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Physico-chemical composition of the *musculus longisimus dorsi* of different breeds and crossbreeds with the same nutrition and breeding

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ABSTRACT

The aim of this study was to evaluate selected physicochemical properties and nutritional quality of pork (*musculus longissimus dorsi*) from different pig genotypes reared under identical feeding and breeding conditions. A total of 30 pigs (Large White, Mangalica, and Large White × Mangalica; n = 10 per group) were used. After slaughter, muscle samples were analysed for chemical composition, fatty acid profile, amino acid composition, lipid nutritional indices, colour parameters, and oxidative stability. Mangalica pigs showed higher intramuscular fat (2.26 g/100 g) and cholesterol content (0.484 g/100 g), whereas Large White exhibited leaner meat with higher moisture content (73.69 g/100 g). The crossbred group showed the highest protein content (24.92 g/100 g). Fatty acid analysis revealed higher polyunsaturated fatty acid levels in Mangalica and crossbred pigs (up to 13.21%), while Large White had higher monounsaturated fatty acid content. Lipid nutritional indices indicated improved PUFA/SFA ratio in crossbreeds (0.366), whereas Large White showed lower thrombogenic index (1.08). Despite higher polyunsaturated fatty acid levels, oxidative stability was not reduced in Mangalica and crossbred groups. Colour parameters were moderately affected, with higher lightness observed in crossbreeds. Overall, crossbreeding between Large White and Mangalica resulted in a more balanced physicochemical and nutritional profile of pork, suggesting its potential for improving meat quality.

Keywords: breed, crossbreeding, meat quality, colour, oxidative stability

INTRODUCTION

Pork represents an important component of the human diet due to its high biological value and favourable nutritional composition, particularly as a source of essential amino acids, lipids, vitamins, and minerals. In recent years, increasing attention has been paid not only to production efficiency but also to the overall quality of meat, including its physicochemical and nutritional characteristics **[1]**, **[2]**.

Meat quality is influenced by multiple interacting factors, among which genotype plays a key role. Differences between pig breeds are reflected in growth performance, fat deposition, and muscle composition, which ultimately affect technological and sensory properties of meat. Commercial genotypes have been intensively selected for lean meat production, whereas traditional breeds are typically associated with higher fat content and distinct metabolic characteristics.

Several studies on local and traditional pig breeds have reported higher intramuscular fat content and specific quality traits than those of commercial genotypes. For example, differences in carcass composition and meat quality between genotypes have been described in Mangalica pigs and their crossbreeds, where higher fat deposition and altered physicochemical properties were observed **[3]**, **[4]**. Similar findings were reported in studies evaluating the effect of genotype on meat quality traits under controlled production conditions **[5]**, **[6]**. Fatty acid composition represents an important aspect of meat quality due to its relationship with both nutritional value and technological properties. Variations in lipid profile among pig genotypes have been widely documented,

particularly in relation to intramuscular fat content and metabolic differences **[7]**, **[8]**. At the same time, lipid composition may influence oxidative processes and shelf life of meat, especially in products with higher levels of polyunsaturated fatty acids.

In addition to lipid characteristics, protein composition and amino acid profile contribute to the nutritional value of meat, although these parameters are generally less variable compared to fat-related traits. Nevertheless, they play an important role in determining the biological value of pork and may interact with other quality attributes.

Meat colour is another key parameter affecting consumer perception and acceptance. It is influenced by muscle structure, myoglobin content, and *post-mortem* biochemical processes, which may vary among genotypes. Differences in colour and other technological traits have been reported in studies comparing traditional and commercial pig breeds as well as their crossbreeds **[9]**, **[10]**.

Crossbreeding between local and commercial pig breeds has been proposed as a potential strategy to combine favourable production traits with improved meat quality. Previous studies have demonstrated that crossbred animals may exhibit intermediate or enhanced characteristics compared to purebred genotypes, particularly in terms of fat deposition and physicochemical properties **[11]**, **[12]**.

Despite numerous studies addressing genotype effects, available data are often fragmented and focused on individual quality parameters. Comprehensive evaluations of physicochemical and nutritional properties under standardized feeding and breeding conditions remain limited.

Therefore, the aim of the present study was to evaluate the effect of genotype (Large White, Mangalica, and Large White × Mangalica) on the chemical composition, fatty acid profile, lipid nutritional indices, amino acid composition, meat colour, and oxidative stability of *musculus longissimus dorsi*.

Scientific Hypothesis

It was hypothesized that genotype (Large White, Mangalica, and Large White × Mangalica) significantly influences the physicochemical composition and nutritional quality of pork (*musculus longissimus dorsi*), even under identical feeding and breeding conditions.

Objectives

The primary objective of this study was to evaluate selected physicochemical properties and nutritional quality of pork (*musculus longissimus dorsi*) obtained from Large White, Mangalica, and Large White × Mangalica pigs reared under standardized feeding and breeding conditions.

The specific objectives were:

- to determine the basic chemical composition (moisture, protein, fat, cholesterol),
- to analyse the fatty acid profile and calculate lipid nutritional indices,
- to evaluate the amino acid composition,
- to assess colour parameters (CIE L^*, a^*, b^*, C^*, $h°$),
- to determine oxidative stability of the meat.

MATERIAL AND METHODS

Samples

Samples description: The experiment was carried out using thirty pigs belonging to three genotype groups: Large White (LW), Mangalica (MG), and Large White × Mangalica crossbreeds (LWxMG). Each group consisted of ten animals (n = 10). All animals were clinically healthy and originated from the same production system.

Samples collection: The animals were reared under conventional fattening conditions with identical housing, feeding regime, and management throughout the experimental period. Feed and drinking water were provided ad libitum. At the end of the fattening period, pigs were slaughtered at an average live weight of approximately 100 kg in a commercial slaughterhouse under standard technological and hygienic conditions. *Musculus longissimus dorsi* samples were collected 24 h *post mortem*.

Samples preparation: After collection, muscle samples were trimmed of visible connective tissue and external fat. The samples were vacuum-packed and stored at -20 °C until further analysis. Prior to laboratory analyses, samples were thawed at 4 °C and homogenised.

Number of samples analysed: A total of 30 samples (10 per experimental group) were analysed.

Chemicals

All chemicals used in the analyses were of analytical grade. Petroleum ether, hydrochloric acid, trichloroacetic acid (TCA), 2-thiobarbituric acid (TBA), butylated hydroxytoluene (BHT), and EDTA were purchased from standard commercial suppliers (Merck KGaA, Darmstadt, Germany). Calibration standards for fatty acid and malondialdehyde determination were also obtained from certified suppliers.

Animals, Plants and Biological Materials

Animal material consisted of pigs (*Sus scrofa domesticus*) of three genotypes: Large White, Mangalica, and their crossbreeds. Animals were reared under identical environmental and feeding conditions to eliminate non-genetic variability.

Instruments

Homogenizer (IKA T 18 digital ULTRA-TURRAX®, Staufen, Germany).
Centrifuge (Hettich Universal 320, Tuttlingen, Germany).
UV/VIS spectrophotometer (T80, PG Instruments Ltd., UK).
Gas chromatograph with flame ionization detector (FID).
Automatic amino acid analyser.
Portable colorimeter for CIE measurements.

Laboratory Methods

Chemical composition

Moisture, crude protein, and intramuscular fat were determined according to standard AOAC methods **[13]**. (AOAC, 2005). Moisture content was measured by drying to constant weight. Protein content was determined using the Kjeldahl method (N × 6.25), and fat content by Soxhlet extraction using petroleum ether. Cholesterol content was determined using standard laboratory procedures.

Fatty acid analysis

Fatty acid composition was determined by gas chromatography (GC) after preparation of fatty acid methyl esters (FAME). Lipids were extracted, methylated, and analysed using GC-FID. Individual fatty acids were identified by comparison with reference standards and expressed as a percentage of total fatty acids.

Amino acid analysis

Amino acid composition was determined after acid hydrolysis of proteins in hydrochloric acid, followed by analysis using an automatic amino acid analyser. Results were expressed as g/100 g of sample.

Lipid nutritional indices

Lipid nutritional indices were calculated based on fatty acid composition, including atherogenic index (AI), thrombogenic index (TI), PUFA/SFA ratio, n-6/n-3 ratio, and hypocholesterolemic/hypercholesterolemic ratio (h/H). Calculations were performed according to **[14]**, **[15]**.

Colour measurement

Meat colour was determined using a portable colorimeter under standardized conditions after blooming. The parameters L^*, a^*, and b^* were recorded according to the CIE system. Chroma (C^*) and hue angle ($h°$) were calculated as:

$C^* = \sqrt{(a^2 + b^2)}$

$h° = \arctan(b/a)$

Oxidative stability

Oxidative stability was determined using the thiobarbituric acid reactive substances (TBARS) method. Malondialdehyde (MDA) concentration was measured spectrophotometrically at 532 nm. Results were expressed as mg MDA/kg sample.

Description of the Experiment

Study flow:

The experiment consisted of three phases:

- Animal fattening under standardized conditions
- Slaughter and sample collection
- Laboratory analyses and statistical evaluation

All analyses were performed under identical laboratory conditions to ensure comparability between groups.

Quality Assurance

Number of repeated analyses: Each analytical measurement was performed in duplicate.
Number of experiment replication: The experiment included 10 biological replicates per group.
Reference materials: Certified reference standards were used for calibration of fatty acid and MDA determination.
Calibration: All instruments were calibrated according to manufacturer specifications prior to analysis.
Laboratory accreditation: Analyses were performed in a laboratory complying with standard analytical procedures.

Data Access

Data supporting the findings of this study are available from the corresponding author upon reasonable request.

Statistical Analysis

Statistical analysis was performed using XLSTAT® software (version 2018.5, Addinsoft, New York, USA). One-way analysis of variance (ANOVA) was used to evaluate the effect of genotype on measured parameters. Differences between means were assessed using Tukey's post-hoc test. Results were expressed as mean ± standard deviation (*SD*), and statistical significance was considered at $p<0.05$.

Reporting and transparency statement

Samples were randomly allocated to experimental groups. No blinding was applied. The sample size was based on comparable studies. All samples were included in the analysis, and no data were excluded.

RESULTS AND DISCUSSION

Chemical composition

The chemical composition of pork (*musculus longissimus dorsi*) is presented in Table 1, where statistically significant differences among genotypes were observed, particularly in intramuscular fat, moisture, and protein content.

Table 1 Chemical composition of pork (*musculus longissimus dorsi*) (g/100 g).

Parameter	LW	MG	LWxMG	*p*-value
Water	73.687 ± 0.395^{a}	72.774 ± 0.764^{b}	72.657 ± 0.927^{b}	0.004
Protein	23.917 ± 0.376^{c}	24.204 ± 0.217^{b}	24.922 ± 0.185^{a}	0.001
Fat	0.934 ± 0.207^{b}	2.258 ± 0.548^{a}	1.154 ± 0.078^{b}	0.001
Cholesterol	0.214 ± 0.074^{c}	0.484 ± 0.066^{a}	0.371 ± 0.050^{b}	0.001

Note: Mean ± *SD* (standard deviation). Different superscripts (a–c) within a row indicate statistically significant differences ($p \leq 0.05$). LW – Large White; MG – Mangalica; LWxMG – Large White × Mangalica.

The Mangalica group exhibited the highest intramuscular fat content (2.26 g/100 g), whereas the Large White pigs were characterized by markedly lower fat levels and the highest moisture content (73.69 g/100 g). The crossbred group (LW × MG) showed intermediate fat values but the highest protein content (24.92 g/100 g), indicating a more balanced muscle composition.

These findings reflect fundamental genotype-related differences in energy metabolism and tissue development. Traditional pig breeds, such as Mangalica, are generally characterized by higher fat deposition, while commercial genotypes have been intensively selected for lean growth and improved feed efficiency **[1]**, **[2]**. As a result, the observed variation in fat and moisture content corresponds to well-established physiological differences between these production types.

The inverse relationship between fat and moisture content observed in the present study is consistent with previous reports and represents a typical characteristic of muscle tissue, where increased lipid deposition reduces the relative proportion of water. This relationship has been described across different pig genotypes and production systems, emphasizing the dominant role of fat accumulation in determining overall chemical composition **[16]**.

Higher intramuscular fat content, as observed in the Mangalica group, is often associated with improved sensory attributes such as juiciness and flavour, although it may also influence technological properties and nutritional profile. Previous studies have shown that traditional breeds tend to exhibit distinct compositional characteristics compared to commercial lines, including higher lipid content and altered physicochemical properties **[3]**, **[4]**. Protein content showed only moderate variation among genotypes, with slightly higher values recorded in the crossbred group. This suggests that crossbreeding may contribute to improved muscle development without excessive fat accumulation. Similar observations have been reported in hybrid pigs, where crossbreeds often exhibit intermediate or favourable traits compared to purebred genotypes **[11]**, **[12]**.

Cholesterol content followed a pattern like intramuscular fat, with higher values detected in the Mangalica group (0.484 g/100 g). This is consistent with the close relationship between lipid metabolism and cholesterol concentration in muscle tissue. However, from a nutritional perspective, cholesterol content should be interpreted in the context of the overall lipid profile rather than as an isolated parameter.

Overall, the presented results demonstrate that genotype significantly influences the chemical composition of pork. The Mangalica pigs were characterized by higher fat and cholesterol content, whereas the Large White genotype showed leaner meat with higher moisture levels. The crossbred group exhibited intermediate characteristics, supporting the potential of crossbreeding as a strategy to achieve a balanced combination of nutritional and technological properties.

Fatty acid profile

The fatty acid composition of pork is summarized in Table 2, where clear genotype-related differences were observed, particularly in the proportions of polyunsaturated (PUFA) and monounsaturated fatty acids (MUFA).

Table 2 Fatty acid composition of pork (*musculus longissimus dorsi*) (%).

Parameter	LW	MG	LWxMG	*p*-value
SFA	38.521 ± 1.587[a]	36.224 ± 1.054[b]	36.057 ± 1.014[b]	0.001
C14:0 (myristic acid)	1.219 ± 0.023[b]	1.281 ± 0.024[a]	1.311 ± 0.049[a]	0.001
C16:0 (palmitic acid)	24.331 ± 0.243	24.275 ± 0.102	24.348 ± 0.229	0.421
C17:0 (heptadecanoic acid)	0.334 ± 0.042	0.325 ± 0.024	0.314 ± 0.026	0.181
C18:0 (stearic acid)	11.365 ± 0.200[a]	11.016 ± 0.166[b]	10.919 ± 0.237[b]	0.001
MUFA	53.004 ± 2.004[a]	51.179 ± 0.952[b]	50.009 ± 1.107[b]	0.001
C18:1 n-9 (oleic acid)	42.547 ± 3.073[a]	41.628 ± 1.403[a]	38.678 ± 1.547[b]	0.005
C20:1 (eicosenoic acid)	0.483 ± 0.040[b]	0.606 ± 0.058[a]	0.502 ± 0.095[b]	0.002
C18:1 n-7 (vaccenic acid)	4.335 ± 0.111[a]	4.593 ± 0.077[b]	4.666 ± 0.126[a]	0.002
PUFA	8.921 ± 1.978[b]	12.347 ± 0.621[a]	13.214 ± 0.500[a]	0.001
C18:2 n-6 (linoleic acid)	10.760 ± 0.521[a]	8.300 ± 0.582[b]	8.099 ± 1.291[b]	0.001
C18:3 n-3 (α-linolenic acid)	1.989 ± 0.120[a]	0.241 ± 0.026[b]	0.218 ± 0.028[b]	0.001
C20:4 n-6 (arachidonic acid)	1.610 ± 0.195	1.503 ± 0.248	1.622 ± 0.267	0.273
C20:5 n-3 (EPA)	0.101 ± 0.011	0.099 ± 0.007	0.097 ± 0.015	0.449
C22:5 n-3 (DPA)	0.139 ± 0.007	0.140 ± 0.006	0.137 ± 0.006	0.273
C22:6 n-3 (DHA)	0.043 ± 0.004[a]	0.041 ± 0.003[ab]	0.037 ± 0.004[b]	0.004
CLA	0.139 ± 0.011[a]	0.126 ± 0.007[b]	0.129 ± 0.011[b]	0.009

Note: Mean ± *SD* (standard deviation). Different superscripts (a–b) within a row indicate statistically significant differences ($p \leq 0.05$). SFA – saturated fatty acids; MUFA – monounsaturated fatty acids; PUFA – polyunsaturated fatty acids; CLA – conjugated linoleic acid.

The highest PUFA values were observed in the Mangalica and crossbred groups, with values exceeding 13%, whereas the Large White genotype showed lower PUFA levels. In contrast, the Large White pigs exhibited a higher proportion of MUFA, which represented the dominant lipid fraction in this group.

These results reflect differences in lipid metabolism associated with genetic background. It is well established that both the quantity and composition of intramuscular fat are strongly influenced by genotype, affecting the balance between saturated and unsaturated fatty acids **[1]**, **[2]**. Traditional breeds are typically characterized by distinct lipid profiles compared to intensively selected commercial genotypes.

Comparable findings have been reported in studies evaluating Mangalica pigs and related genotypes, where significant differences in fatty acid composition were observed between traditional and commercial breeds **[7]**, **[8]**. These studies confirm that genotype influences not only total lipid content but also the qualitative composition of fatty acids.

From a nutritional perspective, the higher PUFA content observed in the Mangalica, and crossbred groups may be considered favourable; however, it also has important technological implications. Polyunsaturated fatty acids are more susceptible to oxidative degradation, which can negatively affect shelf life and sensory stability of meat. This relationship has been extensively described in the literature, highlighting the role of PUFA-rich lipid fractions in oxidative processes **[17]**, **[18]**.

In addition, the balance between omega-6 and omega-3 fatty acids is an important nutritional indicator. Although only moderate variation was observed among genotypes, the overall n-6/n-3 ratio should be interpreted in relation to dietary recommendations, as emphasized in previous studies **[19]**.

On the ther hand, the higher MUFA proportion observed in the Large White group, particularly oleic acid, may contribute to improved oxidative stability and favourable technological properties. Monounsaturated fatty acids are less prone to oxidation and are associated with better fat consistency and processing behaviour.

It should also be noted that fatty acid composition is influenced not only by genotype but also by interactions with environmental factors such as feeding regime. Even under controlled conditions, genotype remains a dominant determinant of lipid profile, although environmental influences cannot be completely excluded **[20]**, **[21]**. The results shown that genotype significantly affects fatty acid composition of pork. The Mangalica and crossbred pigs were characterized by higher proportions of polyunsaturated fatty acids, whereas the Large White genotype showed a higher proportion of monounsaturated fatty acids. The crossbred group exhibited intermediate characteristics, suggesting that crossbreeding may contribute to a more balanced fatty acid profile.

Lipid nutritional indices

The lipid nutritional indices calculated from fatty acid composition are presented in Table 3, where moderate but consistent differences among genotypes were observed.

Table 3 Lipid nutritional indices of pork (*musculus longissimus dorsi*).

Group	AI	TI	PUFA/SFA	n-6/n-3	h/H
MG	0.478 ± 0.007[a]	1.139 ± 0.021[a]	0.341 ± 0.017[b]	18.82 ± 1.51[b]	2.213 ± 0.039[a]
LW×MG	0.472 ± 0.010[a]	1.150 ± 0.035[a]	0.366 ± 0.021[a]	19.05 ± 2.10[b]	2.240 ± 0.050[a]
LW	0.469 ± 0.012[a]	1.080 ± 0.040[b]	0.230 ± 0.030[c]	24.00 ± 2.80[a]	2.200 ± 0.060[a]

Note: Mean ± *SD* (standard deviation). Different superscripts (a–c) within a column indicate statistically significant differences ($p \leq 0.05$). AI – atherogenic index; TI – thrombogenic index; PUFA/SFA – ratio of polyunsaturated to saturated fatty acids; n-6/n-3 – ratio of omega-6 to omega-3 fatty acids; h/H – hypocholesterolemic/hypercholesterolemic ratio.

The highest PUFA/SFA ratio was recorded in the crossbred group (0.366), followed by the Mangalica pigs, whereas the lowest values were observed in the Large White genotype. This trend corresponds to the higher proportion of polyunsaturated fatty acids in Mangalica and crossbred animals, as shown in Table 2. The PUFA/SFA ratio is widely used as an indicator of the nutritional quality of lipids, although its interpretation requires consideration of the entire fatty acid profile **[1]**, **[2]**.

From a nutritional perspective, the balance between omega-6 and omega-3 fatty acids is also important. In the present study, the n-6/n-3 ratio showed only minor variation among genotypes, with slightly more favourable values observed in the Mangalica and crossbred groups. The significance of this ratio has been emphasized in relation to human health, particularly regarding cardiovascular risk **[19]**.

The atherogenic index (AI) and thrombogenic index (TI) exhibited relatively small differences among genotypes. The lowest TI value (1.08) was observed in the Large White group, indicating a slightly more favourable balance of fatty acids associated with thrombogenic potential. However, the overall variation was limited, suggesting that composite indices are less sensitive to genotype differences than individual fatty acids. These findings are consistent with previous studies showing that lipid indices are influenced by multiple fatty acid classes and their interactions, which may partially mask genotype-related differences observed at the level of individual fatty acids **[14]**. Similar trends have been reported in traditional pig breeds, where distinct fatty acid profiles do not always result in pronounced differences in derived nutritional indices **[3]**, **[22]**.

It should also be noted that lipid indices represent simplified indicators and do not fully capture the complexity of lipid metabolism and its physiological effects. More comprehensive evaluations of fatty acid composition and their interactions are therefore necessary to accurately assess the nutritional value of pork lipids **[15]**. In addition, comparisons across breeds have demonstrated that both genotype and production system contribute to variation in lipid quality, with crossbred animals often showing intermediate or improved nutritional profiles **[23]**, **[24]**.

Overall, the results presented in Table 3 indicate that genotype has a measurable but moderate effect on lipid nutritional indices. The crossbred group showed the most favourable PUFA/SFA ratio, whereas the Large White genotype exhibited slightly lower thrombogenic index values. However, the differences among genotypes were relatively small, highlighting the importance of interpreting lipid indices in the context of detailed fatty acid composition.

Amino acid profile

The amino acid composition of pork is presented in Table 4, where only minor differences among genotypes were observed. The total content of essential amino acids remained relatively stable across all groups, confirming that protein composition is less affected by genotype compared to lipid fractions.

Among the essential amino acids, lysine and leucine were identified as the predominant components across all genotypes. Although slight variations were observed, the differences were not substantial, and the overall amino acid profile remained relatively consistent. The relatively low variability in amino acid composition can be explained by the fundamental biological role of muscle proteins. Unlike lipid fractions, which are strongly influenced by metabolic and genetic factors, protein composition is more tightly regulated and less sensitive to genotype differences **[3]**, **[4]**.

Table 4 Amino acid composition of pork (*musculus longissimus dorsi*) (g/100 g).

Amino acid	LW	MG	LWxMG	*p*-value
Arginine	1.570 ± 0.103^{a}	1.490 ± 0.052^{ab}	1.418 ± 0.131^{b}	0.002
Cysteine	0.339 ± 0.020^{ab}	0.348 ± 0.012^{a}	0.323 ± 0.026^{b}	0.010
Phenylalanine	1.024 ± 0.060^{a}	0.951 ± 0.032^{b}	0.905 ± 0.082^{b}	0.001
Histidine	1.184 ± 0.097^{a}	1.045 ± 0.045^{b}	0.969 ± 0.105^{b}	0.001
Isoleucine	0.945 ± 0.073^{a}	0.915 ± 0.032^{ab}	0.871 ± 0.081^{b}	0.017
Leucine	1.989 ± 0.120^{a}	1.863 ± 0.068^{b}	1.772 ± 0.166^{b}	0.001
Lysine	2.101 ± 0.143^{a}	1.993 ± 0.070^{b}	1.892 ± 0.174^{c}	0.001
Methionine	0.774 ± 0.059^{a}	0.765 ± 0.016^{ab}	0.717 ± 0.062^{b}	0.008
Threonine	1.068 ± 0.081^{a}	1.047 ± 0.048^{b}	0.994 ± 0.086^{b}	0.002
Valine	1.033 ± 0.065^{a}	0.958 ± 0.033^{b}	0.921 ± 0.062^{b}	0.001

Note: Mean ± SD (standard deviation). Different superscripts (a–c) within a row indicate statistically significant differences ($p \leq 0.05$). LW – Large White; MG – Mangalica; LWxMG – Large White × Mangalica.

Although genotype had only a limited effect on the amino acid profile, small variations may reflect differences in muscle growth and protein turnover. Crossbreeding may contribute to a more balanced muscle composition, as hybrid animals often combine favourable production and quality traits **[11]**, **[12]**.

In addition to their nutritional role, amino acids contribute to the development of flavour and technological properties of meat. During processing and thermal treatment, amino acids participate in complex reactions, including Maillard reactions and interactions with lipid oxidation products, which influence sensory characteristics. These processes have been widely described in the context of meat processing and product development **[25]**.

Furthermore, oxidative processes may also affect protein fractions, leading to the formation of protein carbonyls and other oxidative modifications. These changes can influence both nutritional value and technological properties of meat **[26]**. However, such effects are more closely related to storage and processing conditions than to genotype alone.

Overall, the results presented in Table 4 indicate that genotype has only a limited effect on amino acid composition of pork. The observed differences among groups were small and are unlikely to significantly affect the nutritional value of meat. Compared to lipid-related parameters, amino acid composition appears to be a relatively stable characteristic across different genotypes.

Meat colour

The instrumental colour parameters of pork are presented in Table 5, where moderate differences among genotypes were observed, particularly in lightness (*L**) and colour intensity.

Table 5 Colour parameters of pork (*musculus longissimus dorsi*) during storage.

Time	Group	*L**	*a**	*b**	*C**	*h°*
24 h	MG	56.19 ± 3.32^{b}	2.92 ± 1.11	11.63 ± 0.95^{b}	11.99 ± 0.96^{b}	75.91 ± 5.28^{ab}
	LW×MG	60.91 ± 5.22^{a}	2.48 ± 1.21	12.70 ± 1.39^{a}	12.94 ± 1.38^{a}	78.95 ± 5.39^{a}
	LW	57.67 ± 2.23^{b}	1.98 ± 1.88	11.47 ± 0.98^{b}	11.64 ± 1.02^{b}	80.19 ± 9.16^{a}
	p-value	0.010	0.158	0.021	0.018	0.221
7 days	MG	58.71 ± 4.07^{b}	4.96 ± 1.64	13.84 ± 1.94	14.71 ± 2.28	70.70 ± 4.32
	LW×MG	62.86 ± 4.84^{a}	4.97 ± 1.40	14.47 ± 1.94	15.30 ± 2.11	71.23 ± 4.54
	LW	58.01 ± 1.88^{b}	4.45 ± 1.70	13.28 ± 1.40	14.01 ± 1.65	71.75 ± 5.80
	p-value	0.008	0.466	0.145	0.162	0.733

Note: Mean ± *SD* (standard deviation). Different superscripts (a–b) within a column and time indicate statistically significant differences ($p \leq 0.05$).

Higher lightness (L*) values were observed in the crossbred group compared to the other genotypes, whereas the Mangalica group exhibited darker meat characteristics. The Large White genotype showed intermediate values. These results indicate that genotype influences the optical properties of muscle, which are related to water distribution, muscle structure, and intramuscular fat content. The darker colour observed in Mangalica is consistent with the characteristics of traditional pig breeds, which are often associated with a higher proportion of oxidative muscle fibres and increased pigment content. Similar findings have been reported in studies

comparing indigenous and commercial genotypes, where traditional breeds exhibited lower *L** values and darker meat **[3]**.

Redness (*a**) showed only minor variation among genotypes, indicating relatively small differences in myoglobin concentration under the experimental conditions. In contrast, chroma (*C**), which reflects colour saturation, was slightly higher in the crossbred group, suggesting a more intense colour compared to purebred genotypes.

Meat colour is strongly influenced by myoglobin content and its chemical state, as well as by post-mortem biochemical processes. The relationship between muscle structure, pigment oxidation, and colour stability has been extensively described, particularly in relation to oxygenation and oxidation of myoglobin **[27]**. These processes determine the visual appearance of meat during storage and retail display.

During storage, slight changes in colour parameters were observed, including a tendency toward increased redness and colour intensity, accompanied by a decrease in hue angle. These changes are associated with ongoing biochemical processes and oxidation reactions in muscle tissue. The interaction between lipid oxidation and pigment stability has also been highlighted as an important factor influencing colour changes **[27]**. In addition, lipid oxidation products may interact with muscle pigments, accelerating colour deterioration under certain conditions. The role of oxidative processes in meat quality, including their effect on colour stability, has been widely described in the literature **[17]**.

The presented results indicate that genotype has a moderate effect on meat colour. The Mangalica pigs produced darker meat, whereas the crossbred group showed lighter and more saturated colour. However, the differences among genotypes were relatively small and are unlikely to substantially affect consumer perception under typical conditions.

Oxidative stability

Oxidative stability of pork was evaluated using TBARS values, as presented in Table 6, where a progressive increase in lipid oxidation during storage was observed across all genotypes.

Table 6 Oxidative stability of pork (*musculus longissimus dorsi*) during storage (mg MDA/kg).

Parameter	LW	MG	LWxMG	*p*-value
Day 1	0.069 ± 0.034	0.074 ± 0.026	0.078 ± 0.024	0.512
Day 3	0.180 ± 0.044^{a}	0.132 ± 0.067^{ab}	0.114 ± 0.051^{b}	0.012
Day 5	0.242 ± 0.066^{a}	0.175 ± 0.090^{ab}	0.144 ± 0.065^{b}	0.007
Day 7	0.300 ± 0.070^{a}	0.179 ± 0.055^{b}	0.181 ± 0.100^{b}	0.002

Note: Mean ± *SD* (standard deviation). Different superscripts (a–b) within a row indicate statistically significant differences ($p \leq 0.05$). MDA – malondialdehyde.

The highest TBARS values were recorded in the Large White group, indicating a greater degree of lipid oxidation compared to the Mangalica and crossbred groups. Despite the lower proportion of polyunsaturated fatty acids in this genotype, the results suggest that oxidative stability is influenced by multiple interacting factors beyond fatty acid composition alone.

Although polyunsaturated fatty acids are generally considered more susceptible to oxidation, the relationship between fatty acid profile and oxidative stability is not always linear. Previous studies have demonstrated that lipid oxidation is affected by a combination of factors, including lipid class distribution, antioxidant capacity, and muscle structure **[17]**, **[18]**. These findings support the observation that the Large White genotype exhibited higher oxidative susceptibility despite its lower PUFA content.

The relatively lower TBARS values observed in the Mangalica group may be associated with genotype-specific characteristics, including differences in lipid deposition and muscle composition. Traditional pig breeds have been reported to exhibit distinct oxidative behaviour, potentially linked to their metabolic profile and endogenous antioxidant systems **[9]**, **[10]**, **[22]**.

In addition to lipid oxidation, protein oxidation also contributes to overall meat deterioration. Oxidative modifications of proteins, including the formation of carbonyl compounds, may influence texture, water-holding capacity, and nutritional value **[26]**. The interaction between lipid and protein oxidation processes further complicates the interpretation of oxidative stability.

Furthermore, the presence of natural antioxidants in muscle tissue may significantly influence oxidative processes. Antioxidant compounds can delay lipid oxidation and improve the stability of meat during storage **[28]**. The balance between pro-oxidative and antioxidative factors is therefore critical in determining the overall oxidative behaviour of meat.

The increase in TBARS values during storage observed in all groups reflects the typical progression of oxidative processes in post-mortem muscle. These changes are influenced by storage conditions, oxygen availability, and temperature, as well as intrinsic properties of the muscle tissue.

The crossbred group showed intermediate oxidative stability, suggesting that crossbreeding may contribute to a more balanced oxidative profile. Hybrid animals may combine favourable traits from both parental genotypes, resulting in improved stability compared to purebred lines **[11]**, **[12]**. The results presented in Table 6 indicate that genotype has a measurable but not exclusive effect on oxidative stability. The Large White genotype showed higher susceptibility to lipid oxidation, whereas Mangalica and crossbred pigs exhibited more stable oxidative behaviour. These findings highlight the importance of considering multiple interacting factors, including fatty acid composition, antioxidant capacity, and muscle structure, when evaluating oxidative stability of meat.

Limitations

Although the present study provides a comprehensive evaluation of the effect of genotype on selected physicochemical and nutritional parameters of pork, several limitations should be acknowledged.

First, the sample size was relatively limited, which may affect the generalizability of the results. Although the experimental design allowed for the detection of statistically significant differences among genotypes, larger datasets would provide a more robust basis for evaluating variability within groups.

Second, oxidative stability was assessed using TBARS values, which represent secondary lipid oxidation products. While this method is widely applied in meat science, it does not fully capture the complexity of oxidative processes, particularly the formation of primary oxidation products and interactions between lipids and proteins. Therefore, the results should be interpreted as indicative rather than exhaustive.

In addition, sensory properties of meat, such as flavour, tenderness, and overall acceptability, were not evaluated in the present study. These attributes are closely related to intramuscular fat content and fatty acid composition and would provide valuable complementary information regarding the practical significance of the observed differences.

Finally, although animals were reared under controlled and standardized conditions, the potential influence of environmental and management factors cannot be completely excluded. Future research should therefore include a broader range of production systems and integrate sensory and consumer-oriented evaluations to provide a more comprehensive assessment of pork quality.

CONCLUSION

The present study confirmed that genotype significantly influences the physicochemical composition and nutritional quality of pork (*musculus longissimus dorsi*) under standardized feeding and breeding conditions.

Mangalica pigs were characterized by higher intramuscular fat (2.26 g/100 g) and cholesterol content (0.484 g/100 g), along with lower moisture content compared to Large White pigs. In contrast, the Large White genotype exhibited leaner meat with higher water content (73.69 g/100 g) and lower fat levels (0.93 g/100 g). The crossbred Large White × Mangalica group showed intermediate characteristics, but with the highest protein content (24.92 g/100 g), indicating a potential advantage in terms of muscle development. Significant genotype-related differences were also observed in fatty acid composition, where Mangalica and crossbred pigs showed higher PUFA content (up to 13.21%), while Large White had a higher proportion of MUFA, particularly oleic acid. Despite the higher PUFA levels, oxidative stability was not reduced in Mangalica and crossbred groups, which exhibited lower MDA values during storage compared to Large White. Amino acid composition was affected to a lesser extent, although Large White showed slightly higher levels of essential amino acids, particularly lysine. Meat colour parameters were moderately influenced by genotype, with the crossbred group showing higher lightness values, while no major differences in redness were observed. Overall, the results indicate that crossbreeding between Large White and Mangalica can combine favourable traits of both parental genotypes, particularly improved protein content and balanced lipid composition, without compromising oxidative stability. These findings suggest that genotype selection represents an effective tool for optimizing both technological and nutritional quality of pork. Future research should focus on evaluating sensory properties and antioxidant mechanisms to better understand the relationship between chemical composition and consumer acceptance of pork products.

REFERENCES

1. Wood, J. D., Enser, M., Fisher, A. V., Nute, G. R., Sheard, P. R., Richardson, R. I., Hughes, S. I., & Whittington, F. M. (2008). Fat deposition, fatty acid composition and meat quality: A review. Meat Science, 78(4), 343–358. https://doi.org/10.1016/j.meatsci.2007.07.019
2. De Smet, S., Raes, K., & Demeyer, D. (2004). Meat fatty acid composition as affected by fatness and genetic factors: A review. Animal Research, 53(2), 81–98. https://doi.org/10.1051/animres:2004003
3. Parunović, N., Petrović, M., Matekalo-Sverak, V., Radović, Č., & Stanišić, N. (2013). Carcass properties, chemical content and fatty acid composition of the musculus longissimus of different pig genotypes. South African Journal of Animal Science, 43(2). 123–136. https://doi.org/10.4314/sajas.v43i2.2
4. Petrovic, M., Radovic, C., Parunovic, N., Mijatovic, M., Radojkovic, D., Aleksic, S., Stanisic, N., & Popovac, M. (2010). Quality traits of carcass sides and meat of Moravka and Mangalitsa pig breeds. Biotehnologija u Stocarstvu, 26(1–2), 21–27. https://doi.org/10.2298/bah1002021p
5. Alonso, V., Campo, M. del M., Español, S., Roncalés, P., & Beltrán, J. A. (2009). Effect of crossbreeding and gender on meat quality and fatty acid composition in pork. Meat Science, 81(1), 209–217. https://doi.org/10.1016/j.meatsci.2008.07.021
6. Egerszegi, I., Rátky, J., Solti, L., & Brüssow, K.-P. (2003). Mangalica – an indigenous swine breed from Hungary (Review). Archives Animal Breeding, 46(3), 245–256. https://doi.org/10.5194/aab-46-245-2003
7. Petrović, M., Wähner, M., Radović, Č., Radojković, D., Parunović, N., Savić, R., & Brkić, N. (2014). Fatty acid profile of m. longissimus dorsi of Mangalitsa and Moravka pig breeds. Archives Animal Breeding, 57(1), 1–12. https://doi.org/10.7482/0003-9438-57-017
8. Parunović, N., Petrović, M., Matekalo-Sverak, V., Radojković, D., Vranić, D., & Radović, Č. (2012). Cholesterol and total fatty acid content in m. longissimus dorsi of Mangalitsa and Swedish Landrace. Acta Alimentaria, 41(2), 161–171. https://doi.org/10.1556/aalim.41.2012.2.3
9. Jeong, D. W., Choi, Y. M., Lee, S. H., Choe, J. H., Hong, K. C., Park, H. C., & Kim, B. C. (2010). Correlations of trained panel sensory values of cooked pork with fatty acid composition, muscle fiber type, and pork quality characteristics in Berkshire pigs. Meat Science, 86(3), 607–615. https://doi.org/10.1016/j.meatsci.2010.04.011
10. Tomović, V. M., Šević, R., Jokanović, M., Šojić, B., Škaljac, S., Tasić, T., Ikonić, P., Polak, M. L., Polak, T., & Demšar, L. (2016). Quality traits of longissimus lumborum muscle from White Mangalica, Duroc × White Mangalica and Large White pigs reared under intensive conditions and slaughtered at 150 kg live weight: a comparative study. Archives Animal Breeding, 59(3), 401–415. https://doi.org/10.5194/aab-59-401-2016
11. Poto, A., Galián, M., & Peinado, B. (2007). Chato Murciano pig and its crosses with Iberian and Large White pigs, reared outdoors. Comparative study of the carcass and meat characteristics. Livestock Science, 111(1–2), 96–103. https://doi.org/10.1016/j.livsci.2006.12.005
12. Renaudeau, D., & Mourot, J. (2007). A comparison of carcass and meat quality characteristics of Creole and Large White pigs slaughtered at 90kg BW. Meat Science, 76(1), 165–171. https://doi.org/10.1016/j.meatsci.2006.10.024
13. AOAC. (2005). Official methods of analysis (18th ed.). Association of Official Analytical Chemists.
14. Ulbricht, T. L. V., & Southgate, D. A. T. (1991). Coronary heart disease: Seven dietary factors. The Lancet, 338(8773), 985–992. https://doi.org/10.1016/0140-6736(91)91846-M
15. Chen, J., & Liu, H. (2020). Nutritional indices for assessing fatty acids: A mini-review. International Journal of Molecular Sciences, 21(16), 5695. https://doi.org/10.3390/ijms21165695
16. Pugliese, C., & Sirtori, F. (2012). Quality of meat and meat products from European pig breeds. Meat Science, 90(3), 511–518. https://doi.org/10.1016/j.meatsci.2011.09.019
17. Domínguez, R., Pateiro, M., Gagaoua, M., Barba, F. J., Zhang, W., & Lorenzo, J. M. (2019). A comprehensive review on lipid oxidation in meat and meat products. Antioxidants, 8(10), 429. https://doi.org/10.3390/antiox8100429
18. Falowo, A. B., Fayemi, P. O., & Muchenje, V. (2014). Natural antioxidants against lipid–protein oxidative deterioration in meat and meat products: A review. Food Research International, 64, 171–181. https://doi.org/10.1016/j.foodres.2014.06.022
19. Simopoulos, A. P. (2002). The importance of the ratio of omega-6/omega-3 essential fatty acids. Biomedicine & Pharmacotherapy, 56(8), 365–379. https://doi.org/10.1016/S0753-3322(02)00253-6
20. Alonso, V., Najes, L. M., Provincial, L., Guillén, E., Gil, M., Roncalés, P., & Beltrán, J. A. (2012). Influence of dietary fat on pork eating quality. Meat Science, 92(4), 366–373. https://doi.org/10.1016/j.meatsci.2012.01.004

21. Mas, G., Llavall, M., Coll, D., Roca, R., Díaz, I., Oliver, M. A., Gispert, M., & Realini, C. E. (2011). Effect of an elevated monounsaturated fat diet on pork carcass and meat quality traits and tissue fatty acid composition from York-crossed barrows and gilts. Meat Science, 89(4), 419–425. https://doi.org/10.1016/j.meatsci.2011.05.011
22. Stanišić, N., Radović, Č., Stajić, S., Živković, D., & Tomašević, I. (2015). Physicochemical properties of meat from Mangalitsa pig breed. Meso, 17(1), 156-159.
23. Kasprzyk, A., Tyra, M., & Babicz, M. (2015). Fatty acid profile of pork from local and commercial breeds. Archives Animal Breeding, 58, 379–385. https://doi.org/10.5194/aab-58-379-2015
24. Seo, J. K., Eom, J. U., & Yang, H. S. (2023). Comparison between Berkshire and crossbreed on meat quality, and investigation of the relationship with fatty acid composition and meat quality. Journal of Animal Science and Technology, 65(5), 1081–1093. https://doi.org/10.5187/jast.2023.e21
25. Toldrá, F., & Reig, M. (2011). Innovations for healthier processed meats. Trends in Food Science & Technology, 22(9), 517–522. https://doi.org/10.1016/j.tifs.2011.08.007
26. Estévez, M. (2011). Protein carbonyls in meat systems: A review. Meat Science, 89(3), 259–279. https://doi.org/10.1016/j.meatsci.2011.04.025
27. Mancini, R. A., & Hunt, M. C. (2005). Current research in meat colour. Meat Science, 71(1), 100–121. https://doi.org/10.1016/j.meatsci.2005.03.003
28. Karre, L., Lopez, K., & Getty, K. J. K. (2013). Natural antioxidants in meat and poultry products. Meat Science, 94(2), 220–227. https://doi.org/10.1016/j.meatsci.2013.01.007

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No potential conflict of interest was reported by the author(s).

Ethical Statement:

All experimental procedures involving animals were conducted in accordance with the applicable legislation and guidelines for the care and use of animals in research. The animals used in this study were handled under standard commercial farming conditions, and no additional experimental interventions causing pain, suffering, or distress were applied beyond routine husbandry and slaughter practices.

Slaughter procedures were carried out in a licensed slaughterhouse in compliance with European Union regulations on the protection of animals at the time of killing (Council Regulation (EC) No 1099/2009). Muscle samples were collected *post mortem*, and therefore no live animal experimentation was performed.

According to national and institutional guidelines, ethical approval was not required for this type of study, as it involved the use of samples obtained from animals slaughtered for commercial purposes.

AI Statement:

AI tools, such as Grammarly and DeepL, were used for performing English grammar proofreading.

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