins and Howe (1946). Data were regressed to equations by Müller (1980) – the model converted the data to values corresponding to the 9<sup>th</sup>, 10<sup>th</sup>, and 11<sup>th</sup> ribs, as follows:

$$\% M = 6.292 + 0.910 X1$$

$$\% B = 2.117 + 0.860 X3$$

$$\% F = 1.526 + 0.913 X2$$

in which:

X1, X2 and X3 represented muscle, fat and bone percentages.

Rates corresponding to the 9<sup>th</sup>, 10<sup>th</sup> and 11<sup>th</sup> ribs were regressed to equations, following Hankins and Howe (1946) to find the percentages of muscle (MUS), fat (FAT) and bone (BON).

$$MUS = 15.56 + 0.81 M;$$

$$FAT = 3.06 + 0.82 F;$$

$$BON = 4.30 + 0.61 B.$$

in which:

M, F and B are the muscle, fat and bone estimates from equations by Müller (1980).

After 24 hours, LM samples were taken by complete cross-section between the 12<sup>th</sup> and 13<sup>th</sup> 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 meat were carried out two months after sampling. The samples were defrosted at room temperature (20°C), ground, homogenized and analyzed in triplicate. Meat moisture and ash contents were determined according to AOAC (1998). Crude protein content was obtained by Kjeldahl method (AOAC, 1998) and total lipids were extracted by Bligh and Dyer (1959) method, with a chloroform methanol<sup>-1</sup> mixture. Cholesterol analysis was carried out by method modified by Rowe et al. (1999). A 60% (w v<sup>-1</sup>) solution of potassium hydroxide was added to the samples in quantities equivalent to 2 mL h<sup>-1</sup> of sample under 1-h reflux. The residue was dissolved again in 2 mL hexane containing 0.2 mg mL<sup>-1</sup> 5- $\alpha$  cholestane internal standard (IS) (Sigma, USA). Cholesterol content was analyzed in 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 0.20  $\mu$ m Ohio Valley-30). Injector, column and detector temperatures were respectively 260, 280, and 280°C. Ultra-pure gas fluxes (White Martins) of 1.5 mL min<sup>-1</sup> H<sub>2</sub> as carrier gas, 30 mL min<sup>-1</sup> N<sub>2</sub> as make-up gas, 300 mL min<sup>-1</sup> synthetic gas, and 30 mL min<sup>-1</sup> N<sub>2</sub> for flame were used. The sample injection split mode was: 1:150. Peak integration was carried out with CG-300 computing integrator (CG Instruments, Brazil) and cholesterol was identified by comparison with standards from Sigma (USA). Sample cholesterol quantification was carried out after verification of method linearity. Standard cholesterol solutions (Sigma, USA) were prepared with concentrations 0.0, 0.4, 0.8, 1.6 and 2.0 mg mL<sup>-1</sup>, containing 0.20 mg mL<sup>-1</sup> 5 $\alpha$ -cholestane (Sigma, USA), and analyzed. The ratio between cholesterol areas and 5- $\alpha$  cholestane was plotted against the cholesterol concentration for injected volumes of 0.0, 2.0, 3.0, 4.0 and 5.0  $\mu$ L. The curve obtained was used for cholesterol analysis in mg 100 g<sup>-1</sup>.

Fatty acid methyl esters (FAME) were prepared by triacylglycerol methylation, according to ISO (1978) method. Fatty acids methyl esters (FAMES) were analyzed in gas chromatograph (Varian, USA) equipped with-flame ionization detector and fused silica capillary column CP-7420 (100 m, 0.25 mm and 0.39  $\mu$ mol day<sup>-1</sup>, Varian, USA) Select Fame. Column temperature was programmed at 165°C for

18 min., 180°C (30°C min.<sup>-1</sup>) for 22 min., and 240°C (15°C min.<sup>-1</sup>) for 30 min., with 45-psi pressure. The injector and detector were kept respectively at 220 and 245°C. The gases fluxes (White Martins) were: 1.4 mL min.<sup>-1</sup> for the carrier gas (H<sub>2</sub>); 30 mL min.<sup>-1</sup> for the make-up gas (N<sub>2</sub>) and 30 mL min.<sup>-1</sup> and 300 mL min.<sup>-1</sup> for H<sub>2</sub> 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 ester standards from Sigma (USA) by spiking samples with standard. The peak areas were determined by Star software (Varian) and data were expressed as percentages of the normalized area of fatty acids.

### Statistical analyses

Statistical analyses were interpreted by analysis of variance and differences evaluated by Tukey's test 5%, analyzed by SAS (2000) program as model:

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

in which:

$Y_{ij}$  "j" is the animal observation subjected to trial "i";

$\mu$  - general constant;

$GG_i$  - trial effect i; i = 1, ..., 4; in which 1 = CAR; 2 = CAN; 3 = CHC and 4 = AAC;

$e_{ij}$  - random error associated with each observation.

### Results and discussion

#### Carcass characteristics

There was no difference ( $p > 0.05$ ) among genetic groups for final live weight and hot carcass weight of bulls slaughtered at 14 months old (Table 3). Although there was no difference among treatments, the slaughter weight of different genetic groups revealed that CAR and CAN genetic bull groups failed to achieve the final weight of 450 kg. In spite of the fact that CHC and AAC genetic groups achieved the final weight of 469 and 461 kg, the two groups did not present adequate finishing level. In fact, such groups have large body frames requiring higher finishing level and body weight.

Carcass dressing and carcass conformation were lower ( $p < 0.05$ ) for CAR genetic group (49.6% and 9.25 points) when compared to CAN (54.5% and 12.4 points), CHC (52.7% and 11.6 points) and AAC (54.0% and 12.0 points) genetic groups. These results show that CAR genetic group may not be slaughtered with 445 kg body weight due to low fat characteristics. However, Rotta et al. (2009a)

evaluated the carcass characteristics of Nellore, Caracu and Holstein bulls finished in feedlot and observed higher rates of carcass dressing (52.8%) and conformation (12.9 points) for Caracu genetic group. Perotto et al. (2000) evaluated the quantitative characteristics of carcasses of Charolais, Caracu and reciprocal cross finished in feedlot and registered higher rates in carcass dressing and conformation to Caracu genetic group. The superior carcass dressing and carcass conformation for CAN, CHC and AAC genetic groups may be explained by their high proportion of British breed genes, as these animals are known for their favorable carcass quality. The less favorable carcass dressing and conformation of the CAR genetic group might be due to higher percentage of tropical breed genes.

**Table 3.** Carcass characteristics of different genetic groups of bulls slaughtered at 14 months old.

Carcass characteristics	Genetic groups				SE <sup>5</sup>
	CAR <sup>1</sup>	CAN <sup>2</sup>	CHC <sup>3</sup>	AAC <sup>4</sup>	
N	8	8	8	8	
Final live weight (kg)	445	443	469	461	5.98
Hot carcass weight (kg)	221	241	247	249	4.10
Hot carcass dressing (%)	49.6b	54.5a	52.7a	54.0a	0.51
Carcass conformation (points)	9.25b	12.4a	11.6a	12.0a	0.33
Fat (mm)	2.50c	3.19b	3.19b	4.38a	0.22
<i>Longissimus</i> muscle area (cm <sup>2</sup> )	57.9	63.1	62.8	63.5	1.06
<i>Longissimus</i> muscle (area <sup>6</sup> )	26.5	27.1	25.4	25.5	0.46
Color (points)	3.50	3.75	3.25	3.88	0.11
Marbling (points)	4.38	4.63	4.38	4.88	0.42
Muscle (%)	58.6	60.7	60.1	62.4	0.29
Fat (%)	24.6	22.9	23.3	22.2	0.89
Bone (%)	16.8	16.4	16.7	15.4	0.91

<sup>1</sup>Caracu, <sup>2</sup>Canchin, <sup>3</sup>Charolais vs. Caracu, <sup>4</sup>Aberdeen Angus vs. Canchin, <sup>5</sup>Standard errors, <sup>6</sup>100 kg of carcass. Means on the same line with different letters are different by Tukey's test ( $p < 0.05$ ).

Fat thickness was highest ( $p < 0.05$ ) in AAC (4.38 mm) genetic group and lowest in CAR (2.50 mm) genetic group. CAN (3.19 mm) and CHC (3.19 mm) genetic groups provided intermediate rates. This fact may be explained by differences in fat accumulation in Aberdeen Angus and Charolais breeds. The fat thickness noted in CAN, CHC and AAC meets the guidelines of the Brazilian market, which requires that fat thickness of carcasses must range between 3 and 6 mm (MÜLLER, 1980). Similar results for fat thickness in CAR genetic group were observed by Rotta et al. (2009a) with 2.88 mm. This shows that CAR genetic group still did not reach 3.0 mm of fat thickness, which is the appropriate slaughter fat in Brazil.

The average for *Longissimus* muscle area and *Longissimus* muscle area 100 kg<sup>-1</sup> carcass were similar ( $p > 0.05$ ) for bulls from four genetic groups (Table 3).

The crossbreed type did not affect ( $p > 0.05$ ) color and marbling of the *Longissimus* muscle (Table 3). According to Müller's scale (1980), the color for all genetic groups may be considered satisfactory, as they

were classified as red-colored. They are therefore within the beef intake standards for the Brazilian market. Further, marbling was classified as average among the different genetic groups. Although medium marbling is well accepted within the Brazilian market, beef should feature more enhanced marbling to reach foreign markets, especially those in North America.

Muscle, fat and bone percentages were not influenced ( $p > 0.05$ ) by genetic groups and showed averages of 60.2, 23.5 and 15.5%, respectively. Although fat thickness was higher than 4.3 mm in AAC genetic group and lower than 2.5 mm in CAR genetic group, it did not influence carcass fat deposition.

### Chemical composition

Differences ( $p > 0.05$ ) existed in moisture, ashes, crude protein, total lipids and total cholesterol among different genetics groups (Table 4) on *Longissimus* muscle.

**Table 4.** Chemical composition of *Longissimus* muscle of different genetic groups of bulls slaughtered at 14 months old.

Parameters	Genetic groups				SE <sup>5</sup>
	CAR <sup>1</sup>	CAN <sup>2</sup>	CHC <sup>3</sup>	AAC <sup>4</sup>	
N	8	8	8	8	
Moisture (%)	72.7	73.3	72.7	72.6	0.17
Ash (%)	1.04	1.03	1.01	1.06	0.11
Crude protein (%)	22.8	22.4	22.8	22.7	0.16
Total lipids (%)	1.38	1.32	1.38	1.39	0.02
Total cholesterol (mg 100 g <sup>-1</sup> muscle)	36.3	36.7	36.5	36.4	0.18

<sup>1</sup>Caracu, <sup>2</sup>Canchin, <sup>3</sup>Charolais *vs.* Caracu, <sup>4</sup>Aberdeen Angus *vs.* Canchin, <sup>5</sup>Standard errors.

The mean rates of moisture, ashes and crude protein were 72.8, 1.03 and 22.7%, respectively. These results were similar to those found by Ducatti et al. (2009) who evaluated chemical and fatty acids composition of different genetic groups (Purunã 1<sup>st</sup> generation; Purunã 2<sup>nd</sup> generation; Caracu; Canchin *vs.* Angus and Charolês *vs.* Caracu) and the mean values observed were 73.3, 0.97% and 22.5%, respectively. According to these results, moisture, ashes and crude protein rates did not show any variations owing to the genetic groups. However, total lipids and total cholesterol rates reported by Ducatti et al. (2009) were higher (2.16% and 42.0 mg 100 g<sup>-1</sup> of muscle) than those in current analysis (1.37% and 36.6 mg 100 g<sup>-1</sup> of muscle). Kazama et al. (2008); Rotta et al. (2009a and b) also reported higher total cholesterol rates when compared to those in current experiment.

### Fatty acid composition

Table 5 shows the composition of fatty acids in the *Longissimus* muscle. Diversity in fatty acids in cattle is partly due to bio-hydrogenation reactions that occur in the rumen (TAMMINGA; DOREAU, 1991).

Palmitoleic acid (C16:1 *n*-7) levels were higher ( $p < 0.05$ ) in CAR bulls and lower in CAN and CHC ones. C17:1 *n*-7 levels were higher ( $p < 0.05$ ) in AAC bulls and lower in CAR and CAN ones. Linoleic acid (C18:2 *n*-6) levels were similar ( $p > 0.05$ ) between CAR and CAN bulls and CHC and AAC bulls, but higher ( $p < 0.05$ ) in CAR and CAN when compared to CHC and AAC bulls. Arachidonic acid (C20:4 *n*-6) levels were similar ( $p > 0.05$ ) in CAN and AAC and CAR and CHC bulls, but superior ( $p < 0.05$ ) in CAN and AAC bulls when compared to those in CAR and CHC bulls. Docosapentanoic acid – DPA (C22:5 *n*-3) levels were higher ( $p < 0.05$ ) in CAN bulls, intermediate in CAR and AAC bulls, and lower in CHC bulls.

**Table 5.** Fatty acid composition in different genetic groups of bulls slaughtered at 14 months old.

Fatty acids	Genetic groups				SE <sup>5</sup>
	CAR <sup>1</sup>	CAN <sup>2</sup>	CHC <sup>3</sup>	AAC <sup>4</sup>	
N	8	8	8	8	
14:0 Miristic acid	2.80	2.36	2.62	2.38	0.07
15:0 Pentadecylic acid	0.24	0.25	0.26	0.27	0.01
16:0 Palmitic acid	29.6	30.2	29.9	33.0	0.21
16:1 <i>n</i> -7 Palmitoleic acid	3.59a	2.66b	2.87b	3.07ab	0.09
17:0 Margaric acid	0.56	0.64	0.60	0.61	0.01
17:1 <i>n</i> -7 Heptadecenoic acid	0.43b	0.42b	0.45ab	0.48a	0.01
18:0 Stearic acid	15.7	15.5	16.5	15.6	0.19
18:1 <i>t</i> -11 Trans vaccenic acid	0.51	0.56	0.47	0.51	0.01
18:1 <i>n</i> -9 Oleic acid	35.1	34.2	36.5	36.2	0.28
18:1 <i>n</i> -7 Cis vaccenic acid	1.19	1.12	1.09	1.08	0.03
18:2 <i>n</i> -6 Linoleic acid	6.04a	6.91a	5.05b	5.13b	0.23
18:3 <i>n</i> -6 Linolenic acid	0.10	0.10	0.10	0.10	0.00
18:3 <i>n</i> -3 $\beta$ -Linolenic acid	0.23	0.35	0.31	0.27	0.02
18:2 <i>c</i> -9, <i>t</i> -11 CLA	0.21	0.25	0.21	0.21	0.01
22:0 Behenic acid	0.04	0.04	0.03	0.08	0.01
20:4 <i>n</i> -6 Arachidonic acid	1.84b	2.41a	1.37b	2.18a	0.11
20:5 <i>n</i> -3 Eicosapentanoic	0.11	0.19	0.15	0.18	0.01
22:5 <i>n</i> -3 Docosapentanoic – DPA	0.40b	0.55a	0.32c	0.46b	0.02
22:6 <i>n</i> -3 Docosahexanoic acid – DHA	0.10	0.10	0.10	0.10	0.00

<sup>1</sup>Caracu, <sup>2</sup>Canchin, <sup>3</sup>Charolais *vs.* Caracu, <sup>4</sup>Aberdeen Angus *vs.* Canchin, <sup>5</sup>Standard errors. Means on the same line with different letters are different by Tukey's test ( $p < 0.05$ ).

Prado et al. (2008a and b) suggested that genetic groups were a major factor associated with variations in the fatty acid profile. The fatty acids 12:0, 14:0 and 16:0 were considered hypercholesterolemic; they increased the quantity of lipoproteins of low density lipoprotein (LDL), which cause heart disease (HMSO, 1994). Food with low amounts of fatty acids is therefore required. In the *Longissimus* muscle of cattle the percentage of 14:0 and 16:0 was considered high (30% of total fatty acids) (PRADO et al., 2008a and b; ROTTA et al., 2009b). Though the fatty acid 18:2 *n*-6 is considered essential, it is related to the imbalance of *n*-6/*n*-3 ratio. This occurs by the high presence of the fatty acid in the *Longissimus* muscle of cattle when compared to *n*-3 fatty acids (ROTTA et al., 2009b). The highest percentage of this fatty acid was founded in CAR

and CAN genetic groups. The fatty acid 18:3 *n*-3 is considered strictly essential and the presence of the fatty acid is important due to its capacity to form other important fatty acids (WOOD et al., 2003).

There was no difference among ( $p > 0.05$ ) genetic groups with regard to saturated fatty acids (SFA) (Table 6). SFA represented approximately 49% of total fatty acid composition analyzed on *Longissimus* muscle of bulls from four genetic groups slaughtered at 14 months old. The MUFA levels were lower ( $p < 0.05$ ) for CAN genetic groups when compared to those of CAR, CHC and AAC genetic groups. However, MUFA levels were similar ( $p > 0.05$ ) among CAR, CHC and AAC genetic groups.

PUFA levels were higher ( $p < 0.05$ ) for CAR and CAN genetic groups. However, CAR and CAN genetic groups and CHC and AAC genetic groups presented no difference ( $p > 0.05$ ) among themselves. Genetic groups with zebu genes in their composition (CAN) showed high percentages of PUFA (ROTTA et al., 2009a). Prado et al. (2008a and b) suggested that zebu genes caused more deposition of connective tissues, with high rates of polyunsaturated fatty acids.

**Table 6.** Fatty acids sum and ratio between the fatty acids of *Longissimus* muscle of different genetic groups slaughtered at 14 months old.

Sums and ratios	Genetic groups				SE <sup>5</sup>
	CAR <sup>1</sup>	CAN <sup>2</sup>	CHC <sup>3</sup>	AAC <sup>4</sup>	
	8	8	8	8	
SFA <sup>6</sup>	49.0	49.1	49.9	48.9	0.34
MUFA <sup>7</sup>	42.0a	40.1b	42.5a	42.5a	0.27
PUFA <sup>8</sup>	9.03ab	10.9a	7.61b	8.63b	0.27
<i>n</i> -6	7.98b	9.42a	6.52c	7.41b	0.31
<i>n</i> -3	0.84b	1.20a	0.88b	1.00b	0.04
PUFA:SFA	0.18b	0.22a	0.15c	0.18b	0.01
<i>n</i> -6: <i>n</i> -3	9.50a	7.85b	7.41b	7.41b	0.26

<sup>1</sup>Caracu, <sup>2</sup>Canchin, <sup>3</sup>Charolais *vs.* Caracu, <sup>4</sup>Aberdeen Angus *vs.* Canchin. <sup>5</sup>Standard errors, <sup>6</sup>Saturated fatty acids, <sup>7</sup>Monounsaturated fatty acids, <sup>8</sup>Polyunsaturated fatty acids. Means on the same line with different letters are different by Tukey's test ( $p < 0.05$ ).

Whereas CAN genetic group presented the highest *n*-6 percentages, CHC had the lowest percentages and CAR and AAC had intermediate percentages (Table 6). The *n*-6 percentage ranged between 6.5 and 9.4%. The genetic groups with zebu genes in their composition showed high percentages of fatty acids in *Longissimus* muscle (PRADO et al., 2008a and b), due to the fact that these genetic groups have more PUFA in their fatty acid profile (ROTTA et al., 2009b).

The *n*-3 percentages were higher ( $p < 0.05$ ) in CAN genetic groups. However, there was no difference ( $p > 0.05$ ) among CAR, CHC and AAC genetic groups.

PUFA:SFA ratio was higher ( $p < 0.05$ ) for CAN genetic group and lower ( $p < 0.05$ ) for CHC

genetic group (Table 6). PUFA:SFA ratio was similar ( $p > 0.05$ ) between CAR and AAC genetic groups. PUFA:SFA ranges between 0.15 and 0.22. PUFA:SFA ratio plays an important role in reducing the risk of coronary heart disease (HU, 2001). The British Health Department (HMSO, 1994) recommended a ratio of 0.45. The genetic groups close to this value were those with zebu genes (CAN) in their composition. However, the observed value in this research is far from recommended.

The *n*-6:*n*-3 ratio was higher ( $p < 0.05$ ) for CAR genetic group. However, there was no difference ( $p > 0.05$ ) among CAN, CHC and AAC genetic groups. According to the British Health Department (HMSO, 1994), the recommended *n*-6:*n*-3 ratio is 4:1. The observed values in this work were higher when compared to the ideal.

## Conclusion

Crossbreeding between European breeds produce higher carcass dressing and carcass conformation due to genetic improvements accumulated over decades. Further, genetic groups have a certain influence on fatty acid profile of the *Longissimus* muscle in bulls finished in feedlot. The difference is related to the origin of the various genetic groups. Cattle with zebu genes have the highest levels of unsaturated fatty acids due to their fiber composition and higher percentage of muscle collagen. However, genetic manipulation only produced a small variation in meat composition.

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