

Article

Growth Performance, Quality and Chemical Composition of the Longissimus Thoracis from Bovine Genetic Groups Selected for the Production of High-Quality Meat

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Simple Summary

The growing consumer demand for high-quality beef has driven interest in genetic crosses that can improve marbling, tenderness, and the nutritional profile of meat. However, the outcomes of combining Wagyu genetics with Brazilian Nellore cattle are still insufficiently characterized. This study compared four Nellore-based genetic groups (crosses with Angus, Japanese Black, and Japanese Brown) finished in commercial feedlots in Brazil, evaluating their growth performance, meat quality traits, and fatty acid profiles. Finishing in feedlots resulted in superior growth for the Angus × Nellore group; however, all genetic groups produced meat with similar quality attributes, including adequate tenderness and moderate to abundant marbling. The fatty acid profiles were largely consistent across groups, with the exception of arachidonic acid, which was higher in the triple cross involving Japanese Brown. All groups presented a high omega-6/omega-3 ratio, a common nutritional limitation of grain-finished beef. It was concluded that, under prolonged feedlot conditions, the extended feeding period and standardized diet are major determinants of meat composition, largely overriding genetic differences, and that diverse crossbreeding strategies can deliver uniform high-quality beef, making future dietary strategies necessary to improve the lipid profile.



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Abstract

The growing demand for high-quality beef has driven the selection of bovine genotypes offering superior marbling and tenderness. This study evaluated meat quality parameters in heifers from four Nellore-based genetic groups: ½ Aberdeen Angus × ½ Nellore (AN), ½ Japanese Brown × ½ Nellore (BN), ½ Japanese Brown × ¼ Aberdeen Angus × ¼ Nellore (TriBAN), and ½ Japanese Black × ¼ Aberdeen Angus × ¼ Nellore (TriJAN). Thirty-two heifers (eight/group) were finished in commercial feedlots. Samples of the longissimus thoracis muscle were analyzed for physical attributes (pH, cooking loss, shear force, marbling, water retention capacity, and colour), chemical composition, and fatty acid profile. In addition, animal performance (daily gain and final weight) was determined. A completely

randomized design was used with analysis of variance followed by Tukey's test ($\alpha = 0.05$). The AN group showed the greatest final weight and daily gain ($p < 0.01$). There were no significant differences among genetic groups for pH, cooking loss, shear force, marbling, water-holding capacity, or colour ($p > 0.05$). Across all groups, the mean ultimate pH was 5.59, shear force (WBSF) averaged 41.11 N, and intramuscular fat (ether extract) content averaged 13.15 g 100 g⁻¹, indicating desirable technological and eating-quality characteristics. Most fatty acids did not differ among treatments ($p > 0.05$), except for arachidonic acid (C20:4 n-6), which was present at higher concentrations ($p < 0.05$) in the TriBAN group than in the other genetic groups. In conclusion, despite differences in productive performance, all genotypes produced meat with consistent quality traits, including tenderness, marbling, and fatty acid profiles associated with high-quality beef.

Keywords: fatty acid profile; feedlot; genetic groups; meat quality; tenderness

1. Introduction

With the increase in the global consumption of beef with sensory characteristics that are superior to the commodity standard, one part of the production chain has been seeking strategies that value not only animal performance and carcass yield, but also sensory and nutritional quality [1,2]. This need is driven by an emerging consumer market that prioritizes products associated with a gourmet culture [3], where the taste experience is paramount.

Meat tenderness and the presence of intramuscular fat (marbling) are critical points in consumer satisfaction [4] that directly influence the purchase decision [5]. Marbling is the most important characteristic of meat quality that affects palatability [6], being the main classification criterion in developed markets and strongly linked to pricing [5]. Nellore cattle, the basic component of Brazilian livestock farming due to their adaptation to tropical conditions and varied production systems [7], represent 80% of the domestic total [8]. However, the meat is tougher with less marbling compared to specialized breeds such as Angus and Wagyu [9,10], which limits its suitability for the gourmet market.

While Angus cattle have been widely adopted in Brazil due to the tenderness and marbling of the meat, rapid growth, and high carcass yield [11], only a small fraction of the carcasses are classified as prime-grade with a high level of marbling [12]. On the other hand, the Wagyu group (Japanese Black and Japanese Brown) is notable for producing meat with an exceptional degree of marbling [10], surpassing Angus cattle even when under the same type of nutritional management [13,14]. Additionally, Wagyu breeds have a distinctive fatty acid (FA) composition, with a high percentage of monounsaturated FA (especially oleic acid) and a high ratio of monounsaturated/saturated FA [15,16], which has a positive impact on sensory quality [17] and raises interest regarding its effect on human health [18].

Although the pure characteristics of these breeds are well established, the outcomes of combining their genetics with Brazilian Nellore cattle remain insufficiently characterized. Therefore, the working hypothesis of this study is that three-way crosses involving Wagyu breeds can achieve satisfactory productive performance, along with meat exhibiting physicochemical and fatty acid profile traits commonly associated with high-quality beef, potentially outperforming conventional industrial crosses.

Based on this premise, the aim of this study was to evaluate the productive performance, qualitative attributes, and fatty acid profile of the longissimus thoracis (LT) muscle from heifers of the following genetic groups: $\frac{1}{2}$ Angus $\times$ $\frac{1}{2}$ Nellore (AN), $\frac{1}{2}$ Japanese Brown

$\times \frac{1}{2}$ Nellore (BN), $\frac{1}{2}$ Japanese Brown $\times \frac{1}{4}$ Angus $\times \frac{1}{4}$ Nellore (TriBAN), and $\frac{1}{2}$ Japanese Black $\times \frac{1}{4}$ Angus $\times \frac{1}{4}$ Nellore (TriJAN), finished in commercial feedlots.

2. Materials and Methods

2.1. Animals and Experimental Design

Samples of the LT muscle were obtained from 32 crossbred heifers ($n = 8$ per genetic group) finished in a commercial feedlot (Beef Passion, Nhandeara, SP, Brazil; 20.6953° S, 50.0416° W). Heifers were used exclusively to standardize the experimental model, controlling for physiological variability associated with sex differences and thus enabling a more consistent comparison among genetic groups. This choice also reflects commercial beef production systems, where females represent a substantial proportion of animals destined for the premium meat market. Four genetic groups were evaluated: $\frac{1}{2}$ Aberdeen Angus $\times \frac{1}{2}$ Nellore (AN), $\frac{1}{2}$ Japanese Brown $\times \frac{1}{2}$ Nellore (BN), $\frac{1}{2}$ Japanese Brown $\times \frac{1}{4}$ Aberdeen Angus $\times \frac{1}{4}$ Nellore (TriBAN), and $\frac{1}{2}$ Japanese Black $\times \frac{1}{4}$ Aberdeen Angus $\times \frac{1}{4}$ Nellore (TriJAN). The animals, with an initial age of 18 months, were kept in covered group pens and received a diet consisting of 430 g/kg of roughage, 105 g/kg of crude protein, and 704 g/kg of total digestible nutrients, expressed on a dry-matter basis. Feed was provided twice daily, with free access to water. The TriJAN group remained under feedlot conditions for 360 ± 72 days, whereas the AN, BN, and TriBAN groups were finished for 273 ± 7 days. This difference resulted from management decisions to achieve the target slaughter endpoint for each genetic group. Because feeding duration was completely associated with genetic group, days on feed was not included as a covariate in the statistical model. The animals were sourced from a commercial feedlot; however, they were the result of routine crossbreeding practices involving multiple sires, which allowed the inclusion of genetic variability representative of commercial production systems rather than a single family line. Although the sample size was not intended to represent the entire genetic spectrum of each breed, the evaluated groups represent genetic compositions commonly used in Brazilian beef production systems.

2.2. Experimental Diet

The experimental diet was formulated to meet the nutritional requirements of feedlot cattle. The main ingredients included corn meal, peanut meal, corn germ, and urea. The ingredient composition of the diet is presented in Table 1.

Table 1. Ingredient composition of the experimental diet (% dry matter basis).

Ingredient	Inclusion (%)
Corn silage	26.44
Corn meal	21.30
Corn germ	18.50
Wet citrus pulp	12.50
Pelleted citrus pulp	10.59
Soybean grain	4.80
Máxima Choice [®] 1	2.65
Peanut meal	2.50
Urea	0.72

¹ Commercial mineral–vitamin supplement.

2.3. Slaughter and Sampling

The animals were slaughtered under the official supervision of the Federal Inspection Service (SIF) in accordance with Brazilian regulations [19]. Samples of the LT muscle from between the 6th and 8th thoracic vertebrae were collected 24 h post-mortem, vacuum-

packed, refrigerated at 4.0 ± 0.5 °C for 7 days to simulate commercial wet aging, and then subjected to laboratory analysis. All samples originated from a commercial slaughterhouse, and the animals were handled and slaughtered following the standards of the Brazilian Industrial and Sanitary Inspection of Animal Products (RIISPOA) [19]. No experimental interventions (e.g., drug administration or dietary manipulations) were performed on live animals for the purposes of this study. As the research exclusively used post-mortem tissues obtained from legally slaughtered animals destined for the human food chain, with no ante-mortem experimental procedures, formal ethical approval was not required under applicable institutional guidelines. Nonetheless, all procedures adhered to internationally recognized principles of animal welfare.

2.4. Evaluating Meat Quality

Colour was measured using a CR410 colorimeter (Konica Minolta, Tokyo, Japan; illuminant D65) after 30 min exposure to atmospheric oxygen, recording the following parameters: L*—lightness, a*—redness index, b*—yellowness index, h°—hue angle, and C*—chroma. The pH was measured using a portable potentiometer (Testo 205, Testo SE & Co. KGaA, Titisee-Neustadt, Germany) in samples kept at 4 °C. Marbling was subjectively evaluated on the cut surface corresponding to the eighth rib according to Müller (1987) [20], using a scoring scale in which 1–3 = traces, 4–6 = slight, 7–9 = small, 10–12 = medium, 13–15 = moderate, and 16–18 = abundant. Marbling was evaluated by three trained panelists blinded to treatments, and the average score was used. To determine the shear force (WBSF), steaks, 2.5 cm thick, were cooked on non-stick aluminum trays at 170 °C until they reached an internal temperature of 70 °C. The steaks were weighed before cooking and again after cooling to room temperature. Cooking loss (CL) was calculated as the difference between the initial and final weight of the samples. The shear force was then determined using a TA.XT2 plus texture analyzer (Stable Micro Systems, Godalming, UK) equipped with a Warner–Bratzler blade and set to a speed of 2 mm/s. Water holding capacity (WHC) was estimated using two methods: (a) filter paper pressure method (FPPM), described by Grau and Hamm [21], using Whatman No. 1 filter paper (Sigma-Aldrich, Barueri, SP, Brazil) and (b) expressible water method (ExpW), based on parameters described by Kauffman et al. [22]. To determine the areas of each image, the ImageJ v.1.54e software (National Institute of Mental Health, Rockville, MD, USA) was used, as described by Smili et al. [23].

2.5. Chemical Composition

The percentage composition was determined in previously lyophilized samples, following official AOAC methods [24]: the moisture content was determined using method 930.15, crude protein (CP) using method 928.08 (using a nitrogen conversion factor of 6.25), ether extract (EE) using method 920.39, and the ash content using method 942.05.

2.6. Fatty Acid Composition

The total lipids were extracted following the Bligh and Dyer method [25], using a mixture of chloroform, methanol, and water. Transesterification was used to obtain the FA methyl esters (FAMES), as per the procedure described by Kramer et al. [26], employing nonadecanoic acid (C19:0, Sigma-Aldrich, St. Louis, MO, USA) as the internal standard. The FAMES were analyzed by gas chromatography, using the Shimadzu GC-2010 PLUS (Kyoto, Japan) equipped with an RT-2560 fused silica capillary column (100 m × 0.25 mm × 0.2 µm). The oven temperature was programmed as follows: initial 100 °C, ramp of 15 °C/min to 200 °C (1 min), ramp of 10 °C/min to 230 °C (1 min), ramp of 0.4 °C/min to 233 °C (3 min), and final ramp of 0.5 °C/min to 240 °C (2 min), with hydrogen (1.2 mL/min) as the carrier gas. Peaks were identified by comparing the retention times with the commercial standards: FAME Mix (code 35077), trans-11-vaccenic acid

(code 46905), and conjugated linoleic acid (code 05632), all from Sigma-Aldrich (St. Louis, MO, USA). Quantification was performed using nonadecanoic acid (C19:0) as the internal standard. Correction factors for the differential response of the flame ionization detector (FID) were applied for each FA based on theoretical response factors for FAMES. The conversion from methyl ester to free FA was performed using molecular weight correction factors specific to each FA, following the procedures described by Kramer et al. [26] and the official AOCS methodology. Quantification, expressed in mg/g of tissue, took into account correction factors for the differential response of the detector and for the conversion of methyl ester into FA. The total saturated FA (SFA), monounsaturated FA (MUFA), and polyunsaturated FA (PUFA), n-6, and n-3 were determined together with the MUFA/SFA, PUFA/SFA, and n-6/n-3 ratios. The atherogenicity (AI) and thrombogenicity (TI) indices were calculated applying the equations proposed by Ulbricht and Southgate [27].

2.7. Statistical Analysis

A completely randomized design was used to analyze the data using analysis of variance (ANOVA) in the PROC MIXED of the SAS v 9.4 software (SAS Institute Inc., Cary, NC, USA). The assumption of normality was evaluated applying the Shapiro–Wilk test, in the PROC UNIVARIATE, and the homogeneity of variances using the REPEATED/GROUP = TREATMENT command in the PROC MIXED of the SAS software. Additionally, outliers and influential values were detected using the RESIDUAL INFLUENCE command in PROC MIXED, and eliminated when the external studentized residuals were greater than 3 and the Cook distances greater than 0.1. Body weight and average daily gain were recorded individually for each animal. Animals were managed under commercial feedlot conditions throughout the experimental period, and performance data were analyzed using individual animal observations. The mean values were compared using Tukey’s test at a significance level of 5% ($\alpha = 0.05$).

3. Results

3.1. Productive Performance

The productive performance parameters are presented in Table 2. The AN group exhibited a higher final body weight (FBW) (712 kg; $p < 0.01$) compared to the BN, TriBAN, and TriJAN groups, which did not differ from each other, with mean values of 623.90, 605.30, and 645.60 kg, respectively.

Table 2. Performance of heifers finished in a feedlot: $\frac{1}{2}$ Angus $\times$ $\frac{1}{2}$ Nelore (AN), $\frac{1}{2}$ Japanese Brown $\times$ $\frac{1}{2}$ Nelore (BN), $\frac{1}{2}$ Japanese Brown $\times$ $\frac{1}{4}$ Nelore $\times$ $\frac{1}{4}$ Angus (TriBAN), and $\frac{1}{2}$ Japanese Black $\times$ $\frac{1}{4}$ Angus $\times$ $\frac{1}{4}$ Nelore (TriJAN).

Variables	Genetic Groups				Mean	SEM	p-Value
	AN	BN	TriBAN	TriJAN			
Final body weight, kg	712.00 a	623.90 b	605.30 b	645.60 b	646.7	18.52	<0.01
Average daily gain, kg/day	0.80 a	0.74 b	0.74 b	0.40 c	0.67	0.25	<0.01
Time in feedlot, days	273	273	273	359	294.5	-	-
Slaughter age, months	26.5	27	27	30.5	27.75	-	-

Means with the same letter within a row are not significantly different (Tukey’s test, $p < 0.05$). SEM: Standard error of the mean.

Regarding average daily gain (ADG), the AN group achieved the highest values (0.8 kg/day), followed by the TriBAN and BN groups (both 0.74 kg/day), and the TriJAN group showed the lowest performance (0.4 kg/day) ($p < 0.01$). The AN group had a 12.3% higher FBW than the average of the other groups. The TriJAN group remained in confinement for an additional 87 days compared to the other groups (360 vs. 273 days).

3.2. Meat Quality Attributes

The physicochemical quality parameters are shown in Table 3. The final pH values ranged from 5.3 to 5.7 across all groups. The average cooking loss (CL) was 22.78 g/100 g, with no significant differences between groups.

Table 3. Meat quality traits of the Longissimus thoracis muscle from heifers of different genetic groups: ½ Angus × ½ Nelore (AN), ½ Japanese Brown × ½ Nelore (BN), ½ Japanese Brown × ¼ Nelore × ¼ Angus (TriBAN), and ½ Japanese Black × ¼ Nelore × ¼ Angus (TriJAN), all finished in a feedlot system.

Variables	Genetic Groups				Mean	SEM	p-Value
	AN	BN	TriBAN	TriJAN			
Final pH	5.568	5.614	5.586	5.557	5.59	0.021	0.078
Cooking loss, g. 100 g ⁻¹	22.31	22.36	23.31	23.12	22.78	0.152	0.761
FPPM (ratio)	3.65	3.69	3.85	3.51	3.68	0.083	0.778
ExpW, g. 100 g ⁻¹	29.86	28.06	31.47	29.9	29.82	1.518	0.714
WBSF, N	34.66	41.49	49.19	39.13	41.11	1.97	0.081
Marbling	14.37	15.00	14.25	15.75	14.84	0.585	0.570
L*	38.88	43.32	42.87	41.15	41.56	0.995	0.342
a*	21.92	22.78	25.46	22.78	23.24	0.864	0.717
b*	11.53	11.92	14.4	11.66	12.38	0.277	0.653
h°	29.72	27.59	27.95	27.04	28.08	0.33	0.181
C*	25.15	25.72	26.63	25.6	25.78	0.519	0.755

FPPM—filter-paper press exudate loss; ExpW—expressible water; WBSF—Warner–Bratzler shear force; Marbling—subjective evaluation according to Müller ([20]). L*—lightness; a*—redness index; b*—yellowness index; h°—hue angle; C*—chroma. Differences in the means across treatments were evaluated using the Tukey’s test at 5% significance. SEM: Standard error of the mean.

Water holding capacity (WHC), assessed by both the filter-paper pressure method (FPPM) and the expressible water method (ExpW), did not differ between genetic groups ($p = 0.778$ and $p = 0.714$, respectively). Although WBSF values did not differ statistically among groups ($p = 0.081$), numerical differences were observed, particularly between AN (34.66 N) and TriBAN (49.19 N), suggesting a potential biological tendency. The overall mean WBSF across all groups was 41.11 N.

Marbling scores, evaluated on the Müller scale, averaged 14.84 across all samples, corresponding to a classification of moderately marbled. No significant differences were observed between groups ($p = 0.570$). However, within the TriJAN group, 6 out of 8 animals (75%) achieved scores > 15 (abundantly marbled), compared to 4 out of 8 (50%) in the AN and BN groups, and 3 out of 8 (37.5%) in the TriBAN group. Overall, 13 out of 32 samples (40.6%) were classified as abundantly marbled.

Colour parameters (L*—lightness, a*—redness, b*—yellowness, h°—hue angle, and C*—chroma) averaged 41.56, 23.24, 12.38, 28.08, and 25.78, respectively, with no statistically significant differences between groups for any of these parameters.

3.3. Chemical Composition

The chemical composition of the LT muscle is presented in Table 4. No significant differences were observed between groups for moisture ($p = 0.736$), ash content ($p = 0.230$), crude protein ($p = 0.227$), or ether extract (EE) ($p = 0.456$).

Table 4. Chemical composition of Longissimus thoracis muscle from feedlot-finished heifers of different crossbreeds: $\frac{1}{2}$ Angus $\times$ $\frac{1}{2}$ Nelore (AN), $\frac{1}{2}$ Japanese Brown $\times$ $\frac{1}{2}$ Nelore (BN), $\frac{1}{2}$ Japanese Brown $\times$ $\frac{1}{4}$ Nelore $\times$ $\frac{1}{4}$ Angus (TriBAN), and $\frac{1}{2}$ Japanese Black $\times$ $\frac{1}{4}$ Angus $\times$ $\frac{1}{4}$ Nelore (TriJAN).

Variables	Treatments				Mean	SEM	<i>p</i> -Value
	AN	BN	TriBAN	TriJAN			
Moisture, g 100 g ⁻¹	66.18	64.94	65.85	65.24	65.55	0.845	0.736
Ash content, g 100 g ⁻¹	1.01	0.99	0.97	0.92	0.97	0.042	0.230
Crude protein, g 100 g ⁻¹	20.93	20.32	20.19	19.88	20.33	0.375	0.227
Ether extract g 100 g ⁻¹	11.88	13.75	12.99	13.96	13.15	1.073	0.456

Differences in the means across treatments were evaluated using the Tukey's test at 5% significance. SEM: Standard error of the mean.

3.4. Fatty Acid Profile

The fatty acid composition of the LT muscle is shown in Table 5. The predominant SFA across all groups were myristic (C14:0), palmitic (C16:0), and stearic (C18:0) acids, with C16:0 being the most abundant. No significant differences were detected for total SFA ($p = 0.856$).

Table 5. Fatty acid profile of Longissimus thoracis from feedlot-finished heifers of different crossbreeds: AN ($\frac{1}{2}$ Angus $\times$ $\frac{1}{2}$ Nelore), BN ($\frac{1}{2}$ Japanese Brown $\times$ $\frac{1}{2}$ Nelore), TriBAN ($\frac{1}{2}$ Japanese Brown $\times$ $\frac{1}{4}$ Nelore $\times$ $\frac{1}{4}$ Angus) and TriJAN ($\frac{1}{2}$ Japanese Black $\times$ $\frac{1}{4}$ Nelore $\times$ $\frac{1}{4}$ Angus).

Fatty Acid (mg/g Tissue)	Treatment				Mean	SEM	<i>p</i> -Value
	AN	BN	TriBAN	TriJAN			
C10:0	0.043	0.034	0.043	0.033	0.038	0.006	0.320
C12:0	0.058	0.046	0.058	0.048	0.052	0.008	0.494
iC14:0	0.027	0.014	0.022	0.025	0.022	0.008	0.762
C14:0	2.582	2.224	2.470	2.770	2.511	0.318	0.634
iC15:0	0.071	0.059	0.082	0.061	0.068	0.009	0.430
aC15:0	0.146	0.121	0.140	0.139	0.136	0.019	0.844
C14:1 c-9	0.580	0.491	0.486	0.632	0.547	0.076	0.456
C15:0	0.200	0.188	0.211	0.177	0.194	0.020	0.720
iC16:0	0.105	0.068	0.090	0.229	0.436	0.010	0.441
C16:0	22.423	20.890	21.533	19.513	21.090	1.903	0.787
iC17:0	0.725	0.137	0.159	0.174	0.299	0.052	0.395
C16:1 c-7	0.131	0.099	0.133	0.263	0.157	0.028	0.405
C16:1 c-9	2.424	2.540	2.678	3.046	2.672	0.369	0.733
aC17:0	0.125	0.103	0.099	0.121	0.112	0.032	0.684
C17:0	0.608	0.537	0.552	0.465	0.540	0.101	0.525
iC18:0	0.074	0.058	0.065	0.069	0.066	0.015	0.880
C17:1 c-9	0.328	0.332	0.344	0.329	0.333	0.060	0.990
C18:0	10.584	9.585	9.524	9.014	9.677	0.733	0.722
C18:1t	1.135	1.151	1.099	3.514	1.725	0.460	0.389
C18:1 c-9	33.874	32.668	32.490	32.374	32.852	2.474	0.987
C18:1 c-11	0.404	0.306	0.397	0.644	0.438	0.056	0.282
C18:2 n-6	0.970	0.936	0.891	0.939	0.934	0.076	0.979
C20:0	0.062	0.055	0.056	0.052	0.056	0.004	0.569
C20:1 c-11	0.071	0.064	0.064	0.074	0.068	0.007	0.871
C18:3 n-3	0.130	0.140	0.134	0.139	0.136	0.017	0.981
CLA, c-9, t-11	0.329	0.263	0.274	0.263	0.282	0.027	0.620

Table 5. Cont.

Fatty Acid (mg/g Tissue)	Treatment				Mean	SEM	p-Value
	AN	BN	TriBAN	TriJAN			
C20:3 n-6	0.035	0.044	0.056	0.044	0.045	0.014	0.310
C20:4 n-6	0.042 a	0.049 a	0.094 a	0.042 a	0.057	0.008	<0.05
Total	83.186	73.203	71.376	75.759	75.881	4.941	0.710
sum:SFA	37.613	34.120	35.896	33.915	35.386	2.172	0.856
sum:MUFA	39.397	37.650	36.237	45.068	39.588	2.785	0.586
sum:PUFA	1.267	1.433	1.449	1.427	1.394	0.127	0.760
sum:UFA	40.664	39.083	37.686	46.495	40.982	2.806	0.764
UFA:SFA	1.081	1.145	1.050	1.371	1.162	0.067	0.225
MUFA:SFA	0.974	1.114	1.068	1.171	1.082	0.065	0.233
PUFA:SFA	0.034	0.042	0.040	0.045	0.040	0.003	0.091
n-6:n-3	9.127	7.933	8.180	9.195	8.609	1.182	0.827
AI	0.826	0.769	0.749	0.825	0.792	0.041	0.443
TI	1.748	1.648	1.722	1.661	1.695	0.059	0.990

Σ SFA = Σ MUFA + Σ PUFA; PUFA/SFA = (C18:2 n-6 + C18:3 n-3)/(C14:0 + C16:0 + C18:0). n-6/n-3 = Σ omega-6 fatty acids/ Σ omega-3 fatty acids. SFA: saturated fatty acids. MUFA: monounsaturated fatty acids. PUFA: polyunsaturated fatty acids. AI: atherogenicity index. TI: thrombogenicity index. Means followed by the same letter in the row do not differ according to Tukey's test at 5% significance. SEM: Standard error of the mean.

Among MUFA, oleic acid (C18:1 cis-9) was the most abundant in all groups. A significant difference was observed for arachidonic acid (C20:4 n-6) ($p < 0.05$), with the TriBAN group showing the highest concentration (0.094 mg/g tissue) compared to the other genetic groups.

Branched-chain fatty acids (BCFAs), particularly iso-C14:0, iso-C16:0, and iso-C17:0, showed notable intra-group variability, especially in the BN group, although mean values did not differ statistically ($p > 0.05$). No significant differences were observed for total PUFA, the n-6/n-3 ratio (mean = 8.609; $p = 0.827$), or the AI ($p = 0.443$) and TI ($p = 0.990$) across the genetic groups.

4. Discussion

4.1. Productive Performance

The superior final body weight and ADG observed in the AN group were consistent with previous findings [14], which reported that Angus cattle surpass Wagyu animals in weight gain when selected for marbling. This difference may be attributed to the higher energy cost associated with fat deposition in breeds more prone to intramuscular fat accumulation, as fat synthesis and storage are metabolically more expensive than muscle deposition [28]. The longer confinement period of the TriJAN group (an additional 87 days) did not compensate for its lower growth rate, reinforcing that the extended feeding period is not sufficient to overcome inherent genetic differences in growth potential.

The requirement for a minimum of 350 days on feed for Wagyu cattle to express their characteristic marbling [29] was met only by the TriJAN group (360 days), while the other groups were confined for 273 days. Despite this, the TriJAN group did not achieve superior final weight or ADG, suggesting that the extended finishing period primarily influences fat deposition rather than overall growth performance.

4.2. Meat Quality Attributes

The pH values (5.3–5.7) are within the ideal range for beef quality [30], ensuring favorable physicochemical characteristics. The lack of differences in cooking loss and water holding capacity across groups indicates that all genetic groups produce meat with similar processing traits, which supports industry standardization [31,32].

The stability of WHC metrics, as expected, is consistent with the normal pH range (5.5–5.8), where the myofibrillar matrix remains stable [33,34]. The mean WBSF value of 41.11 N classifies the meat from all groups as tender (<57.14 N) according to Shackelford et al. [35], and this level of tenderness would satisfy most consumers [36]. The seven-day aging period was effective in optimizing tenderness through proteolysis, as reported by Gagaoua et al. [37], demonstrating that this aging duration is suitable for the LT muscle across all genotypes. Although beef from heifers has been reported to exhibit higher WBSF than beef from steers, this sex-related effect is unlikely to have confounded the present results because all animals belonged to the same sex. Thus, any baseline increase in the SF was equally distributed across treatments, preserving the comparison among genetic groups. Despite all samples being classified as tender, the numerical difference of approximately 10 N observed among some treatment groups may indicate biologically relevant variation in tenderness, even within the range considered acceptable for consumer perception [36]. The absence of statistical significance is likely associated with the high residual variability, which increased the standard errors and reduced the statistical power to detect differences among genetic groups. One possible factor contributing to this variability is the physiological status of the heifers, as hormonal fluctuations associated with the estrous cycle may influence postmortem proteolysis through changes in calpastatin activity [38]. Likewise, Choat et al. [39] reported that physiological differences among heifers may affect meat tenderness. Although these factors were not directly evaluated in the present study, they may have contributed to the residual variability observed in WBSF. Therefore, the observed numerical difference suggests a potentially relevant biological effect that warrants further investigation in studies with larger sample sizes and improved control of physiological variation.

Although no significant differences were found for marbling scores, the numerical tendency toward higher marbling in the TriJAN group (75% of animals with abundant marbling) is noteworthy. The high intra-group variability in marbling, even within homogeneous groups, has been previously reported [40,41] and may have masked statistical significance. Nevertheless, 40.6% of all samples could be classified as prime-grade meat [42], indicating that all genetic groups have the potential to produce high-quality beef under the studied conditions. The mean marbling score obtained using the Müller scale (14.84; “moderately marbled”) was consistent with the mean intramuscular fat content (13.15 g 100 g⁻¹). Although no direct conversion exists between the Müller scale and international grading systems, previous studies have demonstrated strong correlations between subjective marbling scores and chemically determined intramuscular fat content [43–45]. Based on these relationships, the intramuscular fat content observed in the present study is broadly consistent with premium beef categories, corresponding approximately to USDA Choice–Prime and Japanese BMS 4–5 [43–45]. These findings reinforce the commercial potential of all evaluated genetic groups for premium beef production under the finishing conditions adopted. The AN group, despite showing superior growth performance, produced meat with marbling comparable to the Wagyu-influenced groups, reinforcing the hypothesis that prolonged feedlot finishing and high-energy diets are major determinants of intramuscular fat deposition suggesting that prolonged feedlot finishing and high-energy diets may reduce the phenotypic expression of genetic differences in intramuscular fat deposition differences [10]. Furthermore, the fact that 40.6% of samples achieved scores consistent with USDA Prime-grade quality demonstrates the potential of these genetic crosses to supply the high-end beef market, even under commercial production conditions.

The absence of differences in colour parameters is consistent with the lack of variation in pH, WHC, and marbling, which are known to influence meat colour [46]. The L* and a* values were similar to those reported for Wagyu × Angus heifers [47] and F1 Angus-Nellore

animals [47]. The higher b^* value observed in this study (12.38) compared to the average of 8.5 reported by Carvalho et al. [47] may be attributed to greater carotenoid deposition in groups with a higher proportion of Japanese Brown genetics [48].

4.3. Chemical Composition

The similarity in moisture, ash, protein, and ether extract contents across groups is consistent with previous studies evaluating the chemical composition of beef from crossbred cattle finished in feedlot systems [9,10]. The ether extract value for the TriJAN group (13.96%) was slightly above the upper limit of the range (7.58–13.13%) reported for crossbred Wagyu cattle [49], but remained close to previously observed values. The lack of difference in ether extract suggests that the prolonged confinement period and the high-energy diet were key factors in promoting intramuscular fat deposition, overriding genetic differences. Smith et al. [10], who demonstrated that extended grain feeding inherently elevates marbling regardless of genetic background, support this. Interestingly, the additional 87 days of confinement for the TriJAN group did not result in higher ether extract compared to the other groups. This aligns with Pavan et al. [50], who found that longer finishing times increase slaughter weight and subcutaneous fat thickness but do not necessarily enhance marbling, thereby increasing costs without improving intramuscular fat quality.

4.4. Fatty Acid Profile

The predominance of myristic (C14:0), palmitic (C16:0), and stearic (C18:0) acids in the lipid profile is in agreement with the literature for bovine meat [51–53]. The lack of significant differences in total SFA between groups corroborates the findings of Krusinski et al. [54], who observed similar total SFA levels in Red Angus and Akaushi crosses.

Although not statistically significant, the numerically higher MUFA concentration in the TriJAN group (45.068 mg/g) may reflect a trend toward the characteristic FA profile of Japanese Black cattle, which is known for its high oleic acid content [11,54,55]. Oleic acid (C18:1 *cis*-9) is associated with health benefits, including reduced inflammation and improved insulin sensitivity [52], and has been linked to increased fat tenderness and improved sensory quality [56,57].

The significant difference in arachidonic acid (C20:4 n-6) concentration between groups, with the highest level in the TriBAN group, may be related to genetic differences in the expression of elongase and desaturase enzymes (FADS1 and FADS2) [58]. Although arachidonic acid is a precursor of pro-inflammatory eicosanoids [59], the levels observed in this study are within the range reported for feedlot beef [53] and did not compromise the atherogenicity or thrombogenicity indices, which remained similar across groups.

The high intra-group variability in BCFAs, particularly in the BN group, reflects differences in rumen microbiota composition, as BCFAs are primarily synthesized by rumen bacteria from branched-chain amino acids [60,61]. This biological heterogeneity has implications for product consistency, as BCFAs are associated with health benefits in humans, including anticancer and anti-inflammatory properties [53]. The variability suggests that, without greater control over rumen ecology, the predictability of the BCFA profile may be limited, even in specialized genotypes.

The overall homogeneity of SFA, MUFA, and PUFA concentrations across genetic groups can be attributed to the extended confinement period and the standardized high-energy-density diet, which are major determinants of lipogenesis and rumen biohydrogenation [10,62]. Intensive finishing systems tend to homogenize the lipid profile, as both diet and feeding time override genetic differences [50,51].

The mean n-6/n-3 ratio of 8.609 exceeds the recommended upper limit of 4:1 for a balanced diet [63], indicating a nutritional limitation common to grain-finished beef. Elevated n-6/n-3 ratios have been linked to pro-inflammatory conditions and increased risk of chronic diseases [64]. The absence of differences in atherogenicity and thrombogenicity indices across groups suggests that all meats have a similar potential to influence cardiovascular disease risk, reflecting the similarities in fatty acid profiles [64].

5. Conclusions

In the present study, all genetic groups exhibited similar physicochemical characteristics of the longissimus thoracis muscle, indicating that, under the experimental conditions evaluated, the treatments resulted in meat with consistent quality attributes, including marbling and tenderness. However, although the Japanese breeds under test are recognized for their ability to produce meat with fatty acid profiles that are more beneficial to human health, in the present study there was no difference in the fatty acid concentrations of the meat from the Angus $\times$ Nellore cross, a group that also showed superior weight gain performance. The uniformity of the lipid profile under prolonged feedlot conditions and a balanced diet suggests a strong environmental influence on meat composition, contributing to consistent quality-related traits across genetic groups. These characteristics are commonly associated with consumer-valued attributes; however, no sensory evaluation was performed to directly assess consumer perception. Nevertheless, the elevated n-6/n-3 ratio observed across all groups indicates a nutritional limitation, highlighting the need for future genetic and nutritional strategies aimed at improving the lipid profile of beef. Future studies should evaluate the sensory perception of consumers to confirm whether the marbling levels observed translate into superior eating quality attributes such as flavor, juiciness, and overall palatability.

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Informed Consent Statement: Not applicable.

Data Availability Statement: The data presented in this study are available on request from the corresponding author.

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