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Performance, methane production, and beef lipid profile of young bulls finished in feedlot

Abstract – The objective of this work was to evaluate the growth performance, enteric methane production, carcass traits, and fatty acid profile of the *Longissimus thoracis* muscle of young Nellore and Angus x Nellore beef bulls fed with a high-lipid diet and finished in feedlot. Fifty young bulls were evaluated, being divided into two groups: Nellore (n=25) and Angus × Nellore (n=25), randomly assigned to four pens in a completely randomized design. The feedlot phase covered 105 days of feed. The diet (80% concentrate) was formulated to meet or exceed beef cattle requirements to reach an average daily gain of 1.6 kg per day. The crossbred animals showed a higher dry matter intake, feed efficiency, initial body weight, final body weight, average daily gain, average daily carcass gain, hot carcass weight, and percentage of rib. However, dressing percentage was similar for both groups. The Nellore animals produced more enteric methane, expressed in g kg^{-1} average daily gain), but, also, higher concentrations of polyunsaturated fatty acids and conjugated linoleic acid. The two genetic groups show satisfactory growth rates, but the crossbred animals present a better growth performance and produce less methane per unit of beef. The animal's genetic composition modifies its fatty acid profile.

Index terms: animal performance, beef cattle, crossbreeding, meat quality, methane emission, polyunsaturated fatty acids.

Desempenho, produção de metano e perfil lipídico da carne de tourinhos terminados em confinamento

Resumo – O objetivo deste trabalho foi avaliar o desempenho de crescimento, a emissão de metano entérico, as características de carcaça e o perfil de ácidos graxos do músculo *Longissimus thoracis* de tourinhos de corte Nellore e Angus x Nellore alimentados com dieta de alto teor lipídico e terminados em confinamento. Foram avaliados 50 tourinhos, divididos em dois grupos: Nelore (n=25) e Angus × Nelore (n=25), distribuídos aleatoriamente em quatro baias, em delineamento inteiramente casualizado. O confinamento compreendeu 105 dias de alimentação. A dieta (80% de concentrado) foi formulada para atender ou exceder os requisitos dos animais, para atingir uma média diária de ganho de peso de 1,6 kg por dia. Os animais cruzados apresentaram maior consumo de matéria seca, eficiência alimentar, peso vivo inicial, peso vivo final, ganho médio diário, ganho médio diário de carcaça, peso de carcaça quente e percentual de costela. No entanto, o percentual de carcaça foi semelhante para ambos os grupos. Os animais Nelore produziram mais metano entérico, expresso em g kg^{-1} de ganho médio diário, mas, também, maiores concentrações de ácidos graxos poliinsaturados e ácido linoleico conjugado. Os dois grupos têm taxas de crescimento satisfatórias, mas os animais cruzados apresentam melhor desempenho de crescimento e produzem menos metano por unidade de carne produzida. A composição genética do animal modifica seu perfil de ácidos graxos.

Termos para indexação: desempenho do animal, bovinos de corte, cruzamento, qualidade de carne, emissões de metano, ácidos graxos poliinsaturados.

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Introduction

Brazil stands out as one of the most important producers and exporters of beef worldwide. In 2022, according to the Brazilian association of meat exporting industries (ABIEC, 2023), the Brazilian beef cattle herd reached approximately 202 million heads, producing 10.79 million tons of carcasses and exporting 2.26 million tons to over 150 countries. However, despite its importance for food production and income generation, livestock is a major source of concern regarding environmental impacts and climate changes. According to Food and Agriculture Organization of the United Nations (FAO, 2023), ruminant production systems are considered the main source of methane production from enteric fermentation, which represents 54% of the total greenhouse gases emitted by livestock.

In Brazil, to reduce the impacts of livestock production on the environment and greenhouse gas emissions, an efficient use of feed resources and animal management are the most common practices. Another approach for mitigating methane emissions in ruminants is genetic improvement, aiming to improve animal performance (Donoghue et al., 2016). In this case, breeds used in the country should be evaluated. The predominant one for beef cattle is Nellore (*Bos indicus*), which is more adapted to hot climate conditions and more resistant to endo- and ectoparasites. However, many producers have opted for the crossbreeding of Nellore and Aberdeen Angus animals (*Bos taurus*), whose performance is better and meat quality is recognized worldwide.

In addition to genetic improvement, some nutritional strategies, such as the use of lipid sources, have been adopted to mitigate the emission of enteric methane and have also been studied to improve the efficiency and to reduce the environmental impacts of the animal production system (Arndt et al., 2022; Beauchemin et al., 2022). These strategies can also modify the nutritional profile of the produced meat. In this line, Bayat et al. (2015) observed that the inclusion of lipid sources rich in polyunsaturated fatty acids (PUFAs) in cattle diets can improve the fatty acid profile of the meat.

Ruminant meat has been part of the human diet for thousands of years, and its consumption has contributed significantly to the evolution of the species, since it provides essential nutrients of high biological value, such as essential amino acids, fatty acids, and minerals as iron, calcium, zinc, and vitamin B (Vahmani et al., 2020). However, the consumption of beef is associated with an increase in blood cholesterol and cardiovascular diseases. Compared with meat from nonruminant animals, for example, beef has a higher saturated fatty acid (SFA) level, mainly due to the biohydrogenation process of unsaturated fatty acids (UFAs), carried out by ruminal microorganisms. However, not all SFAs are hypercholesterolemic, which is the case of stearic acid that does not alter serum cholesterol levels in humans and is quickly converted to oleic acid in body tissues (Vahmani et al., 2020). It should be noted that the quantity and quality of fatty acids in beef can vary depending on several factors such as type of diet and cattle age, sex class, genetic group, and finishing system (Bressan et al., 2016; Ladeira et al., 2018). This means that distinct genetic groups may present different fat deposition patterns and fatty acid profiles in meat, considering the different times that fat deposition begins.

The objective of this work was to evaluate the growth performance, enteric methane production, carcass traits, and fatty acid profile of the *Longissimus thoracis* muscle of young Nellore and Angus x Nellore beef bulls fed with a high-lipid diet and finished in feedlot.

Materials and Methods

All experimental procedures for animal use were approved by the ethics committee of Universidade Federal de Minas Gerais, under protocol number 71/2019.

At the beginning of the project, 20-month-old young bulls were divided into two groups according to their breed composition, as follows: Nellore (n = 25), with an initial body weight (IBW) of 450±47 kg; and Angus x Nellore crossbred (n = 25), with an IBW of 501.5±45.5 kg, obtained by mating Angus sires with Nellore dams, belonging to different herds. IBW was determined by weighing the animals after 16 hours of water and feed fasting. All animals were sourced from the same breeding season and endured a grazing-growing phase in a pasture of cultivar Mombaça Guinea grass [*Megathyrsus maximus* (Jacq.) B.K.Simon & S.W.L.Jacobs], receiving a protein and energy supplement offered at 0.2% body weight (BW). The average daily gain (ADG) during the rearing phase

was 0.70 kg for Nellore and 0.85 kg for the Angus x Nellore animals.

In the feedlot, the animals were divided into groups according to their breed composition, being allocated into two collective pens measuring 20x24 m, equipped with feed lanes and drinkers. All animals were drenched with an anthelmintic agent prior to the start of the feedlot.

The feedlot period was 126 days, and the animals were adapted to the experimental diets for the first 21 days. The diet was formulated using the Maximum Profit Ration software (RLM Pesquisa em Otimização Agropecuária e Ambiental Ltda, Piracicaba, SP, Brazil) for an ADG of 1.6 kg per day. Initially, 50% sorghum silage and 50% concentrate diet were supplied; the amount of concentrate was increased until the ratio of roughage:concentrate was 20:80 on a dry matter (DM) basis (Table 1). The soybean grain used in the concentrate was ground and passed through a 5.0 mm mesh to increase lipid ruminal availability. The animals were fed three times a day, at 7 a.m., 11 a.m., and 4 p.m. The diet was adjusted daily to maintain 5 to 10% of refusals.

Table 1. Ingredients, chemical composition, and fatty acid profile of the experimental feed.

Ingredient	Composition (% dry matter)
Sorghum silage	20.0
Finely ground corn	57.6
Soybean meal	20.4
Mineral mix	2.0
Nutrient	
Dry matter	66.7
Organic matter	94.7
Crude protein	15.6
Ether extract	7.3
Neutral detergent fiber	23.1
Ash	5.2
Nonfibrous carbohydrates	51.5
Total digestible nutrients*	82.8
Fatty acid profile (g per 100 g fatty acid)	
Myristic acid (C14:0)	0.4
Palmitic acid (C16:0)	13.7
Stearic acid (C18:0)	4.5
Oleic acid (C18:1 c-9)	19.9
Linoleic acid (C18:2 n-6)	49.1
Alpha-linolenic acid (C18:3 n-3)	8.3

(1)Calculated according to National Research Council (NRC, 2001).

Animal growth performance was determined monthly by recording BW after a fast of feed and water for 16 hours. Monthly fasting was chosen in order to maintain consistent and reliable assessment intervals, allowing to closely monitor animal growth patterns and health status, identify earlier trends and anomalies to ensure timely interventions, and improve overall accuracy and performance evaluations. ADG was calculated as the difference between the final BW (FBW) and the IBW, divided by the total number of days on the feedlot.

Titanium dioxide (TiO_2) was used as an internal marker, and 10 g were administered individually to 12 animals of each genetic group once a day, during ten days, through paper cartridges introduced directly into the animal's esophagus at 8 a.m. with the aid of a polyvinyl chloride (PVC) applicator. During the last three days of the dosage period, fecal samples were collected once a day, and these samples at different collection times composed a sample for each animal. The feces were dried at 65˚C until reaching a constant weight. The dried feces were ground through a 1.0 mm screen using a Wiley mill and analyzed through atomic absorption spectrophotometry with the 099-2243 spectrometer (Varian, Palo Alto, CA, USA). The TiO_2 content in the feces (%) was determined according to Myers et al. (2004) at the Animal Nutrition Laboratory of Universidade Federal de Minas Gerais. The standard curve was prepared using 2, 4, 6, 8, and 10 mg TiO_2, and the spectrophotometer readings were recorded at a wavelength of 410 nm. For the calculation of fecal production per animal on a DM basis, the formula used was FP = TS / TF, where FP is the obtained fecal production in gram per day per animal, TS is the amount of TiO_2 supplied to each animal per day (10 g), and TF is the percentage of titanium in the feces.

Fecal production and indigestible neutral detergent fiber (iNDF) were used to estimate dry matter intake (DMI) in kilogram per day for each animal. iNDF was used as the internal marker and obtained after the in situ incubation of the diet (iNDF diet) and feces (iNDF feces) samples for 288 hours in the rumen of a cannulated bovine (Valadares Filho et al., 2010). The equation used to obtain DMI was: DMI = FP x (iNDF feces / iNDF diet). To determine the expected DMI, the used equations were those developed by Azevêdo

et al. (2016) to estimate the DMI of Zebu and crossbred animals according to the BR-Corte system (Pompéu, MG, Brazil), created under Brazilian conditions for beef cattle production.

A day before slaughter, the animals were weighed after a 16 hour-fasting period to obtain FBW and, then, sent to a commercial slaughterhouse, where they were kept fasting for 24 hours with ad libitum water access. According to the humanitarian procedures required by the Brazilian legislation, slaughter was conducted following the official rules of Regulamento da Inspeção Industrial e Sanitária de Produtos de Origem Animal (Brasil, 2017).

Hot carcass weight (HCW) was recorded immediately after the carcass was cleaned. Dressing percentage (DP) was calculated as follows: DP = (HCW / FBW) x 100. The ADG of the carcass (ADGc) was determined using the formula: ADGc = [HCW - (IBW x 50%) / days in feedlot] of Gomide (2006). Maciel et al. (2019) and Monteiro et al. (2022) support the parameter of a carcass yield of 50%.

After cooling and weighing, the carcass was divided into hindquarter, forequarter, and ribs. The weights of these cuts were used to calculate the percentage of each one in relation to the cold carcass.

Carcass pH was measured between the twelfth and thirteenth rib of the cold carcass 24 hours after cooling, using a digital potentiometer equipped with the SG2-ELK Seven Go thermometer (Mettler-Toledo International Inc., Columbus, OH, USA). Prior to pH measurement, the pH meter and electrode were standardized using commercial pH buffers of 4.0 and 7.0 at a room temperature of 23°C.

The emissions of enteric methane were measured using the sulfur hexafluoride (SF_6) tracer gas technique (Primavesi et al., 2004; Berndt et al., 2014). The same animals used for DMI measurements were evaluated daily during five consecutive days. Seven days before sampling, the animals were fit with halters and pre-evacuated PVC sampling canisters for gas collection, in order to be able to adapt to the devices, facilitating handling during the sampling period. Ten days prior to sampling, permeation tubes filled with known quantities of SF_6 and release rates (1,431±59 ng min^{-1}) were administered orally to each of the 24 animals, in order to allow tracer gas flow to stabilize in the rumen.

The gas collection halters and sampling canisters were attached with a capillary tube, with a 0.127 mm diameter, made to be filled up to 50% in 24 hours. The capillary was calibrated so that the vacuum inside the canister remained at the initial 40–60% measured after 24 hours. Gas samples were not collected if the pressure inside the canisters was below or above this range. For the collection of enteric CH_4 and SF_6 samples, the canisters were vacuumed to approximately -12 PSI with a vacuum pump. The collections started at 7 a.m. by taking the animals from their pens to the handling center, in order to facilitate the exchange of the used equipment. After completing the 24 hour collection period, the halters were replaced by new ones and, then, the animals were returned to their original pen. The removed halters were stored for the chromatography analysis. Daily samples were also collected to determine the concentration of CH_4 and SF_6 in the environment. The used pressures and dates and times of container removal were registered for control.

The collected respired air was evaluated immediately after the end of the experimental period. The CH_4 and SF_6 concentrations were analyzed by gas chromatography at Embrapa Pecuária Sudeste, located in the municipality of São Carlos, in the state of São Paulo, Brazil. For the chromatography analysis, the sampling canisters were pressurized with nitrogen (N_2) to approximately 10% above atmospheric pressure, using the GC-2014 chromatograph (Shimadzu Corporation, Kyoto, Japan), following the method described by Johnson & Johnson (1995). The calibration curves were established using standard gas certified by the White Martins company (São Carlos, SP, Brazil), with CH_4 concentrations in ppm (4.85±5%, 9.96±1.65%, and 19.1±3.44%) and SF_6 concentrations in ppt (34±9.0, 91.0±9.0, and 978.0±98.0) according to Johnson et al. (2007).

The CH_4 emissions were calculated using the CH_4:SF_6 ratio in the sampling canister with each of the gases, corrected for background concentrations and the predetermined permeation rate of the SF_6 capsules, using the following equation:

$$RME = RRS \times \frac{(AM - BM)}{(AE - BE)} \times \frac{MM}{ME} \times 1,000$$

where RME is the ruminal methane emission rate (grams per day); RRS is the release rate from the sulfur hexafluoride capsule (milligrams per day); AM

is the methane measured in the animal (ppm); BM is the background concentration of methane (ppm); AE is the enteric methane estimated in the animal (ppt); BE is the background concentration of enteric methane (ppt); MM is the molecular weight of methane, equal to 16; and ME is the molecular weight of sulfur hexafluoride, equal to 146. The factor 1,000 was used to convert the units of RME, in order to express them in grams per day.

To analyze the fatty acid profile of intramuscular fat, samples of the *Longissimus thoracis* muscle, between the twelfth and thirteenth ribs, were taken from the same animals used for DMI and methane measurements. To determine ether extract, the meat samples were lyophilized to obtain homogeneous samples. The analysis was performed according to method 920.85 of Association of Official Analytical Chemists (Helrich, 1990). The samples were identified and stored at -18ºC in individual packages and, then, were thawed at a refrigerated temperature of 5ºC, for 12 hours, and subjected to cleaning for lipid extraction. The fatty acid was extracted according to the methodology described by Folch et al. (1957).

The fatty acid profile was determined using the procedures established by Hartman & Lago (1973). A 5.0 mL sample of the lipid extract was concentrated in a water bath at 45°C, with gaseous nitrogen, followed by saponification with a sodium hydroxide solution in 0.5 mol L^{-1} methanol and by methylation with ammonium chloride, methanol, and sulfuric acid.

After methylation, 5.0 mL hexane were added and stirred for 10 s to separate the esterified fatty acid. Then, 3.0 mL of the supernatant (hexane and methylated fatty acids) were removed and concentrated again in a water bath at 45ºC, with gaseous nitrogen. At the time of injection, this extract was diluted with 1.0 mL hexane, and 1.0 µL of this solution was injected in a gas chromatograph with the GC-2010 flame ionization detector (Shimadzu Corporation, Kyoto, Japan), equipped with the SP 2560 capillary column, with 100 m x 0.25 mm x 0.20 µm (Supelco, Bellefonte, PA, USA).

In the chromatographic oven, temperature conditions were as follows: maintained at 70°C for 4 min, then increased from 13°C min^{-1} to 175°C, which was maintained for 27 min; increased from 4°C min^{-1} to 215°C, held for 9 min; and increased from 7°C min^{-1} to 230°C, maintained for 5 min. The injector temperature was 250°C, and the detector temperature was 300°C.

Several fatty acids were identified by comparing their retention times to the C4:0 to C24:0 chromatographic standard 0, using the 37 Component FAME Mix, packaged in 100 mg neat (Supelco, Bellefonte, PA, USA). Fatty acid concentrations were determined by the peak areas shown in the chromatogram for each acid in relation to fatty acid total area. Fatty acid percentage was obtained through the ChromQuest, version 4.1, software (Thermo Electron Corporation, Waltham, MA, USA).

The activities of the Δ^9 desaturase 16, Δ^9 desaturase 18, and elongase enzymes were determined according to Malau-Aduli et al. (1997), Kazala et al. (1999), and Pitchford et al. (2002), through the following mathematical indexes:

Δ^9 desaturase 16 = 100 [(C16:1 *cis-9*) / (C16:1 *cis-9* + C16:0)]

Δ^9 desaturase 18 = 100 [(C18:1 *cis-9*) / (C18:1 *cis-9* + C18:0)]

Elongase = 100 [(C18:0 + C18:1 *cis-9*) / (C16:0 + C16:1 *cis-9* + C18:0 + C18:1 *cis-9*)]

The atherogenicity index (AI) was calculated using the equation proposed by Ulbricht & Southgate (1991), as an indicator of the risk of cardiovascular disease:

$$AI = \frac{C12:0 + 4 \times C14:0 + C16:0}{\sum \Omega_6 + \sum \Omega_3 + MUFA}$$

where Ω_6 are the omega-6 fatty acids, Ω_3 are the omega-3 fatty acids, and MUFA is the main monounsaturated fatty acid.

The thrombogenicity index (TI) was calculated using the equation of Ulbricht & Southgate (1991), as an indicator of the onset of coronary thrombosis:

$$TI = \frac{C14:0 + C16:0 + C18:0}{0.5 \times \sum MUFA + 0.5 \times \sum \Omega_6 + 3 \times \sum \Omega_3 + \frac{\sum \Omega_3}{\sum \Omega_6}}$$

All analyses were performed using the R statistical software (R Core Team, 2022). The effect of breed on carcass traits, enteric methane emissions, and fatty acid profile was evaluated using the completely randomized design in the one-way analysis of variance. Normality of residues was verified with Shapiro-Wilk's test, and assumptions of homogeneity of variances, by Bartlett's

test. The independence of residues was checked through the graph of residues against predicted values. All assumptions were met. Treatment means were compared by the F-test (α=0.05).

Results and Discussion

Most of the evaluated variables differed between both genetic groups (p<0.01), as shown in Table 2. The crossbred animals had a higher DMI, feed efficiency, IBW, FBW, ADG, ADGc, HCW, and percentage of rib. However, Nellore animals had higher percentages of forequarter and hindquarter. No differences were observed regarding DP and pH at 0 and 24 hours (p>0.05).

The equations developed by Azevêdo et al. (2016) were used to determine the expected DMI. Since they are based on metabolic BW, ADG, and concentrate content in the diet (percentage of total DM in the diet), the expected DMI of the Nellore and Nellore x Angus animals in the present study, with an 80% concentrate in the diet, would be 10.5 and 11.1 kg, respectively. Therefore, for Nellore animals, DMI was similar to that predicted by BR-Corte, but, for the crossbred animals, which consumed 1.5 kg per day, higher than the expected.

Regarding feed efficiency, that of the crossbred animals was higher than that of Nellore. Therefore, it can be supported that the crossbred animals were more efficient, as they gained 156 g live weight for each kilogram of food ingested on a DM basis, while Nellore animals gained 136 g. Similar results were obtained by Maciel et al. (2019) and Dallantonia et al. (2021), who observed a greater feed efficiency in Nellore x Angus animals, compared with Nellore.

The crossbred animals showed a greater growth performance than Nellore animals (total gain of 211.0 kg vs. 150.9 kg), although the growth rates reached by both groups were satisfactory. This result is related to the higher growth rate of the crossbred animals compared with that of Nellore (2.01 vs 1.44 kg per day). It should be noted that the animals from both genetic groups were slaughtered after they reached maturity weight, which was 517 kg for Nellore and 560 kg for the crossbred animals (Marcondes et al., 2016). Furthermore, all animals were slaughtered with a minimum desired subcutaneous fat thickness of 12 mm. The average thickness for Nellore animals was 15.01 mm and for the crossbred animals, 26.33 mm.

Façanha et al. (2014) observed that crosses between Angus and Nellore animals result in heavier progenies, with better carcass characteristics, such as a greater rib eye area, subcutaneous fat thickness, and marbling. Angus animals are known worldwide for their marbling meat and tenderness and are being widely used in Brazil through crosses with Nellore animals. Marcondes et al. (2016) found that, in general, crosses

Table 2. Means, standard error of the means (SEM), and results of the F-test[(1)] for the growth performance and carcass traits of two genetic groups of bulls finished in feedlot.

Item[(2)]	Nellore[(3)]	Nellore x Angus[(4)]	SEM	p-value
DMI (kg per day)	10.6	12.6	0.16	< 0.01
Feed efficiency	0.136	0.156	0.003	< 0.01
IBW (kg)	444.7	509.8	5.75	< 0.01
FBW (kg)	595.6	720.8	10.65	< 0.01
ADG (kg)	1.44	2.01	0.07	< 0.01
ADGc (kg)	1.17	1.46	0.06	< 0.01
HCW (kg)	345.0	404.7	7.63	< 0.01
DP (%)	57.9	56.7	1.05	0.28
Forequarter (%)	41.3	40.0	0.29	< 0.01
Hindquarter (%)	44.7	43.5	0.22	< 0.01
Rib (%)	14.0	16.4	0.27	< 0.01
Carcass pH at 0 hour	6.9	6.9	0.02	0.45
Carcass pH at 24 hours	5.5	5.4	0.04	0.38

[(1)]Treatment means were compared by the F-test (p<0.05). [(2)]DMI, dry matter intake; Feed efficiency, ADG/DMI; IBW, initial body weight; FBW, final body weight; ADG, average daily gain; ADGc, ADG of the carcass; HCW, hot carcass weight; and DP, dressing percentage. [(3)]*Bos indicus*. [(4)]*Bos taurus*.

between different breeds, such as the European and Zebu breeds, produce animals with a greater weight at slaughter when finished with a high-energy diet. In the present study, the differences observed in carcass weight were related to the differences in weight at slaughter.

DP is one of many factors that affect the value of a slaughtered animal, highlighting the importance of understanding slaughter-cattle pricing systems and pricing variability. Despite their lower performance, Nellore animals recovered from an economic point of view since, considering their DP did not differ significantly from that of the crossbred animals (57.9 vs. 56.7%). Similar results were obtained by Monteiro et al. (2022), who did not observe any differences ($p>0.05$) in DP between Nellore (56.2%) and Nellore x Angus (55.9%) animals finished in feedlot, although the crossbred animals showed a higher FBW (633.8 vs. 515.5 kg), ADGc (4.10 vs. 0.89 kg), and HCW (361.6 vs. 285.1 kg).

Lopes et al. (2012a) reported differences ($p<0.01$) in the FBW of Nellore and ¾ *B. taurus* x ¼ *B. indicus* animals, which weighed 482.8 and 519.4 kg, respectively. However, in their study, the DP of Nellore animals was higher ($p<0.01$) than that of the crossbred animals (57.7 vs. 54.7%). Despite the lower DP of the crossbred animals, the authors concluded that the obtained values were satisfactory from a productive point of view, as many slaughterhouses in Brazil consider only 50% of DP when buying an animal based on FBW (Lopes et al. 2012a).

Regarding growth performance and carcass characteristics, Façanha et al. (2014) evaluated ½ Red Angus x ½ Nellore and ¾ Red Angus x ¼ Nellore animals finished in a feedlot. The authors did not find any differences regarding slaughter weight (412.33 vs. 426.53 kg) and DP (52.6 vs 52.9%) between ½ Red Angus x ½ Nellore and ¾ Red Angus x ¼ Nellore animals, respectively, concluding that there were no differences between these genetic groups regarding carcass and meat traits. Despite this, the ½ Red Angus x ½ Nellore cross is recommended, as it would allow of the animals to be slaughtered one generation before the ¾ Angus x ¼ Nellore animals.

Maciel et al. (2019) studied Nellore and Nellore x Angus animals finished in feedlot and also reported differences between the two breed compositions for all variables evaluated. The crossbred animals had a higher FBW, ADG, ADGc, carcass weight, and feed conversion than Nellore, but entered the feedlot at a significantly higher weight, as in the present study.

Considering beef cuts, those in the posterior part of the carcass have a better commercial value (Prado et al., 2015), which is why a higher hindquarter yield is ideal. The Nellore animals showed an excellent ability for muscle development in their hindquarter. However, the crossbred animals had a greater DMI, which results in a larger digestive tract and consequent higher rib percentage (Costa et al., 2017). According to Lopes et al. (2012a), when analyzing cuts (quarters) by weight, a direct influence of slaughter weight is observed, as animals finished with a higher weight result in heavier cuts. Therefore, the comparison in percentage is the most appropriate way to evaluate carcasses of animals with different slaughter weights, as done in the present study.

Regarding carcass pH values at 0 and 24 hours after slaughter, the Nellore and Nellore x Angus animals showed similar results. The pH of the carcasses was within the standard recommended by the meat industry, which considers pH values between 5.5 and 5.7 as normal, resulting in meat with the most desirable quality characteristics (Matarneh et al., 2017). According to these authors, meat with pH 6.0 or higher tend to be darker in color and have a reduced shelf life, whereas meat with $pH<5.4$ is pale in color, has a lower water-holding capacity, and a low protein extraction capacity and yield when processed. Oliveira et al. (2021) did not observe differences ($p>0.05$) between the Nellore, Angus x Nellore, and Canchim x Nellore breeds finished in feedlot regarding carcass pH values at 0 hour (6.68 vs. 6.92 vs. 6.89) and at 24 hours (5.91 vs. 5.98 vs. 5.93).

The rate of carcass pH declined post-mortem, which can be attributed to several factors, including genetics, muscle fiber type, and pre- and post-mortem handling conditions (Matarneh et al., 2017). Despite this decrease, the pH values observed in the present study are an indicative that the glycogen reserve in the muscle tissue was adequate at the time of slaughter for both evaluated genetic groups.

Matarneh et al. (2017) attributed the gradual decrease in carcass pH from about 7.2 in the living tissue to a final value close to 5.6 to the accumulation of the end products of post-mortem glycolysis and adenosine triphosphate hydrolysis, lactate and hydrogen ions,

in the muscle, whose residual glycogen usually stops glycolysis in certain species. Since pH decreases as glycogen increases until a plateau is reached, the relationship between glycogen content and final pH is curvilinear instead of linear.

No difference was observed between the studied groups regarding methane production ($p>0.05$), except for methane expressed as CH_4 in gram per kilogram of ADG ($p<0.01$), as presented in Table 3. Although, in general, larger and fast-growing animals eat more and produce more enteric methane, the crossbred animals produced less methane expressed as CH_4 even though they were heavier and had a higher DMI. Despite this difference in DMI, breed composition did not modify CH4 yield (g CH_4 per unit of DMI).

Methane emissions occur naturally in ruminants but are more accentuated by the consumption of diets with a high content of fibrous carbohydrates. Therefore, the emission of enteric methane can be reduced by improving the composition of the provided diet, reducing fiber content and increasing the concentrations of crude protein and soluble carbohydrates (Berndt & Tomkins, 2013).

One of the most effective ways to reduce enteric CH_4 emissions by ruminants is supplementing diets with lipids. However, due to the toxic action of lipids on ruminal microorganisms, there may be a decrease in digestion, mainly of the fibrous fraction of food, and a consequent drop in the DMI of the diet. Kozloski (2011) and Palmquist & Mattos (2011) added that the UFAs present in lipids are toxic to gram-positive bacteria, protozoa, and archaea methanogenic due to the changes caused in the fluidity of their plasma membrane, leading to cell disruption. In this scenario, National Research Council (NRC, 2016) recommends that the maximum amount of ether extract in the diet of cattle does not exceed 7% of dry matter.

In the rumen, bacteria use hydrogen, by adding it to double bonds, to convert unsaturated fatty acids into saturated fatty acids (biohydrogenation), a process that reduces the amount of hydrogen available for CH_4 synthesis. According to Pereira et al. (2022), the synthesis of CH_4 contributes to the efficiency of rumen fermentation, preventing hydrogen (H_2) concentration from increasing to levels that can inhibit the normal functioning of the rumen and reduce fermentation. These authors highlighted that methane production in the rumen is mainly modulated by the presence of free CO_2 and H_2 produced from the fermentation of feeds; from H_2, CO_2 is reduced by microorganisms, with the consequent formation of CH_4.

In another study, Silva et al. (2018) found that the enteric CH_4 emission of Nellore animals in feedlot (gram per day, kilogram per year, and g kg^{-1} DMI) was not affected by different soybean lipid ($p>0.05$) sources (soybean oil, soybean, and rumen-protected fat based on soybean oil) added to diets containing maize, soybean meal, urea, and crude glycerin. According to the authors, this result might be due to the adaptation of the microbial population and to the partial absorption of the added glycerol by the rumen wall.

Maciel et al. (2019) evaluated the methane production of Nellore and Nellore x Angus groups finished in feedlot, observing that CH_4 g kg^{-1} ADG or CH_4 g per ADGc was significantly lower ($p<0.01$) in the crossbred than in the Nellore animals. For the

Table 3. Means, standard errors of the means (SEM), and results of the F-test[1] for the methane production of two genetic groups of bulls finished in feedlot.

Item[2]	Nellore[3]	Nellore x Angus[4]	SEM	p-value
CH_4 (g per hour)	15.6	14.5	1.43	0.89
CH_4 (g per day)	374.9	348.8	34.4	0.59
CH_4 (kg per year)	127.4	127.3	10.9	0.99
CH_4 (kg DMI^{-1})	35.4	27.7	2.99	0.08
CH_4 (kg BW^{-1})	0.72	0.57	0.06	0.09
CH_4 (g kg $BW_{0.75}^{-1}$)	3.44	2.83	0.30	0.16
CH_4 (g kg ADG^{-1})	266.0	173.4	20.8	< 0.01
CH_4 (g kg CW^{-1})	1.09	0.87	0.09	0.11
CH_4 (g $ADGc^{-1}$)	321.8	247.3	26.5	0.06

[1]Treatment means were compared by the F-test ($p<0.05$). [2]CH_4, methane; DMI, dry matter intake; BW, body weight; $BW_{0.75}$, metabolic body weight; ADG, average daily gain; CW, carcass weight; and ADGc, ADG of the carcass. [3]*Bos indicus*. [4]*Bos taurus*.

authors, these results suggest that the CH_4 production of the crossbred animals is compensated for a better performance, leading to a lower CH_4 per kilogram of meat produced when a feedlot is used in tropical climate conditions.

According to Donoghue et al. (2016), CH_4 emission levels in cattle are heritable traits, meaning that genetic selection has the potential to reduce the emissions of this gas in ruminants, which could result in cumulative and permanent changes in these levels. Therefore, genetic improvement based on testing sires and their progeny in a feedlot trial will lead to a better understanding of genetic correlations, which are usually higher that phenotypic ones, on methane emissions (Herd et al., 2016).

No difference ($p>0.05$) was observed between genetic groups for total fatty acid concentration (TFA), as shown in Table 4. The TFA content found in the present study agrees with those obtained in other works that used identical analytical methods (Lopes et al., 2012b; Bressan et al., 2016; Renna et al., 2019).

A significant difference was observed in lauric and myristic acid concentrations between the evaluated genetic groups ($p<0.01$). The highest levels were obtained for Nellore animals compared with the crossbred animals (0.08 vs. 0.06% and 3.31 vs. 2.63%, respectively). However, the lauric acid percentages were relatively low for both genetic groups, which is considered normal in beef (Liu et al., 2020).

Regardless of the genetic group, the fatty acids found at higher concentrations were the oleic (C18:1 n-9), palmitic (C16:0), and stearic (C18:0) acids. Of the total fatty acids, these represented 75.2 and 77% in the Nellore and crossbred animals, respectively.

For Zebu animals and their crosses, Feitosa et al. (2017) found that intramuscular fat can indicate the fatty acid profile of the meat. Although the adipogenic mechanism is complex, different Zebu genes have been confirmed to be responsible for the fatty acid profile in beef, a genomic information that can help improve this profile and, in the future, be included in breeding programs to obtain quality beef.

Table 4. Means, standard error of the means (SEM), and results of the F-test[(1)] for the concentrations (% of the total fatty acid content) of the total fatty acid and fatty acid profile of the *Longissimus thoracis* muscle of two genetic groups of bulls fed with high-lipid diets and finished in feedlot.

Group	Fatty acid		Nellore	Nellore x Angus	SEM	p-value
	Total fatty acids (g 100 g^{-1} tissue)		1.9	2.2	0.20	0.35
Saturated fatty acid	Lauric	C12:0	0.08	0.06	0.004	< 0.01
	Myristic	C14:0	3.31	2.63	0.13	< 0.01
	Pentadecanoic	C15:0	0.36	0.34	0.02	0.32
	Palmitic	C16:0	23.4	22.6	0.44	0.27
	Margaric	C17:0	0.59	0.74	0.04	0.04
	Stearic	C18:0	13.7	13.6	0.62	0.89
Monounsaturated fatty acid	Myristoleic	C14:1 (*c-9)*	0.81	0.69	0.05	0.07
	Palmitoleic	C16:1 (*c-9)*	3.32	3.00	0.12	0.08
	Heptadecenoic	C17:1	0.57	0.63	0.02	0.08
	Oleic	C18:1 (*c-9)*	38.1	40.8	0.86	0.05
	Vaccenic	C18:1 (*t-11*)	3.12	3.04	0.19	0.76
	Sum of C18:1[(2)]	C18:1	3.38	3.69	0.09	< 0.01
	Elaidic	C18:1 (*t-16)*	0.30	0.23	0.02	0.04
Polyunsaturated fatty acid	CLA[(3)] – rumenic acid	C18:2 (*c-9*, *t-11*)	0.50	0.39	0.03	< 0.01
	Linoleic	C18:2 (omega-6)	4.84	4.12	0.38	0.20
	α-linolenic	C18:3 (omega-3*)*	0.46	0.39	0.02	0.03
	Dihomo-γ-linoleic	C20:3 (omega-6)	0.15	0.12	0.02	0.19
	Arachidonic	C20:4 (omega-6)	0.76	0.73	0.12	0.85
	Docosapentaenoic	C22:5 (omega-3)	0.37	0.33	0.05	0.51

[(1)]The treatment means were compared by the F-test ($p<0.05$). [(2)]Sum of C18:1 *c*-11 + C18:1 *c*-12 + C18:1 *c*-13 + C18:1 *c*-15. [(3)]Conjugated linoleic acid.

No significant effect was observed on palmitic acid concentration (p>0.05) between breeds. According to Shramko et al. (2020), myristic and palmitic acids have hypercholesterolemic potential because they enrich the phospholipids of cell membranes and interfere with low-density lipoprotein (LDL) receptors, reducing their removal and, consequently, increasing their concentration in the blood. However, when compared with palmitic acid, myristic acid has potential to increase fourfold blood cholesterol.

Regarding margaric acid, there was a significant effect (p = 0.04) since the crossbred animals showed the highest concentration of 0.74%. Barcellos et al. (2017) evaluated Nellore animals finished in pasture and Nellore x Angus finished in feedlot, only observing a difference in the concentrations of this acid in intramuscular fat (0.97 vs. 0.86%, respectively).

Regarding stearic acid concentrations, there were no significant differences between the genetic groups (p>0.05). In the animal body, this acid is rapidly metabolized to oleic acid by the Δ^9 desaturase enzyme, a process that helps reduce cholesterol absorption, contributing to the observed cholesterol-lowering effects (Jesch & Carr, 2017).

Oleic acid is the MUFA in beef and, therefore, is found at the highest concentration, corresponding to practically 40% of the total proportion of fatty acids. A significant effect (p = 0.05) was observed between the studied breeds, with higher levels found in the intramuscular fat of Nellore x Angus than in that of Nellore animals (38.1 vs. 40.8%). Oleic acid contributes to an increase in high-density lipoprotein and a decrease in LDL and triglyceride concentrations in the blood plasma, making it possible to prevent cardiovascular diseases (Shramko et al., 2020). Machado Neto et al. (2015) found differences in oleic acid concentration in ¾ *B. taurus* x ¼ *B. indicus* animals fed ground soybean or cottonseed (34.9 vs. 28.7%, respectively). When studying the fatty acid profile of intramuscular fat, Monteiro et al. (2022) observed a difference (p = 0.04) in the concentration of oleic acid between the Angus x Nellore and Nellore breeds, with the crossbred animals showing the highest concentrations (36.7 vs. 41.5%).

As to vaccenic acid concentration (p>0.05), there was no difference between the evaluated genetic groups. As the concentration of vaccenic acid was higher than that of the conjugated linoleic acid (CLA), it is suggested that the first steps of ruminal biohydrogenation occur more quickly than the conversion of vaccenic to stearic acid. Therefore, vaccenic acid accumulates in the rumen and becomes more available for absorption after it reaches the intestine, where it is converted to CLA by the Δ^9 desaturase enzyme (Oliveira et al., 2011).

Table 5. Means, standard error of means (SEM), and results of the F-test[(1)] for the sums of fatty acids, ratios of fatty acids, activities of desaturase enzymes, activities of the elongase enzyme, atherogenicity index, and thrombogenicity index in the intramuscular fat of two genetic groups of bulls fed with high-lipid diets and finished in the feedlot.

Fatty acid, enzyme, and index[(2)]	Nellore	Nellore x Angus	SEM	p-value
Σ SFA[(3)]	42.3	40.1	0.93	0.12
Σ UFA[(3)]	57.2	59.1	0.92	0.19
Σ MUFA[(3)]	49.7	52.4	0.95	0.05
Σ PUFA[(3)]	7.67	6.71	0.73	0.03
Σ omega-3[(3)]	0.68	0.53	0.06	0.02
Σ omega-6[(3)]	6.63	4.89	0.88	0.07
omega-6/omega-3	9.75	9.22	0.02	0.07
Δ^9 Desaturase 16	12.4	11.7	0.38	0.14
Δ^9 Desaturase 18	73.6	75.0	1.09	0.38
Elongase	65.6	67.8	0.65	0.03
Atherogenicity index	0.65	0.57	0.02	0.03
Thrombogenicity index	1.33	1.27	0.05	0.42

[(1)]Treatment means were compared by the F-test (p<0.05). [(2)]ΣSFA, sum of saturated fatty acids; ΣUFA, sum of unsaturated fatty acids; ΣMUFA, sum of monounsaturated fatty acids; ΣPUFA, sum of polyunsaturated fatty acids; Σomega-3, sum of omega-3 fatty acids; Σ omega-6, sum of omega-6 fatty acids; Δ^9 desaturase 16, activity of the enzyme Δ^9 desaturase 16; Δ^9 desaturase 18, activity of the enzyme Δ^9 desaturase 18; and Elongase, activity of the elongase enzyme. [(3)]Values expressed as percentage of the total content of fatty acids.

Regarding the sum of the C18:1 isomer, there was a significant effect between breeds ($p<0.01$), with lower concentrations observed for the Nellore animals. However, Bressan et al. (2016) did not find significant differences in the concentrations of C18:1 *cis*-11, C18:1 *cis*-12, and C18:1 *cis*-13 in the intramuscular fat of different genetic groups (*B. indicus* x *B. indicus* x *B. taurus*).

A significant effect was observed on CLA concentrations ($p<0.01$), which were higher for Nellore animals compared with the crossbred animals (0.50 vs. 0.39%). Contrastingly, Monteiro et al. (2022), evaluating the same genetic groups, found a higher concentration ($p = 0.03$) of CLA in the intramuscular fat of Nellore x Angus than of Nellore animals (0.19 vs. 0.32%).

A factor that influences the production of CLA in fat tissues is ruminal pH. Diets with high levels of concentrate, mainly starch, can decrease rumen pH and reduce lipolysis, an essential step for biohydrogenation (Fiorentini et al., 2018). In the present study, using 80% of concentrate in the diet, a ruminal pH of 5.99 (NRC, 2016) was estimated, as previously described.

The benefits of CLA have been the focus of several researches. Gebauer et al. (2015) and Vahmani et al. (2020), for example, found that CLA has properties that act to reduce body fat, cardiovascular disease, cancer, and blood triglycerides, in addition to preventing fat in the liver and modifying the immune and inflammatory responses of the body.

As to alpha-linolenic acid, the Nellore animals showed higher concentrations than the crossbred animals ($p = 0.03$). However, there was no difference between both genetic groups ($p>0.05$) in the concentrations of linoleic acid, dihomo-γ-linoleic acid, arachidonic acid, and docosapentaenoic acid, which were higher than those reported by Lopes et al. (2012b) for Red Norte and Nellore.

The level of linoleic acid in the tissues was higher than that of alpha-linolenic acid. Wood et al. (2008) attributed this finding to a higher affinity for incorporation into phospholipid molecules and also to a reduced biohydrogenation in the rumen due to a concentrate-rich diet, whose particle size is smaller and rumen transit time is shorter than those of forage diets, limiting microbial biohydrogenation. The elongation and desaturation of the linoleic and alpha-linolenic acids explain these results in the fatty acid profile. Therefore, the higher the concentrations of these two acids, the higher the long-chain fatty acid concentrations derived from them. Moreover, Fiorentini et al. (2015) found that diets with soybean grain have greater linoleic and alpha-linolenic acid deposition than diets with fat protection, also associating a more significant presence of these essential fatty acids with a better meat composition and meat quality.

Breed composition did not affect the sum of SFAs, UFAs, and omega-6 fatty acids ($p>0.05$), but influenced that of MUFAs ($p = 0.05$), PUFAs ($P = 0.03$), and omega-3 fatty acids ($p = 0.02$), as shown in Table 5. Compared with Nellore, the crossbred animals had higher concentrations of MUFAs (49.7 vs. 52.4%) but lower ones of PUFAs (6.71 vs. 7.67%). Generally, animals with a higher Zebu breed percentage have higher concentrations of PUFAs in intramuscular fat due to their fiber composition characteristics and increase in muscle membranes (Ito et al., 2012). Fiorentini et al. (2018) found higher concentrations ($p<0.01$) of PUFAs in the intramuscular fat of animals fed soybean grain (9.40%) instead of protected fat (8.26%). However, supplementation with protected fat increased the concentration of CLA, a result likely related to the lower biohydrogenation of the lipid source.

A significant difference was observed between breed compositions regarding the concentrations of omega-3 ($p = 0.02$), whose sum was 0.15% higher in Nellore animals. However, no difference was observed in the sum of omega-6 and the ratio between omega-6 and omega-3 ($p>0.05$). Knowing the amount of these fatty acids is important due to the growing evidence that the regular consumption of omega-3 is beneficial for the growth and development of humans of all ages, as well as for their health and well-being, helping to prevent diseases such as arthritis, depression, and cancer (Ponnampalam et al., 2018).

According to FAO (2010), there are no recommendations for the intake of the omega-6/omega-3 ratio, as long as omega-6 and omega-3 are within the following consumption values: PUFAs from 6.0 to 11%, total omega-3 intake from 0.5 to 2.0%, and input of omega-6 from 2.5 to 9.0%. To prevent disease development, the recommended daily intake of total fats should be 20 to 30%, and UFA intake should be approximately 10%, whereas the recommended PUFA/SFA ratio is 4 to 5 and the input of *trans*-fatty acid

should not exceed 1%. Consumption should be based mainly on the amount of n-3 present in the food, then on the ratio between omega-6/omega-3.

Bressan et al. (2016) evaluated Nellore and Nellore x Simmental animals and found no significant difference in the omega-6/omega-3 ratio between these genetic groups. However, the authors also analyzed the finishing system (pasture x feedlot), observing that animals finished on pasture showed higher concentrations of omega-3 and a lower ratio of omega-6/omega-3 due to the high levels of alpha-linolenic acid in forages and of linoleic acid in grains. Despite the biohydrogenation of these fatty acids in the rumen, the authors concluded that the used diets influenced the fatty acid profile of the meat.

No differences were observed between the studied genetic groups ($p>0.05$) regarding the activity of the Δ^9 desaturase 16 and Δ^9 desaturase 18 enzymes, despite the considerable differences in the concentrations of oleic acid. However, Bressan et al. (2016) reported a greater activity of Δ^9 desaturase 16 in the intramuscular fat of *B. indicus* animals than in the *B. indicus* x *B. taurus* cross (9.52 vs. 10.30%), with no significant differences between the breeds for the activity of Δ9 desaturase 18. Gama et al. (2013) also concluded that *B. indicus* has a much stronger influence on their crossbred offspring than *B. taurus*, suggesting a solid dominance genetic effect. The Δ^9 desaturase enzyme has been identified as one of the genes associated with the fatty profile of beef (Martins et al., 2018).

The greater proportion of concentrate in the finishing diets promotes Δ^9 desaturase enzyme activity and intramuscular fat deposition. However, the rumen outflow of vaccenic acid frequently is replaced by an isomer of C18:1 *trans*-10, which cannot be converted to CLA, explaining why the occurrence of C18:1 *trans*-10 acid is usually associated with low CLA concentrations in beef (Bessa et al., 2015). According to the same authors, the constraints to the n-3 long-chain PUFA enrichment of beef are mainly associated with the rumen biohydrogenation of PUFAs, the low elongation and desaturation of 18:3 n-3 into n-3 long-chain PUFA, and the capacity of muscle lipids to incorporate n-3 long-chain PUFA.

A significant difference ($p = 0.03$) was observed in the elongase enzyme activity between Nellore and Nellore x Angus animals. This is an indicative that the crossbred animals had a greater capacity to promote elongation from palmitic to stearic acid, although no discrepancies in the concentration of these acids were found. This result shows that the crossbred animals could perform a better fatty acid biosynthesis, mainly through oleic acid. Furthermore, since the animals were slaughtered at a weight heavier than that at maturity, the occurrence of a greater *de novo* synthesis of fatty acids is natural, leading to a greater formation of UFAs through SFAs.

Regarding the AI ($p= 0.03$), the results obtained for the Nellore animals were slightly greater than those for the crossbred animals (0.65 vs. 0.57%). Similarly, Monteiro et al. (2022) did not observe significant differences in this index ($p = 0.16$) between Nellore (0.80%) and Nellore x Angus (0.63%) animals.

The obtained results indicate that the consumption of beef must be stimulated considering the presence of fatty acids beneficial to human health, such as oleic acid and CLA that is only found in animal-origin products, especially from ruminants. Therefore, providing information about the nutritional value of beef to consumers is important, as meat consumption, especially of red meat, is recommended to avoid risks of cancer and metabolic syndromes, as well as obesity (Gebauer et al., 2015; Ponnampalam et al., 2018; Vahmani et al., 2020).

Conclusions

1. Crossbred Nellore (*Bos indicus*) x Angus (*Bos taurus*) young bulls show an enhanced feedlot performance and superior carcass traits.

2. Total methane production is not negatively affected by crossbreeding, but the emissions per unit of beef produced are reduced.

3. Despite being fed the same diet, both breeds show differences in their fatty acid profile and, consequently, in their beef characteristics.

4. Nellore animals exhibit higher concentrations of polyunsaturated fatty acids and conjugated linoleic acid in their intramuscular fat than the crossbred animals.

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