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Diet and genotype effects on the quality index of beef produced in the Argentine Pampeana region

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Abstract

Steers of varying genotypes (Aberdeen Angus, Charolais x AA and Argentine Holstein) in four feeding systems were evaluated. Feeding systems were: S1 = a diet based on pastures only; S2 = a similar forage base as S1 plus a daily supplementation with cracked corn, at 0.7% of l.w./head/day; S3 = a similar forage base as S1 plus a daily supplementation with cracked corn, at 1.0% of l.w./head/day; and S4 = a regular feedlot diet. Tenderness and marbling were not affected by the feeding system. Feedlot meat showed an n-6/n-3 ratio significantly higher than meat produced with the diets based on pastures (S1 = 2.1; S2 = 3.1; S3 = 4.5; S4 = 14.2) ($P < 0.05$), whereas CLA content had an inverse behavior, showing S1 (0.67%) and S2 (0.64%) higher concentrations than S3 (0.55%) and S4 (0.28%) ($P < 0.05$). Diet based on pastures plus a low level of supplementation produced meat with better nutritional characteristics than other productive alternatives, without significant effects of the biotypes.
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Keywords: Bovine meat quality; Feeding systems; CLA; Argentine meat

1. Introduction

Argentine cattle are traditionally fed on pastures. However, the necessity to increase farm productivity in the Pampas region has led to the development of beef production systems characterized by a more intensive use of forage resources, particularly, the incorporation of energy supplements during some months or around the year. Some of these production systems have shown interesting yield and financial benefits (Kloster, Latimori, Amigone, & Ghida Daza, 2003) consequently they were widely adopted by farmers. Energy supplementation in cattle diets has been increased significantly, not only in farms whose products are sent to the domestic market, but also in those that produce meat for export. This raises many questions concerning meat quality, particularly with regard to the profile of the fatty acids in intramuscular fat (IMF) obtained with the high energy feeding systems.

The presence in the human diet of positional and geometric isomers of conjugated linoleic acid (CLA) especially isomer 9 *cis*, 11 *trans* (Parodi, 1999), contributes to health because of their anticarcinogenic and antiatherogenic properties (Ip et al., 1999; Lee, Kritchevssky, & Pariza, 1994). Foods of animal origin are also known as a source of essential fatty acids, particularly omega 3 and omega 6. The long chain omega 3 fatty acids are linked to the development and functionality of nervous and vision systems (Valenzuela & Nieto, 2003) and also to cardioprotective functions (Hu, Manson, & Willett, 2001; Williams, 2000). Although omega 6 fatty acids are precursors of very important molecules, a relationship of omega 6/omega 3 lower than 4 is recommended in human diets. It is suggested that higher rates will be associated with development of tumoral, cardiovascular, inflammatory, autoimmune, and neurodegenerative illnesses (Simopoulos, 2004).

It has been verified that the quantity and composition of fatty acids in foods of animal origin are related to the presence of some of their precursors in the diet, since an important part of dietary fatty acids escapes from the process of

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ruminal biohydrogenation and are absorbed unchanged (French et al., 2000; Wood et al., 2003). In fact, pasture diets allow improving the profile of fatty acids of bovine meat, due to their higher content of precursors of CLA compared with grains based diets (Mandell, Buchanan-Smith, & Campbell, 1998; Raes, De Smet, & Demeyer, 2004). There is some information indicating that meat from steers raised in grazing systems has a more appropriate content of acids for human consumption than meat from feed lot cattle (Latimori, Kloster, & Amigone, 2003; García, Pensel, Margaría, Rosso, & Casal, 2003; García et al., 2005). For this reason, there is a strategic interest to inquire if grain supplementation affects negatively the nutritional value of the meat.

Some authors have found that animal breed affects marbling and thickness of subcutaneous fat (Michal, Zhang, Gaskins, & Jiang, 2006), or the composition of fatty acids in meat (Choi, Enser, Wood, & Scollan, 2000). However, little information is available in Argentina on the interrelationships of animal genotype and dietary fiber to grain ratios.

The aim of this study was to evaluate the effects of four feeding systems, on some attributes of product quality obtained with three different genotypes of steers. The feeding systems described here, represent productive models widespread in Argentina Pampeana region, ranging from pasture exclusive diet, to the feedlot system. The British purebred or their crossbreds, which are the main components of the meat consumed domestically, were represented by Aberdeen Angus steers. The crossbred Charolais x Aberdeen Angus steers represents the most advisable crossbreed for production of heavy steers for export markets, and Holstein steers are potentially adequate for double commercial purpose.

2. Materials and methods

The field work was carried out in the Agricultural Experiment Station of INTA Marcos Juárez during the annual cycles 2001/02 and 2002/03. The Station is located at the southeast of Córdoba province, Argentina, approximately 32.5° South latitude and 62° longitude West, on a typical Argiudol soil, deep and well drained. The climate is temperate with an average temperature of 17 °C and annual precipitations of 885 mm (INTA-SEAG Córdoba, 1978).

One hundred and twenty steers of three genotypes, subjected to four feeding systems were used in this experiment. Genotypes evaluated were Aberdeen Angus (AA), Charolais x Aberdeen Angus (ChxAA) and Argentine Holstein (AH). The four feeding systems were:

S1: steers grazed pasture exclusively.

S2: steers fed with a similar pasture as S1 but supplemented daily with corn grain (0.7% of live weight) with an interruption of the supplement supply between November 15 and February 15.

S3: steers fed with a similar pasture as S1 but supplemented daily with corn grain (1.0% of live weight) without interruption of the supplement supply.

S4: feedlot diet based on corn, alfalfa hay, soybean meal, vitamins and minerals.

The design of three genotypes and four feeding systems were repeated during two years, being analyzed as temporal repetitions. Ten steers for treatment per year were assigned, incoming with 5–7 months of age and an average weight of 185.4 kg. The forage in S1, S2 and S3 were provided by a mixed pasture of alfalfa (*Medicago sativa*) and tall fescue (*Festuca arundinacea Schreb*) grazed under a rotational system of six paddocks with seven days of permanency in each one. The supplement in S2 and S3 was based on cracked corn given once a day, being the quantity adjusted monthly. Hay of pasture was incorporated in S1, S2 and S3 during winter and was given between July 15 and September 30, at a rate of 2.4 kg head/day.

Dry matter (DM) forage allowance (g DM/kg l.w.) was estimated every two weeks before change of paddock. Dried forage samples were used for measuring crude protein (CP), cell wall (NDF), acid detergent fiber (ADF) and DM content. In S4, average daily intake was determined by the difference between offered and refused food. All animals were weighted each 28 days, after an overnight (15–17 h) without food or water.

Steers were conventionally slaughtered in a commercial abattoir at a similar degree of finishing estimated by visual evaluation. Six of them were taken at random from each treatment and, 48 hours after slaughter, their left carcasses were processed. Steaks of *Longissimus dorsi* muscles at the 11th and 13th rib were dissected, frozen and stored at −20 °C until posterior analysis. Physical and chemical analysis performed in *Longissimus dorsi* muscles were tenderness, marbling, muscle color, pH and intramuscular fat content and composition.

2.1. Tenderness and marbling

Thick steaks of 2.5 cm were obtained from the 13th rib for WBSF using the same electric saw. Once thawed, they were deboned, weighed and placed in a pre-heated Philips electric grill until they reached a final internal temperature of 71 °C (AMSA, 1995). Cooked steaks were weighed and cooled to <10 °C. Eight 1.3 cm diameter cores were obtained form each steak parallel to the muscle fibre orientation and sheared once across the middle using a Warner-Bratzler shear machine (model 3000; G-R Manufacturing CO., Manhattan, Kansas, USA). Shear force was expressed in Newton (N).

To determine marbling, *Longissimus dorsi* (rib eye) samples corresponding to 11th rib were compared using the scale of marbling of USDA.

2.2. Muscle colour and pH

Colour measurements were carried out using a ByK Gardner Colour View Spectrophotometer (model 9000, USA) following the recommendations of AMSA (1991). Determinations were done in 2.5 cm thick steaks obtained

from the 13th rib. CIE Lab system provides the values of three colour components; L^* (black–white component, lightness), and the chromatic coordinates, a^* (+red to –green component) and b^* (+yellow to –blue component). The instrumental conditions were large area aperture (5 cm diameter), D65-artificial and 10° standard angle observer. The measuring aperture was covered with a glass plate (ByK Gardner Inc., USA), and the instrument was calibrated against a white plate. Each sample was allowed to bloom for 45 min prior to the first measurement, and four scans from each steak were averaged for statistical analysis.

pH was measured using a pH meter (Thermo Orion model 420, USA) with a standardized combination electrode which was inserted into *Longissimus dorsi* muscle (4.0 and 7.0 buffers).

2.3. Intramuscular fat content and composition

Intramuscular fat (IMF) was measured in *Longissimus dorsi* at 12th rib with determination of saturated fatty acids (SFA) (14:0 + 16:0 + 18:0), monounsaturated fatty acids (MUFA) (16:1 + 18:1) and polyunsaturated (PUFA) (n-3 + n-6). n-6 Fatty acid (18:2 + 18:3 + 20:3 + 20:4 + 22:4), n-3 (18:3 + 20:5 + 22:5 + 22:6), n-6/n-3 ratio and conjugated linoleic acid (CLA).

Aliquot samples of 10 g each, trimmed of external fat, were minced, dried and extracted in a Tekator apparatus using hexane as the extraction solvent according to official methods (AOAC, 1992) were used to determine total intramuscular fat (IMF). Other aliquot samples of 5 g each were extracted using the Folch, Lees, and Stanley (1957) method. Fatty acid methylesters were prepared according to the method of Pariza, Park, and Cook (2001) and analyzed for GLC (García & Casal, 1993) using a Chrompack CP 900 equipment with a capillary column CP-Sil 88.

Individual fatty acids were identified by comparing relative retention times with individual fatty acids standard (PUFA-2 Animal Source. Supelco). Analytic results were expressed as percentages of total fatty acids. Statistical analyses were performed using GLM procedures (SAS, 1999) and means were compared with Duncan test.

3. Results and discussion

In Table 1, the forage allowance for each treatment during the two years of evaluation, are shown.

Quality forage index as CP, NDF and ADF (average of 23.97%, 42.44% and 27.43%, respectively) did not present differences among treatments within each season ($P > 0.05$)

These results suggested an appropriate homogenization of forage allowance and forage quality among treatments S1, S2 and S3. It should be stated that the values of forage allowance presented, are the average of the three grazing treatments. In S4 the same concentrate diet was used for the three genotypes, some of whose characteristic are shown in Table 2.

Table 1
Forage allowance (g DM/kg l.w.) to each genotype

Genotype	Autumn	Winter	Spring	Summer	Mean (annual)
AA	25.35	13.55	17.36	20.29	18.57[a]
	(6.06)	(2.11)	(1.86)	(5.28)	(5.57)
ChxAA	29.93	18.19	19.13	19.73	21.00[a]
	(4.98)	(4.60)	(5.04)	(7.78)	(6.92)
AH	28.73	14.28	19.83	19.49	19.84[a]
	(5.06)	(3.75)	(6.52)	(8.58)	(7.65)

Within columns means without common superscript are significantly different ($P < 0.05$).
Standard deviation for each mean value is indicated between brackets.

Feed intake measurements of feedlot steers were similar in all groups and rounded about 2.9% of live weight. In Table 3 the analysis of daily weight gains (DWG) among groups is presented.

Daily weight gain (DWG) performance progressed according to the energy concentration of the given diets (Table 3). When DWG was compared among genotypes inside diet, significant differences were also detected among groups, according to the potential mature size of genotypes (Webster, 1989). As expected, these differences in DWG among treatments, generated differences in the fattening period (days from entrance to slaughter). Although this was not considered as an analyzed variable, it is mentioned as a descriptive issue, that the duration of the fattening period in S1, considering the three genotypes, was 379 days, in S2 359 days, in S3 333 days and in S4 was only 171 days.

3.1. Tenderness and marbling

Results of tenderness assessed by Warner Bratzler shear force are shown in Table 4.

This variable did not present significant differences ($P > 0.05$) neither among diets nor among genotypes, all qualifying as tender meats.

Longissimus dorsi (rib eye) samples corresponding to 11th rib were compared using the scale of marbling according to the USDA (Table 5).

Feeding systems did not generate differences in marbling. Considering the genotypes like variation source, it was observed that the groups AA had a significantly higher fatty infiltration than ChxAA and AH.

3.2. Muscle colour and pH

Colour parameters and pH values are shown in Table 6.

L^* parameter (lightness) showed significant differences ($P < 0.05$) among diets, with the highest value for S4. Even though no significant differences were found ($P > 0.05$) in the other parameters, S4 samples tended to less redness. No differences were observed between genotypes ($P > 0.05$). Samples from ChxAA tended to be brighter and more yellow. pH values were in the expected range for fresh meat.

Table 2
Composition of S4 diet

Component	(% of DM)	EM (Mcal/kgDM)	CP (%)	NDF (%)	ADF (%)
Corn grain	82.5	3.25	9.2	–	–
Soybean meal	8.4	2.90	48.6	23.3	11.4
Alfalfa hay	8.6	2.30	23.5	41.8	24.6
Vitamins, minerals	0.5	–	–	–	–
Total	100	3.15	13.7	5.6	3.1

Table 3
Daily weight gain (g/day) according to diet and genotype

Genotype	S1 (pasture)	S2 (suppl. 0.7%)	S3 (suppl. 1.0%)	S4 (feedlot)
AA	$546 \pm 71^{c\,C}$	$675 \pm 123^{c\,C}$	$808 \pm 88^{b\,C}$	$1055 \pm 107^{a\,AB}$
ChxAA	$707 \pm 102^{bc\,ABC}$	$787 \pm 73^{bc\,BC}$	$871 \pm 99^{b\,BC}$	$1222 \pm 190^{a\,A}$
AH	$800 \pm 83^{c\,AB}$	$875 \pm 111^{c\,AB}$	$983 \pm 86^{b\,AB}$	$1093 \pm 202^{ab\,AB}$

Within rows and columns means without common superscript are significantly different (Duncan, $P < 0.05$).

Table 4
Warner Bratzler shear force (Newton) according to diet and genotype

Genotype	S1 (pasture)	S2 (suppl. 0.7%)	S3 (suppl. 1.0%)	S4 (feedlot)	Mean genotype
AA	32.38 ± 4.36	29.76 ± 4.89	33.72 ± 55.6	30.51 ± 7.52	31.58 ± 7.92^{A}
ChxAA	33.14 ± 6.27	30.78 ± 2.53	32.07 ± 5.83	31.36 ± 4.89	31.84 ± 4.98^{A}
AH	29.58 ± 5.69	29.45 ± 3.38	29.54 ± 4.40	32.07 ± 7.87	30.16 ± 5.51^{A}
Mean diet	31.71 ± 5.56^{a}	29.98 ± 3.65^{a}	31.76 ± 8.32^{a}	31.31 ± 6.72^{a}	

Within rows and columns means without common superscript are significantly different (Duncan, $P < 0.05$).

Table 5
Marbling score in *Longissimus dorsi* according to diet and genotype

Genotype	S1 (pasture)	S2 (suppl. 0.7%)	S3 (suppl. 1.0%)	S4 (feedlot)	Mean genotype
AA	2.00 ± 0.43	1.96 ± 0.26	2.04 ± 0.40	2.04 ± 0.54	2.01 ± 0.41^{A}
ChxAA	1.63 ± 0.64	1.63 ± 0.48	1.71 ± 0.40	1.96 ± 0.62	1.73 ± 0.55^{B}
AH	1.54 ± 0.45	1.46 ± 0.33	1.67 ± 0.33	1.83 ± 0.54	1.63 ± 0.43^{B}
Mean diet	1.72 ± 0.54^{a}	1.68 ± 0.42^{a}	1.81 ± 0.40^{a}	1.94 ± 0.56^{a}	

Within rows and columns means without common superscript are significantly different (Duncan, $P < 0.05$).

Table 6
Colour parameters and pH according to diet and genotype

Diet	L^*	a^*	b^*	pH
S 1 (pasture)	33.93 ± 3.34^{a}	19.12 ± 2.23^{a}	17.07 ± 1.87^{a}	5.69 ± 0.14
S 2 (0.7%)	34.57 ± 3.86^{a}	19.76 ± 2.51^{a}	18.06 ± 2.01^{a}	5.70 ± 0.15^{a}
S 3 (1.0%)	33.26 ± 5.20^{a}	20.50 ± 3.07^{a}	18.30 ± 2.53^{a}	5.73 ± 0.20^{a}
S 4 (feedlot)	37.17 ± 5.03^{b}	18.99 ± 2.82^{a}	18.28 ± 2.38^{a}	5.65 ± 0.16^{a}
Genotype				
AA	33.90 ± 5.13^{a}	20.16 ± 2.22^{a}	17.63 ± 2.30^{a}	5.73 ± 0.20^{a}
ChxAA	36.34 ± 4.50^{a}	19.14 ± 2.67^{a}	18.27 ± 2.04^{a}	5.65 ± 0.15^{a}
AH	33.97 ± 3.87^{a}	19.53 ± 3.17^{a}	17.95 ± 2.40^{a}	5.70 ± 0.14^{a}

Within columns means without common superscript are significantly different (Duncan, $P < 0.05$).

3.3. Fatty acids

Fatty acids analysis of meat samples are shown in Tables 7 and 8.

Table 7 shows that only pasture (S1) samples had significantly lower percentages of intramuscular fat ($P < 0.05$) than meat from other feeding systems, whereas no differences could be attributed to the genotype ($P > 0.05$). In contrast, genotype influenced the percentage of saturated fatty acids. Muscles from AH presented the lowest levels ($P < 0.05$), while SFA was not affected by feeding system. No significant differences were observed among treatments

Table 7
Intramuscular fat (g/100 g of tissues); saturated fatty acids (SFA); monounsaturated fatty acids (MUFA); and polyunsaturated fatty acids (PUFA) in *Longissimus dorsi* muscle between 9° and 11° rib according to diet and genotype

Genotype	S1 (pasture)	S2 (suppl. 0.7%)	S3 (suppl. 1%)	S4 (feedlot)	Mean genotypes
Intramuscular fat (%)					
AA	2.91 ± 0.91	3.54 ± 1.14	3.74 ± 1.66	4.12 ± 1.05	3.57 ± 1.26^{A}
ChxAA	2.93 ± 1.00	3.98 ± 1.82	4.33 ± 1.30	3.95 ± 1.39	3.80 ± 1.46^{A}
AH	2.82 ± 0.73	3.22 ± 0.91	4.68 ± 2.21	3.66 ± 0.99	3.59 ± 1.48^{A}
Mean diet	2.89 ± 0.86^{c}	3.58 ± 1.35^{b}	4.25 ± 1.76^{a}	3.91 ± 1.40^{b}	
SFA					
AA	41.1 ± 4.1	41.1 ± 2.9	39.2 ± 3.4	37.3 ± 4.4	39.7 ± 4.0^{A}
ChxAA	39.7 ± 2.8	39.6 ± 1.1	38.9 ± 2.7	37.9 ± 3.0	39.0 ± 2.5^{A}
AH	36.6 ± 1.4	36.4 ± 1.8	38.4 ± 3.5	37.1 ± 3.2	37.1 ± 2.7^{B}
Mean diet	39.2 ± 3.5^{a}	39.0 ± 2.8^{a}	38.8 ± 3.2^{a}	37.4 ± 3.5^{a}	
MUFA					
AA	35.5 ± 2.0	39.1 ± 3.2	38.5 ± 2.4	39.9 ± 4.0	38.2 ± 3.4^{B}
ChxAA	39.0 ± 3.0	39.9 ± 4.5	41.5 ± 2.5	39.4 ± 3.0	40.0 ± 3.4^{B}
AH	40.2 ± 2.2	42.0 ± 2.8	43.5 ± 2.4	42.3 ± 2.2	42.0 ± 2.6^{A}
Mean diet	38.2 ± 3.1^{b}	40.3 ± 3.7^{ab}	41.2 ± 3.2^{a}	40.5 ± 3.3^{ab}	
PUFA					
AA	9.6 ± 2.1	7.8 ± 1.8	8.9 ± 1.7	9.3 ± 2.5	8.9 ± 2.1^{A}
ChxAA	8.1 ± 2.0	8.0 ± 3.3	8.4 ± 1.1	9.2 ± 2.3	8.4 ± 2.3^{A}
AH	9.2 ± 1.9	8.6 ± 2.5	7.6 ± 2.4	9.1 ± 1.4	8.6 ± 2.1^{A}
Mean diet	9.0 ± 2.1^{a}	8.1 ± 2.5^{a}	8.3 ± 1.9^{a}	9.2 ± 2.1^{a}	

Within rows and columns means without common superscript are significantly different (Duncan, $P < 0.05$). SFA = 14:0 + 16:0 + 18:0; MUFA = 16:1 + 18:1; PUFA = n-3 + n-6; $n = 12$.

Table 8
n-3 and n-6 fatty acids; n-6/n-3 ratio and CLA in *Longissimus dorsi* muscle between 9° and 11° rib according to diet and genotype

Genotype	S1 (pasture)	S2 (suppl. 0.7%)	S3 (suppl. 1.0%)	S4 (feedlot)	Mean genotypes
n-3 (%)					
AA	3.1 ± 0.7	1.9 ± 0.6	1.9 ± 0.5	0.9 ± 0.4	1.9 ± 1.0^{A}
ChxAA	2.7 ± 0.8	1.7 ± 0.5	1.4 ± 0.3	0.9 ± 0.5	1.7 ± 0.8^{AB}
AH	2.8 ± 0.8	1.7 ± 0.4	1.2 ± 0.3	0.8 ± 0.4	1.6 ± 0.9^{B}
Mean diet	2.9 ± 0.8^{a}	1.8 ± 0.5^{b}	1.5 ± 0.5^{b}	0.8 ± 0.4^{c}	
n-6 (%)					
AA	6.2 ± 1.6	5.5 ± 1.1	6.6 ± 1.3	8.0 ± 2.2	6.6 ± 1.8^{A}
ChxAA	5.1 ± 1.3	5.9 ± 3.2	6.6 ± 1.0	8.1 ± 2.3	6.4 ± 2.3^{A}
AH	6.0 ± 1.4	6.1 ± 2.0	5.6 ± 1.6	8.2 ± 1.3	6.5 ± 1.9^{A}
Mean diet	5.8 ± 1.5^{b}	5.9 ± 2.2^{b}	6.3 ± 1.4^{b}	8.1 ± 1.9^{a}	
Ratio: n-6/ n-3					
AA	2.1 ± 0.9	3.2 ± 0.9	3.7 ± 1.4	12.6 ± 9.5	5.4 ± 6.3^{A}
ChxAA	2.0 ± 0.3	3.4 ± 1.2	4.8 ± 1.3	13.9 ± 12.2	6.0 ± 7.6^{A}
AH	2.2 ± 0.7	3.9 ± 1.6	4.9 ± 1.3	16.1 ± 10.6	6.8 ± 7.6^{A}
Mean diet	2.1 ± 0.6^{b}	3.5 ± 1.2^{b}	4.5 ± 1.4^{b}	14.2 ± 10.6^{a}	
CLA (%)					
AA	0.61 ± 0.12	0.59 ± 0.09	0.51 ± 0.08	0.30 ± 0.08	0.50 ± 0.15^{B}
ChxAA	0.69 ± 0.14	0.63 ± 0.10	0.57 ± 0.09	0.29 ± 0.10	0.54 ± 0.19^{AB}
AH	0.73 ± 0.11	0.71 ± 0.15	0.58 ± 0.07	0.26 ± 0.04	0.57 ± 0.21^{A}
Mean diet	0.67 ± 0.13^{a}	0.64 ± 0.12^{a}	0.55 ± 0.08^{b}	0.28 ± 0.08^{c}	

n-3 = 18:3 + 20:5 + 22:5 + 22:6; n-6 = 18:2 + 18:3 + 20:3 + 20:4 + 22:4; $n = 12$.
Within rows and columns means without common superscript are significantly different (Duncan, $P < 0.05$).

($P > 0.05$). Neither MUFA nor PUFA showed to be modulated by diet or genotype, except the cuts obtained from HA that were higher in MUFA percentage than the other genotypes.

Table 8 shows the percentages of polyunsaturated n-3, n-6 and CLA fatty acids. These components are very important for human nutrition because of their antiatherogenic and anti cancer properties (Ip et al., 1999; Lee et al., 1994). Therefore, they are considered as nutraceuticals. Percentages of n-3 were higher when participation of fresh forage increased in the diet ($P < 0.05$), while n-6 levels were similar for the three treatments that included fresh forage, but they were lower than in feedlot diet ($P < 0.05$). Except for the lower levels of n-3 observed in HA, it seemed to be no biologically important differences among genotypes. The n-6/n-3 ratio remained within the levels recommended for human consumption in S1 and S2 (<4:1), while meat produced in feedlot (S4) showed the highest values, being S3 intermediate. No differences were found among genotypes ($P > 0.05$).

The highest CLA levels in meat were obtained in exclusive pasture diet (S1) and in pasture diet with low supplementation (S2). Lowest levels were produced in feedlot system (S4) and intermediate levels in the system with high supplementation (S3). On the other hand, AA steers produced CLA levels statistically lower ($P > 0.05$) than the other genotypes.

Genetic and nutritional approaches have been widely studied in relation to fatty acid composition of beef. Indeed, genetic factors generally provide smaller differences than dietary handling. These results strongly agree with this observation (De Smet, Raes, & Demeyer, 2004). Nevertheless, as concluded by these authors, breed reflects differences in underlying gene expression or enzymes involved in fatty acid synthesis. This could be the case for the differences found in AA steers for CLA production.

4. Conclusions

The exclusive pasture diet, or the same forage diet with a low level of grain supplementation, generated meat with better nutritional characteristics than the other productive alternatives, without strong evidence of significant effects on the studied physical characteristics. There were no significant differences among breeds under the evaluated productive conditions, suggesting that the intensified productive systems that assure post weaning to slaughtering periods lower than 12–14 months, could hide potentials genetic differences in characteristic as tenderness, colour and marbling, among studied racial groups.

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