

Article

Meat Quality of Two ECC-Approved Chicken Genotypes with Different Growth Rates Subjected to Moderate Kinetic Activity and Compared with a Fast-Growing Genotype

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Abstract

Over the years, poultry supply chains have prioritized highly productive genetic lines to meet consumer demand, often at the expense of meat quality, animal welfare, and animal health. Recently, however, industry trends have shifted toward a greater awareness of welfare, reduced farming intensity, and improved product quality. In response, the European Chicken Commitment (ECC) has advocated for the use of slower-growing genotypes, even within conventional production systems. This study aimed to evaluate the meat quality of two ECC-approved chicken genotypes with differing growth rates—slow-growing (SG: 30–40 g/day, Kabir) and medium-growing (MG: 40–50 g/day, Ranger Gold) in comparison with a fast-growing strain (FG: >65 g/day, Ross 308). A total of 300 chickens were assigned to two experimental conditions: a control group (C), with spontaneous activity, and a treatment group (M), subjected to induced moderate kinetic activity. The results demonstrated that genotype influenced the meat quality of chickens raised indoors more significantly than kinetic activity. Comparisons revealed that SG and MG chickens exhibited superior meat quality, particularly regarding protein content, oxidative status, and a more suitable fatty acid profile. Overall, our findings support the adoption of ECC-approved genotypes in indoor systems to simultaneously improve animal welfare and enhance the nutritional and technological quality of poultry meat.

Keywords: European Chicken Commitment (ECC); poultry; slow-growing genotypes; meat quality



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1. Introduction

In recent decades, the poultry industry has gained significant attention due to several factors. Poultry meat is considered more affordable and healthier than other animal protein sources, and poultry farming is recognized for its high production efficiency, contributing substantially to the global meat supply. In Italy, per capita consumption increased from 14.5 kg in 2011 to an estimated 21.4 kg in 2025 [1]. Globally, poultry production has also risen significantly, reaching approximately 137.8 million tons in 2021; according to UNAITALIA [2], production is projected to reach approximately 406 million tons by 2034.

As one of the leading sources of meat production worldwide, poultry has attracted considerable interest from consumers and the public. Recently, various organizations have

developed a heightened awareness of both animal and human welfare, prompting interest in rearing systems, the quality of animal-derived products, and environmental impact. Consequently, alternative rearing systems are being explored to replace conventional methods, offering substantial management and genetic changes that enhance animal welfare and, subsequently, result in higher-quality products.

To address these concerns, the European Chicken Commitment (ECC) and the Better Chicken Commitment (BCC)—scientific policies endorsed by animal protection organizations—have introduced new guidelines for broiler production. These represent a set of scientifically grounded criteria aimed at improving chicken welfare. Key recommendations include: the use of slower-growing (SG) genotypes suited to less-intensive systems; reduced stocking density (from 42 to 33 kg/m²); environmental enrichment (e.g., straw bales, perches, and branches); and a regulated circadian rhythm (at least 6 h of darkness). To date, 380 European food companies have committed to the ECC, with the goal of transforming global conventional poultry production by 2026.

These ECC guidelines not only significantly affect living conditions but also influence the quality of the final product. It is well established that different rearing systems impact meat characteristics. Slower-growing chickens require a longer rearing period to reach standard live weight compared to fast-growing (FG) ones. However, they often yield superior meat quality, characterized by higher protein content, lower fat levels [3], and a more suitable fatty acid profile (higher polyunsaturated fatty acids, PUFA; lower saturated fatty acids, SFA; and an n-6/n-3 ratio close to 4) [4]. These differences are often attributable to intrinsic factors, such as metabolic variations [5], which can be further enhanced through optimized management practices and feeding plans. Beyond rearing systems, environmental and management factors—such as temperature, light intensity, photoperiod, and sex—have also been shown to affect meat quality. Moreover, numerous studies [6] have demonstrated that growth rate plays a crucial role in determining carcass and meat quality traits.

While most ECC-approved genotypes are already utilized in outdoor rearing systems [7], it is well documented that combining SG strains with organic or free-range systems positively influences meat quality by reducing fat content and increasing vitamin and mineral levels compared to conventional systems. These improvements are attributed to increased kinetic activity, grazing behavior, and a higher intake of bioactive compounds. However, limited knowledge exists regarding the performance of ECC genotypes reared indoors. Accordingly, this study aimed to evaluate the meat quality (breast and drumstick) of two ECC-approved broiler strains characterized by intermediate and slow growth rates, with and without the induction of kinetic activity; results were compared to a fast-growing genotype under the same conditions.

2. Materials and Methods

2.1. The Ethics

All methods are reported following ARRIVE guidelines for the reporting of animal experiments. This study was carried out in accordance with the Guiding Principles in the Use of Animals for Scientific Purposes. It was approved by the Animal Bioethics Monitoring Committee of the University of Perugia (authorisation n° 79751 of 22 February 2024, protocol n. 10/2024).

2.2. Animals and Diets

Two ECC-approved genotypes were evaluated: a slow-growing strain (SG: 30–40 g/d; Kabir) and a medium-growing strain (MG: 40–50 g/d; Ranger Gold). These were compared to a fast-growing genotype (FG: >65 g/d; Ross 308) for meat quality assessment.

A total of 300 one-day-old chicks from the three aforementioned genotypes (Figure 1) were housed at the experimental farm of the University of Perugia. The birds were distributed into 12 pens (25 animals per pen), each measuring 3 m × 3 m, maintaining a maximum stocking density of 30 kg live weight/m² in accordance with ECC guidelines. The animals were sourced from an Italian hatchery (AVIZOO, Italy). The farmhouse environment was maintained under controlled conditions following standard poultry management guidelines.

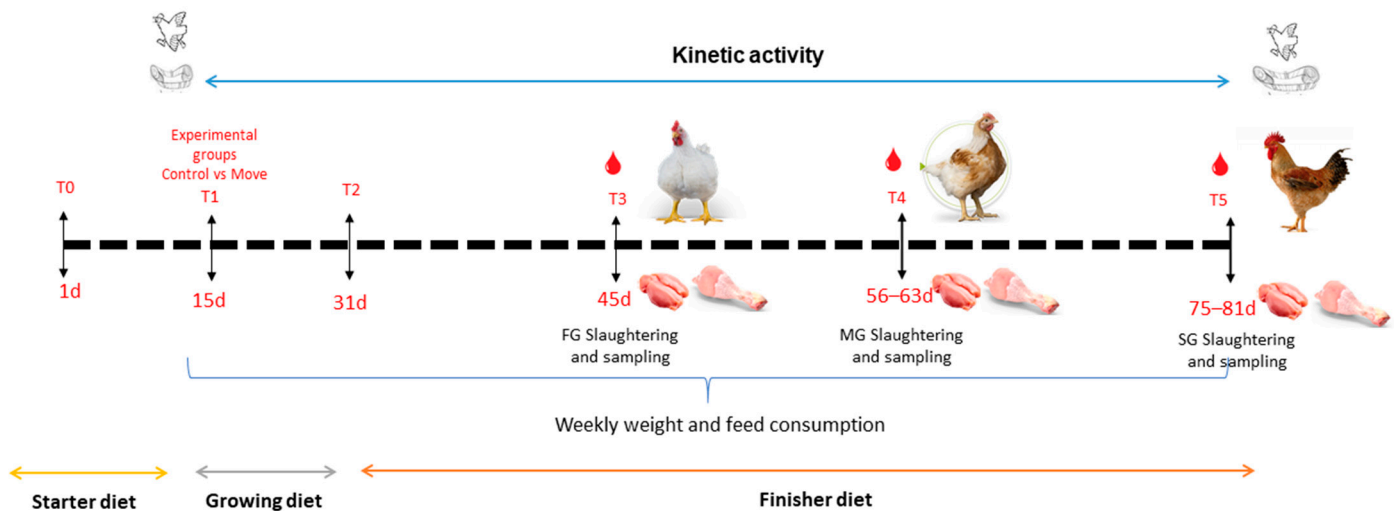


Figure 1. Experimental protocol. A total of 300 birds—comprising 100 slow-growing (SG), 100 medium-growing (MG), and 100 fast-growing (FG) chickens—were housed from one day of age. The animals were divided into two experimental groups: a control group (C), which received no stimulated exercise, and a treatment group (M), in which kinetic activity was induced daily (1 h at 4 km/h) by operators, starting from day 15. All animals were fed according to a commercial dietary plan consisting of a starter diet (days 1–15), a grower diet (days 16–31), and a finisher diet (from day 32 until slaughter). Each genotype was slaughtered upon reaching commercial target weight: 45 days for FG, 56–63 days for MG, and 75–81 days for SG.

The animals were divided into two experimental groups (25 birds per group, with 4 replicates per genotype): a control group (C), which received no stimulated exercise, and a treatment group (M). In the M group, daily locomotory activity (1 h at 4 km/h) was induced starting from 15 days of age. Following the methodology of Mattioli et al. [8], operators walked behind the animals within the pens to promote exercise. All animals were fed a commercial dietary plan (Table 1):

- Starter diet from 1 to 15 days.
- Grower diet from 16 to 31 days.
- Finisher diet from day 32 until slaughter.

Different genotypes were slaughtered upon reaching the commercial weight (~2800 g; estimated as 70% of adult body weight), particularly, at 45 days for FG, 56–63 days for MG, and 75–81 days for SG.

2.3. Slaughtering and Sampling

At slaughter, six animals per replicate, genotype, and treatment were randomly selected and slaughtered. The birds were electrically stunned (110 V; 350 Hz) and then slaughtered. After bleeding, the carcasses were scalded in hot water (56.5 °C for 1 min) and plucked. The non-edible viscera (proventriculus, intestines, gallbladder, spleen, esophagus, and full crop) were removed, and the carcasses were stored for 24 h at 4 °C to obtain the cold carcass weight. Breast and drumstick muscles were immediately collected for physi-

cal evaluation. Furthermore, a 30 g aliquot of the main cuts (breast and drumstick) was sampled and stored at -20°C for chemical analysis, which was performed two weeks later.

Table 1. Ingredients (%) and chemical composition (%) of experimental diets.

	Starter	Grower	Finisher
Ingredients (%)			
Corn	25.05	43.89	53.25
Soybean meal	22.90	21.80	19.00
Wheat	7.02	12.50	3.90
Maize meal	24.00	3.00	4.00
Gluten feed	15.00	15.50	15.70
Soybean oil	1.32	0.62	0.62
Vitamin-mineral premix ^a	0.68	0.42	0.72
Dicalcium phosphate	0.73	-	0.84
Calcium carbonate	2.70	2.00	1.50
NaCl	0.21	0.15	0.24
Sodium bicarbonate	0.10	0.12	0.10
Lys + Met	0.27	-	0.13
Chemical composition (%)			
Moisture	11.60 $\pm$ 0.12	12.00 $\pm$ 0.20	12.00 $\pm$ 0.21
Crude protein	24.77 $\pm$ 1.07	21.87 $\pm$ 1.03	20.51 $\pm$ 1.02
Ether extract	4.52 $\pm$ 1.04	3.73 $\pm$ 0.98	3.84 $\pm$ 0.96
Ash	8.04 $\pm$ 0.25	6.75 $\pm$ 0.36	6.99 $\pm$ 0.41
NDF	15.22 $\pm$ 2.12	18.33 $\pm$ 1.97	17.44 $\pm$ 1.96
ADF	7.26 $\pm$ 1.25	7.49 $\pm$ 2.36	7.57 $\pm$ 1.41
ADL	1.32 $\pm$ 0.25	1.17 $\pm$ 0.32	1.17 $\pm$ 0.74
Cellulose	5.94 $\pm$ 1.04	6.32 $\pm$ 1.17	6.40 $\pm$ 0.98
Hemicellulose	7.96 $\pm$ 0.78	10.84 $\pm$ 0.14	9.87 $\pm$ 0.86
Vitamins (mg/kg D.M.)			
Vitamin A	21.06 $\pm$ 3.25	21.66 $\pm$ 2.14	22.37 $\pm$ 2.10
Vitamin E	47.55 $\pm$ 3.47	63.56 $\pm$ 5.41	64.78 $\pm$ 4.89
Carotenes	41.16 $\pm$ 4.22	40.57 $\pm$ 3.86	40.46 $\pm$ 4.32
Fatty acid profile (g/kg D.M.)			
C14:0	0.21 $\pm$ 0.04	0.07 $\pm$ 0.01	0.07 $\pm$ 0.01
C16:0	8.89 $\pm$ 1.04	9.47 $\pm$ 0.32	9.65 $\pm$ 0.14
C16:1	0.15 $\pm$ 0.01	0.10 $\pm$ 0.01	0.10 $\pm$ 0.01
C17:0	0.09 $\pm$ 0.01	0.07 $\pm$ 0.01	0.06 $\pm$ 0.02
C18:0	0.09 $\pm$ 0.02	0.07 $\pm$ 0.01	0.06 $\pm$ 0.01
C18:1	16.51 $\pm$ 1.14	17.94 $\pm$ 1.20	18.24 $\pm$ 1.41
C18:2	33.37 $\pm$ 2.47	37.94 $\pm$ 1.33	37.71 $\pm$ 1.47
C18:3	2.10 $\pm$ 0.98	2.98 $\pm$ 0.74	2.56 $\pm$ 0.76
SFA	9.20 $\pm$ 1.04	9.62 $\pm$ 0.98	9.79 $\pm$ 0.97
MUFA	16.67 $\pm$ 1.54	18.04 $\pm$ 1.80	18.35 $\pm$ 1.70
PUFA	35.47 $\pm$ 3.45	40.93 $\pm$ 3.24	40.28 $\pm$ 4.01
n-6	33.37 $\pm$ 2.87	37.94 $\pm$ 2.47	37.71 $\pm$ 1.87
n-3	2.10 $\pm$ 0.98	2.98 $\pm$ 0.74	2.56 $\pm$ 0.47
n-6/n-3	15.90 $\pm$ 1.13	12.73 $\pm$ 1.41	14.73 $\pm$ 1.74
Metabolizable energy (Kcal/Kg)	3245 $\pm$ 268	3195 $\pm$ 346	1976 $\pm$ 141

^a Amount per kg; vitamins, pro-vitamins: retinyl acetate: 4800 IU; vitamin D3—cholecalciferol 1800 IU; iron sulfate monohydrate—Fe: 37.5 mg, manganese sulfate, monohydrate—Mn: 54 mg, copper sulfate pentahydrate—Cu: 6.0 mg, zinc oxide—Zn 36 mg, potassium iodide 66 mg, and sodium selenite—Se 0.12 mg; butylated hydroxytoluene: 43.5 mg, butylated hydroxyanisole: 30 mg, sepiolite: 600 mg, lutein: 18.0 mg, and zeaxanthin: 4.5 mg.

2.4. Physico-Chemical Determination of Feed and Meat

The pH after 24 h was measured with a Knick digital pH meter (Broadly Corp., Santa Ana, CA, USA) after homogenization of 1 g of meat for 30 s in 10 mL of 5 M iodoacetate [9].

The water-holding capacity (WHC) of breast and drumstick was estimated according to Nakamura [10] by centrifuging $1 \times g$ of the samples placed on tissue paper inside a tube for 4 min at $1500 \times g$. The remaining water after centrifugation was quantified by drying the samples at 70°C overnight. The WHC was calculated as follows: (weight after centrifugation – weight after drying)/initial weight $\times 100$.

For cooking loss (CL), whole samples of both muscles (about 20 g) were placed in open aluminum pans and roasted in an electric oven (pre-heated to 200°C) for 15 min to an internal temperature of 80°C [11]. Cooking loss was estimated as the percentage of the weight of the roasted samples (cooled for 30 min to about 15°C and dried on the surface with a paper towel) with respect to the raw ones.

The color, L^* (lightness), a^* (redness), and b^* values (yellowness) were measured (after 24 h) on the cut surface of each filet using a tristimulus analyzer (Minolta Chroma meter CR-200, Osaka, Japan), following the CIELab color system [12].

Estimation of myoglobin (Mb) was done following the method reported by Krzywicki [13] after the absorbance spectra recording (from 500 to 550 nm (Equations (1)–(3))) using the CIELab color system previously reported.

In particular:

$$\text{meta-Mb: } -0.1 \times (550 \text{ nm}) - 0.57 \times (540 \text{ nm}) + 0.15 \times (500 \text{ nm}) \quad (1)$$

$$\text{oxy-Mb: } -0.116 \times (550 \text{ nm}) + 0.165 \times (540 \text{ nm}) - 0.052 \times (500 \text{ nm}) \quad (2)$$

$$\text{Total Mb: (meta-Mb) + (oxy-Mb)} \quad (3)$$

The moisture, ash, and total nitrogen of feed and meat were evaluated using AOAC methods (AOAC 1995 No. 950.46B, 920.153, and 928.08, respectively [14]). Total proteins were calculated with Kjeldahl using a conversion factor of 6.25. Lipids were extracted in duplicate from 5 g of each homogenized sample and calculated gravimetrically [15].

2.5. Fatty Acid Profile of Meat and Diets and Meat Estimated Indices

Total lipids were extracted from 10 g of each homogenized meat sample and 6 g of grounded feed, according to Folch [15] and esterified according to Christie [16]. One ml of each solution containing fatty acid esters was transferred to vials for gas chromatography analysis. Fatty acid ester separation (FAME) was performed using a Varian gas chromatograph (CP-3800; Milan, Italy) equipped with a flame ionization detector (FID) and an Agilent capillary column ($100 \text{ m} \times 0.25 \text{ mm}$, CPS Analytica, Milan, Italy) coated with a DB-Wax stationary phase (film thickness of $0.25 \mu\text{m}$). The injector and detector temperatures were set at 270°C and 300°C , respectively. The carrier gas was helium at a flow rate of 0.6 mL/min . The oven temperature was programmed as follows: 40°C (1 min hold) to 163°C (10 min hold) with a ramp of 2°C/min , to 180°C (7 min hold) with a ramp of 1.5°C/min , at 187°C (maintenance of 2 min) with a ramp of 2°C/min and at 230°C (maintenance of 25 min) with a ramp of 3°C/min . Individual fatty acid methyl esters were identified by comparing their retention time with the retention time of a commercially available FAME standard mixture (FAME Supelco 2560 mixture, Merck, Darmstadt, Germany). C21:0 methyl ester (CAS number 2363-71-5; Merck H5149, Darmstadt, Germany), eluted under the same conditions as the samples, was used as internal standard ($1 \text{ mg}/100 \mu\text{L}$ of added solution). The area of each peak was used to calculate the proportion of fatty acids. For quantitative analysis ($\text{mg}/100 \text{ g}$ meat), the calculation method reported by [17] was applied. Total saturated fatty acids (SFA), total monounsaturated fatty acids (MUFA), total polyunsaturated fatty acids (PUFA), and total n-6 and n-3, as well as n-6/n-3 ratios, were also calculated [18].

Based on the fatty acid profile, the healthy fatty Index (HFI) (Equation (4)) was also calculated. This index evaluates dietary lipid intake not only from a nutritional perspective but also in terms of human health implications [19]:

$$\text{HFI} = ((\text{mg}/100 \text{ g MUFA} \times 2) + (\text{mg}/100 \text{ g n-6} \times 4) + (\text{mg}/100 \text{ g n-3} \times 8) + (\text{mg}/100 \text{ g n-3}/\text{mg}/100 \text{ g n-6})) / ((\text{mg}/100 \text{ g SFA}) + (\text{mg}/100 \text{ g MUFA} \times 0.5) + (\text{mg}/100 \text{ g n-6} \times 0.25) + (\text{mg}/100 \text{ g n-3} \times 0.125) + (\text{mg}/100 \text{ g n-6}/\text{mg}/100 \text{ g n-3})) \quad (4)$$

Estimated $\Delta 5$ - and $\Delta 6$ -desaturase was calculated according to [20] (Equation (5)); these calculated activities can be used as surrogates for the true measure of desaturase activity. To evaluate the activities of both $\Delta 5$ - and $\Delta 6$ -desaturase, the enzymes that catalyze the formation of long-chain n-6 and n-3 polyunsaturated fatty acids (PUFA) starting from the precursors linoleic (C18:2n-6, LA) and alpha-linolenic (C18:3n-3, ALA) acid, the following equation was used:

$$\Delta 5\text{-Desaturase} + \Delta 6\text{-Desaturase} = (\text{C20:2n-6} + \text{C20:4n-6} + \text{C20:5n-3} + \text{C22:5n-3} + \text{C22:6n-3}) / (\text{LA} + \text{ALA} + \text{C20:2n-6} + \text{C20:4n-6} + \text{C20:5n-3} + \text{C22:5n-3} + \text{C22:6n-3}) \quad (5)$$

2.6. Antioxidant Profile and Oxidative Status

Tocopherols (α - δ - γ tocopherol, α -tocotrienol) and carotenes of feed and retinol of meat were quantified by a HPLC system according to Hewavitharana [21]. In detail, 5 mL of distilled water and 4 mL of ethanol were added to 2 g of the meat/feed sample and vortexed for 10 s. After mixing, 4 mL of hexane containing BHT (200 mg/L) was added, and the mixture was shaken and centrifuged. Three milliliters of supernatant was dried under a stream of nitrogen and then redissolved in 300 μ L of acetonitrile. Fifty microlitres were injected into the HPLC system (Hitachi Primade, Milan, Italy, comprising a cooling autosampler 1210, pump 1110, fluorimetric detector-FD 1440, and diode array detector 1430, and a Synergi Hydro-RP column, Phenomenex, Bologna, Italy). Tocopherols and tocotrienols were identified using the FD, previously reported and emission wavelengths of 295 nm and 328 nm, respectively, and they were quantified using external calibration curves prepared with increasing amounts of pure standards in ethanol.

The main carotenes were determined by the same HPLC system previously described. The solvent system consisted of solution A (methanol/water/acetonitrile, 10:20:70, *v/v/v*) and solution B (methanol/ethyl acetate, 70:30, *v/v*). The volume of injection was 10 μ L, the flow rate was 1 mL min⁻¹, and the elution program was a gradient starting from 90% A in a 20 min step to 100% B and then a second isocratic step of 10 min. The detector was a diode set at a wavelength of 450 nm for lutein, zeaxanthin, astaxanthin, and apo- β -carotene. Retinol was analyzed with the same HPLC system using a diode array detector set at λ 325 nm. The different carotenoids and retinol were identified and quantified by comparing the sample with pure commercial standards (Sigma-Aldrich, Steinheim, Germany; Extrasynthese, Genay, France).

The meat lipid oxidation was evaluated according to Ke [22] by a spectrophotometer set at 532 nm (Shimadzu Corporation UV-2550, Kyoto, Japan), which measured the absorbance of TBARS. Oxidation products were quantified as μ g of malondialdehyde (MDA) per g of muscle.

Carbonyl derivatives of proteins were evaluated according to Lushchak [23] using 1 mL of 10 mM DNPH in 2 M HCl as a reagent. The carbonyl content in the supernatant was evaluated spectrophotometrically (Shimadzu Corporation UV-2550, Kyoto, Japan) at 370 nm using a molar extinction coefficient of 22,000 1/M $\times$ cm; values were expressed as nmol carbonyl/mg protein in guanidine chloride solution. Protein concentrations were evaluated according to the Bradford method with Coomassie Brilliant Blue G-250 [24] using

bovine serum albumin as a standard. The same trichloroacetic acid extract was also used to measure thiol groups based on the 5,5' dithio-bis-2-dinitrobenzoic acid assay, with an extinction coefficient of 13,600 1/M $\times$ cm and expressed as μ mol group SH/g of wet tissue.

With the aim to clarify the degree of cross-reactivity due to peroxide/aldehyde-protein interaction, which could lead to an underestimation of TBARS values, the lipid-protein cross-reactive level was reported as TBARS/Carbonyls ratio.

2.7. Statistical Evaluation

Data were analyzed using IBM SPSS v18. A two-way ANOVA was applied to assess the effects of genotype, treatment, and their interaction. The Root Mean Square Error (RMSE), which measures the average magnitude of prediction errors by taking the square root of the mean of squared differences between predicted and observed values, was reported as an indicator of model accuracy. Tukey post hoc test was used for pairwise comparisons between experimental groups (genotype, treatment, and their interaction), with significance set at $p < 0.05$.

3. Results

3.1. Physical Traits of Meat

The physical traits of the two primary meat cuts (Table 2) demonstrate that genotype significantly influences quality characteristics. As expected, notable differences were observed between breast and drumstick samples. Regarding genotype, FG birds exhibited the lowest ultimate pH values in both meat cuts. Water-holding capacity (WHC) also appeared to be genotype-dependent ($p < 0.05$); however, it was not significantly affected by treatment ($p > 0.05$), with SG chickens tending toward lower values. Interestingly, FG chickens showed lower cooking loss (CL) compared to the other two genotypes. Although FG birds had a lower ultimate pH, this result is often associated with a faster onset of *rigor mortis*, which accelerates the rate of pH decline. In terms of meat color, FG birds exhibited higher lightness (L), resulting in paler meat, which correlates with their lower myoglobin content.

Table 2. Physical characteristics (mean $\pm$ standard deviation) of breast and drumstick meat of slow-growing (SG; Kabir), medium-growing (MG; Ranger Gold), and fast-growing (FG; Ross 308) chicken genotypes subjected to induced kinetic activity (M) or not (C).

	Genotype (GEN)			Treatment (T)		p Value			RMSE
	FG	MG	SG	C	M	G	T	GxT	
breast									
ultimate pH	5.61 $\pm$ 0.03 a	5.91 $\pm$ 0.05 b	5.95 $\pm$ 0.04 b	5.87 $\pm$ 0.04 y	5.78 $\pm$ 0.05 x	0.000	0.025	0.143	0.177
WHC, %	42.49 $\pm$ 1.18 c	40.29 $\pm$ 0.85 b	37.22 $\pm$ 1.43 a	40.99 $\pm$ 0.92	39.01 $\pm$ 1.41	0.000	0.069	0.127	0.857
Cooking loss, %	35.54 $\pm$ 1.80 a	36.36 $\pm$ 0.85 a	38.23 $\pm$ 1.41 b	36.47 $\pm$ 1.69	36.94 $\pm$ 2.26	0.000	0.941	0.096	1.181
L	52.99 $\pm$ 2.38 b	48.88 $\pm$ 0.77 ab	44.83 $\pm$ 1.57 a	49.57 $\pm$ 1.58	48.22 $\pm$ 1.54	0.007	0.495	0.221	1.054
a*	3.17 $\pm$ 0.53	4.06 $\pm$ 0.59	6.37 $\pm$ 0.25	1.84 $\pm$ 0.55	2.73 $\pm$ 1.50	0.062	0.571	0.349	0.901
b*	6.36 $\pm$ 1.32 a	5.38 $\pm$ 1.07 a	9.93 $\pm$ 0.73 b	12.70 $\pm$ 1.32	11.75 $\pm$ 1.30	0.000	0.211	0.189	0.786
Total myoglobin	2.06 $\pm$ 0.21 a	2.04 $\pm$ 0.20 a	3.12 $\pm$ 0.22 b	2.39 $\pm$ 0.24	2.42 $\pm$ 0.30	0.000	0.415	0.598	0.851
drumstick									
ultimate pH	6.14 $\pm$ 0.03 a	6.35 $\pm$ 0.05 ab	6.62 $\pm$ 0.04 b	6.49 $\pm$ 0.06 y	6.25 $\pm$ 0.06 x	0.000	0.021	0.128	0.203
WHC, %	52.55 $\pm$ 1.07 b	50.98 $\pm$ 0.90 ab	49.36 $\pm$ 1.26 a	51.19 $\pm$ 1.29	50.72 $\pm$ 1.28	0.000	0.091	0.257	0.933
Cooking loss, %	31.28 $\pm$ 0.95 a	30.21 $\pm$ 1.13 a	33.02 $\pm$ 1.17 b	30.29 $\pm$ 1.70	32.08 $\pm$ 2.15	0.000	0.056	0.164	1.164
L	56.11 $\pm$ 1.07 c	45.59 $\pm$ 1.08 b	42.97 $\pm$ 1.23 a	48.64 $\pm$ 1.61	47.81 $\pm$ 1.68	0.000	0.542	0.620	1.073
a*	2.20 $\pm$ 0.53 a	6.53 $\pm$ 0.59 c	10.01 $\pm$ 0.25 b	3.17 $\pm$ 0.62	3.32 $\pm$ 0.76	0.000	0.798	0.833	0.695
b*	17.64 $\pm$ 1.30 c	13.29 $\pm$ 1.04 b	7.63 $\pm$ 0.41 a	12.65 $\pm$ 1.30	13.06 $\pm$ 1.13	0.000	0.751	0.898	0.958
Total myoglobin	1.92 $\pm$ 0.18 a	2.43 $\pm$ 0.23 b	3.15 $\pm$ 0.29 c	2.40 $\pm$ 0.20	2.60 $\pm$ 0.23	0.000	0.810	0.625	0.789

a, b, c for GEN effect ($p < 0.05$); x, y for T effect ($p < 0.05$).

3.2. Chemical Composition of Meat

The chemical composition of poultry meat is a key determinant of its nutritional value and technological quality, factors that are strongly influenced by genetics, rearing conditions, and slaughter age. As shown in Table 3, the levels of lipids, proteins, moisture, and ash were significantly affected by genotype and kinetic activity, as well as the interaction between these two factors. The chemical composition data (specifically lipid content, Table 3) confirm that SG birds had a lower polyunsaturated fatty acid (PUFA) content (mg/100 g meat) in both experimental series. Specifically, in both the breast and drumstick, lipid content was higher in FG and MG birds compared to SG birds. In contrast, SG birds exhibited higher moisture levels than FG and MG birds ($p < 0.05$) and higher protein levels than FG ones.

Table 3. Chemical composition (%; mean $\pm$ standard deviation) of breast and drumstick of slow-growing (SG; Kabir), medium-growing (MG; Ranger Gold), and fast-growing (FG; Ross 308) chicken genotypes subjected to induced kinetic activity (M) or not (C).

	Genotype (GEN)			Treatment (T)		<i>p</i> Value			RMSE
	FG	MG	SG	C	M	GEN	T	G×T	
breast									
Moisture	73.83 $\pm$ 1.71 a	73.24 $\pm$ 1.05 a	75.95 $\pm$ 1.12 b	74.1 $\pm$ 1.20	73.8 $\pm$ 1.25	0.000	0.360	0.125	0.300
Protein	21.60 $\pm$ 0.85 a	23.15 $\pm$ 1.04 b	23.33 $\pm$ 1.24 b	22.66 $\pm$ 1.10	22.73 $\pm$ 1.54	0.000	0.803	0.555	0.435
Lipids	2.12 $\pm$ 0.25 c	1.06 $\pm$ 0.09 b	0.65 $\pm$ 0.20 a	1.24 $\pm$ 0.33	1.31 $\pm$ 0.14	0.000	0.100	0.000	0.335
Ash	1.27 $\pm$ 0.25 a	1.41 $\pm$ 0.25 b	1.20 $\pm$ 0.98 a	1.28 $\pm$ 0.21	1.31 $\pm$ 0.32	0.000	0.339	0.593	0.141
drumstick									
Moisture	73.59 $\pm$ 0.41 a	74.35 $\pm$ 0.13 ab	75.41 $\pm$ 0.25	74.60 $\pm$ 0.60	74.50 $\pm$ 0.12	0.042	0.105	0.365	0.303
Protein	18.10 $\pm$ 1.25 a	20.78 $\pm$ 1.03 b	21.04 $\pm$ 0.98 b	20.18 $\pm$ 0.32 y	19.77 $\pm$ 0.14 x	0.000	0.000	0.000	0.480
Lipids	5.41 $\pm$ 0.22 b	3.44 $\pm$ 0.41 a	3.47 $\pm$ 0.14 a	4.17 $\pm$ 0.30 y	4.04 $\pm$ 0.10 x	0.000	0.000	0.000	0.397
Ash	1.11 $\pm$ 0.04 a	1.16 $\pm$ 0.13 b	1.12 $\pm$ 0.04 a	1.13 $\pm$ 0.03	1.13 $\pm$ 0.04	0.000	0.518	0.000	0.072

a, b, c for GEN effect ($p < 0.05$); x, y for T effect ($p < 0.05$).

3.3. Fatty Acid Profile of Breast and Drumstick

In our study, we evaluated the effects of genotype and treatment on the fatty acid composition of both breast and drumstick muscles (Tables 4 and 5). Genotype significantly influenced the content of fatty acid classes: monounsaturated (MUFA), polyunsaturated (PUFA), and saturated fatty acids (SFA), with the highest levels observed in FG chickens, followed by MG and SG birds.

To further explore the lipid profile from a qualitative perspective, we analyzed the n-6/n-3 ratio, a key indicator of the balance between these two PUFA classes. No significant differences were observed in the drumstick, whereas in the breast, both genotype and the $G \times T$ influenced this ratio. In this muscle, the FG chickens showed a ratio of 9.01, while MG and SG birds had values of 6.26 and 5.84, respectively. Furthermore, to assess the lipid profile from a nutritional standpoint, we also calculated the HFI, which integrates the relative proportions of SFA, MUFA, and PUFA, particularly the n-6/n-3 balance, to evaluate the health-promoting potential of meat lipids. According to our results (Table 5), MG (3.67) and SG (3.65) genotypes showed the highest HFI values in the breast, with no significant effect of treatment and not even of the interaction between factors.

In the drumstick (Table 6), only MG birds maintained a high HFI (3.70), while SG chickens did not follow the same trend observed in the breast. This difference was likely due to the higher activity levels of SG birds, which, as previously mentioned, led to greater utilization of PUFA and, consequently, affected the HFI of meat.

Table 4. Major fatty acids (mg/100 g of meat; mean $\pm$ standard deviation) and healthy fatty index (HFI) of breast of fast-growing (FG; Ross 308), medium-growing (MG; Ranger Gold), and slow-growing (SG; Kabir) broiler chicken genotypes, indoor-reared and subjected to induced (M) or not (C) kinetic activity.

Breast	Genotype (GEN)			Treatment (T)		<i>p</i> Value			RMSE
	FG	MG	SG	C	M	G	T	GxT	
C14:0	8.70 $\pm$ 1.36 b	3.72 $\pm$ 0.83 a	2.72 $\pm$ 1.55 a	4.93 $\pm$ 1.17	5.17 $\pm$ 0.98	0.000	0.369	0.000	0.702
C16:0	388.65 $\pm$ 55.61 c	192.24 $\pm$ 31.74 b	129.18 $\pm$ 48.40 a	227.20 $\pm$ 41.86 x	246.18 $\pm$ 36.04 y	0.000	0.007	0.000	4.550
C16:1	64.43 $\pm$ 9.93 c	24.21 $\pm$ 6.48 b	16.55 $\pm$ 2.05 a	34.11 $\pm$ 1.32	36.02 $\pm$ 0.85	0.000	0.490	0.000	2.016
C18:0	139.02 $\pm$ 12.3 c	94.95 $\pm$ 5.32 b	51.3 $\pm$ 4.20 a	90.39 $\pm$ 6.21	99.83 $\pm$ 4.23	0.000	0.198	0.001	2.720
C18:1	608.15 $\pm$ 26.25 c	242.77 $\pm$ 12.42 b	149.57 $\pm$ 13.45 a	326.97 $\pm$ 13.17	340.03 $\pm$ 21.47	0.000	0.415	0.000	6.052
C18:2n-6	371.52 $\pm$ 23.70 c	179.78 $\pm$ 16.25 b	108.72 $\pm$ 13.45 a	213.36 $\pm$ 3.25	226.66 $\pm$ 24.07	0.000	0.080	0.000	4.472
C18:3n-3	21.84 $\pm$ 2.14 c	6.81 $\pm$ 3.12 ab	4.17 $\pm$ 1.20 a	10.56 $\pm$ 0.45	11.31 $\pm$ 3.25	0.000	0.277	0.000	1.182
C20:3n-3	6.39 $\pm$ 0.14 b	7.70 $\pm$ 3.25 b	4.76 $\pm$ 3.36 a	5.61 $\pm$ 2.15	6.95 $\pm$ 1.96	0.111	0.236	0.000	0.839
C20:4n-6	55.74 $\pm$ 15.20 b	55.90 $\pm$ 10.25 b	35.52 $\pm$ 3.45 a	48.55 $\pm$ 10.22	49.56 $\pm$ 11.36	0.004	0.848	0.005	1.816
C20:5n-3	15.06 $\pm$ 3.24 b	15.56 $\pm$ 4.12 b	10.37 $\pm$ 4.21 a	13.38 $\pm$ 3.25	13.94 $\pm$ 3.41	0.012	0.704	0.003	0.954
C22:5n-3	3.61 $\pm$ 1.24	4.35 $\pm$ 1.36	3.16 $\pm$ 0.65	3.75 $\pm$ 0.64	3.67 $\pm$ 0.67	0.084	0.866	0.007	0.495
C22:5n-6	7.06 $\pm$ 0.36 b	7.83 $\pm$ 0.12 b	4.74 $\pm$ 0.14 a	6.40 $\pm$ 1.14	6.68 $\pm$ 1.74	0.003	0.687	0.002	0.674
C22:6n-3	3.73 $\pm$ 1.10 a	6.63 $\pm$ 0.78 b	4.92 $\pm$ 1.25 ab	5.37 $\pm$ 0.14	4.82 $\pm$ 0.41	0.009	0.450	0.015	0.659
SFA	550.30 $\pm$ 25.51 c	299.52 $\pm$ 17.84 b	187.65 $\pm$ 36.20 a	330.14 $\pm$ 34.10 x	361.50 $\pm$ 24.36 y	0.000	0.008	0.000	5.340
MUFA	681.48 $\pm$ 51.29 c	280.95 $\pm$ 27.36 b	168.60 $\pm$ 22.41 a	366.04 $\pm$ 34.25	387.98 $\pm$ 27.80	0.000	0.162	0.000	6.360
PUFA	489.76 $\pm$ 38.41 c	290.25 $\pm$ 28.41 b	180.29 $\pm$ 17.10 a	312.07 $\pm$ 22.45	328.13 $\pm$ 12.57	0.000	0.203	0.000	4.932
n-3	50.64 $\pm$ 5.10 c	41.05 $\pm$ 6.41 b	27.38 $\pm$ 2.78 a	38.68 $\pm$ 3.01	40.70 $\pm$ 4.12	0.000	0.477	0.000	1.594
n-6	439.13 $\pm$ 32.45 c	249.21 $\pm$ 34.10 b	152.91 $\pm$ 12.44 a	273.40 $\pm$ 20.74	287.43 $\pm$ 19.87	0.000	0.176	0.000	4.707
n-6/n-3	9.01 $\pm$ 0.75 c	6.26 $\pm$ 0.53 b	5.84 $\pm$ 0.42 a	7.27 $\pm$ 0.34	6.81 $\pm$ 0.87	0.000	0.186	0.033	0.546
HFI	3.46 $\pm$ 0.08 a	3.67 $\pm$ 0.25 b	3.65 $\pm$ 0.21 b	3.59 $\pm$ 0.44	3.52 $\pm$ 0.32	0.003	0.410	0.325	0.570
Δ^5/Δ^6 de-saturase index	9.81 $\pm$ 0.12 a	18.90 $\pm$ 2.36 b	19.60 $\pm$ 1.52 b	15.90 $\pm$ 4.50	16.31 $\pm$ 3.52	<0.001	0.787	0.427	1.018

a, b, c, for GEN effect ($p < 0.05$); x, y for T effect ($p < 0.05$).

Table 5. Major fatty acid profile (mg/100 g of meat; mean $\pm$ standard deviation) and healthy fatty index (HFI) of drumstick meat of slow-growing (SG; Kabir), medium-growing (MG; Ranger Gold), and fast-growing (FG; Ross 308) chicken genotypes subjected to induced kinetic activity (M) or not (C) (values below 1% have not been reported).

Drumstick	Genotype (GEN)			Treatment (T)		<i>p</i> Value			RMSE
	FG	MG	SG	C	M	G	T	GxT	
C14:0	23.74 $\pm$ 0.12 c	14.18 $\pm$ 0.14 a	20.50 $\pm$ 0.20 b	19.53 $\pm$ 0.13	19.41 $\pm$ 1.14	0.000	0.820	0.088	0.849
C16:0	1000.57 $\pm$ 65.47 b	613.73 $\pm$ 22.45 a	683.49 $\pm$ 37.80 a	779.67 $\pm$ 12.14 y	752.19 $\pm$ 13.45 x	0.000	0.019	0.005	5.404
C16:1	192.53 $\pm$ 16.35 c	118.92 $\pm$ 22.40 a	148.29 $\pm$ 13.25 b	161.32 $\pm$ 10.41	145.17 $\pm$ 17.63	0.000	0.146	0.629	2.710
C18:0	409.96 $\pm$ 12.41 b	214.19 $\pm$ 10.42 a	254.19 $\pm$ 13.35 a	294.80 $\pm$ 10.52	290.76 $\pm$ 22.47	0.001	0.918	0.077	4.930
C18:1	1501.76 $\pm$ 62.12 b	968.49 $\pm$ 32.41 a	833.93 $\pm$ 41.02 a	1141.52 $\pm$ 65.74	1061.27 $\pm$ 41.70	0.000	0.152	0.509	7.456
C18:2n-6	1009.78 $\pm$ 66.23 b	648.47 $\pm$ 33.14 a	691.32 $\pm$ 47.12 a	782.32 $\pm$ 32.41	784.06 $\pm$ 33.14	0.000	0.921	0.000	5.419
C18:3n-3	59.38 $\pm$ 13.74 b	31.87 $\pm$ 7.84 a	38.75 $\pm$ 8.99 a	43.16 $\pm$ 10.14	43.50 $\pm$ 13.25	0.000	0.874	0.038	1.501
C20:3n-3	17.62 $\pm$ 3.54 b	13.69 $\pm$ 1.85 a	12.46 $\pm$ 2.12 a	13.21 $\pm$ 3.24	15.97 $\pm$ 1.25	0.056	0.124	0.287	0.975
C20:4n-6	120.57 $\pm$ 14.87 b	105.12 $\pm$ 12.33 ab	84.21 $\pm$ 22.10 a	99.10 $\pm$ 10.47	107.49 $\pm$ 14.87	0.014	0.383	0.650	2.273
C20:5 n-3	32.99 $\pm$ 7.52	29.06 $\pm$ 3.25	28.62 $\pm$ 3.10	29.09 $\pm$ 14.20	31.36 $\pm$ 3.54	0.364	0.411	0.400	1.163
C22:5 n-3	8.47 $\pm$ 2.36	7.89 $\pm$ 1.24	7.03 $\pm$ 3.25	7.56 $\pm$ 2.41	8.03 $\pm$ 0.35	0.360	0.566	0.368	0.634
C22:5 n-6	16.25 $\pm$ 1.52 b	14.19 $\pm$ 3.25 b	10.73 $\pm$ 3.52 a	13.21 $\pm$ 6.25	14.24 $\pm$ 3.24	0.003	0.401	0.304	0.837
C22:6 n-3	8.68 $\pm$ 1.14	10.29 $\pm$ 2.65	9.03 $\pm$ 2.22	9.09 $\pm$ 1.45	9.58 $\pm$ 3.56	0.359	0.610	0.377	0.687
SFA	1465.67 $\pm$ 74.02 b	862.89 $\pm$ 65.74 a	976.97 $\pm$ 71.54 a	1118.05 $\pm$ 66.25	1085.64 $\pm$ 45.07	0.000	0.435	0.012	7.031
MUFA	1712.24 $\pm$ 64.74 b	1097.60 $\pm$ 75.32 a	995.52 $\pm$ 66.47 a	1317.30 $\pm$ 67.12	1219.61 $\pm$ 64.42	0.000	0.094	0.439	7.774
PUFA	1286.75 $\pm$ 63.25 b	872.95 $\pm$ 67.10 a	894.49 $\pm$ 42.25 a	1006.71 $\pm$ 70.14	1029.41 $\pm$ 54.85	0.000	0.392	0.010	5.929
n-3	127.14 $\pm$ 13.77 b	92.79 $\pm$ 10.41 a	95.89 $\pm$ 6.52 a	102.11 $\pm$ 10.70	108.44 $\pm$ 9.78	0.000	0.263	0.406	1.940
n-6	1152.09 $\pm$ 150.47 b	771.27 $\pm$ 24.36 a	789.60 $\pm$ 17.84 a	898.57 $\pm$ 61.10	910.08 $\pm$ 66.45	0.000	0.590	0.002	5.661
n-6/n-3	9.25 $\pm$ 2.25	8.51 $\pm$ 1.03	8.30 $\pm$ 1.24	8.94 $\pm$ 1.41	8.44 $\pm$ 3.34	0.139	0.218	0.105	0.462
HFI	3.43 $\pm$ 0.12 a	3.70 $\pm$ 0.30 b	3.49 $\pm$ 0.08 a	3.48 $\pm$ 0.07	3.57 $\pm$ 0.09	0.048	0.107	0.750	0.647
Δ^5/Δ^6 desaturase index	8.72 $\pm$ 1.12 a	11.51 $\pm$ 2.32 b	10.12 $\pm$ 1.14 b	9.58 $\pm$ 2.10	10.67 $\pm$ 1.24	0.037	0.209	0.575	0.670

a, b, c, for GEN effect ($p < 0.05$); x, y for T effect ($p < 0.05$).

Table 6. Antioxidants and main oxidative traits (mean $\pm$ standard deviation) of breast and drumstick meat of slow-growing (SG; Kabir), medium-growing (MG; Ranger Gold), and fast-growing (FG; Ross 308) chicken genotypes subjected to induced kinetic activity (M) or not (C).

		Genotype (GEN)			Treatment (T)		p Value			RMSE
		FG	MG	SG	C	M	GEN	T	GxT	
breast	Unit									
Carbonyls	nmol/mg proteins	3.59 $\pm$ 0.67	3.94 $\pm$ 1.13	4.89 $\pm$ 1.01	3.42 $\pm$ 0.51 x	4.86 $\pm$ 0.95 y	0.570	0.170	0.048	0.739
Lipid oxidation	μ g MDA/g	0.15 $\pm$ 0.01 b	0.08 $\pm$ 0.01 a	0.13 $\pm$ 0.02 b	0.13 $\pm$ 0.20	0.12 $\pm$ 0.13	0.018	0.385	0.097	0.109
Lipid–protein cross-reactive	-	0.06 $\pm$ 0.10	0.05 $\pm$ 0.15	0.04 $\pm$ 0.01	0.05 $\pm$ 0.01	0.04 $\pm$ 0.01	0.549	0.525	0.078	0.081
Thiols	μ mol SH-group/g tissue	2.21 $\pm$ 1.66	1.58 $\pm$ 0.09	2.28 $\pm$ 0.34	2.12 $\pm$ 0.24	1.93 $\pm$ 0.12	0.071	0.477	0.441	0.370
α -T3	μ g/g	1.04 $\pm$ 0.21	1.62 $\pm$ 0.84	0.77 $\pm$ 0.17	0.89 $\pm$ 0.14	1.41 $\pm$ 0.57	0.494	0.383	0.266	0.542
γ -T	μ g/g	0.62 $\pm$ 0.10 b	0.34 $\pm$ 0.09 a	0.33 $\pm$ 0.43 a	0.35 $\pm$ 0.09	0.51 $\pm$ 0.11	0.021	0.090	0.096	0.230
δ -T	μ g/g	1.15 $\pm$ 0.12 c	0.66 $\pm$ 0.05 b	0.33 $\pm$ 0.06 a	0.68 $\pm$ 0.05	0.75 $\pm$ 0.09	0.000	0.488	0.117	0.273
α -T	μ g/g	4.72 $\pm$ 0.44 c	2.88 $\pm$ 0.38 b	1.35 $\pm$ 0.17 a	2.99 $\pm$ 0.47	2.98 $\pm$ 0.40	0.000	0.989	0.122	0.553
Σ Antioxidants	μ g/g	7.53 $\pm$ 0.69 c	5.49 $\pm$ 0.91 b	2.78 $\pm$ 0.32 a	4.90 $\pm$ 0.58	5.64 $\pm$ 0.84	0.000	0.372	0.933	0.712
drumstick	Unit									
Carbonyls	nmol/mg proteins	3.94 $\pm$ 0.47	6.76 $\pm$ 1.33	4.57 $\pm$ 0.65	6.44 $\pm$ 0.76 y	3.74 $\pm$ 0.65 x	0.060	0.009	0.877	0.739
Lipid oxidation	μ g MDA/g	0.18 $\pm$ 0.01 b	0.12 $\pm$ 0.01 a	0.11 $\pm$ 0.01 a	0.10 $\pm$ 0.01 x	0.16 $\pm$ 0.01 y	0.030	0.045	0.014	0.083
Lipid–protein cross-reactive	-	0.04 $\pm$ 0.01	0.03 $\pm$ 0.01	0.03 $\pm$ 0.01	0.02 $\pm$ 0.01 x	0.04 $\pm$ 0.01 y	0.871	0.025	0.600	0.064
Thiols	μ mol SH-group/g tissue	2.28 $\pm$ 0.14 b	1.90 $\pm$ 0.11 ab	1.43 $\pm$ 0.16 a	1.95 $\pm$ 0.17	1.80 $\pm$ 0.09	0.000	0.321	0.018	0.314
α -T3	μ g/g	0.930.26	1.38 $\pm$ 0.31	0.68 $\pm$ 0.24	1.21 $\pm$ 0.30	0.77 $\pm$ 0.10	0.211	0.181	0.776	0.403
γ -T	μ g/g	0.51 $\pm$ 0.15	0.60 $\pm$ 0.40	0.41 $\pm$ 0.12	0.60 $\pm$ 0.26	0.41 $\pm$ 0.12	0.523	0.151	0.458	0.256
δ -T	μ g/g	1.29 $\pm$ 0.12	1.17 $\pm$ 0.13	1.11 $\pm$ 0.07	1.33 $\pm$ 0.12	1.05 $\pm$ 0.04	0.878	0.344	0.171	0.381
α -T	μ g/g	5.19 $\pm$ 0.49	3.85 $\pm$ 0.46	4.38 $\pm$ 0.43	4.56 $\pm$ 0.36	4.38 $\pm$ 0.42	0.094	0.716	0.016	0.526
Σ Antioxidants	μ g/g	7.92 $\pm$ 0.75	6.99 $\pm$ 1.22	6.57 $\pm$ 0.66	7.71 $\pm$ 0.76	6.61 $\pm$ 0.57	0.543	0.286	0.098	0.721

a, b, c, for GEN effect ($p < 0.05$); x, y for T effect ($p < 0.05$).

Overall, our findings underscore the important role of genotype in shaping the qualitative fatty acid profile of chicken meat, with significant implications for human health. The MG chickens, due to their physiological and metabolic traits, offer a more favorable lipid profile, contributing to enhanced nutritional value.

The analysis of desaturase activity in breast and drumstick muscles revealed that genotype significantly influenced enzymatic activity [20], whereas kinetic activity had no notable effect. Notably, MG and SG chickens tend to have a higher proportion of membrane lipids, which are naturally rich in PUFA. Consequently, in the breast muscle (Table 5), these genotypes exhibited higher $\Delta 5$ and $\Delta 6$ -desaturase activities—the enzymes responsible for converting precursors such as linoleic acid and alpha-linolenic acid into long-chain PUFA (LC-PUFA). This enzymatic pattern is also reflected in the lipid health indices (HFI), where MG and SG birds displayed more suitable values than FG birds, characterized by a higher concentration of beneficial fatty acids. A similar trend was observed in the drumstick, although only the $\Delta 5/\Delta 6$ -desaturase index showed significant genotype-related differences. These findings support our earlier observations that slower-growing chickens possess a greater capacity for the enzymatic conversion of essential PUFA into LC-PUFA (≥ 20 C).

3.4. Oxidative Status and Vitamin Profile of Meat

The antioxidant profile of chicken meat is a critical indicator of both oxidative stability and nutritional quality. Multiple factors influence the oxidative status and vitamin composition of meat, including the rearing system, dietary characteristics, lipid profile, kinetic activity, and genotype.

In the present study (Table 6), genotype exerted a major effect on tocopherols, total antioxidant capacity, and lipid oxidation, particularly in the breast muscle. FG birds exhibited higher lipid oxidation (TBARS) despite having elevated concentrations of fat-soluble antioxidants. This apparent contradiction may be explained by the tendency of FG animals to accumulate vitamins A and E within adipose tissue; consequently, measured antioxidant levels in the muscle may not accurately reflect the antioxidants available *in situ* to inhibit lipid peroxidation. Furthermore, the higher intramuscular fat content in FG meat

likely increased its susceptibility to peroxidation, rendering the existing antioxidant pool insufficient to prevent the generation of malondialdehyde (MDA).

SG birds displayed lower antioxidant levels, which may indicate a greater consumption of these compounds to counteract oxidative stress; nonetheless, TBARS values in SG meat were comparable to those of FG meat, suggesting similar net lipid peroxidation under these experimental conditions. Conversely, MG birds displayed a good oxidative balance, characterized by relatively low lipid oxidation and an antioxidant reserve that appeared to be effectively mobilized to mitigate oxidative stress.

4. Discussion

It is widely established that chicken strain significantly affects both productive performance and welfare. The performance of the three genotypes evaluated in this study, as detailed in a companion paper [25], highlights critical genotype-specific trade-offs between growth efficiency and animal welfare.

The fast-growing strain exhibited the highest growth performance (daily weight gain—DWG: 55.33 g/day; feed-to-conversion ratio—FCR: 2.07); however, this was accompanied by an increased incidence of footpad dermatitis, sternal lesions, and myopathies, along with a reduction in comfort behaviors. Conversely, slow-growing birds expressed the highest proportion of comfort behaviors, albeit with lower productive efficiency (DWG: 34.55 g/day; FCR: 3.40). Medium-growing birds displayed intermediate performance levels [25].

Induced exercise elicited further genotype-specific responses: in FG chickens, it reduced daily weight gain and worsened the feed conversion ratio due to increased daily feed intake and eating time. In contrast, MG and SG birds maintained stable performance under the exercise protocol. These findings underscore the complexity of balancing meat quality, growth efficiency, and animal welfare within a sustainable poultry production system. Furthermore, it should be noted that the applied induced exercise may be comparable, from a human endpoint, as a trained kinetic activity (chronic input, every day for 1h/day; [26]), and thus could have given rise to phenomena of adaptability, especially in slow-growing genotypes [8].

However, while our previous study focused attention on the physiological response of chickens [8], the present study was specifically designed to evaluate meat quality endpoints. A robust trade-off analysis under commercial production conditions is necessary to quantify the practical implications for sustainable poultry systems. For these reasons, we investigated the “commercial-oriented product” and thus slaughtered the chickens at the same weight of about 2800 g.

Poultry meat quality is influenced by multiple factors, including genotype, farming system, and both pre- and post-mortem conditions, as well as the chickens' maturity. Among these, physical traits such as ultimate pH, water-holding capacity (WHC), cooking loss (CL), and color are key indicators of technological and sensory quality. As confirmed by numerous studies [27], the inherent differences among slow-, medium-, and fast-growing genotypes led to significant variations in these parameters. These differences are primarily attributable to physiological and metabolic factors, including growth rate, muscle fiber morphometry, and varying responses to transport and slaughter stress.

Regarding pH, the observed trends align with Devatkal [26], who suggested that rapid muscle development can lead to a degree of tissue hypoxia. This condition triggers anaerobic metabolism, increasing lactate production and causing a subsequent drop in pH. However, Taylor [27] proposed an alternative hypothesis: intensive genetic selection may enhance post-mortem glycolysis, accelerating the release of pyruvic acid and potentially decreasing pH values. This trait was also significantly affected by kinetic activity; the

treatment (M) group showed even lower pH levels, with the most pronounced differences observed in the drumstick, the muscle most involved in movement. Induced movement has been shown to promote mitochondrial biogenesis in alpha-white (α W) fibers, transitioning them toward alpha-red (α R) fibers. This transition is accompanied by an enhancement of the aerobic catabolism of pyruvate and a glycogen-sparing effect, as the oxidative pathway is more efficient for energy production. The potentially greater availability of glycogen resulting from this metabolic shift could explain the lower ultimate pH values observed in birds subjected to induced activity.

SG chickens tended to exhibit lower water-holding capacity (WHC), as confirmed by Fanatico [28] and Devatkal [26]. This is likely attributable to their smaller muscle fiber diameter, which may release more water compared to FG genotypes [29]. Additionally, SG birds are often more susceptible to pre-slaughter stress, further compromising WHC and resulting in firmer, drier meat than that of FG birds. Our findings confirm the correlation between WHC, pH, and water loss previously reported by Berri [30].

Regarding color, our results are supported by the literature [31] indicating that highly selected, fast-growing genotypes produce less myoglobin. In contrast, SG genotypes tend to accumulate more myoglobin as they age, resulting in darker, redder meat [32]. However, some studies [33] have suggested that the thinner muscle fibers of SG chickens may occasionally exhibit higher L (lightness) values than those of FG genotypes.

Taken together, these traits demonstrate that the physical profile of chicken meat is strongly modulated by genetic factors: FG birds showed lower pH and cooking loss (CL) along with paler meat, while SG birds exhibited higher pH, darker meat, and lower WHC. Notably, MG chickens displayed intermediate characteristics, representing a remarkable balance between growth efficiency and meat quality.

The trend in lipid content is linked to the tendency of highly selected genotypes to deposit more fat in the breast muscle, as demonstrated by several studies [33,34]. In contrast, SG birds exhibited higher moisture levels than FG and MG birds ($p < 0.05$) and higher protein levels than FG birds. This is likely due to their slower maturity rate, despite being slaughtered at a chronologically older age [34]. Indeed, in this study, FG birds reached commercial weight at 45 days, while MG and SG birds were slaughtered at 63 and 81 days, respectively. Some authors have attributed the higher protein content and lower fat percentage of MG and SG birds to outdoor rearing systems, where increased kinetic activity is expected [35].

Low stocking density and outdoor access, two factors that allow the chickens kinetic activity, are known to favor myogenesis over lipogenesis, driven partly by exercise and diversified diets (forage plus compound feed). However, in the present study, birds had no outdoor access; therefore, the observed differences are probably attributable to their specific muscle fiber structure, lower degree of physiological maturity (age), and intrinsically higher kinetic activity. Furthermore, Petracci [36] reported that FG chickens often display abnormal muscle fiber morphology (e.g., myopathies), a feature frequently associated with increased fat infiltration.

Although most available data on poultry meat quality focus primarily on the breast, the drumstick was also significantly influenced by genotype and the rearing system in a consistent manner. Accordingly, FG birds showed higher lipid content [37], while SG and, to a lesser extent, MG birds exhibited higher levels of moisture, protein, and ash. Mikulski [38] observed that SG chickens reared outdoors had higher thigh protein content than FG chickens raised in conventional systems.

This pattern was also evident in the drumstick, where a Genotype $\times$ Treatment ($G \times T$) interaction emerged: FG birds in the control group showed the greatest lipid accumulation, likely because they did not utilize these substrates for energetic purposes. In contrast,

chickens subjected to kinetic activity appeared to utilize dietary energy to sustain their metabolic demands and, when necessary, mobilized stored lipids.

The fatty acid profile of both breast and drumstick is influenced by multiple factors, including diet, pasture access [34,39], genotype [40], production system [20], sex [41,42], age [43], and stress [44]. The fatty acid composition of chicken meat is a critical determinant of its nutritional value, sensory quality, and overall implications for consumer health. In recent years, there has been growing interest in understanding how genetic selection for growth rate affects the lipid profile, particularly polyunsaturated fatty acids (PUFAs) and the n-6/n-3 ratio. These differences extend beyond basic science, influencing essential fatty acid intake in humans, the risk–benefit assessment of meat consumption, and the production strategies required to optimize both meat quality and nutritional value.

The fatty acid profile is shaped by a complex interplay of physiological, biochemical, and nutritional factors across genotypes. Specifically, this study focused on the mechanisms linking kinetic activity to lipid deposition and PUFA content, the oxidative degradation of PUFA, the antioxidant demand, and the nutritional significance of the n-6/n-3 ratio in both breast and drumstick muscles.

Our results were consistent across both muscle types and aligned with the findings of Wattanachan [44]. The observed pattern likely reflects differing dietary energy allocation among genotypes, with FG birds directing more energy toward fat accumulation, while MG and SG birds prioritize kinetic activity and metabolic functions. Mattioli [40] previously demonstrated that SG chickens possess a more favorable fatty acid profile, largely due to reduced lipid deposition compared with FG birds [45]. This reduced fat deposition in SG chickens likely reflects their greater kinetic activity, which enhances PUFA utilization in locomotor muscles such as drumsticks. However, the increased oxidative degradation of PUFA under high activity and oxidative stress [20,46] necessitates greater antioxidant consumption, thereby depleting their reserves, as observed in the more active groups.

Drumstick meat typically contains higher total fat, a higher proportion of alpha-linolenic acid and PUFA, and a slightly higher n-6/n-3 ratio compared to breast meat. These differences can be attributed to the distinct physiological roles and phospholipid content of the two muscle types; the drumstick is richer in oxidative fibers, whereas the breast is composed primarily of glycolytic ones. Furthermore, they differ in their metabolic pathways (aerobic vs. anaerobic metabolism) and primary energy substrates (lipids vs. glycogen) [47].

Regarding the n-6/n-3 ratio, a value of approximately nine indicates an imbalance favoring the storage of n-6 fatty acids, which are typically overrepresented in human diets and are therefore considered less beneficial from a nutritional standpoint. In contrast, a ratio closer to six suggests a higher content of n-3 fatty acids, which are known for their anti-inflammatory properties [48]. Similar findings were reported by Meluzzi [49], who also observed a more suitable n-6/n-3 ratio in SG compared to FG birds, indicating a healthier lipid profile in the former. In addition, the estimation of desaturase activity also suggested that FG chickens had metabolic preferences (n-6) previously demonstrated by Castellini [48] and Boschetti [50] in rabbit and poultry, respectively. SG animals exhibited higher $\Delta 6$ -desaturase enzyme activity and prioritized ALA as a substrate. In contrast, FG animals showed higher desaturase activity with a preference for LA. This suggests that genetic selection for rapid growth rate may inadvertently influence the animal's preference for desaturating either LA or ALA.

Muscle fiber composition also plays a crucial role: FG chickens generally possess a higher proportion of glycolytic fibers, which are less efficient in fatty acid oxidation. Conversely, SG birds exhibit a greater content of oxidative fibers, which are associated with a slower metabolism and reduced fat deposition. This physiological makeup allows for

a more efficient conversion of essential fatty acids into long-chain polyunsaturated fatty acids (LC-PUFA). To better understand how lipid metabolism is influenced by genotype and kinetic activity, we estimated the activity of the key enzymes ($\Delta 5/\Delta 6$ -desaturase) involved in fatty acid conversion. Several studies have highlighted the importance of these enzymes in enhancing meat nutritional quality. For instance, Tosi [51] demonstrated that $\Delta 5$ - and $\Delta 6$ -desaturases are essential for the synthesis of eicosapentaenoic (EPA, C20:5n-3) and docosahexaenoic (DHA, C22:6n-3) acids from ALA. Similarly, Tosi [51] showed that $\Delta 9$ -desaturase promotes monounsaturated fatty acid accumulation, thereby improving oxidative stability and extending the shelf-life of the meat.

In summary, these results corroborate earlier analyses: genotype is the predominant factor determining the fatty acid profile and associated enzymatic activity, which collectively define the qualitative characteristics of chicken meat.

The meat oxidative status suggested that MG was a better compromise from a technological point of view, as it showed a good conservation potential in terms of lipid–protein oxidation and antioxidant balance, which should be further explored. Lipid peroxidation generates reactive oxygen species (ROS) and secondary aldehydes capable of oxidizing amino acid side chains, leading to the formation of protein carbonyls. Conversely, protein oxidation can impair endogenous antioxidant enzymes (e.g., catalase or glutathione peroxidase), thereby compromising the system's ability to counteract subsequent lipid oxidation. Moreover, the interactions between lipid and protein oxidation are complex and bidirectional. To accurately interpret these phenomena, it is essential to evaluate the lipid–protein cross-reactions, as evaluating a single process in isolation can be misleading if the synergistic nature of oxidative stress is not considered.

In the breast muscle, oxidative indices were significantly affected by genotype, following the trend $FG > MG > SG$. Protein thiols and carbonyls serve as complementary oxidative markers: the loss of thiols reflects early, potentially reversible oxidation, whereas carbonyl formation indicates more advanced and often irreversible protein damage. In our study, the breast muscle showed genotype-driven effects on both markers, which is consistent with the lipid-driven oxidative pattern described above.

In the drumstick, only the interaction Genotype $\times$ Treatment ($G \times T$) emerged as significant, with the highest lipid oxidation values observed in FG birds subjected to exercise, whereas carbonyl value (protein oxidation) was mainly affected by kinetic activity.

This discrepancy likely reflects the drumstick's primary role in locomotion and its distinct fiber composition. Notably, protein carbonyls were higher in the control group than in the active groups, suggesting that limited physical activity may favor the accumulation of oxidative products. Thiol concentrations in the drumstick were genotype $\times$ treatment-dependent, with FG birds exhibiting higher values due to the movement.

In conclusion, birds with limited physical activity (FG) tend to accumulate more lipids and fat-soluble antioxidants; however, this accumulation provides only partial protection against oxidative damage. More active birds (MG and especially SG) appear to consume their antioxidant reserves to maintain oxidative homeostasis. Muscles with higher lipid content generate more oxidative products because free radicals preferentially target lipids; the resulting reactive compounds, such as aldehydes, subsequently bind to proteins, inducing carbonylation and other secondary modifications. The elevated carbonyl levels observed in FG animals are consistent with previous scientific reports.

5. Conclusions

This study demonstrates that genotypes, and to a lesser extent kinetic activity, are the primary factors affecting meat quality in chickens reared indoors under the European Chicken Commitment (ECC) guidelines. Compared to FG birds, SG and MG genotypes

produced meat with superior protein content, a more favorable oxidative status, and a healthier fatty acid profile. In contrast, FG birds accumulated higher levels of fat and displayed a less desirable fatty acid composition. The MG birds (Ranger Gold) showed an intermediate, well-balanced profile that offers a robust and practical compromise between growth performance and meat quality. It should be acknowledged, however, that the present study assessed genotype effects from a commercial perspective, comparing product quality at a standard market weight but at different ages. Several limitations arise from this approach. In particular, differences in physiological maturity inevitably influenced muscle development and metabolism, thereby affecting many technological and qualitative traits, as previously discussed.

Nonetheless, the use of ECC-approved slow-growing genotypes in indoor production systems does not impose a uniform slaughter age. Instead, it allows each company to adopt the most suitable standard based on animal welfare considerations, performance goals, and the desired nutritional and technological quality of meat.

Furthermore, it is important to recognize that not all ECC-approved strains perform in a comparable manner. Although grouped under the general category of “slower-growing,” strains such as Kabir and Ranger Gold exhibited marked differences in meat quality, partly because growth rate also determines different slaughter age and thus the degree of physiological maturity at processing. Indeed, differences in slaughter age influenced both quality outcomes (as extensively demonstrated) and the overall sustainability of the production system, including cycle length, feed-to-gain ratio, and manure output. Nevertheless, from a commercial perspective and under the conditions of this study, Ranger Gold (MG) delivered the most balanced performance across production efficiency, meat quality, metabolic resilience, and welfare indicators [52].

Therefore, careful genotype selection is essential to optimize results for specific rearing systems. Future production models must integrate appropriate feeding strategies and management practices to ensure the synergy between animal welfare and high-quality, sustainable food products.

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Abbreviations

The following abbreviations are used in this manuscript:

ECC	European Chicken Commitment
FG	Fast-growing genotypes
MG	Medium-growing genotypes
SG	Slow-growing genotypes
LA	Linoleic acid
ALA	Alpha-linolenic acid
NDF	Neutral detergent fiber
ADF	Acid detergent fiber
ADL	Acid detergent lignin
WHC	Water-holding capacity
DL	Drip loss
FAME	Fatty acid methylesters
PUFA	Polyunsaturated fatty acids
MUFA	Monounsaturated fatty acids
SFA	Saturated fatty acids
HFI	Healthy fatty index
α -T3	α -Tocotrienol
γ -T	γ -Tocopherol
δ -T	δ -Tocopherol
α -T	α -Tocopherol
Mb	Myoglobin
MDA	Malondialdehyde

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