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Chemical and Fatty Acid Composition of *Longissimus* Muscle of Crossbred Bulls Finished in Feedlot

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ABSTRACT : This work was carried out to study the chemical and fatty acid composition of *Longissimus* muscle (LM) of crossbred young bulls finished in a feedlot. After weaning (at 8 months old), the bulls were kept in a feedlot for 180 days. The bulls were kept in individual pens and fed (twice daily) with corn silage, soybean hulls, cracked corn, limestone, urea and mineral salt. The bulls were slaughtered with a final weight of 464 kg. Forty bulls were used: 10 Caracu (CAR), 10 Canchim (CAN), 10 Caracu vs. Charolais (CCH) and 10 Canchim vs. Aberdeen Angus (CAA). The percentages of moisture, ash, crude protein, total lipids, as well as the fatty acid composition, were measured in the LM. The moisture percentage was lower ($p<0.05$) for bulls from CAA genetic group (71.2%) in comparison to bulls from CAR (74.2%), CAN (74.9%) and CCH (74.7%) genetic groups. On the other hand, there was no difference ($p>0.05$) among bulls from CAR, CAN and CCH genetic groups. Ash percentage was lower ($p<0.05$) for CAR bulls (0.96%) in comparison with the other genetic groups. There was no difference ($p>0.05$) among CAN, CCH and CAA genetic groups. Similarly, there was no difference ($p>0.05$) in crude protein among the different genetic groups. Total lipids percentage was higher ($p<0.05$) for CAA bulls (5.35%) and lower ($p<0.05$) for CAN (1.85%) and CCH (1.41%) genetic groups. Genetic group has little effect on the fatty acid composition of *Longissimus* muscle of bulls. However, CLA (C 18:2 *c*-9 *t*-11) percentage was higher ($p<0.05$) for CAR (0.33%) and CCH (0.37%) in comparison to CAN (0.27%) and CAA (0.29%) genetic groups. Saturated, monounsaturated and polyunsaturated fatty acids, *n*-6 and *n*-3 percentages did not differ ($p>0.05$) among genetic groups. PUFA/SFA ratio ranged from 0.10 to 0.15, with no difference ($p>0.05$) among genetic groups. Similarly, *n*-6/*n*-3 ratio ranged from 12.6 to 16.3, without difference ($p>0.05$) among genetic groups. (**Key Words :** Cattle, Crossbreeding, Fatty Acids, Meat Quality)

INTRODUCTION

For the modern consumer, taste and nutritional value are two important quality attributes of meat. Today, the tendency is to focus on the production of lean beef with a minimum of visible excess of fat (Abrahão et al., 2005; Padre et al., 2006; Macedo et al., 2008; Prado et al., 2008a;b;c;d; Maggioni et al., 2009), but in some areas like Japan and Korea, grading and trading standard for beef is intramuscular fat. Nevertheless, the fact remains that fat in meat contributes to eating quality (Kazama et al., 2008). It is also widely accepted that the amount and type of fat influence the major components of meat quality, namely tenderness and flavor (Webb, 2006).

In Brazil, Zebu breeds are used for meat production. European breeds are well known for their highly marbled meat, while Zebu breeds feature less fat and more connective tissue (Moreira et al., 2003; Rotta et al., 2009). In warmer regions of Brazil, adapted cattle breeds are primarily limited to Zebu cattle - such as the Nellore breed - as the European breeds are less adapted to tropical climates in function of the high temperatures.

Researchers have been conducting studies since the 1980s on the crossbreeding system with the objective of increasing animal production (Perotto et al., 2000; 2001) and meat quality (Padre et al., 2007; Aricetti et al., 2008; Prado et al., 2009a;b). Crossbreeds between Zebu and European specimens can be slaughtered at 20 to 24 months and feature better meat quality and low total cholesterol percentage (Prado et al., 2008b). Fat percentage is very important to meat quality, as the fatty acid composition of

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Table 1. Percentage composition of experimental diets (% DM)

Parameters	DM (%)
Corn silage	39.0
Cracked corn	21.0
Soybean meal	5.00
Soybean hulls	33.0
Limestone	0.60
Mineral salt	0.60
Urea	0.80
Total	100

animals can make a considerable difference on product quality (Padre et al., 2006).

Meat fat is quite important to the consumer, as the fat percentage will influence the quality and price of meat. On the other hand, a higher fat percentage will also represent a higher production cost, as it will require high energy density in the diet in order to achieve high fat deposition (Moreira et al., 2003).

Beef is regarded as one of the factors that may lead to the development of cardiovascular disease, obesity, hypertension and cancer in humans, especially due to the presence of saturated fat and cholesterol. Nevertheless, fat contents lower than 5% of muscle weight and cholesterol contents lower than 50 mg per 100 g of muscle have been reported in literature (Greghi et al., 2003; Padre et al., 2007; Ducatti et al., 2009; Rotta et al., 2009), which represents a third to a half of the daily intake by humans.

The objective of this study was to evaluate chemical and fatty acid composition of LM of crossbred young bulls finished in feedlot.

MATERIAL AND METHODS

Animal management and sampling

The committee of Animal Production at the State University of Maringá approved this study (CIOMS/OMS, 1985), which was carried out at the Experimental Farm of the Agronomic Institute of Paraná, in the city of Ponta Grossa, Paraná, south Brazil.

Forty bulls were used: 10 Caracu (CAR), 10 Canchim (CAN), 10 Caracu vs. Charolais (CCH), and 10 Canchim vs. Aberdeen Angus (CAA), with an initial average age between 8 and 10 months. The bulls were kept separate in individual pens (8 m^2 for each animal) and fed twice a day.

The bulls had access to a diet formulated to meet requirements for fattening beef cattle (NRC, 1996), and gain 1.5 kg/d. The bulls were fed with corn silage and a concentrate diet. Corn silage was provided *ad libitum*, with adjustments made according to the previous day's intake (Table 1). Around 5% to 10% extra was left in the trough, in order not to limit intake. The bulls were fed with the objective of achieving an intake around 2.5% of dry matter-to-live body weight ratio. Water was given *ad libitum*.

The bulls were weighed at the beginning of the experiment. Thereafter, they were weighed every 28 days, observing a 16-h fast, accomplished by removing all feed at 4 p.m. on the day prior to weighing. The total experimental period lasted 180 days, during which the animals reached an average final live weight of 464 kg.

The development of fat thickness 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.

The determination of total digestible nutrients (TDN) of soybean meal and cracked corn were estimated using an equation for roughage feeds by Kearl (1992). The chemical composition of the foods and diets (% DM) used are shown in Table 2.

The bulls were slaughtered at a commercial slaughterhouse 90 km away from the Ponta Grossa farm, in Curitiba, Paraná, following the usual practices of the Brazilian beef industry. The animals were stunned using a captive bolt stunner. Next, they were bled through exsanguinations by cutting the neck vessels, and removal of the head, hide, viscera, tail, legs, diaphragm and excess internal fat. Afterward, the carcass was divided medially from the sternum and spine, resulting in two similar halves, which were weighed to calculate hot carcass weight. Next, the half-carcasses were washed, identified and stored in a chilling chamber at 4°C, where they remained for a 24-h period. Twenty-four hours later, after chilling, LM samples were taken between the 12^{th} and 13^{th} ribs. The samples were identified and stored in closed plastic bags, then immediately taken to the Food Analysis Laboratory of the Chemistry Department at the State University of Maringá,

Table 2. Chemical composition of the ingredients and experimental diets (% DM)

Parameters	DM	CP	NDT	NDF	EE	Ca	P
Corn silage	27.0	7.90	60.0	59.0	3.00	0.25	0.22
Cracked corn	88.6	7.00	80.0	9.00	3.70	0.02	0.31
Soybean hulls	92.5	72.0	72.0	68.6	1.36		
Soybean meal	88.6	45.0	78.0	36.0		0.50	0.20
Limestone	98.0					28.0	
Mineral salt	98.0					23.0	17.0
Urea	98.0	262					

Data obtained from the Laboratory of Feed Analyses and Animal Nutrition, State University of Maringá.

Table 3. Chemical composition in *Longissimus* muscle of crossbred bulls

Parameters	CAR[1]	CAN[2]	CCH[3]	CAA[4]	P<F
Moisture (%)	74.2±0.73a	74.9±1.62a	74.7±1.09a	71.2±0.60b	0.05
Ash (%)	0.96±0.04b	1.07±0.05a	1.13±0.06a	1.05±0.05a	0.05
Crude protein (%)	21.4±0.59	21.2±0.83	22.2±0.72	21.4±0.81	ns
Total lipids (%)	2.68±0.15b	1.85±0.56c	1.41±0.26c	5.35±0.15a	0.05

[1] Caracu, [2] Canchim, [3] Caracu vs. Charolais, [4] Canchim vs. Aberden Angus, ns: non-significant.

where they were frozen at -18°C for later analysis. At the start of the analyses, the meat samples were unfrozen at room temperature and homogenized using a meat grinder. Next, tests were conducted to analyze the levels of moisture, ash, crude protein, total lipids and fatty acid composition.

Chemical composition

Beef analyses were carried out in laboratory conditions two months later. The samples were thawed at room temperature (20°C), ground, homogenized and three replications were used to estimate the traits.

Beef moisture and ash contents were determined according to AOAC (1980); crude protein was obtained through the Kjeldahl method (Cunnif, 1998); total lipids were extracted by the Bligh and Dyer (1959) method using a mixture of chloroform/methanol; fatty acid methyl esters (FAME) were prepared by triacylglycerol methylation, according to the ISO method (1978).

Fatty acid methyl esters analysis

Fatty acid methyl esters (FAMEs) were analyzed in a gas chromatograph (Varian, USA) equipped with a flame ionization detector and a fused silica capillary column CP-7420 (100 m, 0.25 mm, and 0.39 μm o.d., Varian, USA) Select Fame. Column temperature was programmed at 165°C for 18 min, 180°C (30°C/min) for 22 min, and 240°C (15°C/min) for 30 min at 45 psi. The injector and detector were kept at 220°C and 245°C, respectively. The gas flows (White Martins) used were: carrier gas (H_2), 1.4 ml/min; make-up gas (N_2), 30 ml/min; H_2 and synthetic flame gas, 30 ml/min and 300 ml/min, respectively. Sample injection split mode was 1:80. Fatty acids were identified by comparing relative FAME peak retention times of samples and fatty acids methyl ester standards from Sigma (USA) by spiking samples with standards. The peak areas were determined by Star software (Varian). The data were expressed as percentages of normalized fatty acid area.

Experimental design and statistical analysis

The experimental design consisted of 4 treatments: 10 Caracu (CAR), 10 Canchim (CAN), 10 Caracu vs. Charolais (CAC) and 10 Canchim vs. Aberdeen Angus (CAA). The data were submitted to an analysis of variance (F-test), using SAS (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 to 4;

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

RESULTS AND DISCUSSION

Chemical composition

The percentage of moisture was similar ($p>0.05$) among Caracu (CAR), Canchim (CAN) and Caracu vs. Charolais (CCH) genetic groups (Table 3). Canchim vs. Aberdeen Angus (CAA) genetic group showed the lowest ($p<0.05$) percentage of moisture in comparison with the other genetic groups.

The values found for moisture are close to those observed by Prado et al. (2008a;b;c;d). The average moisture level found by Moreira et al. (2003) for crossbreeds was 71.0%, almost similar to that observed for the CAA genetic group. Among the factors that determined the variations in moisture percentages of beef are: age (Di Marco, 1998), level of carcass dressing (Luchiari Filho, 2000) and physiological condition (Marques et al., 2006; Prado et al., 2009a). In general, moisture levels observed in literature for the LM of cattle finished under various systems have varied between 72.8% (Prado et al., 2008a;b) and 76.2% (Aricetti et al., 2008). The variation in moisture levels can also occur as a result of total lipid content in the muscle (Moreira et al., 2003; Rotta et al., 2009). The higher percentage of total lipids in the muscle represents the lower percentage of water in *Longissimus* muscle.

The average of ash percentage observed in the different genetic groups (1.05%) is near the value found in the LM without cover fat in bulls (Ducatti et al., 2009; Rotta et al., 2009), heifers (Marques et al., 2006) and young bulls (Prado et al., 2008b;c;d). Consequently, it can be concluded that ash levels vary little, regardless of genetic group or finishing system (pasture or feedlot).

Total protein percentage varies little in beef, with observed values close to 21% in composition on LM without cover fat, regardless of diet, breed, genotype or physiological condition (Marques et al., 2006; Padre et al., 2006; Macedo et al., 2007; Prado et al., 2009a).

The higher percentage of total lipid is associated with animals from CAA genetic group is related to the lower moisture percentage by this genetic group, as result of the specific breeds involved in this crossbreeding. In general, animals that feature more significant British bloodlines have greater fat deposition, as result of the genetic selection imposed upon these animals for decades. Thus, animals from the CAA (Aberdeen Angus vs. Canchim) genetic group should feature higher adipose tissue accumulation, which in turn reflects the higher total lipids percentage on LM. On the other hand, animals that feature pronounced Charolais heritage in their genetic makeup have lower total lipids percentages - which were the case with animals from CAN - Canchim and CCH - Caracu vs. Charolais genetic groups. There is wide variation in total lipids percentages for meat (Aricetti et al., 2008; Kazama et al., 2008; Prado et al., 2008a;b;c;d). Total lipids percentages are influenced by several factors, such as gender, genetic groups and diet, as well as the anatomical location of the meat cut (Moreira et al., 2003; Macedo et al., 2008; Aricetti et al., 2008; Rotta et al., 2009).

Fatty acid composition

The percentages of C 14:0, C 14:1 *n*-7, C 16:0, C 16:1 *n*-7, C 16:1 *n*-9, C 17:0, C 17:1 *n*-7, C 18:1 *n*-7, C 18:1 *n*-9, C 18:2 *t*-6, C 18:2 *n*-6, C18:2 *t*-10 *c*-12, C 18:3 *n*-3, C 18:3 *n*-6, C 20:1 *n*-9, C 20:5 *n*-3, C 22:0, C 22:6 *n*-3 and C 23:0 fatty acids were similar (p>0.05) among animals from CAR, CAN, CCH and CAA genetic groups, respectively (Table 4).

Animals from CAR and CCH groups featured higher (p<0.05) percentages of C 15:0, C 15:1 *n*-7, C 18:2 *c*-9 *t*-11 and C 20:0 fatty acids in relation to animals from CAN and CAA genetic groups. However, animals from CAN and CAR genetic groups featured higher (p<0.05) percentages

Table 4. Fatty acid composition and 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 *Longissimus* muscle of crossbred bulls

Fatty acids	CAR[1]	CAN[2]	CCH[3]	CAA[4]	P<F
C 14:0	2.53±0.25	1.89±0.34	2.21±0.97	1.71±0.41	ns
C 14:1 *n*-7	0.35±0.10	0.28±0.09	0.31±0.14	0.27±0.08	ns
C 15:0	0.41±0.07a	0.26±0.03b	0.36±0.08a	0.24±0.08b	0.05
C 15:1 *n*-7	0.26±0.04a	0.18±0.03b	0.23±0.06a	0.18±0.05b	0.05
C 16:0	25.6±1.46	24.9±2.68	25.3±2.52	25.2±0.76	ns
C 16:1 *n*-7	2.45±0.44	2.35±0.42	2.55±0.34	2.72±0.47	ns
C 16:1 *n*-9	0.55±0.09	0.47±0.10	0.51±0.11	0.50±0.11	ns
C 17:0	0.89±0.13	0.79±0.06	0.78±0.14	0.70±0.14	ns
C 17:1 *n*-7	0.61±0.11	0.61±0.08	0.66±0.07	0.61±0.06	ns
C 18:0	21.4±2.10a	22.3±2.98a	19.5±2.40b	20.5±1.98b	0.05
C 18:1 *n*-7	0.94±0.15	0.91±0.26	0.89±0.12	0.73±0.15	ns
C 18:1 *n*-9	34.7±1.51	36.5±2.60	35.3±4.09	38.0±2.10	ns
C 18:2 *t*-6	0.25±0.11	0.36±0.11	0.31±0.10	0.23±0.11	ns
C 18:2 *n*-6	3.84±1.26	4.12±1.69	5.07±1.62	3.81±1.48	ns
C 18:2 *c*-9 *t*-11	0.33±0.03a	0.27±0.06b	0.37±0.04a	0.29±0.09b	0.05
C 18:2 *t*-10 *c*-12	0.09±0.01	0.09±0.02	0.09±0.02	0.10±0.02	ns
C 18:3 *n*-3	0.19±0.02	0.19±0.04	0.18±0.05	0.17±0.05	ns
C 18:3 *n*-6	0.07±0.01	0.07±0.02	0.10±0.07	0.08±0.04	ns
C 20:0	0.39±0.14a	0.30±0.10b	0.38±0.08a	0.25±0.09b	0.05
C 20:1 *n*-9	0.14±0.01	0.17±0.04	0.16±0.04	0.19±0.05	ns
C 20:3 *n*-6	0.14±0.04c	0.34±0.09a	0.21±0.07b	0.26±0.03a	0.05
C 20:5 *n*-3	0.09±0.06	0.11±0.06	0.08±0.03	0.06±0.04	ns
C 22:0	0.98±0.30	1.20±0.26	1.31±0.31	1.29±0.36	ns
C 22:6 *n*-3	0.06±0.01	0.07±0.06	0.09±0.04	0.06±0.04	ns
C 23:0	0.13±0.07	0.16±0.09	0.28±0.13	0.19±0.03	ns
SFA	51.4±2.61	51.8±4.02	50.1±2.19	50.1±2.19	ns
MUFA	39.4±1.59	41.5±2.65	40.6±4.17	43.2±2.16	ns
PUFA	5.06±1.27	5.62±1.70	6.50±1.67	5.06±1.27	ns
n-6	4.30±1.27	4.89±1.70	5.69±1.66	4.38±1.48	ns
n-3	0.34±0.07	0.37±0.09	0.35±0.06	0.29±0.07	ns
PUFA/SFA	0.10±0.02	0.15±0.02	0.13±0.03	0.10±0.02	ns
n-6/*n*-3	12.6±1.85	13.2±1.25	16.3±1.98	15.1±1.39	ns

[1] Caracu, [2] Canchim, [3] Caracu vs. Charolais, [4] Canchim vs. Aberden Angus, ns: non-significant.

of C 18:0 fatty acid as compared to animals from CAA and CCH genetic groups. The percentage of C 20:3 *n*-6 fatty acid was the highest ($p<0.05$) to animals from CAN and CAA genetic groups. This percentage was intermediary for animals from CCH genetic group; it was the lowest to animals from CAR genetic group. Therefore, it was observed that the fatty acid composition of the LM changes little in function of genetic group; only 6 of the 25 fatty acids analyzed presented differences among the different genetic groups.

Linoleic (C 18:2 *n*-6) and alpha-linolenic (C 18:3 *n*-3) acids are polyunsaturated fatty acids, classified as essential - their intake is vital, as the cells of mammals are unable to synthesize them (Smith, 2007). Linoleic and alpha-linolenic acids are precursors of arachidonic (C 20:4 *n*-6) and eicosapentaenoic (C 20:5 *n*-3) acids, which have long-chain fatty acids formed by the action of elongase and desaturase enzymes present in the endoplasmic reticulum of cells (Smith, 2007). The percentages of C 20:4 *n*-6 and C 20:5 *n*-3 fatty acids on LM of bulls can vary as results of the total lipids percentages on LM (Moreira et al., 2003; Kazama et al., 2008; Prado et al., 2008b;c;d).

Oleic acid raises the levels of HDL (high density lipoprotein) cholesterol and lowers the concentration of LDL (low density lipoprotein) cholesterol in the bloodstream (Katan et al., 1994). Studies have demonstrated a close relationship between LDL cholesterol levels and cardiovascular disease in humans, whereas HDL cholesterol has an inverse relation with the risk of cardiovascular diseases (Kwiterovich, 1997).

The percentages of saturated fatty acids (SFA), monounsaturated fatty acids (MUFA), polyunsaturated fatty acids (PUFA), *n*-6 and *n*-3, as well as PUFA/SFA and *n*-6/*n*-3 ratios can be found on Table 4.

Genetic groups had no effect ($p>0.05$) on the percentages of SFA, MUFA, PUFA, n-6 and n-3, or on PUFA/SFA and *n*-6/*n*-3 ratios. The majority of fatty acids found on LM of bulls were SFA, followed by MUFA. Likewise, Aricetti et al. (2008) and Prado et al. (2008a; b) observed similar percentages of SFA and MUFA in bulls from different crossbreeding systems, finished under similar diets and handling as in this experiment. Thus, SFA and MUFA percentages vary little as functions of genetic groups. PUFA percentage was 5.5%. Similar values are found on LM of bulls finished in feedlot (Aricetti et al., 2008; Prado et al., 2008a;b). PUFA/SFA ratio was 0.13. This ratio is below the value observed in cattle finished under pasture (Padre et al., 2007). Furthermore, it is below the value considered ideal for human health (Department of Health, 1994). *n*-6/*n*-3 ratio was close to 15:1. However, in other studies conducted with animals from industrial crossbreeding systems and finished under similar conditions, *n*-6/*n*-3 ratio was below 5/1. Still, the ratio in this experiment is above the values recommended as beneficial for human health (Department of Health, 1994).

IMPLICATIONS

Crossbreeding between European breeds resulted in meat with higher levels of total lipids, which feature higher fat percentages as the result of genetic improvements applied over decades. The higher carcass fat level improves more flavors to beef, increasing its palatability. However, in terms of consumer health, the increase in fat content could be harmful. The fatty acid composition showed higher PUFA and lower SFA for crossbreds as compared to purebred cattle. On the other hand, crossbreeding between European genetic groups increased PUFA/SFA ratio and reduced *n*-6/*n*-3 ratio. Neither PUFA/SFA nor *n*-6/*n*-3 ratios meet the requirements for preserving human health.

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