Vol: 4, No: 2, (2025)

Antakya Veteriner Bilimleri Dergisi
The Journal of Antakya Veterinary Science
https://dergipark.org.tr/tr/pub/antakyavet

Araştırma makalesi / Research article

Determination of white striping development in Broiler chicken breast meats using some meat quality parameters: ROC Analysis Approach

Ufuk KAYA[1a], Erva ESER[2b*], Eren KUTER[3c], Ahmet Gökhan ÖNOL[4d]

[1] *Hatay Mustafa Kemal University, Faculty of Veterinary Medicine, Department of Biostatistics, 31060, Hatay, Türkiye*
[2] *Kırıkkale University, Faculty of Veterinary Medicine, Department of Biostatistics, 71410, Kırıkkale, Türkiye*
[3] *Burdur Mehmet Akif Ersoy University, Faculty of Veterinary Medicine, Department of Animal Nutrition and Nutritional Diseases, 15030, Burdur, Türkiye*
[4] *Aydın Adnan Menderes University, Faculty of Veterinary Medicine, Department of Animal Nutrition and Nutritional Diseases, 09016, Aydın, Türkiye*

MAKALE BİLGİSİ:
ARTICLE INFORMATION:

Geliş / Received:
10.10.2025
Revizyon/Revised:
25.10.2025
Kabul / Accepted:
05.12.2025
ORCIDS:
[a] 0000-0002-4805-0993
[b] 0000-0002-9827-6288
[c] 0000-0003-4536-9058
[d] 0000-0002-7520-7423

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Abstract:

White striping (WS) in broiler chicken breast meat is an important quality problem that causes significant economic losses. The nutrient composition of breast meat varies according to the severity of WS, but it is not clearly known whether this condition can be identified using the Receiver Operating Characteristic (ROC) analysis, a statistical diagnostic approach. This study aimed to determine whether biochemical parameters such as fat, dry matter, ash, and protein could predict WS occurrence through ROC analysis. Thirty male Ross 308 broilers were evaluated, including 15 normal (score 0) and 15 moderately affected (score 1) fillets. The diagnostic performance of each parameter was assessed using ROC curves, and correct classification rates were calculated. ROC analysis revealed that fat ($P < 0.001$), dry matter ($P = 0.021$), ash ($P = 0.003$), and protein ($P < 0.001$) contents could successfully discriminate WS status. Among these parameters, fat (AUC = 0.933) and protein (AUC = 0.787) showed the highest classification power. The optimal cut-off points were identified as fat > 5.81% and protein < 86.63%. Validation metrics supported these findings, with a Gini index of 0.724 and a model quality score (Q = 0.77; mean of sensitivity and specificity), indicating strong discriminatory performance. In conclusion, the results demonstrate that the nutrient composition of broiler breast meat can serve as a reliable predictive tool for WS detection. Increasing the sample size and incorporating additional biochemical or molecular markers in future studies may enhance the precision and applicability of ROC-based models.

Keywords: Broiler chickens, correct classification rate, nutrient composition, ROC analysis

Bazı et kalitesi parametrelerini kullanarak Broiler tavuk göğüs etlerinde beyaz şeritlenme gelişiminin belirlenmesi: ROC Analizi Yaklaşımı

Özet:

Broiler tavuk göğüs etlerinde görülen beyaz şeritlenme (White Striping, WS), endüstride önemli ekonomik kayıplara yol açan ciddi bir et kalitesi sorunudur. Göğüs etinin kimyasal bileşiminin WS şiddetine göre değiştiği bilinmekle birlikte, bu değişimlerin Alıcı Çalışma Karakteristiği (Receiver Operating Characteristic, ROC) analizi gibi istatistiksel tanı yaklaşımlarıyla güvenilir biçimde tespit edilip edilemeyeceği yeterince açıklığa kavuşmamıştır. Bu çalışma, yağ, kuru madde, kül ve protein gibi bazı biyokimyasal parametrelerin ROC analizi aracılığıyla WS oluşumunu tahmin etme potansiyelini değerlendirmeyi amaçlamıştır. Araştırmada, 15 normal (skor 0) ve 15 orta düzeyde etkilenmiş (skor 1) olmak üzere toplam 30 erkek Ross 308 broiler örneği değerlendirilmiştir. Her bir parametrenin tanısal performansı ROC eğrileri yardımıyla analiz edilmiş ve doğru sınıflandırma oranları hesaplanmıştır. ROC sonuçları, yağ ($P < 0{,}001$), kuru madde ($P = 0{,}021$), kül ($P = 0{,}003$) ve protein ($P < 0{,}001$) içeriklerinin WS durumunu anlamlı düzeyde ayırt edebildiğini göstermiştir. Bu parametreler arasında yağ (AUC = 0,933) ve protein (AUC = 0,787) en yüksek sınıflandırma gücünü sergilemiştir. Optimum kesim noktaları yağ> %5,81 ve protein <%86,63 olarak belirlenmiştir. Modelin doğrulama ölçütleri, Gini indeksi (0,724) ve model kalitesi (0,77) değerleri ile güçlü bir ayırt edici performans ortaya koymuştur. Sonuç olarak, broiler göğüs etinin besin bileşiminin, WS'nin tespiti ve sınıflandırılması için güvenilir bir tahmin aracı olarak kullanılabileceği belirlenmiştir. Gelecekte yapılacak çalışmalarda örneklem büyüklüğünün artırılması ve ek biyokimyasal veya moleküler belirteçlerin dahil edilmesi, ROC tabanlı modellerin hassasiyetini ve uygulanabilirliğini daha da güçlendirebilir.

Anahtar kelimeler: Broiler tavuklar, doğru sınıflandırma oranı, ROC analizi, besin madde bileşimi

Sorumlu Yazar / Corresponding Author: ervaeser@kku.edu.tr

How to cite this article: Kaya U, Eser E, Kuter E & Önol AG (2025). Determination of white striping development in Broiler chicken breast meats using some meat quality parameters: ROC Analysis Approach. J. Antakya Vet. Sci., 4(2), 1–9.

Introduction

The rapid growth of the global population has continuously increased the demand for animal-derived protein sources, positioning the poultry sector as a major contributor to meeting this demand (Alexandratos & Bruinsma, 2012). Over the past five decades, the poultry industry has surpassed the red meat sector globally, becoming the leading source of animal-based food production (Alexandros & Bruinsma, 2012; Mottet & Tempio, 2017). Broiler meat is widely preferred due to its affordability, high nutritional value, low-fat content, and lower association with obesity and cardiovascular disease risk compared with red meat (Kuttappan et al., 2012; Petracci & Cavani, 2012).

The expansion of the broiler industry is largely attributed to genetic progress. Selective breeding programmes have been shown to reduce rearing time, improve feed efficiency, and increase slaughter weight (Zuidhof et al., 2013; Petracci et al., 2015). However, these achievements have also given rise to the emergence of growth-related muscular abnormalities. Among the aforementioned conditions, white striping (WS) has become one of the most prevalent myopathies to affect the pectoralis major muscle in modern broiler chickens (Kuttappan et al., 2016).

White striping is characterized by white striations running parallel to the pectoralis major muscle fibers, impairing carcass appearance and causing reductions in water-holding capacity, processability, sensory quality, and shelf life, thereby leading to significant economic losses (Kuttappan et al., 2012; Kuttappan et al., 2013; Baldi et al., 2018; Che & Hall, 2024). Studies have reported WS prevalence rates ranging between 10% and 80%, with a higher incidence in fast-growing commercial lines (Kuttappan et al., 2013; Alnahhas et al., 2016; Russo et al., 2015; Dalle Zotte et al., 2015, Pekel et al., 2020). When co-occurring with other myopathies, such as woody breast (WB) and spaghetti meat (SM), the economic and qualitative losses become even more pronounced (Kuttappan et al., 2016; Baldi et al., 2018).

Recent multicenter and large-scale studies have provided deeper insights into the role of growth rate, carcass and fillet traits, sex, and genotype in the development of WS, WB, and SM. These studies emphasize the importance of integrating both flock-level and individual-level data for accurate evaluation (Zampiga et al., 2023). In addition, recent field studies and meta-analyses have further elucidated the economic consequences and co-occurrence dynamics of these myopathies, showing substantial reductions in carcass yield and quality classification when WB and SM are present simultaneously (Petracci & Soglia, 2024). Even when occurring alone, WS has been associated with global economic losses reaching hundreds of millions of dollars annually (Zhang et al., 2024). These recent findings underscore the urgent need for objective and early diagnostic approaches across the poultry production chain.

Although the precise etiology of WS remains unclear, it is generally associated with rapid muscle growth, metabolic imbalance, oxidative stress, and histopathological alterations (Petracci et al., 2015; Kuttappan et al., 2016; Alnahhas et al., 2016). Previous research has shown that WS-affected fillets tend to exhibit higher lipid content, lower protein levels, and variable changes in dry matter and ash contents (Kuttappan et al., 2012; Ferreira et al., 2014; Baldi et al., 2018; Kuter and Önol, 2021; Kuter et al., 2022). These biochemical alterations suggest that basic nutritional components may serve as potential biomarkers for identifying WS in broiler meat.

Furthermore, metabolomic and proteomic approaches have recently provided strong molecular evidence supporting these biochemical observations. Circulating metabolites related to histidine and sphingolipid metabolism have been significantly associated with WS and WB, while reduced phospholipid and elevated neutral lipid concentrations have been linked to impaired sensory and functional meat quality (Kuttappan et al., 2022; Papah et al., 2023). Targeted proteomic analyses have confirmed upregulated pathways related to muscle degeneration, fibrosis, and oxidative stress in WS-affected muscles (Zhang et al., 2024). Together, these findings strengthen the rationale for using chemical composition indicators, such as fat, protein, ash, and dry matter, as biochemically supported diagnostic variables in WS detection.

At present, WS diagnosis relies primarily on macroscopic scoring systems, which are inherently subjective and may vary among evaluators (Kuttappan et al., 2013; Russo et al., 2015). Consequently, the application of statistical diagnostic tools has become increasingly important. The Receiver Operating Characteristic (ROC) curve analysis is a robust and widely used statistical method for assessing diagnostic performance by determining sensitivity, specificity, and area under the curve (AUC) values to establish optimal cutoff thresholds (Alpar, 2013; Akçay & Demirel, 2011). Although ROC analysis has been successfully applied in various medical and veterinary contexts (Akçay & Demirel, 2011; Özlüer Başer et al., 2021), its use in the prediction of WS occurrence remains limited.

Recent reviews have emphasized that selective breeding and optimized management strategies are pivotal in controlling breast myopathies, and that defining objective diagnostic thresholds, such as those derived from ROC-based approaches, can support decision-making in both breeding and nutritional management (Petracci & Soglia, 2024). Moreover, mounting evidence indicates that WS has a heritable component, with moderate-to-high heritability estimates suggesting that genetic selection could effectively reduce its prevalence (Alnahhas et al., 2016).

Therefore, the present study aimed to predict the occurrence of white striping in broiler breast meat using biochemical composition parameters, specifically dry matter, ash, protein, and fat, through ROC curve analysis. The study's objective was to move beyond subjective macroscopic scoring toward objective, quantitative, and practically applicable threshold values, thereby contributing to both scientific understanding and industrial quality control processes in poultry meat production.

Materials and Methods

Experimental design and ethical approval

This study was conducted at the Poultry Research Unit of the Faculty of Veterinary Medicine, Aydın Adnan Menderes University (Aydın, Türkiye). All experimental procedures were approved by the Animal Experiments Local Ethics Committee of Aydın Adnan Menderes University (Approval No: 64583101/2016/168) and carried out in accordance with EU Directive 2010/63/EU on the protection of animals used for scientific purposes.

Animals and sampling

A total of 30 male Ross 308 broiler chickens were used in the experiment. The statistical power of the ROC analysis was estimated a priori using MedCalc software. Assuming an expected AUC of 0.80, a null hypothesis value of 0.50, $\alpha = 0.05$, and a total sample size of 30 (15 per group), the achieved power $(1-\beta)$ was approximately 0.81, indicating sufficient sensitivity for detecting differences in classification performance. After a 49-day rearing period under standard commercial conditions, the birds were euthanized by decapitation. Carcasses were defeathered, eviscerated, and chilled at 4 °C for 24 h. The pectoralis major (breast fillets) was then excised and photographed. White striping (WS) scoring was performed visually by a single trained observer following the classification criteria described by Kuttappan et al. (2013). To minimize observer bias, all samples were randomly coded before evaluation, and the scorer was blinded to the group identity of the samples. Fillets without visible white striations were classified as normal (score 0), whereas fillets with thin but distinct white striations were classified as moderate (score 1).

Chemical analysis

Samples were taken from the proximal one-third portion of each fillet for nutritional composition analysis. The parameters analyzed included dry matter (DM), crude ash (CA), crude protein (CP), and crude fat (fat). All analyses were performed following the standard procedures described by the Association of Official Analytical Chemists (AOAC, 2012). Measurements were conducted in duplicate, and mean values were used for statistical evaluation.

Statistical analysis

Statistical analyses were performed using IBM SPSS Statistics 27.0 (IBM Corp., Armonk, NY, USA) and MedCalc 9.2 (MedCalc Software Ltd., Ostend, Belgium). Descriptive statistics were presented as Mean ± Standard Error (SE). Prior to inferential analyses, data normality was assessed using the Shapiro–Wilk test, and homogeneity of variances was examined with Levene's test. For the comparison of nutrient composition (DM, CA, CP, and fat) between the normal (score 0) and moderate (score 1) WS groups, the Independent Samples t-test was applied. Receiver Operating Characteristic (ROC) curve analysis was applied to evaluate the diagnostic performance of DM, CA, CP, and fat contents in distinguishing WS-affected (1) and normal (0) fillets. Sensitivity, specificity, 95% confidence intervals (CI), and area under the curve (AUC) were calculated. AUC values were interpreted as follows: 0.5–0.6 = poor, 0.6–0.7 = fair, 0.7–0.8 = acceptable, 0.8–0.9 = good, and > 0.9 = excellent (Mandrekar, 2010; Hajian-Tilaki, 2013; Sun et al., 2024). The optimal cut-off points (thresholds) for each parameter were determined using the Youden index ($J = \text{Sensitivity} + \text{Specificity} - 1$). Differences between the AUC values of the parameters were compared using the DeLong test (DeLong et al., 1988). To further validate the classification performance, several complementary indices were calculated. The Precision–Recall (PR) analysis was employed to evaluate the trade-off between precision (the proportion of true positives among all predicted positives) and recall (sensitivity), providing a robust measure of classifier reliability, particularly in datasets with imbalanced group sizes. The Gini index, defined as twice the AUC minus one ($\text{Gini} = 2 \times \text{AUC} - 1$), was used to quantify the overall discriminatory power of the model on a 0–1 scale, where higher values indicate greater separability between classes. The Kolmogorov–Smirnov (K–S) statistic was computed to determine the maximum divergence between the cumulative distributions of predicted probabilities for positive and negative cases; larger K–S values correspond to superior model discrimination. The overall model quality (Q) was calculated as a composite index representing the average of sensitivity and specificity (Q = (Sensitivity + Specificity) / 2). This metric provides a balanced assessment of the model's ability to correctly classify both positive and negative cases, independent of prevalence. In addition, the correct classification rate (Accuracy, %) was derived from ROC-based classifications to indicate the proportion of correctly identified cases among all observations. Statistical significance was accepted at P < 0.05.

Results

Descriptive statistics of the nutritional composition parameters of breast fillets with white striping (WS) scores of 0 (normal) and 1 (moderate) are presented in Table 1.

Table 1. Descriptive statistics of nutritional composition according to white striping scores

Parameter	Score 0 (Normal) (n=15)	Score 1 (Moderate) (n=15)	P
Crude Fat (%)	5.76 ± 0.23	8.29 ± 0.36	0.003
Dry Matter (%)	97.95 ± 0.05	97.78 ± 0.05	0.701
Crude Ash (%)	4.65 ± 0.04	4.49 ± 0.03	0.169
Crude Protein (%)	86.65 ± 0.32	84.41 ± 0.33	0.625

An increase in WS score was associated with higher fat content and a lower protein content. The mean fat percentage was 5.76% in the normal group and 8.29% in the moderate group, and this difference was statistically significant (P = 0.003). Although the protein content tended to be decreased from 86.65% in the normal group to 84.41% in the moderate group, the difference was not statistically significant (P=0.625). Similarly, no statistically significant differences observed between groups for DM (P=0.701) and ash levels (P=0.169).

The diagnostic performance of the nutritional parameters in predicting the occurrence of white striping was evaluated using ROC analysis, and the results are presented in Table 2.

According to the ROC analysis, the fat parameter exhibited the highest discriminative ability (AUC = 0.862; 95% CI: 0.77–0.99; P < 0.001). The sensitivity and specificity for fat were 93.33% and 66.67%, respectively, with a Youden index of 0.60, indicating the highest diagnostic accuracy among all parameters. The positive likelihood ratio (LR+) was 2.80, while the negative likelihood ratio (LR−) was 0.10, suggesting that a negative test result strongly ruled out the presence of WS.

The protein parameter ranked second in discriminative performance (AUC = 0.787; 95% CI: 0.66–0.91; P < 0.001), with 93.33% sensitivity, 56.67% specificity, a Youden index of 0.50, LR+ = 2.15, and LR− = 0.12.

Although dry matter and ash parameters exhibited lower AUC values compared to fat and protein, both were found to be statistically significant predictors (P = 0.021 and P = 0.003, respectively). The AUC values for DM and ash were 0.662 (95% CI: 0.51–0.81) and 0.701 (95% CI: 0.55–0.84), with 76.67% sensitivity, 60.00% specificity, and a Youden index of 0.367 for both.

Figure 1 presents the ROC curves for fat, DM, ash, and protein parameters. The largest area under the curve was obtained for fat, followed by protein, ash, and DM, respectively.

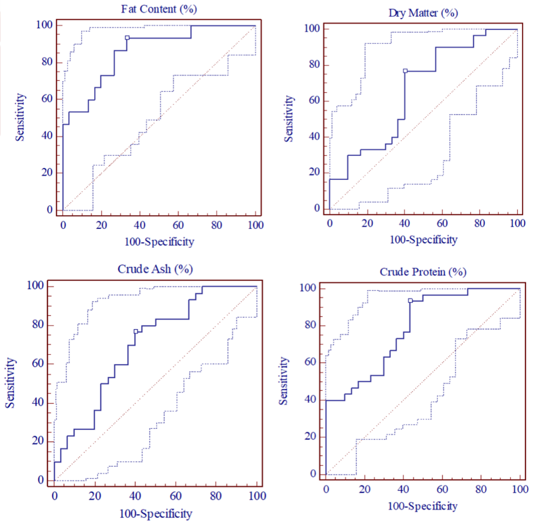

Figure 1. ROC curves for fat, dry matter (DM), ash, and protein parameters

Table 2. Results of ROC analysis

Parameter	Cut-off Value	Sensitivity (%)	95% CI (Sensitivity)	Specificity (%)	95% CI (Specificity)	AUC	P-value	Youden Index	LR+	LR−
Crude Fat (%)	> 5.81	93.33	77.9–99.0	66.67	47.2–82.7	0.86	<0.001	0.60	2.80	0.10
Dry Matter (%)	≤ 97.93	76.67	57.7–90.0	60.00	40.6–77.3	0.66	0.021	0.36	1.92	0.39
Crude Ash (%)	≤ 4.61	76.67	57.7–90.0	60.00	40.6–77.3	0.70	0.003	0.36	1.92	0.39
Crude Protein (%)	≤ 86.63	93.33	77.9–99.0	56.67	37.4–74.5	0.78	<0.001	0.50	2.15	0.12

CI: Confidence Interval, AUC: Area Under the Curve, LR: Likelihood Ratio (positive and negative)

Correct classification rates obtained from ROC analysis are shown in Table 3. The fat parameter demonstrated the highest correct classification rate (80.0%), followed by protein (73.3%), dry matter (66.7%), and ash (63.3%).

Table 3. Correct classification rates based on ROC analysis

Parameter	Correct Classification Rate (%)*
Fat (%)	80.00
Dry Matter (%)	66.71
Crude Ash (%)	63.32
Crude Protein (%)	73.34

The results of the Classifier Evaluation Metrics analysis are presented in Table 4. This analysis was conducted to evaluate the discriminatory capability of the model for each nutritional parameter.

Table 4. Classifier Evaluation metrics

Test Result Variable(s)	Gini Index	Max K–S	Cutoff
Fat content (%)	0.72	0.60	6.26
Dry matter (%)	–0.32	0.00	99.29
Crude ash (%)	–0.40	0.00	6.26
Crude protein (%)	–0.57	0.00	91.45

K-S: Kolmogorov-Smirnov test statistics

The parameter of fat content percentage exhibited the most marked discriminative ability, with a Gini index of 0.724 and a K–S statistic of 0.600, indicating a robust and reliable model performance. Conversely, negative Gini values observed in the remaining variables suggest that their classification performance was below that of random prediction, thereby highlighting that only fat content provided meaningful separation within the model.

The overall performance of the model is presented in Figure 2.

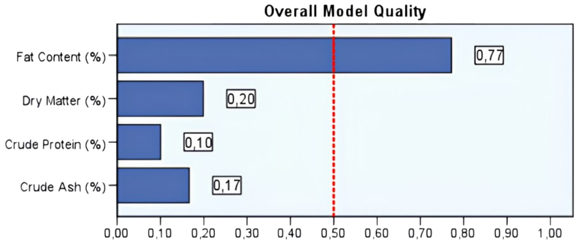

Figure 2. Overall model quality for the ROC-based classification of white striping

The model quality was calculated as 0.77, which is above the 0.5 threshold, indicating that the model provides a significantly better classification than random prediction. This result supports the robustness of the classification, confirming that the model successfully distinguishes the target class based on the fat content parameter.

The Precision–Recall curve supported the ROC findings and demonstrated that the highest discriminative ability was again achieved for fat content (%) (Figure 3).

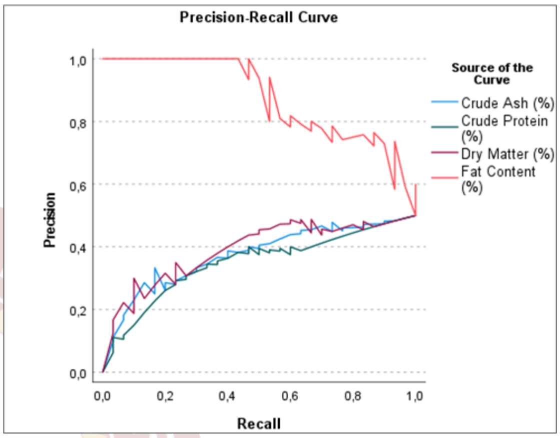

Figure 3. Precision–Recall curves for fat, dry matter, ash, and protein parameters in predicting white striping

Across the entire curve, fat content (%) exhibited consistently high precision and recall values, confirming it as the most accurate parameter for classifying the presence of the white stripe pattern. Precision values above 0.8 indicate a very low probability of false classification for positive (white-striped) samples. In contrast, other parameters (dry matter, ash, and protein) produced lower and more scattered curves, suggesting limited reliability in identifying the white stripe feature. This finding confirms that fat content serves as the most consistent and reliable biomarker not only in the ROC analysis but also within the Precision–Recall framework.

Discussion

White striping (WS) myopathy in broiler chickens is recognized as one of the most critical quality challenges in modern poultry production (Kuttappan et al., 2016; Lee & Mienaltowski, 2023). Characterized by white striations running parallel to the muscle fibers of the pectoralis major, WS results from an imbalance between muscle hypertrophy and the metabolic and vascular capacities of the tissue (Petracci & Cavani, 2012; Boerboom et al., 2018). Continuous genetic selection for rapid growth and high breast yield has exceeded the adaptive capacity of the muscle, leading to local hypoxia, mitochondrial dysfunction, and oxidative imbalance (Bailey, 2023; Baldi et al., 2018; Kong et al., 2023). Consequently, lipid peroxidation and protein degradation are accelerated, resulting in myofiber degeneration and fat infiltration (Ferreira et al., 2014; Fraga et al., 2021; Kato et al., 2023).

The findings of the present study are consistent with these mechanisms. The increase in fat content and decrease in protein concentration with higher WS scores align with earlier reports describing increased intramuscular lipid deposition and reduced protein density in WS-affected fillets (Kuttappan et al., 2012; Kuttappan et al., 2013; Kuter et al., 2022). This confirms that WS is not merely a morphological abnormality but also a biochemical disorder.

The reduction in protein content observed in WS fillets may be attributed to excessive activation of proteolytic systems. Soglia et al. (2023) and Kong et al. (2024) reported that the ubiquitin–proteasome system and calpain pathway are hyperactivated in affected tissues, leading to sarcomere degradation. In the current study, the strong negative association between protein concentration and WS presence, supported by ROC-derived cutoff values (fat >5.81%; protein <86.63%), reflects these molecular processes. These biochemical thresholds serve as quantifiable indicators of metabolic disruption and oxidative injury at the cellular level.

According to these results, higher fat content and lower protein levels were strongly associated with the presence of white striping. This finding is consistent with previous reports by Kuttappan et al. (2012, 2013) and Baldi et al. (2018), which described similar biochemical alterations characterized by increased intramuscular fat deposition and decreased protein density in WS-affected fillets.

White striping is increasingly viewed as a chronic fibrotic and inflammatory condition rather than solely a metabolic one (Bailey, 2023; Muñoz-Lapeira et al., 2025). The resulting extracellular matrix (ECM) remodeling leads to increased tissue stiffness and altered muscle integrity (Fraga et al., 2021; Padilha et al., 2024). In this context, the significant differences in ash and dry matter contents observed in this study may reflect ionic and osmotic imbalances resulting from ECM alterations (Russo et al., 2015; Kuter et al., 2022). Reduced mineral equilibrium, particularly of Ca^{2+} and Mg^{2+}, may compromise muscle excitability and water-holding capacity, linking biochemical composition to the characteristic texture of WS fillets.

From a methodological standpoint, the present research contributes to the literature by combining ROC analysis with machine learning–based diagnostic metrics in poultry meat evaluation. ROC analysis is widely applied in medical diagnostics to evaluate classification performance (Mandrekar, 2010; Hajian-Tilaki, 2013; DeLong et al., 1988), and it is increasingly employed in animal science and food quality research (Richardson et al., 2024; Sun et al., 2024). In this study, the integration of AUC values, Gini indices, and Precision–Recall curves provided a multidimensional assessment of model robustness, with fat content showing the strongest discriminative capacity.

The high precision values (>0.8) observed for fat content confirm its reliability as a biomarker for WS classification. This indicates that ROC-based diagnostic modeling can be effectively integrated into automated, AI-assisted quality control systems. Indeed, recent advances in imaging technologies such as optical coherence tomography (Ekramirad et al., 2024) and hyperspectral imaging, combined with supervised learning models (Özlüer Başer et al., 2021), may enable real-time, non-destructive detection of WS using fat and protein ratios as reference inputs.

From an industry perspective, WS causes substantial economic losses due to downgraded products, reduced water-holding capacity, and lower consumer acceptance (Mottet & Tempio, 2017; Petracci et al., 2015). The implementation of quantitative biochemical thresholds such as fat >5.81% and protein <86.63% could standardize quality grading, minimizing subjectivity and product rejection (Bailey, 2023; Lee & Mienaltowski, 2023). This would contribute to more consistent carcass evaluation and facilitate the integration of early metabolic screening into poultry management.

This study demonstrated that the ROC analysis approach is an effective, objective, and practical method for determining the presence of white striping (WS) in broiler breast meat using nutritional composition parameters. Among the tested variables, fat and protein contents exhibited the highest sensitivity and significant discriminative power (AUC), indicating their potential as reliable biochemical biomarkers for WS detection. In contrast, dry matter (DM) and ash levels showed limited but complementary discriminative ability.

The additional validation metrics including the Precision–Recall curve, Gini index, and Kolmogorov–Smirnov (K–S) statistic further supported these findings. The high Gini index (0.724) and overall model quality (0.77) obtained for the fat parameter confirmed that the classification performance was substantially superior to random prediction. Similarly, the Precision–Recall analysis revealed that fat maintained high precision values across all sensitivity ranges, reinforcing its strong diagnostic reliability alongside protein.

These results not only support the biochemical mechanisms underlying WS reported in previous literature but also provide objective and practical cut-off values applicable to industrial quality control. Fat content above 5.81% and protein content below 86.63% may serve as reference thresholds for distinguishing WS-affected fillets. Further studies with larger populations are warranted to validate these thresholds and enhance the generalizability of ROC-based diagnostic accuracy.

In summary, WS represents a multifactorial condition influenced by nutritional, environmental, and genetic interactions. While the present study provides valuable insights, it should be noted that the sample size (n = 30) was relatively limited for ROC-based analyses, and this should be considered when interpreting the results. Future research with larger populations is recommended to strengthen statistical power and external validity. Future research should integrate metabolomic, proteomic, and histopathological data with ROC- and machine learning–based models to enhance diagnostic precision (Che & Hall, 2024; Zampiga et al., 2023). Longitudinal studies focusing on gene–nutrition interactions during early muscle development will further elucidate causal mechanisms, ultimately contributing to improved welfare, meat quality, and sustainability in poultry production.

Future research should integrate additional indicators including blood metabolites, carcass traits, histopathological alterations, and omics-based (metabolomic/proteomic) profiles within the ROC and complementary diagnostic frameworks. Such multimodal approaches will facilitate the early, objective, and multidimensional detection of WS, thereby improving both industrial quality management and breeding program efficiency. Consequently, ROC-based biomarkers could serve as sustainable decision-support tools to enhance production efficiency and animal welfare in the poultry industry.

Acknowledgement: We would like to thank Prof. Dr. Ahmet Gökhan ÖNAL and Assoc. Prof. Dr. Eren KUTER for providing the data for this study and allowing its use.

Funding: The author(s) received no financial support for the research, authorship, and/or publication of this article.

Ethical Approval: All experimental procedures were approved by the Local Ethics Committee for Animal Experiments of Aydın Adnan Menderes University (Approval No: 64583101/2016/168).

Conflict of Interest: The authors declare that there is no conflict of interest among the authors.

Author Contributions: Conceptualization: Ufuk Kaya,Eren Kuter, Erva Eser; Methodology: Ufuk Kaya, Erva Eser; Software and Statistical Analysis: Ufuk Kaya, Erva Eser; Validation: Ufuk Kaya, Erva Eser, Ahmet Gökhan Önol; Formal Analysis: Ufuk Kaya, Erva Eser, Eren Kuter; Investigation: Eren Kuter, Ahmet Gökhan Önol; Resources: Eren Kuter, Ahmet Gökhan Önol; Data Curation: Eren Kuter; Writing – Original Draft: Erva Eser, Ufuk Kaya; Writing – Review & Editing: Ufuk Kaya, Erva Eser, Ahmet Gökhan Önol; Visualization: Erva Eser, Ufuk Kaya; Supervision: Ufuk Kaya, Ahmet Gökhan Önol; Project Administration: Ufuk Kaya, Ahmet Gökhan Önol; Funding Acquisition: Ahmet Gökhan Önol.

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