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Review

Spoilage Biomarkers in Poultry Meat: A 25 Years Overview

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Abstract

Meat spoilage remains one of the major challenges affecting food quality, shelf life, and economic sustainability worldwide. Over the last 25 years, significant advances have been made in understanding the biochemical, microbiological, and environmental mechanisms responsible for spoilage in fresh and processed meat products. Spoilage is primarily driven by microbial proliferation, particularly psychrotrophic and mesophilic bacteria such as *Pseudomonas* spp., *Brochothrix thermosphacta*, lactic acid bacteria, and members of *Enterobacteriaceae*, whose dominance depends strongly on storage temperature, oxygen availability, pH, and packaging conditions. These microorganisms promote proteolysis, lipolysis, and the production of volatile organic compounds (VOCs), biogenic amines (BAs), sulphur-containing metabolites, and other compounds associated with undesirable odour, discoloration, slime formation, and texture deterioration. Attempting to identify biomarkers that allow for the early detection of these compounds may be essential to help prevent their deterioration and subsequent disposal. Parallel progress in preservation technologies has shifted from conventional refrigeration, vacuum packaging, and modified atmosphere packaging toward innovative strategies such as biopreservation, antimicrobial coatings, essential oils, and high-pressure processing, aiming to extend shelf life while maintaining sensory quality. In addition, intelligent packaging systems and non-destructive monitoring tools based on biosensors, spectroscopy, and nanomaterials have emerged as promising approaches for real-time spoilage detection. Despite these advances, spoilage remains highly variable across meat types, processing environments, and supply chains, emphasizing the need for integrated control strategies. Future research should focus on predictive microbiology, sustainable preservation systems, and microbiome-guided interventions to reduce meat losses and improve food safety across global markets.

Keywords: biomarkers; spoilage; shelf life; poultry

1. Introduction

Over the years, meat production has increased globally, reaching 371 million tons in 2023. Among all types of meat, poultry registers the highest global production, with a total of 146 million tonnes (FAO, 2024). Despite all the efforts undertaken by several organizations to prompt a paradigm shift regarding consumption patterns, meat remains a key provider of essential nutrients for human health, and it is highly appreciated by consumers (Bohrer, 2017; FAO, 2024; Pereira & Vicente, 2013). Among the most consumed meat and meat products is poultry, as it is cheaper, recognized as healthier and the one producing the lower water footprint (FAO, 2024; Gerbens-Leenes et al., 2013). These attributes set poultry meat at the top of the consumers' preferences and justify all the efforts to increase meat quality and decrease waste (FAO, 2024). According to a recent study, 23% of all meat produced is lost and wasted (Karwowska et al.,

2021), particularly at the consumption stage within households (Caldeira et al., 2019). Nevertheless, incorrect meat processing and lack of precautions during packaging, transport and storage can lead to meat spoilage. Moreover, beyond the economic impact, meat production is linked to several environmental issues (Kilibarda et al., 2023). In 2013, it was estimated that poultry production contributed for 8.7% of total greenhouse gas emissions (Gerber et al., 2013). Moreover, a recent study forecasts an increase in poultry meat production, potentially reaching 50% of total meat production by 2030, potentially aggravating existing environmental challenges and food waste concerns (Kang et al., 2025).

Meat spoilage results from a series of complex physicochemical transformations which lead to undesirable changes in meat. These alterations are mostly related to changes in colour and texture and/or the development of slime and off-odours and off-flavours (Zhu et al., 2022). Additionally, meat provides a proper environment for microbial proliferation, including pathogens, compromising meat quality and safety (Labadie, 1999).

Spoilage starts in the slaughterhouse and ends in the consumer's house at the cooking time (Kilibarda et al., 2023). From the animal slaughter, a series of events related to systems failure occurs as a result of pre-slaughter stress. Specifically, during this process, ATP synthesis ceases, oxygen delivery impairs, vitamins and antioxidants become depleted, nervous regulation and respiration cease and glycogen depletion leads to a pH decrease (Addis, 2015). Such events culminate in the failure of the reticuloendothelial system which makes the cells unable to phagocyte foreign bodies, providing a highly susceptible niche for microbial invasion and growth (Uribe-Querol & Rosales, 2017). Additionally, inadequate sanitary conditions at the slaughterhouse, improper handling, processing and transportation conditions, as well as storage and packaging features can promote microbial growth (Dave & Ghaly, 2011; Kilibarda et al., 2023).

Spoilage rate is highly influenced by several factors such as temperature, pH, bacterial activity, water, nutrient availability and storage conditions (Luong, Coroller, et al., 2020). According to the European Union legislation (Regulation (EC) No. 853/2004), after post-mortem inspection, slaughtered animals must be cooled to a temperature below 4 °C as fast as possible, emphasizing the impact of temperature in meat spoilage (European Parliament & Council of the European Union, 2004). Also, it is known that a slight temperature change during meat transport and storage can significantly impact bacterial growth rates, compromising meat shelf life (Ghollasi-Mood et al., 2017; Zhang et al., 2012).

Meat spoilage is driven by multiple interconnected mechanisms (Luong et al., 2020a), detailed in Section 2. However, microbial spoilage is the leading cause of meat spoilage, as a result of substrate metabolization that leads to major sensorial alterations perceptible by the consumers (Zhu et al., 2022). The most frequently identified microorganisms in spoiled meat are *Pseudomonas* spp., some genus of the *Enterobacteriaceae* family, lactic acid bacteria (LAB) and *Brochothrix thermosphacta* (Fraqueza et al., 2012; Mikš-Krajnik et al., 2016). The microbial population evaluation and its prevalence is a major indicator of meat quality (Balamatsia et al., 2006). However, to assess the microbiological content of meat samples, it is necessary to conduct cell culture procedures which require time for the colony proliferation. As this analysis does not detect early spoilage, several authors have associated meat deterioration with the formation of different volatile organic compounds (VOCs) and non-volatile, in particular biogenic amines (BAs) and total volatile basic nitrogen (TVB-N) (Balamatsia et al., 2006; Baston et al., 2010). Biogenic amines formation occurs through the enzymatic decarboxylation of free amino acids due to the enzymatic activity of the microbial population present in the meat and it is highly dependent on the environmental conditions, namely presence of O₂, temperature and pH (Balamatsia et al., 2006; Fraqueza et al., 2012). Besides assessing freshness, this analysis also provides an indication of the product's toxicity, representing a key parameter in evaluating livestock quality (Balamatsia et al., 2006). Therefore, there is an urgent need to develop new tools

to effectively evaluate these parameters in meat, in order to assess its quality (Chen et al., 2024; Wojnowski et al., 2018).

Considering the complexity of the meat spoilage phenomenon, its dimension and major impact on climate changes and economic systems driven by significant meat losses, it is crucial to deeply comprehend the entire spoilage process, including the microorganisms involved and potential biomarkers for early spoilage detection and thus reducing the burden of this public health hazard. Therefore, a very large number of studies were dedicated to this thematic. The target of the published literature includes: identification of the main spoilage bacteria (Mikš-Krajnik et al., 2016), evaluation of the impact of storage parameters in spoilage (Balamatsia et al., 2007), detection of meat spoilage accurately through standard techniques and/or new approaches as spectrophotometric or imaging methods (Acquaticci et al., 2024), characterization and quantification of spoilage biomarkers (Acquaticci et al., 2024), assessment of alternatives to prevent spoilage (Chouliara et al., 2007), among others.

In this context, the aim of this study was to review: i) the main microorganisms associated with poultry spoilage (prevalent species, its corresponding meat alterations and relation with storage conditions) and ii) the main spoilage biomarkers (techniques employed, biomarkers and their correlation with bacterial species and biomarkers fluctuations through the supply chain). Some concluding remarks and future perspectives will also be included.

2. Mechanisms of Meat Spoilage

Meat spoilage is driven by multiple interconnected mechanisms that begin before slaughter and progress throughout the supply chain until the point of consumption. Three main mechanisms are traditionally recognized: (i) microbial contamination from various sources, (ii) lipid oxidation and other natural meat processes, and (iii) a series of autolytic enzymatic reactions that occur in muscle cells after slaughtering (Luong, Coroller, et al., 2020). However, additional factors such as protein and pigment photo-oxidation also contribute to quality deterioration during storage and retail display. In this section, these mechanisms are presented following the chronological sequence of the spoilage process: starting with pre-slaughter stress and its immediate post-mortem consequences (Section 2.1), followed by the autolytic enzymatic reactions triggered upon slaughter (Section 2.2), the progressive microbial contamination from various sources (Section 2.3), the chemical degradation of lipids through oxidation (Section 2.4), and finally, the photo-oxidative changes induced by environmental factors during storage and retail (Section 2.5). This sequential approach provides a comprehensive understanding of how each mechanism builds upon the previous, collectively driving meat deterioration.

2.1. Pre-Slaughter Stress and Post-Mortem Changes

The first element that impacts meat quality is the slaughter process itself, as animals inevitably undergo a stress period prior to and during slaughter. The physiological response to stress triggers the release of catecholamines and accelerates muscle glycogen breakdown, with direct consequences on post-mortem meat quality. Depending on the duration and intensity of the stress, two distinct conditions can arise, both detrimental to meat quality (Dave & Ghaly, 2011). When animals are subjected to prolonged or chronic stress, muscle glycogen reserves become significantly depleted before slaughter. As a result, post-mortem lactic acid production is insufficient, leading to a high ultimate pH (typically above 6.0). Under these conditions, meat becomes dark, firm and dry (DFD), a condition characterized by a closed muscle structure that retains water internally but presents a dry, sticky surface. DFD meat is particularly problematic because the elevated pH creates a favourable environment for microbial proliferation, considerably shortening its shelf life (Addis, 2015; Dave & Ghaly, 2011). Conversely, when animals experience acute, short-duration stress immediately before slaughter, a rapid post-

mortem glycolysis occurs while the carcass temperature is still elevated. This combination of low pH and high temperature promotes the denaturation of myofibrillar proteins, resulting in pale, soft and exudative (PSE) meat. PSE meat exhibits poor water-holding capacity, leading to significant drip loss, reduced juiciness and an unattractive pale appearance that diminishes consumer acceptance (Addis, 2015; Miller, 2002). In both conditions, the altered physicochemical properties of meat, particularly pH deviations and compromised protein structure, create a highly susceptible niche for microbial invasion and growth, ultimately accelerating the spoilage process (Addis, 2015; Dave & Ghaly, 2011; Miller, 2002).

2.2. Autolytic Enzymatic Reactions

A series of autolytic enzymatic reactions are triggered upon slaughter, as the cessation of blood flow deprives tissues of oxygen, nutrients and, consequently, energy. These reactions play a critical role in post-mortem changes, contributing to meat spoilage (Dave & Ghaly, 2011). After slaughter, the muscle metabolism shifts from aerobic to anaerobic pathways and several enzymes initiate different biochemical reactions - glycolysis, proteolysis and lipolysis (Abril et al., 2023). During glycolysis, the depletion of glycogen triggers enzymes (e.g. glucose 6-phosphate and phosphocreatine kinase) to reduce ATP, converting glucose in pyruvate and, consequently, forming lactic acid, which drops the pH of meat. As described previously, muscle acidification has impact on meat quality, namely in the susceptibility to microbial proliferation (Abril et al., 2023; Amaral et al., 2018). In parallel, proteolytic enzymes (e.g. calpains, cathepsins, aminopeptidases) are responsible for the autolysis of meat post-mortem, considering their role in the digestion of myofibrillar proteins, contributing for tenderization and texture changes (Abril et al., 2023; Dave & Ghaly, 2011). Finally, degradation of lipids by muscle lipases and phospholipases can compromise the flavour of meat due to the production of volatile compounds (Tatijaborworntham et al., 2022). All the processes described accelerate meat spoilage, considering the reaction products formed and multiple physicochemical alterations, namely in texture, flavour, odour, colour and contamination susceptibility (Dave & Ghaly, 2011).

2.3. Microbial Contaminations

Meat is not considered sterile after slaughtering, as the environment and conditions inherent to the process favour microbial contamination (Salama & Chennaoui, 2024; Zhu et al., 2022). Contamination can originate from multiple sources throughout the production chain. At the slaughterhouse, the animal's skin, feathers, gastrointestinal tract and respiratory system constitute primary reservoirs of microorganisms. During processing steps such as de-feathering, evisceration and carcass washing, bacteria can be transferred to the meat surface through direct contact or cross-contamination via equipment, water and workers' hands (Dave & Ghaly, 2011; Kilibarda et al., 2023). Furthermore, inadequate sanitary conditions at the processing facilities, including poorly sanitized surfaces and utensils, can further increase the microbial load (Moazzami et al., 2025; Rouger et al., 2017). Beyond the slaughterhouse, the extent of contamination is influenced by multiple factors along the supply chain, including the type of meat, further processing conditions, packaging, distribution and storage (Zhu et al., 2022). Processed meat products, particularly ground meat, have been shown to present higher contamination levels and a greater incidence of pathogens compared to primary cuts, due to the additional handling and increased surface area exposed to microbial colonization (Álvarez-Astorga et al., 2002). Although microbial contamination is inevitable, it is well established that certain parameters throughout the supply chain, from slaughter to the end-user, can effectively delay spoilage, particularly through the use of appropriate packaging and proper storage conditions (Demirhan & Candoğan, 2017; Miller, 2002). Importantly, within the microbial diversity present in meat, some pathogenic species may also occur, namely *Salmonella* spp.,

Campylobacter jejuni and *Listeria monocytogenes*, posing a significant risk for foodborne illnesses in the population (Moazzami et al., 2025; Zhu et al., 2022). A detailed analysis of the specific spoilage organisms in poultry meat and their prevalence under different conditions is presented in Section 3.

2.4. Lipid Oxidation and Natural Processes

Lipid oxidation is a major chemical process that accelerates meat spoilage and constitutes one of the primary causes of quality deterioration in muscle foods. Following slaughter, blood stops circulating, compromising all metabolic processes, including the antioxidant defence systems that normally protect cell membranes from oxidative damage. As a consequence, fatty acid oxidation is promoted, particularly in polyunsaturated fatty acids, which are highly susceptible to oxidative attack due to the presence of multiple double bonds in their structure (Amaral et al., 2018). This process proceeds through three sequential stages: initiation, propagation and termination. During initiation, the removal of a hydrogen atom from an unsaturated fatty acid generates a lipid free radical, which rapidly reacts with molecular oxygen to form peroxy radicals. These radicals, in turn, abstract hydrogen atoms from adjacent fatty acids, generating hydroperoxides and propagating the oxidative chain reaction. Hydroperoxides are inherently unstable and undergo further decomposition, producing a wide range of secondary oxidation products, including aldehydes (e.g. hexanal, pentanal, malondialdehyde), ketones and alcohols, among others (Dave & Ghaly, 2011; Ladikos & Lougovois, 1990). Notably, some of these secondary products, such as 4-hydroxy-2-trans-nonenal and malondialdehyde, are highly reactive and can interact with proteins and other cellular components, further contributing to quality decline. The accumulation of these compounds has significant implications for meat quality, as they are directly responsible for the development of rancid off-flavours and off-odours, colour changes, particularly through the oxidation of myoglobin, and loss of nutritional value, namely through the degradation of essential fatty acids and fat-soluble vitamins (Dave & Ghaly, 2011). Moreover, the rate and extent of lipid oxidation are influenced by several factors, including the fatty acid composition of the meat, the presence of pro-oxidant metals (e.g. iron released from myoglobin and haemoglobin), oxygen availability, temperature and light exposure (Amaral et al., 2018). Poultry meat, given its relatively high content of polyunsaturated fatty acids compared to red meats, is particularly susceptible to lipid oxidation, which makes this mechanism especially relevant in the context of poultry spoilage (Ladikos & Lougovois, 1990).

2.5. Photo-Oxidation and Environmental Factors

Beyond endogenous biochemical processes, external environmental factors encountered during storage, transport and retail display also contribute to meat spoilage. Photo-oxidation occurs when light energy, especially ultraviolet (UV) and visible wavelengths from retail lighting, interacts with photosensitive compounds naturally present in meat, such as riboflavin and myoglobin (Faustman & Cassens, 1990; Suman & Joseph, 2013). This interaction generates reactive oxygen species (ROS), including singlet oxygen (1O_2), which initiate oxidative reactions affecting both pigments and lipids (Lund et al., 2011). Myoglobin, the primary pigment responsible for meat colour, is particularly susceptible: under light exposure, oxymyoglobin (Fe^{2+} , bright red) is oxidized to metmyoglobin (Fe^{3+} , brown), leading to surface discolouration that negatively impacts consumer acceptance and increases product waste (Suman & Joseph, 2013). Additionally, singlet oxygen reacts directly with unsaturated fatty acids, producing hydroperoxides at a faster rate than conventional autoxidation, and generating secondary products responsible for rancid off-flavours (Lund et al., 2011). Protein oxidation also contributes to quality decline. Reactive oxygen species can modify amino acid side chains through carbonylation and promote disulfide bond formation, leading to decreased protein solubility, reduced water-holding capacity and texture deterioration (Estévez, 2011; Lund et al., 2011). Other

environmental factors further accelerate spoilage, including inadequate humidity control, which promotes surface dehydration and texture hardening, and improper frozen storage, which may cause freezer burn through ice sublimation (Jay et al., 2005). Together with temperature fluctuations during transport and storage (Ghollasi-Mood et al., 2017; Zhang et al., 2012), these environmental factors act synergistically with endogenous spoilage mechanisms, reinforcing the importance of controlling storage conditions, packaging integrity and retail display parameters to preserve poultry meat quality.

3. Literature Overview

Based on the research terms “spoilage”, refined results within “chicken”, and “microbial”, 482 publications related to the subject were obtained from the Web of Science database on 15 January 2026, and all records were exported in a plain text file format. The term “poultry” was not addressed in the database because it was found to reduce the number of studies, as chicken meat is actually the most reported. The data were later processed in the VOSviewer software (version 1.6.20 for Windows) based on the all-keyword co-occurrence full counting method for analysis to create a network view map based on that bibliographic data, presented in Fig. 1. The minimum occurrence was defined to be five (software standard), and terms were extracted from the titles and abstracts of the articles. Of 2151 keywords, 205 were found to meet the threshold for the analysis. A thesaurus file (optional) was applied to merge synonyms, unify bacterial nomenclature, and remove irrelevant terms to improve network clarity. In the network view, the extracted items (n=93) are represented by a label, and each circle (node) size is defined by the item's frequency of occurrence. The colour defines the cluster (n=6) to which an item is inserted, while the lines represent the links (co-occurrence relationships) between the items. As shown in Fig. 2, it was possible to verify that the most frequently occurring items (largest circles) were spoilage, shelf-life, meat, chicken, and quality. The red cluster constituted the largest group with 23 items, comprising terms more focused on microbiological quality and the associated microorganisms, such as *Listeria*, *Salmonella*, *E. coli* and *Campylobacter*. On the other hand, the green cluster grouped 20 terms related to storage. The dark blue cluster grouped terms more related to shelf-life and preservation. This cluster contained 19 items in total. The yellow cluster, which had 17 items, grouped terms mostly concerning to spoilage. By selecting the term “sensory properties”, 11 linked items were highlighted, such as lipid oxidation, colour, and freshness. The lowest cluster, light blue, grouped the three items: chemical composition, stability, and physicochemical properties.

Following the same principle described before (Figure 1), based on the research terms “spoilage”, refined results within “chicken”, and “biogenic”, 92 publications related to the subject were obtained from the Web of Science database, on 15 January 2026. Of the 591 keywords, 35 were found meet the threshold for the analysis. After the thesaurus file application, in the network view, the objects of interest (n = 24) are represented in Figure 2(a). Four clusters were detected, where cadaverine, putrescine, and histamine were the BAs related to spoilage.

Based on research terms “microbial”, refined results within “chicken”, and “compounds”, 172 publications related to the subject were obtained from the Web of Science database, on 15 January 2026. Of 1030 keywords, 68 meet the threshold for the analysis. After the thesaurus file application, in the network view, the objects of interest (n = 33) are shown in Figure 2(b). The colours define the clusters (n=5), where the terms lactic-acid bacteria, packaging, bacterial community, freshness, preservation, and stability seem to be directly related to volatile organic compounds.

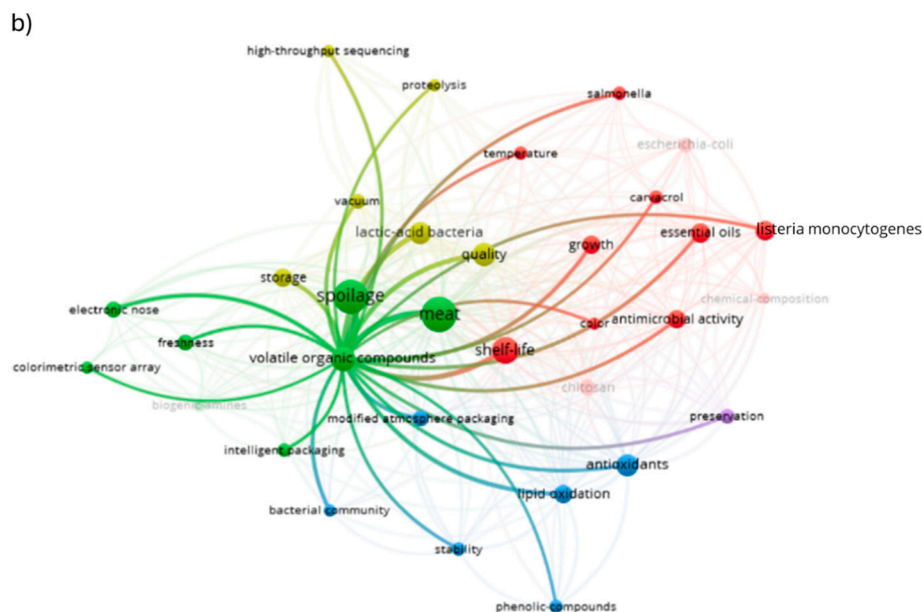


Figure 2. Network view maps generated in VOSviewer. Selection of the “biogenic amines” (a) and “volatile organic compounds” terms (b), in the bibliometric mapping and highlighting of the most connected items from the Web of Science database.

4. Microbial Spoilage

The process of meat spoilage is characterized by several sensorial alterations that decrease meat quality, namely through the production of off-flavours, mucus and exudates, as well as physical alterations (e.g. colour, texture). This process is mainly driven by specific spoilage organisms (SSO). These microorganisms, initially present in low number within a substrate, are capable of rapidly proliferating under favourable conditions, considering their ability to metabolize the available substrate and produce metabolites that change meat properties (Huis in't Veld, 1996; Zhu et al., 2022). According to the UK Health Security Agency, raw meat that presents more than 10^7 CFU per gram must undergo a microbial assessment, in order to fully characterize the microbiota (UK Health Security Agency, 2024). Considering the global scale of poultry meat consumption and its considerable levels of waste, extensive efforts have been undertaken to identify and characterize microbial species present in poultry livestock, namely in chicken, turkey, duck and quail. Tables 1 and 2 summarize studies that describe the microbial population detected in different types of poultry, under diverse experimental conditions (e.g. packaging, storage, natural preservatives, among others). From the 54 studies compiled, 80% correspond to chicken, 11% to turkey and 2% to poultry (unspecified) (see Figure 3A). The remaining 7% focus on more than one type of poultry. Regarding studies conducted on chicken, many do not clearly specify the anatomical part analysed, often referring to 'carcasses' or 'chicken'. However, a significant number of studies focused specifically on breast meat (43%) and leg or wing portions (7%), ensuring some consistency between experiments. These studies focused on examining the microbiological diversity of different types and cuts of poultry (see Figure 3B), along with their sensorial properties, in order to determine which parameters can improve product shelf life and quality, thereby reducing waste and foodborne illnesses. Across all studies, the most frequently reported were *Pseudomonas* species and LAB detected in 52% and 54% and of the cases, respectively. Additionally, other microorganisms were detected, including those belonging to the *Enterobacteriaceae* family (37%), which includes *Salmonella* spp. (19%), and coliforms, namely *E. coli* (20%); *Listeriaceae* family, that includes *B. thermosphacta* (24%), and *Listeria* spp. (13%). Among others, *Staphylococcus* spp. and *Carnobacterium* spp. were present.

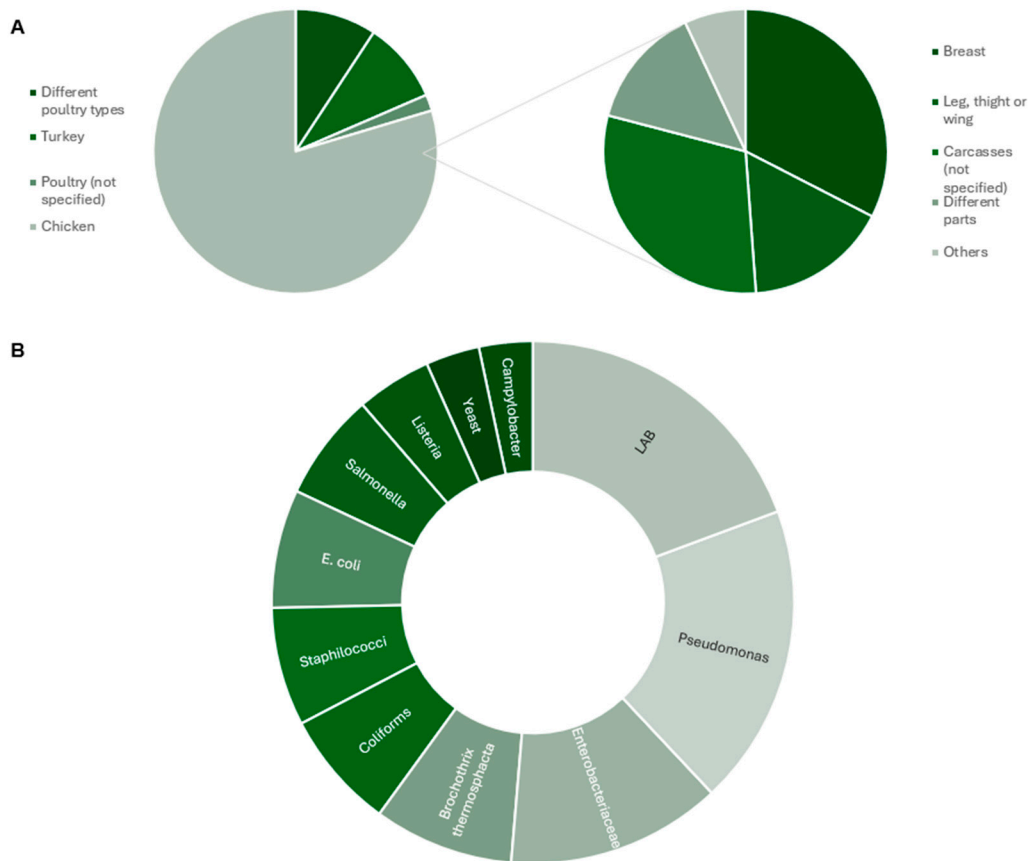


Figure 3. Microbiological assessment of poultry meat. **(A)** Incidence of the different poultry types and cuts analysed and **(B)** microbiological populations identified.

Considering that each microorganism has its ideal growth conditions, factors such as meat processing, packaging and storage play a critical role in the microbial population diversity and prevalence. Moreover, each species promotes different meat alterations.

Regarding the predominant species found in poultry meat (Figure 3B), *Pseudomonas* species, such as *P. fragi*, *P. fluorescens* and *P. lundensis* are dominant under aerobic conditions. On the other hand, *B. thermosphacta*, *E. coli*, *Staphylococcus* spp., *Listeria* spp. and LAB, including *Lactobacillus* spp., are facultative anaerobic bacteria which promote meat spoilage in different packaging. LAB, in particular, has showed adaptability to different temperature ranges (Zhang et al., 2012). Finally, anaerobic species, such as *Clostridium* spp. do not rely on oxygen (Rouger et al., 2017; Salama & Chennaoui, 2024; Zhu et al., 2022).

Results presented in Figure 3 showcase the wide microbiological diversity associated with poultry meat and underscore the importance of addressing SSO, whose selective activity largely drives product deterioration, thereby impacting both quality and shelf life.

These studies mainly investigate the composition and growth dynamics of microbial populations under different conditions, particularly focusing on packaging strategies, such as air, vacuum and modified atmospheres (MAP). Air-packaging is known to cause colour changes, production of undesirable flavours and odours, while promoting growth of aerobic microorganisms and spoilage through oxidative reactions (Doulgeraki et al., 2012; Zouharová et al., 2023). In contrast, different vacuum and MAP-packaging evaluations showed the potential of these types of packaging in promoting shelf-life extension and preservation of meat quality. In vacuum packaging, air is removed before sealing, providing an O₂-depleted environment that limits aerobic microbial growth. On the other hand, MAP allows different gas mixtures, using O₂, carbon dioxide (CO₂), nitrogen (N₂) or even inert gases, such as argon (Ar) (Luong et al., 2020;

Zouharová et al., 2023). Particularly, CO₂ and N₂ are commonly used, given their bacterial proliferation inhibition potential and prevention of oxidative reactions in meat, respectively (Zouharová et al., 2023). Nevertheless, these O₂-deprived atmospheres promote the proliferation of facultative anaerobic microorganisms, which grow under both aerobic and anaerobic conditions (Doulgeraki et al., 2012).

Among the 54 studies, 23 included MAP packaging. Different authors evaluated microbial populations of chicken meat packed in MAP with high N₂ content (Balamatsia et al., 2007; Balamatsia et al., 2006; Gallas et al., 2010; Rossaint et al., 2015). These studies investigated chicken breasts stored at low temperatures (2-4 °C), over several days, to assess how different atmospheres influence product quality. Results showed the presence of different species, namely *Pseudomonas* spp., *B. thermosphacta* and LAB, being the latter one predominant. Considering LAB are facultative anaerobic microorganisms, their growth is enhanced under anaerobic or CO₂-enriched environments (Herbert et al., 2013). Moreover, when compared with air-packaging, MAP delayed aerobic microorganisms' growth due to its inhibitory effects on microbial growth, by reducing the proliferation rate (Farber, 1991).

Herbert et al. (2013) focused on comparing six different combinations of Ar or N₂-enriched atmospheres on chicken breasts stored at low temperatures, investigating microbial proliferation throughout a 24-day storage. Results revealed no significant differences in microbial growth between the tested atmospheres, with exception of LAB, which were favoured under Ar and N₂-enriched environments, depleted from oxygen. This outcome is consistent with those reported previously. Additionally, samples packed in MAP with 15% Ar showed improved colour preservation, a key factor influencing consumers' initial impression of meat and potentially contributing to the reduction of food waste. Similarly, Fraqueza et al. (2009) evaluated the microbial growth of turkey breasts packed under different MAP conditions, using CO₂, Ar and N₂. Compared with air-packaging, all MAP conditions extended the products' shelf life. However, packages containing CO₂ proved more effective at delaying bacterial growth, particularly when combined with Ar. On the other hand, Balamatsia et al. (2007) evaluated the microbial composition of chicken breast fillets stored at low temperatures and packed under different conditions as air, vacuum and MAP packaging with N₂ and CO₂-enriched atmospheres. All approaches contributed to extending meat shelf life comparatively with air-packaging, particularly CO₂-enriched atmosphere. Notably, this packaging better preserved sensory quality, which play a decisive role in consumer choice. Importantly, vacuum and CO₂-enriched packaging presented lower growth of *Pseudomonas* spp., due to the CO₂ bacteriostatic effect explained previously (Balamatsia et al., 2007).

Similar to the different types of packaging, several researchers are focused on understanding the impact of storage conditions on meat quality. A study using chicken breast assessed the effect of temperature fluctuations (0-4 °C, 4 °C and 4-10 °C) during several days, revealing that some bacterial populations were affected by these variations (Zhang et al., 2012). As expected, *Pseudomonas* spp., LAB and *Enterobacteriaceae* showed greater counts when exposed to variations between 4-10°C, whereas 0-4°C fluctuations retarded microbial growth. Additionally, variations at higher temperatures induced more microbiological diversity. Therefore, these results highlight the importance of temperature monitoring and proper storage conditions at low temperatures to ensure product quality.

Additionally, different studies assessed the microbial population of air-packed chicken breasts stored at low and high temperatures (Ghollasi-Mood et al., 2017; Mikš-Krajnik et al., 2016). Results showed that *Pseudomonas* spp. was dominant in all conditions and presented a higher correlation with spoilage, revealing a critical role in meat deterioration (Ghollasi-Mood et al., 2017). Moreover, it was shown that this SSO exhibits enhanced ability to proliferate at low temperatures, compared to other species, due to their capacity to metabolize the available

substrates, which can compromise meat quality despite proper storage conditions (Cortez-Vega et al., 2012; Ghollasi-Mood et al., 2017).

On the other hand, different studies focused on investigating new approaches to extend meat shelf life, in order to reduce large amounts of waste. Chouliara et al. (2007) assessed the combination of different MAP atmospheres (N₂ and CO₂-enriched) and oregano essential oil, as a natural preservative, for shelf-life extension of chicken breast. The phenolic composition of this oil provides anti-microbial properties that enhance its preservative properties (Juliano et al., 2000). Results showed that both MAP packaging and oregano oil at 1% concentration presented the greatest shelf-life extension and reduced microbial counts, particularly *Pseudomonas* spp., LAB and *B. thermosphacta*, showing the enhanced potential of this natural preservative in meat quality.

Nevertheless, despite all the efforts, it is important to emphasize that slaughtering conditions and subsequent meat handling strongly influence the initial microbial population, indicating that meat quality and shelf life depend on multiple factors beyond storage and packaging conditions (Morshdy et al., 2025; Rouger et al., 2017). A recent study conducted in Swedish slaughterhouses reported the prevalence of different bacteria, namely *C. jejuni* and *L. monocytogenes*, proving the lack of hygiene prevalent in many facilities, compromising meat quality and food safety (Moazzami et al., 2025). Moreover, another study conducted on chicken cuts and by-products revealed that processed meat, particularly ground meat, presented higher contamination levels and incidence of pathogens compared to primary cuts (Álvarez-Astorga et al., 2002). The multiplicity of contamination sources has attracted significant scientific attention, thus driving efforts to mitigate meat contamination, improving public health by reducing foodborne diseases.

Table 1. Microorganisms associated with chicken meat under different storage and packaging conditions.

Sample	Packaging/Storage environment	Experimental conditions	Microorganisms	Reference
Ten packages of cooked chicken product (not specified)	MAP (80% N ₂ , 20% CO ₂)	3 storage temperatures: 4-6 °C, 7-9 °C, 11-13 °C Different time points (T0 - eight days prior to their expiration date; T1 - at the expiration date; T2 - four days after the expiration date; and T3 - eight days after the expiration date)	<i>Carnobacterium divergens</i> (n=149) <i>Carnobacterium maltaromaticum</i> (n=39) <i>Lactobacillus sakei</i> (n=4) <i>Hafnia alvei</i> (n=1) <i>Rahnella aquatilis</i> (n=113) <i>Serratia proteamaculans</i> (n=188)	Geeraerts et al. 2019
Carcasses (n=n.d.)	Unpacked; Air-packaging (PAP) and MAP (80% CO ₂ , 20% N ₂)	Stored at 4 °C Unpacked (control): Day 0 Air-packaging: Day 4 MAP: Day 8	Lactid acid bacteria <i>Aeromonas</i> spp. <i>Acinetobacter</i> spp. <i>Escherichia coli</i> <i>Streptococcus</i> spp. <i>Pseudomonas fragi</i> <i>Pseudomonas fluorescens</i> <i>Lactococcus raffinolactis</i> <i>Serratia liquefaciens</i> <i>Shewanella</i> spp. <i>Carnobacterium maltaromaticum</i>	Wang et al., 2017

Carcasses (n=80)	Unpacked	Two-stage sampling (washed and pre-washed carcasses) Stored at 0-4°C; Day 0	<i>Salmonella spp.</i> <i>Escherichia coli</i>	Mpundu et al., 2019
Carcasses (n=40)	Unpacked (n=10) Air-packed (n=30)	Stored at 4°C Day 1 for the fresh group and day 1 and 12 for the packed group	Aerobic bacteria (APC) <i>Campylobacter spp.</i> <i>Pseudomonas spp.</i>	Chen et al., 2020
Carcasses (n=1 707)	Unpacked	Stored at <4°C	Aerobic bacteria (APC) <i>Salmonella spp.</i> <i>Escherichia coli</i> <i>Enterococcus spp.</i> <i>Staphylococcus aureus</i>	Klaharn et al., 2022
Carcasses (n=1754)	Unpacked	Fresh (n=996), chilled (n=185) and frozen (n=573) Stored on ice Day 0 (immediately after arrival)	Aerobic bacteria (APC) <i>Salmonella spp.</i> <i>Escherichia coli</i>	Li et al., 2019
Carcasses (n=50)	Unpacked	Day 0 (within 24h)	<i>Salmonella spp.</i> <i>Escherichia coli</i>	Kumar et al., 2014
Breast (n=45)	Unpacked	Stored at 1-5.7°C for 8h for ageing purposes	<i>Aerobic mesophiles</i> <i>Escherichia coli</i> <i>Pseudomonas</i> <i>Coliforms</i>	Moreira et al., 2028

<p>Carcasses (n=636)</p>	<p>Unpacked</p>	<p>Chilling for 1 year Samples with temperature ≤10°C</p>	<p><i>Aerobic microorganisms</i> <i>Enterobacteriaceae</i> <i>Enterococcus</i> <i>Coagulase-positive Staphylococcus</i> <i>spp.</i> <i>Escherichia coli</i> <i>Campylobacter</i> <i>Clostridium perfringens</i></p>	<p>Lindblad et al.,2006</p>
<p>Carcasses (n=63)</p>	<p>Unpacked</p>	<p>Refrigerated Day 0 (immediately after arrival)</p>	<p><i>L. monocytogenes</i> <i>L. innocua</i> <i>L. welshimeri</i> <i>L. seeligeri</i></p>	<p>Antunes et al., 2002</p>
<p>Carcasses (n=144)</p>	<p>Does not specify</p>	<p>Does not specify</p>	<p><i>Campylobacter jejuni</i> <i>Salmonella enterica serotype</i> <i>Enteritidis</i> <i>Listeria monocytogenes</i> <i>Escherichia coli</i></p>	<p>Dan et al., 2015</p>
<p>Carcasses (n=100)</p>	<p>Does not specify</p>	<p>Transported on ice Day 0 (within 4h)</p>	<p><i>Listeria spp.</i> <i>Listeria monocytogenes</i> <i>L. innocua</i> <i>L. welshimeri</i> <i>L. grayi</i> <i>L. ivanovii</i></p>	<p>Capita et al., 2001b</p>

<p>Carcasses (n=40)</p>	<p>Does not specify</p>	<p>Transported under refrigeration Day 0 (within 4h)</p>	<p><i>Psychrotrophs</i> <i>Pseudomonads</i> <i>Fluorescent pseudomonads</i> <i>Enterococci</i> <i>Micrococcaceae</i> <i>Staphylococcus aureus</i> Yeasts and molds</p>	<p>Capita et al., 2001a</p>
<p>Carcasses (n=n.d.)</p>	<p>MAP1 - 62%CO₂, 8%O₂,30%N₂ MAP2 - 20% CO₂, 80% N₂</p>	<p>Stored at 1°C Day 0, 8, 12 and 15</p>	<p>Coliforms <i>Escherichia coli</i> <i>Pseudomonas</i> spp. <i>Brochothrix thermosphacta</i> Lactid acid bacteria <i>Staphylococcus aureus</i> Aerobic mesophilic bacteria</p>	<p>Saucier et al., 2000)</p>
<p>Carcasses (n=n.d.)</p>	<p>Vacuum-packaging CO₂-packaging</p>	<p>Stored at -1,5 and 3°C Vacuum-packaged samples from both storage temperatures, as well as CO₂ packaged samples stored at 3°C, were analyzed weekly Vacuum-packaged samples stored at -1.5°C were analyzed in 2-week intervals</p>	<p>Enterobacteria <i>Enterococci</i> <i>Pseudomonads</i> <i>Bacilli</i></p>	<p>Gill et al., 1990</p>

Half carcasses (n=84)	Air-packaging MAP1 - 80% CO ₂ , 20% N ₂ MAP2 - 30% CO ₂ , 70% N ₂	Stored at 4°C Day 0, 2, 4, 6, 8, 10 and 12	<i>Pseudomonas</i> spp. Lactid acid bacteria	Zhang et al., 2015
Carcasses (n=99)	Not specified	Fresh and frozen Frozen samples were thawed at room temperature Fresh samples: day 0 (3h postmortem) Frozen samples: day 1	<i>Salmonella</i> spp. <i>Listeria monocytogenes</i> <i>Campylobacter</i>	Nierop et al.,2005
Carcasses (n=193), ground meat (n=106) and ready-to-use products (n=323)	Packed but not specified	Stored at 4°C Day 0	<i>Campylobacter</i> spp.	Mackiw et al., 2011

Carcasses with neck skin (n=96)	Packed vs. tradicional slaughtering (manual processing)	Sampling during hot and cold season (2-week intervals) Stored at 4°C Day 0 (within 2h)	Aerobic bacteria (APC) <i>Escherichia coli</i> <i>Staphylococcus aureus</i> <i>Clostridium perfringens</i> <i>Salmonella</i> spp. <i>Listeria monocytogenes</i> Coliforms	Cohen et al., 2007
Breast with bone (n=n.d.)	MAP: 60% N ₂ , 40% CO ₂	Marinated samples Stored at -23°C and thawed at 5°C Day 1, 6, 11, 14 and 19	Yeast Mold Coliforms Lactic acid bacteria Psychrotrophic bacteria <i>Pseudomonas</i> spp. <i>Brochothrix thermosphacta</i>	Randell et al., 1995
Breast (n=44)	Air-packaging	Stored at 0, 4, 10 and 15°C At least 100 h	<i>Pseudomonas</i> spp. <i>Enterobacteriaceae</i> Lactic acid bacteria	Ghollasi-Mood et al., 2017
Breast (n=20)	Aerobically stored	Thawed at 4°C Every 2 days for 17 days	<i>Enterobacteriaceae</i> Aerobic mesophilic bacteria	Lázaro et al., 2015

Breast (n=n.d.)	Biopackaging comparing traditional PET – MAP: 70% O ₂ , 20% CO ₂ , 10% N ₂	Stored at 4°C Day 0, 3, 6, 10 and 14	Total aerobic mesophile Mesophilic Lactid acid bacteria <i>Enterobacteriaceae</i> <i>Pseudomonas</i> spp. Coagulase-positive <i>Staphylococcus</i> spp.	Alessandroni et al., 2022
Breast (n=36)	Aerobically stored and MAP: 30% CO ₂ , 70% N ₂	Stored at 4°C Day 0, 5, 8, 11, 14 and 17	<i>Pseudomonas</i> spp. Lactid acid bacteria <i>Enterobacteriaceae</i>	Balamatsia et al., 2006)
Breast (n=n.d.)	MAP1: 30% CO ₂ , 65%N ₂ , 5% O ₂ MAP2: 65% CO ₂ ,30% N ₂ , 5% O ₂ ; Vacuum-packaging; Aerobically stored	Stored at 4°C Day 1, 3, 5, 7, 11 and 15	<i>Pseudomonas</i> spp. Lactid acid bacteria <i>Brochothrix thermosphacta</i> <i>Enterobacteriaceae</i> Yeast	Balamatsia et al., 2007

<p>Breast (n=n.d.)</p>	<p>MAP1- 15% Ar, 60% O₂, 25% CO₂ MAP2 - 15% N₂, 60% O₂, 25% CO₂ MAP3 - 25% Ar, 45% O₂, 30% CO₂ MAP4 - 25% N₂, 45% O₂, 30% CO₂ MAP5 - 82% Ar; 18% CO₂ MAP6 - 82% N₂, 18% CO₂</p>	<p>Stored at 4°C 0-570 h</p>	<p><i>Lactobacillus</i> spp. <i>Brochothrix thermosphacta</i> <i>Pseudomonas</i> spp. <i>Enterobacteriaceae</i></p>	<p>Herbert et al., 2013</p>
<p>Breast (n=72)</p>	<p>Air packaging</p>	<p>Storage: 4°C, fluctuations between 0-4°C, fluctuations between 4-10°C Day 0 (before packaging), 1, 2, 3 and 4</p>	<p><i>Pseudomonas</i> spp. Lactid acid bacteria <i>Enterobacteriaceae</i> <i>Staphylococcus</i> spp. <i>Shewanella</i> spp. <i>Psychrobacter</i> sp. <i>Acinetobacter</i> sp. <i>Carnobacterium</i> spp. <i>Aeromonas</i> spp. <i>Weissella</i> spp.</p>	<p>Zhang et al., 2012</p>

Breast (n=80)	MAP1 - 25% CO ₂ , 75% O ₂ ; MAP2 - 25% CO ₂ , 75% N ₂	Stored 2-4°C Day 0, 3, 9 and 14	Psychrotrophic bacteria <i>Brochothrix thermosphacta</i> Lactic acid bacteria Coliforms (not detected on day 0)	Gallas et al., 2010
Breast (n=n.d.)	Aerobically packaged Aerobically packaged + oregano oil 0.1% w/w vs 1%w/w MAP1 (30% CO ₂ ,70%N ₂) vs. MAP2 (70% CO ₂ ,30%N ₂) MAP 1 + oregano oil 0.1% MAP 1 + oregano oil 1% MAP 2 + oregano oil 0.1% MAP 2 + oregano oil 1%	Stored at 4°C Day 0, 3, 6, 9, 12, 15, 20 and 25	<i>Pseudomonas</i> spp. Lactic acid bacteria <i>Brochothrix thermosphacta</i> <i>Enterobacteriaceae</i> Yeast	Chouliara et al., 2007
Breast (n=42)	Aerobically packaged and MAP (30% CO ₂ , 70%N ₂)	Precooked (fried) Stored 4°C Day 0, 4, 8, 12, 15, 19 and 23	<i>Pseudomonads</i> Lactic acid bacteria	Patsias et al., 2006
Breast with skin (n=n.d.)	Treated with 1% acetic acid solution vs. untreated MAP (70% CO ₂ , 30% N ₂)	Stored at 4°C Day 0, 3, 7, 14 and 21	<i>Pseudomonads</i> <i>Lactobacilli</i> <i>Enterobacteriaceae</i>	Jimenez et al., 1999

Raw boneless and skinless Breasts (n=8)	Aerobically stored	Microbiological analysis: samples stored at 4°C and 10°C - 7 days, in 24h- intervals. Samples stored at 21°C 3 days - each 3h during the first 12h and each 24h at the 1st,2nd,3rd days	Psychrotrophs <i>Pseudomonas</i> spp. Lactic acid bacteria <i>Brochothrix thermosphacta</i> H ₂ S producing bacteria Coliforms	Mikš-Krajnik et al., 2016
Boneless and skinless Breasts (n=54)	Air-packaging; MAP (High O ₂) and Vacuum-packaging	Stored at 2.2°C and 3.3°C Day 1, 3, 6, 7 and 8	<i>Pseudomonas</i> spp. <i>Enterobacteriaceae</i> Lactic acid bacteria	Chmiel et al., 2020
Boneless and skinless breast (n=8)	MAP1 - 70% O ₂ ,30% CO ₂ ; MAP2- 70% N ₂ ,30% CO ₂	Stored at 4°C Day 0, 3, 6, 9, 12, 15 and 20	<i>Lactobacillus</i> spp. <i>Brochothrix thermosphacta</i> <i>Pseudomonas</i> spp. <i>Enterobacteriaceae</i>	Rossaint et al., 2015
Boneless and skinless fillets and legs (n=n.d.)	MAP under mixtures of CO ₂ (35-70%) and N ₂	Raw and marinated Stored at 6°C Sampled on their labeled use-by date or within 1-4 days after this date	<i>Enterobacteriaceae</i> : <i>Hafnia</i> spp. <i>Serratia</i> spp. <i>Rahnella</i> spp. <i>Yersinia</i> spp.	Säde et al., 2013

Breasts without skin (n=21), breasts with skin (n=19) and ground meat (n=26)	Not specified	Fresh (4°C) and frozen (-18°C) samples	<i>Salmonella</i> spp. <i>Staphylococcus aureus</i> <i>Listeria monocytogenes</i> <i>Enterobacteriaceae</i> Sulphite-reducing clostridia Total aerobic mesophilic bacteria	Kozacinski et al., 2006
Breast and legs (thighs and drumsticks) (n=n.d.)	Aerobically stored	Stored at 4°C Day 1, 3, 5 and 7	<i>Psychrotrophic microorganisms</i>	Baston et al., 2010
Drumsticks (n=71), breasts (n=69) and thighs (n=70)	Not specified	Day 0 (immediately after arrival)	<i>Listeria monocytogenes</i>	Goh et al., 2012
Drumsticks (n=n.d.)	MAP - 70% CO ₂ , 15% O ₂ , 15% N ₂ ; MAP+CO ₂ 3-h soluble gas stabilization treatment	Stored 3°C Day 0, 4, 7 and 11	Total aerobic bacteria <i>Pseudomonas</i> spp. Coliforms <i>Escherichia coli</i> <i>Salmonella choleraesuis</i> subsp. <i>arizonae</i>	Al-Nehlawi et al., 2013

<p>Breast and thigh (n=16)</p>	<p>Chicken breast fillets were supplied in plastic packages (width: 25 cm; thickness: 90 µm; permeability of ca. 25 cm³, 90 cm³, and 6 cm³ m⁻²day⁻¹bar⁻¹ at 20 °C and 50%RHforCO₂,O₂, andN₂, respectively), while thigh fillets were separately placed in Styrofoam trays and manually wrapped with air-permeable polyethylene cling film.</p>	<p>Stored at 0, 5 and 10°C Day 0 and day 5</p>	<p><i>Pseudomonas</i> spp. Lactid acid bacteria <i>Brochothrix thermosphacta</i> <i>Rubrivivax</i> <i>Burkholderiales</i> <i>Pelomonas</i> <i>Flavobacterium</i> <i>Acinetobacter</i> <i>Serratia</i> <i>Shewanella</i>, <i>Psychrobacter</i> <i>Vibrionaceae</i></p>	<p>Dourou et al., 2021</p>
<p>Thigh (n=n.d.)</p>	<p>Aerobically packaged MAP (70% CO₂, 30% N₂) only or combined with 3 different oxygen scavengers</p>	<p>Stored at 4°C (dark) Day 0, 1 and then 3-day for 19 days</p>	<p><i>Mesophilic bacteria</i> <i>Pseudomonas</i> spp. Coliforms Lactid acid bacteria</p>	<p>Demirhan & Candoğan, 2017</p>

<p>Strings (n=51)</p>	<p>Aerobically stored</p>	<p>Stored at 4°C Day 0, 1, 2, 3, 4, 5, 6, 7, 8, 10 and 15</p>	<p><i>Acinetobacter</i> spp. <i>Carnobacterium</i> spp. <i>Rahnella</i> spp. <i>Pseudomonas</i> spp. <i>Brochothrix</i> spp. <i>Weissella</i> spp.</p>	<p>Liang et al., 2012</p>
<p>Legs (n=10)</p>	<p>MAP enriched and devoid in O₂</p>	<p>Stored at 4°C</p>	<p>Mesophilic bacteria <i>Pseudomonas</i> spp. Lactic acid bacteria <i>Brochothrix thermosphacta</i> <i>Carnobacterium</i> spp.</p>	<p>Rouger et al., 2018</p>
<p>Legs (n=66)</p>	<p>Unpacked; Treated with different decontamination solutions vs. untreated</p>	<p>Stored at 3°C Day 0, 1, 3 and 5</p>	<p>Psychrotrophs <i>Enterobacteriaceae</i> Coliforms <i>Micrococcaceae</i> Enterococci <i>Brochothrix thermosphacta</i> <i>Pseudomonas</i> spp. Lactic acid bacteria Moulds and yeasts</p>	<p>del Río et al., 2007</p>

<p>Cooked legs (n=n.d.)</p>	<p>MAP – 40% CO₂, 60% N₂</p>	<p>Steam-cooked samples Stored at 3.5°C Weekly analysis for 7 weeks</p>	<p><i>Lactococcus raffinolactis</i> <i>C. divergens</i> <i>Carnobacterium piscicola</i> <i>Lactococcus garvieae</i> <i>Lactococcus lactis</i> <i>Enterococcus faecalis</i></p>	<p>Barakat et al., 2000</p>
<p>Legs, wings, giblets and derived products (hamburgers and sausages) (n=15)</p>	<p>Unpacked</p>	<p>Stored at 2°C Day 0 (4h post mortem)</p>	<p>Mesophiles Psychrotrophs Coliforms <i>Escherichia coli</i> <i>Staphylococcus aureus</i></p>	<p>Álvarez-Astorga et al., 2002</p>
<p>Undamaged, farm damaged and machine damaged wings (n=264)</p>	<p>Unpacked</p>	<p>Transported on ice Day 0 (1h post mortem)</p>	<p>Coliforms <i>Enterobacteriaceae</i> <i>Pseudomonas</i> spp. <i>Staphylococcus aureus</i> <i>Salmonella</i> spp. (in 0.8% of the samples)</p>	<p>Malpass et al., 2010</p>

n.d. – not defined.

Table 2. Microorganisms associated with poultry meat (other than chicken) under different storage and packaging conditions.

Meat type	Sample	Packaging/Storage environment	Experimental conditions	Microorganisms	Reference
Duck	Carcasses (n=577)	Unpacked	Fresh, chilled and frozen Stored on ice Day 0 (immediately after arrival)	Aerobic bacteria (APC) <i>Salmonella</i> spp. <i>Escherichia coli</i>	Li et al., 2019
	Breast (n=10)	Aerobically stored	Frozen samples and thawed at 4°C Every 2 days for 17 days	<i>Enterobacteriaceae</i> Aerobic mesophilic bacteria	Lázaro et al., 2015
Turkey	Carcasses with neck skin	Packed vs. tradicional morrocon slaughtering (manual processing)	Sampling during hot and cold season (2-week intervals) Stored at 4°C Day 0 (within 2h)	Aerobic bacteria (APC) <i>Escherichia coli</i> <i>Staphylococcus aureus</i> <i>Clostridium perfringens</i> <i>Salmonella</i> spp. <i>Listeria monocytogenes</i> Coliforms	Cohen et al., 2007
	Thighs (n=16)	Packaged under mixtures of CO ₂ (35- 70%) and N ₂	Raw and marinated Stored at 6°C Sampled on their labeled use-by date or within one to four days after this date	<i>Enterobacteriaceae</i> : <i>Hafnia</i> spp. <i>Serratia</i> spp. <i>Rahnella</i> spp. <i>Yersinia</i> spp.	Såde et al., 2013
	Breast (n=n.d.)	Air-packaging MAP1 - 50% N ₂ ,50% CO ₂ MAP2-0.5%CO/50%CO ₂ , 49.5%N ₂ MAP3-50% Ar, 50% N ₂	0° C in the dark Day 0, 5 and 12 (+ day 19 and 25 for MAP packaging)	<i>Enterobacteriaceae</i> <i>Pseudomonas</i> spp. <i>Brochothrix thermosphacta</i> Lactic acid bacteria	Fraqueza et al., 2012

		MAP4-0.5%CO, 80%CO ₂ , 19.5%N ₂ MAP5 - 100% N ₂ MAP6 - 50% Ar, 50% CO ₂		Mesophilic, anaerobic and psychrotrophic counts	
Breast (n=n.d.)	Aerobically packed MAP1: 100% N ₂ MAP2: 50% Ar, 50% N ₂ MAP3: 50% Ar, 50% CO ₂ MAP 4: 50% N ₂ , 50% CO ₂	Stored at 0°C in the dark for 12-25 days Day 0, 5, 12 (and 19 and 25 for MAP)		<i>Pseudomonas</i> spp. <i>Enterobacteriaceae</i> <i>Brochothrix thermosphacta</i> LAB Mesophilic, anaerobic and psychrotrophic counts	Fraqueza & Barreto, 2009
Carcasses (n=n.d.)	MAP1 - 62% CO ₂ , 8% O ₂ ,30% N ₂ MAP2 - 20% CO ₂ , 80% N ₂	Stored at 1°C Day 0, 8, 12 and 15		Coliforms <i>Escherichia coli</i> <i>Pseudomonas</i> spp. <i>Brochothrix thermosphacta</i> Lactic acid bacteria <i>Staphylococcus aureus</i> Aerobic mesophilic bacteria	Saucier et al., 2000
Meat (n=115)	Not specified	Transported on iced Day 0		<i>Listeria monocytogenes</i> <i>L. innocua</i> <i>L. welshimeri</i> <i>L. grayi</i>	Aras & Ardic, 2015
Ground meat (n=240)	Air-packaging (not specified)	Transported under refrigeration Day 0 (within 2h)		<i>Salmonella</i> spp.	Iseri & Erol, 2010
Sausages (n=n.d.)	Air-packaging (21% O ₂ , 78% N ₂) MAP1 - 70% O ₂ , 30% CO ₂	Stored at 4°C until day 5. Stored at 8°C until day 22		Lactic acid bacteria Mesophilic bacteria	Luong, Jeuge, et al., 2020

		MAP 2- 50% CO ₂ , 50% N ₂	Microbiological assessment at day 2, 8, 15 and 22		
Quail	Carcasses (n=20)	Aerobically stored	Frozen samples and thawed at 4°C Every 2 days for 17 days	<i>Enterobacteriaceae</i> Aerobic mesophilic bacteria	Lázaro et al., 2015
Poultry	Carcasses (n=15)	Unpacked	Day 0 (1h post mortem)	Aerobic mesophilic bacteria <i>Enterococcus faecium</i> <i>Enterococcus faecalis</i> <i>Enterococcus casseliflavus</i> <i>Enterococcus durans</i> <i>Enterococcus spp.</i>	Krocko et al., 2007

n.d. – not defined.

5. Spoilage Biomarkers

Beyond direct microbiological analysis, spoilage can be monitored through other parameters (Balamatsia et al., 2006). Indeed, a major sensorial change in spoiling meat is the presence of off-odours and flavours like VOCs and BAs (Mikš-Krajnik et al., 2016).

Volatile organic compounds are mainly produced during the spoilage process as a result of microbial activity, but also due to other natural processes such as meat ageing and lipidic oxidation (Acquatucci et al., 2024; Mikš-Krajnik et al., 2016). Different authors, table 3, have reported certain VOCs as crucial biomarkers in detecting spoilage in meat. Additionally, these biomarkers are presented as critical to understand the microorganisms responsible for contamination and in the prevention of foodborne illnesses (Acquatucci et al., 2024; Carraturo et al., 2020; Mikš-Krajnik et al., 2016). Regarding BAs, these low molecular weight compounds are mainly produced during the enzymatic decarboxylation of amino acids caused by bacteria, natural tissue processes and the amination and transamination of aldehydes and ketones (Nuñez et al., 2016; Santos, 1996). However, they can also be endogenous, considering their presence in non-fermented foods at low concentrations (Santos, 1996). These compounds can be classified according to their precursor (aliphatic, aromatic and heterocyclic) or number of amine groups (monoamines, diamines and polyamines) (Nuñez et al., 2016). The production of different BAs depends on the available substrate, along with other environmental conditions previously described for affecting the bacterial metabolism (e.g. pH, presence of O₂, temperature, etc.) (Fraqueza et al., 2012; Wójcik et al., 2022). Moreover, it is known that improper storage conditions lead to an increased production of these compounds (Danchuk et al., 2020). Considering their toxicity at higher levels, particularly when ingested, it is recommended to restrict the intake of foods rich in these biomolecules (Wójcik et al., 2022). Similarly with VOCs, BAs are recognized as important spoilage biomarkers, giving crucial highlights regarding meat freshness and the contribution of certain microbial strains to their production (Fraqueza et al., 2012; Lázaro et al., 2015; Zamfir et al., 2025). However, the detection of these biomarkers in food is complex due to the interference of other present compounds, requiring sensitive methods (Danchuk et al., 2020; Nuñez et al., 2016). Mass-spectrometry (MS) is a powerful tool capable of identifying different molecules within a substrate, profiling its fingerprint (Ali et al., 2023; T. Zhang, Chen, et al., 2021). It is commonly combined with liquid-chromatography (LC) or gas-chromatography (GC), as effective separation methods to facilitate further analyses (Cunsolo et al., 2014). Given the versatility, sensitivity and precision of these techniques, MS has become vital in the food industry (Ali et al., 2023; Cunsolo et al., 2014).

Among the 23 studies summarized in Table 3, 65% focused on the detection of VOCs, 9% in BAs and 13% assessed both these biomarkers in poultry. The remaining 13% focused on the analysis of different metabolites, namely lipids, lipopeptides, amino acids, nucleotides, among others. Regarding the techniques used in combination with MS, 70% of the studies used GC, whereas 13% used LC. The remaining 17% used other techniques, that do not rely on chromatographic separation to detect poultry spoilage biomarkers, particularly proton transfer reaction MS (PTR-MS) and headspace analysis with cryoadsorption. Figure 4 presents the relationship between the biomarkers analysed and each of the detection techniques used.

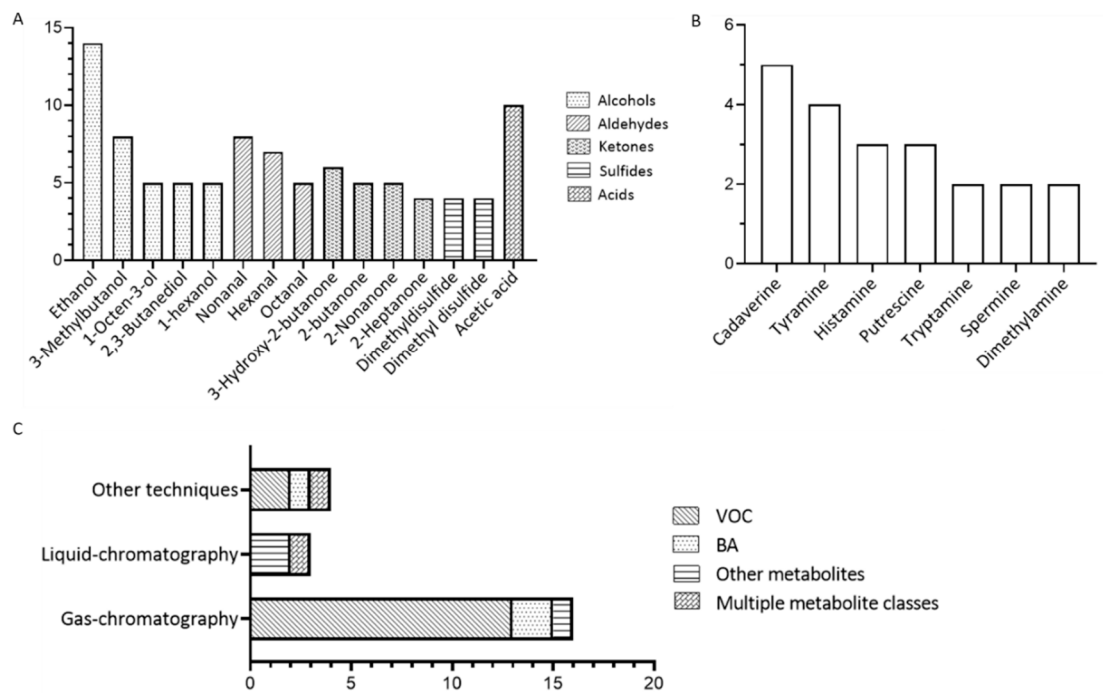


Figure 4. Biomarkers identified, (A) VOCs and (B) BAs, and (C) corresponding separation techniques used prior MS analysis.

Published literature investigated different conditions affecting meat spoilage and its biomarkers, namely, extended meat storage and the impact of storage temperature, considering that high temperatures naturally accelerate microbial growth and spoilage (Geeraerts et al., 2019; Lovestead & Bruno, 2010; Mikš-Krajnik et al., 2015; Mikš-Krajnik et al., 2016; Tománková et al., 2012; T. Zhang et al., 2020). Some studies induced spoilage by inoculating specific microorganisms into poultry meat, in order to comprehend the association between each microbial strain and biomarkers production (Carraturo et al., 2020; Klein et al., 2018; Wang et al., 2017; Wang et al., 2025). Although most studies were conducted using poultry, one study focused uniquely on evaluating the biosurfactant produced by bacteria, recognised as a critical element in bacterial growth (Wang et al., 2025).

Studies focused chicken breast employed different strategies to accelerate meat spoilage, namely high temperature (Mikš-Krajnik et al., 2015) and bacterial inoculation (Klein et al., 2018; Wang et al., 2017).

Across the published literature using bacterial inoculation, the main compound classes detected were alcohols, ketones and sulphides. Alcoholic compounds are commonly detected in spoiled meat, considering their role in anaerobic metabolism of glucose and some amino acids (Casaburi et al., 2015; Klein et al., 2018). Moreover, during spoilage, protein degradation releases amino acids, namely leucine, which is subsequently metabolized, producing 3-methyl-1-butanol (Nychas et al., 2008). This compound was found in the three studies, and it was highly associated with *E. coli*, *S. liquefaciens* 17 and *Pseudomonas* strains. Chicken samples inoculated with *E. coli* (Klein et al., 2018), *Aeromonas salmonicida* and *Serratia liquefaciens* 17 (Wang et al., 2017) also presented higher production of alcoholic compounds, given their facultative anaerobic metabolism. Dimethyl disulfide, a key sulphur-containing compound for spoilage assessment, was also detected. It was already reported that storage extension and temperature increase the concentration of this molecule, therefore promoting meat spoilage (Eilamo et al., 1998). Indeed, dimethyl disulfide is also present in non-inoculated samples with increasing concentration over time (Klein et al., 2018; Mikš-Krajnik et al., 2015). Inoculation with *E. coli*, *P. fluorescens* (Klein et

al., 2018) and *S. liquefaciens* (Wang et al., 2017) also enhanced the production of this biomarker. Regarding ketones, 2-butanone and acetoin were found samples inoculated with *E. coli* and *P. fluorescens* (Klein et al., 2018), revealing an increasing concentration during storage time. Moreover, 2-heptanone and 2-nonanone were found in samples inoculated with *Pseudomonas* strains and *S. liquefaciens* 17, whereas acetoin was present on samples inoculated with *A. salmonicida* 35 and *S. liquefaciens* 17 (Wang et al., 2017). Acetoin, or 3-hydroxy-2-butanone, is particularly important for meat spoilage detection. It is mainly linked to LAB and *Enterobacteriaceae*, formed through pyruvate metabolization, that provides a butter-like flavour (Ardö, 2006; Casaburi et al., 2015; Y. Wang et al., 2025). It can be reduced into 2,3-butanediol, also associated with poultry spoilage and microbial growth (Geeraerts et al., 2019). Acetic acid was also detected in some of these studies (Mikš-Krajnik et al., 2015; Timsorn et al., 2016; G.-Y. Wang et al., 2017).

VOCs production was also evaluated on skinless and boneless chicken breasts using high temperatures to induce meat spoilage (Chmiel et al., 2020; Lovestead & Bruno, 2010; Mikš-Krajnik et al., 2016). The compounds that were detected in, at least, two of these studies were dimethyl disulphide, dimethyl trisulphide, 3-methyl-1-butanol, propanoic acid and butanoic acid. The latter two compounds are included in the volatile acids group, generally formed through the lipolysis of triglycerides and phospholipids, amino acids degradation and ketone oxidation (Toldra', 1998). These events result in off-flavours, impacting meat quality and consumption (Chmiel et al., 2020). Chmiel et al. (2020) reported that higher concentrations of propanoic acid were found in air-packaged samples stored at low temperatures comparatively with O₂-enriched MAP packaging. Regarding sulphur-containing compounds, Mikš-Krajnik et al. (2016) showed that these compounds were strongly linked to microbial growth under 4 and 10 °C temperatures. Finally, Mikš-Krajnik et al. (2016) showed a high correlation between 3-methyl-1-butanol production and LAB and *B. thermosphacta*, which aligns with the findings reported previously regarding the role of facultative anaerobic microorganisms in the production of alcoholic compounds. Moreover, Chmiel et al. (2020) reported higher levels of 3-methyl-1-butanol on air-packaging and exposed to light samples comparatively with O₂-enriched MAP packaging. Although it is not a key compound in these studies, it is important to note that ethanol was one of the main biomarkers found in one of the studies, strongly related to *Pseudomonas* spp. growth, but also with facultative anaerobic microorganisms (Mikš-Krajnik et al., 2016). These results show that ethanol can be produced through both aerobic and anaerobic pathways.

Ioannidis et al. (2018) focused on developing a non-destructive technique to measure VOCs production over 15 days on skinless chicken stored at 4 °C on MAP. From the poll of metabolites analysed, this study revealed a clear concentration increase over storage time for ethanol and dimethyl sulphide. 2-propanol was also detected in higher concentrations at the end storage. Regarding aldehydes, results showed that 3-methylbutanal increased its concentration over time, with a particular increase on day 6, thereby demonstrating potential as a biomarker for early spoilage detection. Finally, acetoin exhibited a peak concentration on day 9, followed by a sharp decrease, associated with the production of 2,3 butanediol (Geeraerts et al., 2019). Similarly, Tománková et al. (2012) evaluated VOCs production during 20 days of storage on chicken hindquarters with bone and skin, stored at 4°C in two types of MAP. Different sulphur-compounds were found on samples packed on Ar-enriched MAP, namely dimethyl sulphide, dimethyl disulphide, dimethyl trisulphide and dimethyl tetrasulphide, and showed higher content on day 16. On the other hand, pentamethylheptane and ammonia exhibited similar content for both MAP packages. Overall, O₂-enriched MAP delayed LAB and coliform growth and decreased the production of off-flavours.

In a similar context, a research team focused on studying the impact of different storage temperatures on VOCs formation using skinless chicken breasts fillets, thighs and wings and boneless chicken (Senter et al., 2000). Different VOCs classes were found, namely alcohols,

ketones, esters and sulphur-containing compounds. Particularly, ethanol, acetone, methyl ethyl ketone and carbon disulphide were present in all samples. Additionally, ethyl acetate, hydrogen sulphide and dimethyl sulphide were also consistently detected, therefore were considered relevant VOCs for chicken spoilage. Interestingly, results revealed that a short duration storage on high temperatures increased aerobic plate counts and may render the meat unfit for consumption, pointing out the importance of adequate storage conditions.

Different research teams assessed volatile production in different cooked chicken samples using high storage temperatures (Geeraerts et al., 2019; Jia et al., 2024) and bacterial inoculation (Wang et al., 2025) to induce meat spoilage. The main compounds detected were 1-octen-3-ol, phenol, acetic acid, acetoin, 2-butanone, 2,3-butanedione, hexanal, nonanal, limonene and cymene. Firstly, regarding the alcoholic compound 1-octen-3-ol, higher concentrations of this molecule were found in chicken samples with extended storage and inoculated with *B. thermosphacta* and co-culture of *B. thermosphacta* and *Latilactobacillus curvatus*, two facultative anaerobe strains (Wang et al., 2025). Phenol was also reported in these studies. However, despite its high content, it was not considered a proper candidate for spoilage biomarker, since it increases variability in MS data (Geeraerts et al., 2019). Regarding acetic acid production, it is known to be closely related to fermentation processes. Geeraerts et al. (2018) showed that its concentration increases with higher storage temperatures and as the expiration dates is approached and, eventually, exceeded. Despite being mentioned as a potential candidate for spoilage biomarker (Mikš-Krajnik et al., 2015; Mikš-Krajnik et al., 2016), Geeraerts et al. (2018) reported that high content of this molecule can increase data fluctuations, similarly to phenol. Regarding ketones, higher concentrations of these compounds were found in samples inoculated facultative anaerobic microorganisms (Wang et al., 2025), corroborating the results previously reported (Mikš-Krajnik et al., 2016; Wang et al., 2017). Particularly, 2,3-butanedione content increased with storage time for all samples (Wang et al., 2025). Interestingly, for aldehydes, Wang et al. (2025) showed that hexanal content decrease along storage time, whereas an opposite pattern was detected for nonanal. Additionally, hexanal is known to produce off-flavours, as showed by Geeraerts et al. (2018). Limonene and cymene concentrations were inferior in spoiled chicken samples, comparatively with control group (Jia et al., 2024). Additionally, *Lactobacillus* presented negative correlation with these molecules, according to Pearson's correlation. Finally, Geeraerts et al. (2018) revealed that increasing temperatures and extended storage increase VOCs concentration, namely the afore mentioned biomarkers.

Finally, two research teams used unspecified parts of chicken to assess VOCs formation, whereas Carraturo et al. (2020) resorted to microbial-incubated samples and Acquaticci et al. (2024) focused on air-packaged samples stored at 4°C. Inoculation with three different microbial strains resulted on the production of different VOCs (Carraturo et al., 2020). *S. Typhimurium* inoculated samples produced high content of 1-butanol 3-methyl, 2,3-dithiobutane and dimethyl trisulfide, whereas *C. jejuni* resulted in the production of benzyl disulfide, butanoic acid ethyl ester and dimethyl trisulfide. Finally, meat spiked with *S. aureus* presented higher production of ethanol and 3-methyl-1-butanol and more similarities with the negative control group. Regarding Acquaticci et al. (2024) study, several compounds were evaluated in order to detect their content trend trough several days. For aldehydes, nonanal increased its concentration from day 0 to 9, whereas hexanal and octanal decreased their content from day 0 to day 6 and 9, respectively. This dropout may be associated with their transformation to carboxylic acid. Regarding alcohols, 1-pentanol and 2-octen-1-ol increased their content from day 0 to 9, due to oxidation processes. Acetoin content also increased from day 0 to 9. Overall, results showed that different molecules may be considered key biomarkers, despite their concentration trend over time. Particularly, 1-butanol, 3-methylbutanol, 1-hexanol, 1-octen-3-ol, linalool, 2-nonanone e nonanal were considered important biomarkers for spoilage detection on chicken samples.

Focusing on BAs and their critical role on assessing meat freshness, different studies evaluated the presence of these compounds on chicken breast samples stored under refrigerated conditions (Wojnowski et al., 2019a; Wojnowski et al., 2019b; Wojnowski et al., 2018b). Results showed that cadaverine, putrescine, tyramine and histamine presented increasing concentrations over time across all studies. Cadaverine and putrescine production result from microorganisms' activity, leading to the exacerbation of the toxic effects of excessive histamine and tyramine content (Wójcik et al., 2022). Interestingly, cadaverine and 2-phenylethylamine were not detected on day 1 and also day 3, regarding the latter one, despite presenting increasing content over time (Wojnowski 2019b). Furthermore, results showed that total viable aerobic bacteria counts and cadaverine concentration increased after the second day of storage, corroborating the connection between BAs formation with microbial activity (Wojnowski et al., 2018b). Additionally, one of the studies stated that the biogenic amines index (BAI), defined by the sum of histamine, tyramine, cadaverine and putrescine in a sample (Wójcik et al., 2022), presented a substantial increase after the second day under refrigerated storage, mostly due to cadaverine production. BAI plays a key role on the assessment of meat freshness, but also in the prevention of foodborne illnesses (Wójcik et al., 2022). It is recognized that fresh meat should not exceed 5 mg/kg, whereas low quality meat is classified between 20-50 mg/kg and spoiled meat with values superior to 50 mg/kg (Esposito et al., 2022). Overall, these studies showed that MS is a useful tool to assess BAs content in livestock samples and that this parameter is key to assess poultry freshness.

Considering the importance of these two types of biomarkers, a study investigated the presence of VOCs and BAs in chicken and turkey breasts stored at 4 °C for 5 days (Wojnowski et al., 2018a). Results showed that both total viable counts and volatile compounds content had an increase over storage time. Particularly, turkey samples presented a less noticeable increase in the concentration of the biomarkers, since it is a leaner meat and, consequently, with decreased lipid oxidation. A more detailed analysis in chicken samples revealed an overall increase in several compounds namely, allyl radical, ethanol, butadiene, acrolein, 3-methyl-1-butyne/2-methyl-1-butyne, benzene, diethyl sulphide, toluene, heptanol and cadaverine. As showed previously, cadaverine was not detected on day 1. This work showed that MS approaches combined with machine learning algorithms can be useful tools to complement current meat quality assessment methodologies.

A more comprehensive analysis was conducted using chicken breasts stored under low temperatures during several days, in order to characterize the metabolomic profile of chicken meat throughout storage (Zhang et al., 2020). The first results revealed a total of 37 potential metabolomic biomarkers, in which 27 were increased and the remaining 10 were depleted over storage time. SSO resource to the substrates present in meat to proliferate, thus possibly contributing to the depletion of certain metabolites during storage. For instance, gluconic acid presented decreasing concentration over storage, since it is substrate for microbial growth. Moreover, results identified indole-3-carboxaldehyde, uridine monophosphate, *s*-phenylmercapturic acid, gluconic acid, tyramine and serylphenylalanine as potential freshness biomarkers for chilled chicken. Tyramine was already reported for its increasing concentration over time (Wojnowski, Kalinowska, et al., 2019a; Wojnowski et al., 2019b; Wojnowski 2018b). In this study, tyramine content increased significantly on day 5, supporting the aforementioned results.

A different approach was used to assess the metabolomic profile of chicken. Lv et al. (2023) investigated the lipidomic profile of vacuum-packed chicken breasts stored under low temperatures. Results revealed that a total of 492 lipid species were detected. On day 0, the lipid profile was composed of predominantly present were triacylglycerols and phosphatidylcholines, with a total abundance above 78%. However, by day 6, a marked reduction in the content of these two lipid classes were observed, contributing to an overall decrease of almost 17% in total lipid content. Regarding microbial assessment, results showed an increase of total viable counts over

storage time. Results showed that a total of 12 molecules could be considered spoilage biomarkers, mainly associated with glycerophospholipid and linoleic acid metabolisms.

Other study was conducted to characterize and correlate chicken breasts microbiome and metabolome, in order to understand the mechanisms behind spoilage (Zhang et al., 2021). Results showed a particular predominance of some bacterial species, namely *Photobacterium*, *Carnobacterium*, *Brochothrix*, *Pseudomonas* and *Serratia*, revealing a potential correlation of these species with spoilage processes. However, other species may have a role in chicken spoilage mechanisms, given their enrichment over storage time, namely *Acinetobacter*, *Kurthia*, *Shewanella*, and *Obesumbacterium*. Regarding metabolome, results demonstrated that chicken's metabolomic profile across storage days, in which samples from day 0 and 3 presented different profile comparatively with samples from day 5 and 7. Overall, a total of 10 pathways were identified as responsible for chilled chicken spoilage, with particular focus on histidine and purine metabolisms. In particular, histidine pathway results in decarboxylation that produces histamine, a critical BAs present in spoiled meat (Moro et al., 2020).

Overall, this analysis allowed to identify several key biomarkers for poultry freshness and spoilage assessment, including VOCs, BAs and other types of metabolites. It was possible to verify that different MS approaches were efficient in the detection of these compounds. In particular, MS analysis combined with a microbial profiling of meat provided a more comprehensive analysis of the biomarkers associated with meat spoilage.

Table 3. Poultry spoilage biomarkers detected using mass-spectrometry.

Compound class	Poultry sample	Experimental conditions	Technique used	Compounds found	Reference
VOCs	Chicken breasts	Aerobically packed T= 21°C Evaluation days: Every 3-hours during the first 12 hours and every 24h for day 1, 2 and 3.	HS-SPME-GC-MS	Alcohol Sulphides Esters Free fatty acids Others	Mikš-Krajnik et al., 2015
	Chicken breast	Inoculation: <i>Pseudomonas fluorescens</i> and <i>Escherichia coli</i> (10 ⁶ CFU/mL) Storage: Stainless-steel container for Control and <i>P. fluorescens</i> . Dessicator for <i>E. coli</i> . Evaluation time: 2-10	TD-GC-MS	Control group: Hydrocarbons, Alcohols, Aldehydes, Ketones, Ester, Sulfur-containing compounds, Ethers <i>Ps. fluorescens</i>-inoculated: Hydrocarbons, Alcohols, Aldehydes, Ketones, Sulfur-containing compounds Esters, Ethers <i>E.coli</i> inoculated: Hydrocarbons, Alcohols, Aldehydes, Ketones, Sulfur-containing compounds, Esters, Ethers	Klein et al., 2018

Chicken breasts	T= 8°C for 7 days Inoculation: <i>Aeromonas salmonicida</i> 35, <i>Pseudomonas fluorescens</i> H5, <i>Pseudomonas fragi</i> H8 and <i>Serratia liquefaciens</i> 17 (10 ³ CFU/g)	GC-MS	Control: Alcohols, Aldehydes, Ketones <i>A. salmonicida</i> inoculated: Alcohols, Aldehydes, Ketones, Others <i>P. fluorescens</i> inoculated: Alcohols, Ketones, Others <i>P. fragi</i> inoculated: Alcohols, Ketones, Others <i>S. liquefaciens</i> inoculated: Alcohols, Aldehydes, Ketones, Others	Wang et al., 2017
Sliced chicken breasts	Temperature: 4 or 30°C for 5 days	Electronic nose GC-MS	Aldehydes Alcohols and diols Esters Alkenes Fatty acids Amides Others	Timsorn et al., 2016
Skinless chicken breast	MAP 40% CO ₂ , 30% N ₂ , 30% O ₂ Temperature: 4°C Evaluated days: 2, 9, 15	SPME-SIFT-MS with HS-TD-GC-MS	Acids Alcohols Aldehydes Ketones Sulfur-compounds	Ioannidis et al., 2018
Boneless and skinless chicken breasts	Temperature: 25°C for 2 weeks	Cryoadsorption on short alumina open tubular column and GC-MS	Sulphides Thioester Others	Lovestead & Bruno, 2010

	Boneless and skinless chicken breasts	Aerobically packed T= 4, 10, 21°C Evaluation days: Every 24h for 7 days (4 and 10°C). Every 3h during the first 12h and each 24h at the 1st,2nd,3rd days (21°C)	HS-SPME-GC-MS	Alcohol Sulphides Esters Hydrocarbons Free fatty acids Others	Mikš-Krajník et al., 2016
	Boneless and skinless chicken breasts	Air, MAP enriched with O ₂ and vacuum-packed Temperature: 2.2°C and 3.3°C	GS-MS	Alcohols Aldehydes Acids Others	Chmiel et al., 2020
	Chicken hindquarters with bone and skin	MAP 70% O ₂ , 30% CO ₂ and 70% Ar, 30% CO ₂ ; T= 4°C Evaluation days: 0, 4, 8, 12, 16, and 20	GC-MS	Hydrocarbons Sulphides Others	Tománková et al., 2012
	Skinless chicken breasts fillets, thighs and wings and boneless chicken breasts with skin	Temperature: 4°C for 5 days; 13°C for 2 days; 4°C for 3 days, followed by 1 day at 13°C and finally 4°C for 1 day	HS-SPME-GC-MS GC-MS GC-SCD	Alcohols Ketones Esters Sulfur-containing compounds	Senter et al., 2000
	Chicken	Air-packaged Temperature: 4°C Evaluation days: 0,2 and 5	HS-SPME-GC-MS	Alcohols Aldehydes Ketones Others	Acquatucci et al., 2024

	Chicken	Temperature: 4°C Inoculation: <i>Salmonella Typhimurium</i> (S), <i>Campylobacter jejuni</i> (C), <i>Staphylococcus aureus</i> (A) (10 ⁶ CFU/mL)	HS-SPME-GC-MS	All groups: Alcohols Control, Meat+S+C and Meat+C+S: Alkane	Carraturo et al., 2020
	Cooked chicken	MAP 80% N ₂ and 20% CO ₂ Temperature: 4-6°C, 7-9°C, 11-13°C Evaluation time: 8 days before expiration date, expiration day, 4 and 8 days after expiration day	SIFT-MS HS-SPME-GC-TOF-MS	Alcohols Aldehydes Ketones Sulphur-containing volatiles Terpenes	Geeraerts et al., 2019
	Braised chicken	Vacuum-packaged Temperature: 4°C for 12 days Inoculation: <i>Lactobacillus curvatus</i> , <i>Brochothrix thermosphacta</i> and co-culture (10 ⁵ -10 ⁶ CFU/mL)	HS-SPME-GC-MS	All groups: Alcohol, Aldehydes, Ketone, Esters Control: Aromatic alcohols L. curvatus inoculated: Fatty acid, Ketone B. thermosphacta inoculated: Aromatic alcohols, Ketone, Aldehyde Inoculated with mixture: Aromatic alcohols, Fatty acid, Acids, Ketone	Wang et al., 2025
	Ready to eat chicken feet	Vacuum-packaged Temperature: 25 °C	HS-SPME-GC-MS	Alcohols Acids Ketones Alkenes Alkanes Esters Aldehydes Others	Jia et al., 2024

BAs	Ground chicken breasts	Temperature: 4°C Evaluation days: 0-5	DLLME-GC-MS	Cadaverine Histamine Putrescine Tyramine	Wojnowski et al., 2018b
	Chicken breast	Aerobically or vacuum-packaged Temperature: 4°C Evaluation days: 1, 3 and 5	DLLME-GC-MS	2-phenylethylamine Cadaverine Dimethylamine Histamine Putrescine Spermine Tryptamine Tyramine	Wojnowski et al., 2019b
	Chicken breasts	Aerobic-like packaged Temperature: 4°C	Eletronic nose DLLME-GC-MS	Cadaverine Histamine Putrescine Tyramine	Wojnowski et al., 2019a
VOCs and BAs	Chicken and turkey breasts	Temperature: 4°C for 5 days Evaluation days: 1-5	PTR-TOF	Radical (Allyl radical) Alcohols Hydrocarbons Aldehydes Sulfur-compounds Amine (Cadaverine)	Wojnowski et al., 2018a

VOCs, BAs, aminoacids, peptides, nucleotides and organic acids	Chicken breasts	Temperature: 4°C for 1, 3, 5 or 7 days	GC-MS	Aminoacids Peptides Nucleotides Organic acids BAs (Tyramine, Cadaverine, Indole-3-carboxaldehyde, 3-Methylxanthine, Nicotyrine, Idazoxan) VOC (Amine, nitrile, 1-benzopyran, benzene)	Zhang et al., 2020
Lipids	Chicken breast	Vacuum-packed Temperature: 4°C Evaluation days: 0, 3 and 6	UHPLC-MS/MS	Phosphatidylcholine Phosphatidylethanolamine Lysophosphatidylethanolamine Lysophosphatidylcholine Free fatty acid Sphingomyelin Cholesterol Ester	Lv et al., 2023
Lipopeptides	Biosurfactant from spoiled chicken	Analysis of the biosurfactant produced by <i>P. fragi</i> NMC25 obtained from spoiled chicken	GC-MS	Fatty acids Amino acids	Wang et al., 2025

Metabolites	Chicken breast	T= 4°C Evaluation days: 0, 3, 5, 7	UHPLC-MS/MS	Inosine L-5-oxoproline D-serine Phosphatidylcholine lyso 18:1 PC (O-14:0/2:6) Alanine 2-hydroxycinnamic acid Tyrosine 2'-aminoacetophenone L-lysine L-pipecolic acid Glutamate	T. Zhang, Ding, et al., 2021
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DLLME-GC-MS: dispersive liquid-liquid microextraction-gas chromatography-mass spectrometry; GC-SDC: Gas Chromatography – chemiluminescence detection; HS-SPME-GC-MS: headspace solid-phase microextraction coupled with gas chromatography-mass spectrometry; HS-SPME-GC-TOF-MS: headspace solid-phase microextraction coupled with gas chromatography time-of flight mass spectrometry; HS-TD-GC-MS: head space thermal desorption gas chromatography; PTR-TOF: proton transfer reaction mass spectrometer with time-of flight; SPME-SIFT-MS: solid-phase microextraction coupled with a selected ion flow tube mass spectrometer; UHPLC-MS/MS: ultra-high-performance liquid chromatography-mass spectrometry; TD-GC-MS: thermal desorption-gas chromatography-mass spectrometry.

6. Conclusions and Future Perspectives

This review provided a comprehensive overview of the mechanisms, microbiology and biomarkers associated with poultry meat spoilage over the last 25 years. From the analysis of 54 microbiological studies and 23 biomarker-focused studies, several key conclusions can be drawn. Meat spoilage is a complex, multifactorial process that begins before slaughter and progresses throughout the entire supply chain. Pre-slaughter stress conditions directly influence post-mortem meat quality, potentially leading to DFD or PSE conditions that increase susceptibility to microbial colonization (Addis, 2015; Dave & Ghaly, 2011). Following slaughter, autolytic enzymatic reactions, lipid oxidation and environmental factors such as photo-oxidation act synergistically to accelerate quality deterioration (Amaral et al., 2018; Luong et al., 2020). Moreover, slaughter and processing conditions have major implications on the initial microbial load, highlighting the critical importance of hygiene practices at the slaughterhouse level (Moazzami et al., 2025; Morshdy et al., 2025; Rouger et al., 2017).

Regarding microbial spoilage, the most frequently identified organisms in poultry were lactic acid bacteria, *Pseudomonas* spp., members of the *Enterobacteriaceae* family and *B. thermosphacta*. Their prevalence is strongly dependent on packaging and storage conditions. Air-packaged samples consistently presented shorter shelf life due to the promotion of aerobic microbial growth and oxidative reactions, whereas CO₂-enriched MAP demonstrated a clear bacteriostatic effect, delaying microbial proliferation and extending poultry shelf life (Balamatsia et al., 2007; Chouliara et al., 2007; Fraqueza & Barreto, 2009). Vacuum packaging also proved effective in limiting the growth of aerobic species, particularly *Pseudomonas* spp. (Balamatsia et al., 2007). Notably, apart from *Pseudomonas* spp., the predominant spoilage organisms are facultative anaerobes, conferring them adaptability to proliferate under both aerobic and anaerobic conditions, which poses a persistent challenge across different packaging strategies (Zhang et al., 2012). Low storage temperatures consistently delayed microbial growth, whereas temperature fluctuations significantly compromised meat quality, reinforcing the need for strict cold chain management throughout distribution and retail (Ghollasi-Mood et al., 2017; Zhang et al., 2012).

Concerning spoilage biomarkers, this review evidenced that VOCs, BAs and other metabolites constitute valuable indicators of poultry freshness. Key VOCs identified across multiple studies include dimethyl disulphide, dimethyl trisulphide, 3-methyl-1-butanol, acetoin, ethanol and acetic acid, many of which showed strong correlations with specific spoilage organisms. Among BAs, cadaverine, putrescine, tyramine and histamine exhibited consistent increases over storage time, with the BAI emerging as a practical tool for freshness assessment (Wojnowski et al., 2018; Wójcik et al., 2022). Mass spectrometry, particularly when coupled with gas or liquid chromatography, proved to be a versatile and sensitive analytical platform for the detection and quantification of these biomarkers (Acquaticci et al., 2024). Furthermore, metabolomic approaches revealed broader biochemical pathways involved in spoilage, including histidine and purine metabolisms, offering deeper insights into the mechanisms underlying meat deterioration (Zhang et al., 2021).

Despite the significant progress achieved over the past decades, spoilage remains highly variable across meat types, processing environments and supply chains. Future research should focus on the development of rapid, non-destructive and cost-effective monitoring tools, such as biosensors and intelligent packaging systems, capable of real-time spoilage detection at the consumer level. Additionally, predictive microbiology models integrating storage conditions, microbial dynamics and biomarker production could provide more accurate estimations of remaining shelf life. The application of microbiome-guided interventions, combined with sustainable preservation strategies such as biopreservation, antimicrobial coatings and natural preservatives, holds considerable promise for reducing poultry meat losses while maintaining food safety and quality across global markets.

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