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Proteomics-Discovered Quality Biomarkers for Chilled/Frozen Meat and Aquatic Products: Translational Barriers from Lab to Industry and Breakthrough Directions

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Abstract

Over the past decade, proteomics has identified numerous differentially abundant proteins and post-translational modifications in chilled and frozen meat and aquatic products, holding promise as molecular markers for quality monitoring. Yet, these candidates have rarely been used in commercial cold-chain surveillance or rapid testing. This review asks a more practical question: what prevents proteomic findings from moving into industrial use? To keep the discussion focused, candidate biomarkers are grouped into three types: degradation fragments (e.g. the 30 kDa troponin-T fragment), oxidized proteins (e.g. carbonylated creatine kinase), and abundance-changed enzymes/chaperones (e.g. Hsp27/Hsp70). Across the literature, four barriers appear repeatedly: (1) insufficient validation of storage-condition universality; (2) difficulty migrating quantitative methods from mass spectrometry to rapid detection formats; (3) lack of quantitative models linking biomarker changes to sensory/textural quality indices; and (4) scarcity of cross-species and cross-processing stability data. The main purpose of this review is to map where translation breaks down between discovery and application. Rather than treating proteomic identification as an endpoint, it examines the points where potential markers fail to become workable tools for quality monitoring. That gap matters. A candidate may perform well under controlled experimental conditions and still be difficult to apply in routine commercial testing. Based on this, the review organizes a specific set of translational problems and a research agenda that may help move freshness/freeze-thaw history markers closer to practical cold-chain quality control in the food industry.

Keywords

protein biomarkers, proteomics, chilling/freezing, meat and aquatic products, translational gaps

1. Introduction

Over the past fifteen years, proteomic approaches have been extensively applied to chilled and frozen meat and aquatic products, generating a wealth of data on differentially expressed proteins and modification sites associated with post-mortem degradation and oxidation [1, 2]. Numerous candidate biomarkers have been proposed, including troponin-T degradation fragments, carbonylated creatine kinase, and heat shock proteins (Hsp27, Hsp70). However, these findings have had almost no effect on routine industry practice. At the fresh

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meat counter, quality assessment still depends on sensory inspection, expiration date labels, and total volatile basic nitrogen (TVB-N) measurements. The gap between laboratory findings and industrial use remains large.

Why focus specifically on translational barriers? Simply producing longer lists of differential proteins without validation is likely to give less and less useful return. In clinical proteomics, Chen & Zheng (2020) [3] note that the complexity and low throughput of discovery-phase methods create extra obstacles for translation. Similar problems appear in food proteomics as well. A systematic review of these barriers may help reduce repeated studies and guide limited resources toward the applications with the best practical potential.

This review has three purposes: (i) to categorize candidate quality biomarkers identified from chilled/frozen meat and aquatic products; (ii) to identify key translational barriers from four perspectives (condition universality, technological migration, quantitative linkage to quality indices, and coverage breadth); and (iii) to propose priority solutions for bridging the gap from discovery to industrial deployment.

2. Theoretical Background

2.1 What is a Quality Protein Biomarker?

A biomarker is a measurable molecular indicator that reflects biological states or responses to external factors [3]. In meat science, a protein biomarker refers to one whose abundance, structure, or post-translational modifications change quantifiably during storage, temperature shifts, or freeze-thaw cycles, and these changes can be linked to quality traits like tenderness, water-holding capacity, color stability, and spoilage [1, 4]. However, not every changing protein makes a useful marker. A practical biomarker must meet several requirements: it should respond specifically to the quality changes of interest with minimal interference from the muscle matrix; behave consistently across breeds, production systems, and storage conditions; correlate quantitatively with measures like shear force, drip loss, or sensory scores to support clear thresholds; and be compatible with low-cost, rapid on-site tests rather than mass spectrometry. Developing such biomarkers matters for the cold chain industry. Current practices rely on subjective sensory checks, sell-by dates that assume ideal conditions, and TVB-N measurements that only rise at later spoilage stages [5]. Reliable protein biomarkers could turn “freshness” into measurable signals, enabling dynamic shelf-life estimation, freeze-thaw history identification, and early warning of temperature abuse, thus providing the foundation for data-driven cold chain management—and identifying the barriers to this translation is precisely why this review was written.

2.2 Two Major Protein Changes During Chilling/Freezing

Protein degradation and oxidation are the two primary pathways that generate measurable changes in muscle proteins during storage, forming the molecular basis for most candidate biomarkers reported to date.

For degradation, troponin-T (TnT) is arguably the most studied example. TnT is a structural protein of the thin filament that regulates muscle contraction through calcium-dependent interactions. After slaughter, ATP depletion raises intracellular calcium levels, activating calpains—endogenous proteases that preferentially cleave TnT at specific sites in its N-terminal region, generating a ~30 kDa fragment that is consistently observed. TnT has become a focal point for biomarker research because it is highly sensitive to calpain activity, degrades early post-mortem, and yields a stable fragment detectable by standard immunoassays. Multiple studies have confirmed this fragment as a reliable indicator of proteolysis and tenderization [6-9].

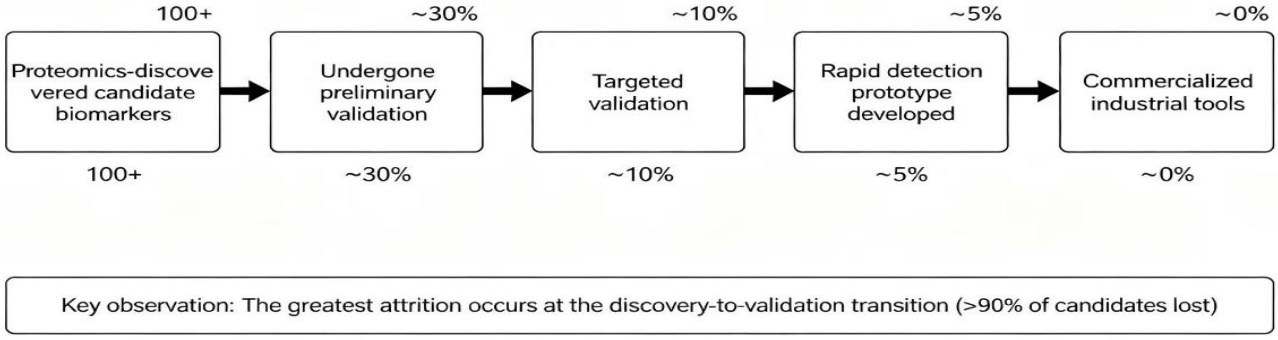
For oxidation, carbonylation is a key modification pathway. Reactive oxygen species attack amino acid side chains—particularly lysine, arginine, proline, and threonine—introducing carbonyl groups irreversibly. Creatine kinase has emerged as a prominent target because its active-site cysteine is highly vulnerable to oxidation and because the enzyme is abundant in muscle and central to energy metabolism. Carbonylation of creatine kinase has been documented in poultry and fish [10, 11], and protein carbonyl accumulation has been linked to reduced water-holding capacity, texture deterioration, and flavor loss [12]. Together, degradation and oxidation provide complementary molecular readouts of quality loss during cold storage.

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2.3 The Technical Chain from Proteomics to Biomarkers

The typical pipeline consists of three stages: discovery (identification of differential proteins/modifications using TMT, label-free, etc.), targeted validation (quantification of candidates by PRM/MRM or immunoassays), and translation (adaptation to rapid formats such as lateral flow strips or ELISA kits). Gagaoua and Picard [1] illustrated this chain, highlighting that most studies remain at the discovery stage, few enter targeted validation, and very rare examples reach translation. Chen and Zheng [3] pointed out that the complexity and low throughput of proteomics methods create additional hurdles for translation. The skewed distribution of publications across these three stages is summarized in Figure 1.

Figure 1: Distribution of publications across the three stages of the proteomics-to-biomarker translational pipeline



3. Literature Review

To derive the barriers in this review in a systematic way, we carried out a structured literature search in Web of Science, PubMed, and Scopus for publications from January 2000 to December 2025. The search terms covered proteomics ("proteomics," "mass spectrometry"), food matrices ("meat," "pork," "beef," "chicken," "fish," "aquatic products"), storage conditions ("chilled," "frozen," "cold storage," "freeze-thaw"), and quality indicators ("freshness," "tenderness," "biomarker"). We included only peer-reviewed original articles and reviews in English. After screening titles, abstracts, and full texts, 19 articles were finally retained.

The four translational barriers discussed in Sections 3.2-3.5 did not come from any single published framework. They were developed through inductive coding during the reading process. As we reviewed the studies, we noted factors that authors repeatedly identified as limiting practical application, then compared these points across papers and grouped them into recurring themes. Four themes appear repeatedly in independent studies: condition universality, technological migration, quantitative linkage, and coverage breadth.

This approach was built from the literature itself. It was not imposed in advance from prior assumptions.

3.1 Overview of Candidate Biomarkers Emerged from Proteomics Data

Several studies have pointed to the same candidates. Troponin-T degradation fragments, especially the ~30 kDa peptide, are widely used as signs of post-mortem proteolysis and tenderness [6-9]. Heat shock proteins Hsp27 and Hsp70 have also been examined as freshness markers.

Lomiwes et al. [13] reviewed the role of small heat shock proteins (sHSPs), including Hsp27, in tenderness development. Their review linked the anti-apoptotic and chaperone functions of these proteins during the conversion of muscle to meat with quality traits such as tenderness, colour, and juiciness. The picture is not consistent, though. Moncau et al. [14] found low correlations between Hsp27/Hsp70 concentrations and beef tenderness in crossbred cattle, which suggests that their value may depend on breed.

Carbonylated creatine kinase was identified in chicken [12] and in mackerel surimi [11]. Peptidomic profiling also suggested that peptides derived from creatine kinase may indicate lipid oxidation in aged meat. Table 1 summarizes the four most frequently reported candidate biomarker categories and their current translational status. Even so, most of these candidates are still only at the "suggested" stage, with little follow-up validation or rapid test development.

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Table 1: Summary of candidate biomarker categories and their current translational status

Biomarker type	Specific name	Species/matrix	Discovery method	Targeted validation	Rapid prototype	References
Degradation fragment	Troponin-T 30 kDa fragment	Beef	Immunoblotting	Yes (ELISA)	Lab ELISA	Tsitsilonis et al., 2002
Degradation fragment	Troponin-T 30 kDa polypeptide	Beef	Immunological	No	No	Negishi et al., 1996
Oxidative modification	Carbonylated creatine kinase	Chicken, mackerel	Proteomics + immunodetection	No	No	Stagsted et al., 2004; Pazos et al., 2013
Abundance change	Hsp27 / Hsp70	Beef	Proteomics / immunoblotting	Partial (correlation)	No	Lomiwes et al., 2014

3.2 Barrier 1: Insufficient Condition Universality

Most candidate biomarkers have been reported under single species and single temperature conditions; whether they remain valid when switching to another breed or storage regime is unknown. Moncau et al. [14] provided a cautionary example: Hsp27 and Hsp70 concentrations showed low correlation with beef tenderness in a specific crossbred population, indicating that promising markers in one genetic background may fail in another. Kominami et al. [7] demonstrated that proteolysis kinetics are dynamic and non-constant, varying with thawing and aging conditions. Zhao et al. [15] examined peptide and metabolite markers for pork freshness under four different temperatures (−2, 4, 10, 25 °C)—a rare multi-condition validation, but such comprehensive studies are exceptional. As Chen and Zheng (2020)[3] argued regarding clinical translation, the complexity and low throughput of discovery-phase methods themselves hinder broad validation. The lack of cross-species and cross-condition validation prevents industry from investing in assay development.

3.3 Barrier 2: Difficulty in Migrating from Mass Spectrometry to Rapid Detection

Proteomics relies on high-resolution mass spectrometry, whereas industry needs immuno-strips or handheld sensors. Key bottlenecks include: lack of high-specificity antibodies against specific modification sites (e.g., a particular carbonylated lysine), and the need for antibody pairs to distinguish degradation fragments from full-length proteins—an expensive development process.

Despite these bottlenecks, a few studies have successfully developed ELISA-based methods for TnT fragments and citrate synthase[16], though none have reached commercial products. A lateral flow immunoassay for meat authentication [17] showed that point-of-care technology is feasible for species identification, but similar formats for freshness biomarkers are lacking.

3.4 Barrier 3: Lack of Quantitative Links Between Biomarker Changes and Macroscopic Quality Indices

Even when a biomarker changes significantly, industry cannot determine “pass/fail” without a quantitative relationship to texture, water-holding capacity, or sensory scores. Most studies report only qualitative statements such as “protein A is negatively correlated with shear force.” Tsitsilonis et al. [18] is a rare exception that correlated TnT fragment levels with tenderness. A proteomics and metabolomics profiling of pork exudate [15] identified peptides and metabolites that significantly differed between fresh and spoilt pork and observed significant correlations with quality parameters. In a different approach, gene expression has been used as a predictor in generalized linear models to classify pork quality grades—a framework that could be adapted for protein biomarkers. While such modelling approaches have been applied to transcriptomic data, analogous quantitative frameworks linking specific protein abundance or modification levels to consumer-relevant quality endpoints remain largely absent from the proteomics literature. Studies that simultaneously collect proteomics data and a full set of quality indices (texture, WHC, sensory) in the same experiment are extremely scarce. Soladoye et al. [10] provided the mechanistic basis linking carbonyls to quality traits, but quantitative models are missing.

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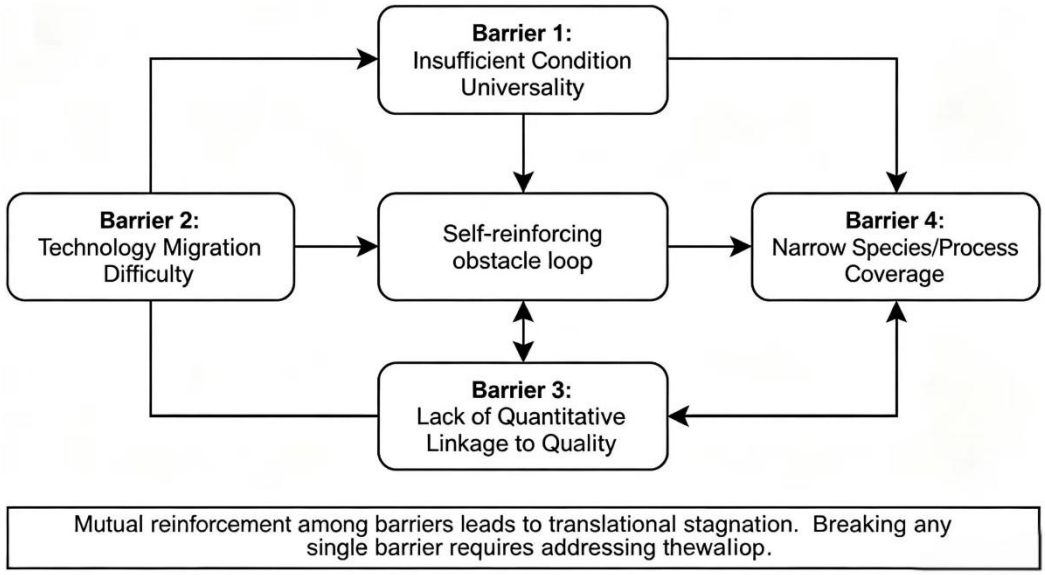
3.5 Barrier 4: Narrow Species and Processing Coverage, Lack of Standardization

Existing data are heavily concentrated on pork, chicken, and large yellow croaker, with most studies using untreated raw muscle. Very little work covers processed products (marinated, pre-cooked). A lateral flow immunoassay study analysed multiple meat species for authentication [17] demonstrating that cross-species detection is feasible; yet, no similar scale of study exists for freshness or freeze-thaw biomarkers. The cold chain packaging and intelligent monitoring review [5] noted that cold chain integrity is rarely maintained in practice, which is directly linked to the lack of validated biomarkers for processed products. Standardization of sample preparation and reporting guidelines is absent, making cross-laboratory comparison difficult.

4. Interconnections Among the Four Barriers

Figure 2 illustrates how the four barriers reinforce each other. Insufficient universality prevents industry from investing in validation; difficulty in technological migration hinders the accumulation of universality data; lack of quantitative models makes all candidates unconvincing; and narrow species coverage limits generalizability. This creates a self-reinforcing obstacle loop. Thomas et al. [4] comprehensively reviewed the entire chain from discovery to detection, and Ren et al. [5] emphasized the industrial consequences. Breaking this loop requires targeted interventions.

Figure 2: Schematic illustration of the self-reinforcing cycle among the four translational barriers



4.1 The Core Bottleneck: Discovery-to-Validation Cliff

Our literature screening revealed a striking pattern: the vast majority of proteomics studies in this field lack any targeted validation experiment, and reports that include a rapid detection prototype are even rarer. This suggests that the discovery-to-validation transition represents the most fragile link in the entire chain.Chen and Zheng (2020) [3] noted that in clinical proteomics, the vast majority of candidate biomarkers never reach validation; the situation in food proteomics is likely even worse because of lower funding and fewer commercial incentives.

4.2 Positive Attempts in Existing Studies

Despite the barriers, some studies provide instructive examples. The TnT ELISA by Tsitsilonis et al. [18] the SOD-based ELISA for frozen-thawed lamb [19], the citrate synthase ELISA for frozen pork [16], and the lateral flow immunoassay for meat authentication [17] all demonstrate that technical migration is possible. Common features of these successful cases include: (i) they started from a well-validated candidate; (ii) they developed immuno- or targeted methods with reasonable performance; (iii) they established a link with macroscopic quality. The success of these studies suggests three enabling factors: (i) the biomarkers were

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selected from well-replicated proteomic discoveries rather than single studies; (ii) the assay formats were chosen with end-user feasibility in mind from the outset; and (iii) the researchers established correlations with industry-relevant quality metrics early in the development process. These cases show that translation is not impossible—the key is designing experiments with an application-oriented mindset from the beginning.

5. Priority Recommendations for Breaking the Barriers

To break the self-reinforcing loop described above, we propose four priority actions, each targeting one of the four barriers identified in Section 4. The recommendations follow a logical sequence: first validate what works across conditions, then build quantitative models, next convert candidates into field-deployable formats, and finally establish consensus standards. Each recommendation is followed by an assessment of the expected improvements it would bring.

The next stage should focus on validation across laboratories and species, especially for the candidates reported most often. The TnT 30 kDa fragment and carbonylated creatine kinase are the clearest starting points. They need systematic testing across multiple storage temperatures, major commercial species, and different muscle types. DIA mass spectrometry looks like the most practical option here because it offers higher throughput and better reproducibility than targeted approaches. If this is done well, it could produce the first public reference database showing the range in which each biomarker remains reliable. That step addresses the current problem of "unknown universality," which appears to be one reason industry has been slow to invest.

A second priority is to build quantitative models that connect biomarker levels to actual quality outcomes. Proteomics data should be collected alongside conventional quality measurements such as shear force, drip loss, and sensory scores from the same samples. Without that link, the markers remain hard to use. Machine learning methods such as random forest or LASSO regression could then be used to identify the smallest marker set that predicts each endpoint with acceptable accuracy. This would move the field beyond broad claims of "correlation" and toward defined thresholds for "pass/fail" decisions. In practice, that would make the results easier for quality control personnel to use without needing bioinformatics training.

The third priority is the development of rapid detection prototypes. After candidates have been validated and tied to quality endpoints, they should be adapted into lateral flow assays or ELISA kits. That stage depends on antibodies that can distinguish degradation fragments from intact proteins or detect specific modification sites. Industry involvement is needed early, because performance specifications have to match commercial conditions rather than ideal laboratory settings. If those requirements are built in from the start, the result could be the first commercially viable, field-deployable tests for freshness and freeze-thaw history. This matters if biomarker testing is expected to replace the expensive, laboratory-bound mass spectrometry workflows currently used.

The fourth area is standardization. Industry and academic laboratories should develop standard protocols for sample preparation, threshold values, and quality control. These protocols need to specify sampling procedures, reference materials, positive/negative cut-off values, and batch-to-batch quality control requirements. At present, differences in method make cross-study comparison difficult. Common standards would also make it easier to test processed products and minor species, both of which remain underrepresented in current research. That would help cross-laboratory comparison, support regulatory acceptance, and give the food industry a more realistic basis for adopting protein biomarker testing in routine quality assurance.

Taken together, these four priorities provide a practical roadmap for dealing with the main steps in the translational barrier cycle. For that reason, it may be worth slowing purely descriptive differential protein discovery work and putting more effort into validation and translation. One might expect new candidate discovery to remain the main priority, but the larger problem now seems to be limited follow-through on markers already proposed. Funding agencies could help by creating programs that require both targeted quantification and a rapid detection prototype as deliverables.

6. Conclusion

Proteomics has generated a long list of candidate quality biomarkers for chilled and frozen meat and aquatic products, yet their path to application is blocked by four major barriers: insufficient condition universality,

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difficulty in migrating from mass spectrometry to rapid detection, lack of quantitative links to macroscopic quality indices, and narrow species and processing coverage. These barriers form a self-reinforcing cycle, with the discovery-to-validation gap as its most vulnerable node. This review shifts the focus from "finding more biomarkers" to "making existing ones usable" and proposes four interconnected priority actions in response: multi-laboratory, multi-species validation of the most frequently reported candidate; construction of quantitative models linking proteomic data to quality endpoints; development of field-deployable rapid detection prototypes; and establishment of consensus standards for sample preparation, threshold values, and quality control.

If these actions are carried out consistently, especially by refining standardized protocols and widening sample coverage to include more species, storage conditions, and processing types, validation data should build up over time across different biological and technological settings. That would help balance the industry's continuing concern over whether the same biomarkers can be applied universally.

On that basis, the quantitative models and rapid test formats developed from these data could shift current analytical workflows away from expensive mass spectrometry and lab-based settings toward lower-cost, on-site testing tools. The shift will not be quick.

Moving from laboratory discovery to industrial use is still difficult, but coordinated work by academia, industry, and funding agencies may allow proteomics to provide practical tools for monitoring freshness and freeze-thaw history. If that happens, cold-chain quality management may move from an experience-based approach to a more data-driven o*ne.*

References

[1] M. Gagaoua and B. Picard, "Current Advances in Meat Nutritional, Sensory and Physical Quality Improvement," Foods, vol. 9, no. 3, p. 321, Mar. 2020, doi: 10.3390/foods9030321.

[2] G. Paredi, M.-A. Sentandreu, A. Mozzarelli, S. Fadda, K. Hollung, and A. M. de Almeida, "Muscle and meat: new horizons and applications for proteomics on a farm to fork perspective," J Proteomics, vol. 88, pp. 58–82, Aug. 2013, doi: 10.1016/j.jprot.2013.01.029.

[3] J. Chen and N. Zheng, "Accelerating protein biomarker discovery and translation from proteomics research for clinical utility," Bioanalysis, vol. 12, no. 20, pp. 1469–1481, Oct. 2020, doi: 10.4155/bio-2020-0198.

[4] R. Thomas, D. Sharma, R. Thomas, D. Bharadwaj, J. N. Vishwakarma, and V. K. Gupta, "Exploring potential biomarkers in foods of animal origin," J Food Sci Technol, vol. 62, no. 10, pp. 1825–1841, Oct. 2025, doi: 10.1007/s13197-025-06412-x.

[5] Q.-S. Ren, K. Fang, X.-T. Yang, and J.-W. Han, "Ensuring the quality of meat in cold chain logistics: A comprehensive review," Trends in Food Science & Technology, vol. 119, pp. 133–151, Jan. 2022, doi: 10.1016/j.tifs.2021.12.006.

[6] N. Soltanizadeh, M. Kadivar, J. Keramat, and M. Fazilati, "Comparison of fresh beef and camel meat proteolysis during cold storage," Meat Sci, vol. 80, no. 3, pp. 892–895, Nov. 2008, doi: 10.1016/j.meatsci.2008.04.007.

[7] Y. Kominami, T. Hayashi, T. Tokihiro, and H. Ushio, "Peptidomic analysis characterising proteolysis in thaw-aging of beef short plate," Food Chem (Oxf), vol. 3, p. 100051, Dec. 2021, doi: 10.1016/j.fochms.2021.100051.

[8] H. Negishi, E. Yamamoto, and T. Kuwata, "The origin of the 30 kDa component appearing during post-mortem ageing of bovine muscle," Meat Sci, vol. 42, no. 3, pp. 289–303, Mar. 1996, doi: 10.1016/0309-1740(95)00044-5.

[9] C. Y. Ho, M. H. Stromer, and R. M. Robson, "Identification of the 30 kDa polypeptide in post mortem skeletal muscle as a degradation product of troponin-T," Biochimie, vol. 76, no. 5, pp. 369–375, Jan. 1994, doi: 10.1016/0300-9084(94)90110-4.

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[10] J. Stagsted, E. Bendixen, and H. J. Andersen, “Identification of specific oxidatively modified proteins in chicken muscles using a combined immunologic and proteomic approach,” J Agric Food Chem, vol. 52, no. 12, pp. 3967–3974, Jun. 2004, doi: 10.1021/jf035503d.

[11] M. Pazos, R. Maestre, J. M. Gallardo, and I. Medina, “Proteomic evaluation of myofibrillar carbonylation in chilled fish mince and its inhibition by catechin,” Food Chem, vol. 136, no. 1, pp. 64–72, Jan. 2013, doi: 10.1016/j.foodchem.2012.07.109.

[12] O. P. Soladoye, M. L. Juárez, J. L. Aalhus, P. Shand, and M. Estévez, “Protein Oxidation in Processed Meat: Mechanisms and Potential Implications on Human Health,” Compr Rev Food Sci Food Saf, vol. 14, no. 2, pp. 106–122, Mar. 2015, doi: 10.1111/1541-4337.12127.

[13] D. Lomiwes, M. M. Farouk, E. Wiklund, and O. A. Young, “Small heat shock proteins and their role in meat tenderness: a review,” Meat Sci, vol. 96, no. 1, pp. 26–40, Jan. 2014, doi: 10.1016/j.meatsci.2013.06.008.

[14] C. T. Moncau, A. F. Rosa, J. P. Eler, and J. C. C. Balieiro, “Proteínas de choque térmico na qualidade da carne,” Pesquisa Agropecuaria Brasileira, pp. 90–96, Feb. 2018, doi: 10.1590/S1678-3921.pab2018.v53.24794.

[15] F. Zhao et al., “Proteomics and Metabolomics Profiling of Pork Exudate Reveals Meat Spoilage during Storage,” Metabolites, vol. 12, no. 7, p. 570, Jun. 2022, doi: 10.3390/metabo12070570.

[16] T. S. Anand et al., “Development and validation of mitochondrial citrate synthase enzyme-based sandwich ELISA for reliable authentication of fresh vs frozen thawed pork meat,” Food Control, vol. 180, pp. 111672–111672, Jan. 2026, doi: 10.1016/j.foodcont.2025.111672.

[17] R. Banerjee et al., “Lateral flow immunoassay-based absolute point-of-care technique for authentication of meat and commercial meat products,” J Food Sci Technol, vol. 60, no. 2, pp. 772–782, Feb. 2023, doi: 10.1007/s13197-022-05663-2.

[18] O. E. Tsitsilonis et al., “A skeletal muscle troponin T specific ELISA based on the use of an antibody against the soluble troponin T (16-31) fragment,” J Immunol Methods, vol. 268, no. 2, pp. 141–148, Oct. 2002, doi: 10.1016/s0022-1759(02)00186-2.

[19] C. K. F. Rahman et al., “ELISA-based detection of fresh and frozen-thawed lamb meat: a promising analytical approach for meat authentication,” Anal Methods, vol. 16, no. 37, pp. 6364–6372, Sep. 2024, doi: 10.1039/d4ay00874j.

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Conflicts of Interest

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