A Review on Contamination and Spoilage Mechanisms in Meat and Fish Products: Implications for Food Safety

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Abstract—The contamination and spoilage of meat and fish present significant food safety challenges. This review examines the microbial mechanisms behind spoilage, highlighting key pathogens like *Salmonella*, *E. coli*, *Listeria*, and *Vibrio*, which pose risks at various stages of the supply chain, including slaughter, processing, and storage. Spoilage is driven by microbial activity, leading to sensory changes such as off-flavors, discoloration, and texture loss. Environmental factors like temperature, moisture, and handling practices influence microbial growth, with refrigeration, hygiene, and packaging technologies playing critical roles in mitigating spoilage. The review also discusses food safety regulations, preventive measures, and the need for ongoing research into new technologies to improve the safety, shelf life, and quality of meat and fish products. Addressing these challenges is key to reducing foodborne illness and waste.

Index Terms—Spoilage mechanism, pathogens, Meat and Fish Products, Food borne illnesses

I. CONTAMINATION AND SPOILAGE OF MEAT

Meat spoilage (MS) is a complex microbial process that presents health risks and contributes to significant food waste and economic losses across production, storage, and distribution. Understanding spoilage microorganisms and strategies to mitigate their impact is essential for developing effective preservation methods. This review examines the microorganisms responsible for spoilage in meat from livestock, poultry, and fish, and explores strategies to extend product shelf life. Meat is a vital source of nutrients like protein, fatty acids, vitamins, and minerals, and is a staple in human diets (Geiker et al., 2021; Wyness, 2016). However, with global meat production increasing (Godfray et al., 2018), around 23% of meat is wasted annually (Karwowska et al., 2021), largely due to spoilage during storage (Lipinski, 2020). Its high nutritional value and water activity make meat particularly susceptible to microbial contamination by bacteria, yeasts, and molds (Fernandes, 2009; Sofos et al., 2013).

II MICROBIOLOGICAL CONTAMINATION IN MEAT

Microbial contamination in meat production often originates from microorganisms naturally present in animals. Factors such as rearing conditions, transportation, slaughtering, and processing practices, along with hygiene standards at slaughterhouses, influence the microbial quality of fresh meat. While the natural flora of animals doesn't typically cause spoilage, microorganisms from their intestinal or respiratory tracts are a common source of contamination. Hides, hooves, and hair can carry microorganisms from soil, manure, feed, and water, including spoilage organisms. The skin of meat animals may harbor *Micrococci*, *Staphylococci*, and *Streptococci*, which can contaminate the final product during slaughter. Fecal matter and materials from the gastrointestinal tract are common sources of enteric pathogens, such as *Salmonella*. Though workers at meat processing plants can occasionally be vectors for foodborne pathogens, their role in contamination is generally minimal (Frazier & Westhoff, 1999).

Surveillance of emerging contaminants and strict inspection protocols are essential for minimizing microbial contamination risks, protecting public health, and fostering economic benefits through job creation and improved trade relations. These efforts rely on rigorous testing and inspection by both exporting and importing countries. Microbial contamination in meat mainly occurs on the surface,

leading to spoilage and potential transmission of foodborne pathogens (Singh et al., 2019; Sofos, 2014). The primary contamination source is typically the animal itself, with microorganisms from hides, fleece, skin, or feathers being transferred during slaughter. These surfaces often carry animal feces, soil, and feed residues, which can contaminate the carcass.

Spillage of intestinal contents during evisceration is a significant contributor to carcass contamination (Berends et al., 1997; Brizio et al., 2015; Fernandes, 2009; Sheridan, 1998; Sofos, 2014). Other contamination sources include the processing environment, equipment, workers, and external vectors such as insects, rodents, and birds (Singh et al., 2019; Sofos, 2014). Contamination can persist during storage and distribution (Sung et al., 2013). The types of microorganisms in meat products depend on factors like the animal's physiological state, processing methods, hygiene practices, surface area, storage temperature, and the presence of competitive microorganisms (Rawdkuen, Punbusayakul, & Lee, 2016). To control microbial growth, ensure safety, and extend shelf life, both traditional and novel techniques are used.

III MICROBIAL DETECTION METHODS

Microbial detection methods are divided into traditional and rapid techniques (Law et al., 2014). Traditional culture-dependent methods typically take 2 to 7 days for results, while rapid methods use nucleic acids (genosensors), biosensors, or immunological assays (Zhao et al., 2014). Electrochemical-based methods have gained significant attention. Advanced technologies such as computer vision (Jackman et al., 2011), proteomics and mass spectrometry (Mora et al., 2018), Raman spectroscopy (Herrero, 2008), and chromatography (Marques et al., 2011) are also used for microbial detection.

Improving contamination monitoring with advanced detection methods allows the meat industry to better manage microbial risks, enhancing food safety and extending shelf life. Numerous techniques exist for enumerating and isolating microbial contaminants, with widely accepted methods from the American Public Health Association (APHA, 1984) and the International Commission on Microbiological Specifications for Foods (ICMSF, 1978) for bacterial enumeration. Novel methods, including immunological assays, PCR, biosensors, and nucleic acid probes, have been developed for monitoring pathogens in meat (Fung, 1995). However, challenges remain, such as difficulties in recovering bacterial species from complex food matrices due to co-extraction issues (Duffy et al., 1999). Despite these challenges, traditional culture-based and serological methods remain essential, though new technologies like PCR and biosensors offer faster, more accurate alternatives.

IV INCIDENCES OF CONTAMINANTS IN MEAT

The microbiological profile of meat is crucial for determining the safety and quality of fresh meat products. The presence of pathogens or microorganisms in meat is a significant food safety concern. Meat is considered wholesome when harmful pathogens are absent or present in minimal amounts, depending on their toxins and metabolites. Several studies have documented microbial contamination in meat, noting the microorganisms associated with different types. For example, Vanderlinde et al. (1998) studied the microbial quality of beef carcasses in retail and export markets, while Biswas et al. (2008) found that buffalo meat from Indian packing plants generally contained fewer microorganisms than beef from other regions.

Ziauddin et al. (1994) reported varying bacterial counts across different regions of beef carcasses, with Standard Plate Count (SPC) ranging from 4.52 to 5.49 log10 cfu/cm². Contamination indicators, such as *Streptococcus faecalis* (linked to fecal contamination), help assess meat quality (Gill, 1998). Studies also highlight the prevalence of *Coagulase-positive Staphylococcus* and *Listeria monocytogenes* in beef, with regional variations. For example, Vanderlinde et al. (1998) found a 4.1% incidence of *Listeria monocytogenes* on beef carcasses in Australia, while none were detected in Northern Ireland (Madden et al., 2001). The presence of pathogens like *Salmonella*, *Listeria*, and *Staphylococcus* spp. poses significant public health risks, making monitoring bacterial counts such as SPC and APC essential for ensuring meat safety and quality.

Salmonella is widespread in food animals, and outbreaks of salmonellosis linked to beef are well-documented. Prevalence rates of *Salmonella* in beef vary, from 0.22% in Australia (Vanderlinde et al., 1998) to 5.2% in fed-beef trimmings in the USA (Scanga et al., 2000). *Escherichia coli*, especially pathogenic strains like *E. coli* O157:H7, is a major concern due to its pathogenicity in both humans and animals. Contamination often occurs through carcass soiling and processing environment contamination with fecal material during slaughter (Johnson et al., 1996). The presence of verotoxigenic *E. coli* (VTEC) is a global issue, with alarmingly high contamination rates reported in India, highlighting the need for improved surveillance and control (Rathore, 2000; Banerjee et al., 2001; Hazarika et al., 2005).

V. CONTAMINATION AND SPOILAGE OF FISH AND FISH PRODUCTS

Historically, studies on fish-associated microorganisms relied on culture-dependent techniques, focusing mainly on aerobic heterotrophic bacteria and often neglecting eukaryotes and anaerobes due to culturing challenges. However, recent advancements in molecular and culture-independent methods have greatly expanded our understanding of fish microbiota, revealing a broad range of uncultured organisms, including anaerobes, particularly in the digestive tracts of both freshwater and marine fish. This updated article provides an overview of current knowledge on fish-associated bacteria, their abundance, characteristics, and roles in healthy fish, noting that certain pathogens can be present in healthy fish without causing disease.

The nature of fish-microbe associations—whether they represent asymptomatic carrier states, pre-pathogenesis stages, or forms of commensalism or synergism—remains unclear. For example, *Flavobacterium psychrophilum*, the causative agent of coldwater disease in salmon and trout, has been found in healthy Baltic salmon, suggesting that pathogenic bacteria can sometimes be present without causing illness (Salmo salar et al., 1999). Fish are constantly exposed to microorganisms from their environment, such as water, sediment, sewage, and fecal matter, which influence microbial communities. The external surfaces, including the gills and digestive tract, are especially prone to microbial colonization, starting at the egg or larval stage and continuing throughout development, influenced by microorganisms in the surrounding environment (Olafsen, 2001).

Fish microbiota can be manipulated using prebiotics or probiotics to enhance fish health and potentially reduce disease susceptibility (Robertson et al., 2000). There are three key outcomes of bacterial interactions with fish: *External Colonization*, where microorganisms may colonize external surfaces, especially in areas with damage; *Ingestion and Digestion*, where microorganisms enter the digestive tract via water or food; and *Inhibition by Resident Microflora*, where the resident microbiota may prevent the growth of incoming microorganisms, offering natural protection (Austin, 1987). The global demand for fish continues to rise, with production reaching around 179 million tons in 2018 (FAO, 2020), largely driven by aquaculture expansion.

By 2050, aquaculture is expected to double its output to meet rising protein demands. In the U.S., major aquaculture species include catfish and Atlantic salmon, with significant fish imports. In 2018, the U.S. imported 6.1 billion pounds of fish valued at $22.4 billion (NOAA, 2020). While fish muscles are often considered sterile, this is debated (Austin, 2006; Novoslavskij et al., 2016). Pathogenic microorganisms can be present on both external and internal surfaces, often linked to foodborne illnesses. Fish have been involved in outbreaks of diseases caused by bacteria, viruses, and parasites, including *Vibrio spp.*, *Salmonella spp.*, and *Clostridium botulinum* (Novotny et al., 2004). Spoilage bacteria can also produce histamine, leading to scombroid poisoning, especially in certain fish species (Colombo et al., 2018).

Antibiotic resistance (AMR) in fish-associated microorganisms is a growing concern, as many bacteria found in fish, particularly those linked to foodborne illnesses, exhibit resistance to common antibiotics, posing significant health risks (Brunton et al., 2019; Watts et al., 2017). Modern sequencing techniques have provided deeper insights into the fish microbiome, revealing sources of pathogenic and spoilage microorganisms (Brugman et al., 2018). To address contamination and spoilage, various decontamination methods, including physical, chemical, and biological interventions, have been explored (Kuebutornye et al., 2020; Kumar et al.,

2020). Innovative approaches like photodynamic inactivation of bacteria and the use of natural antimicrobials show promise for enhancing fish safety.

VI MICROBIOLOGICAL SAFETY OF FISH AND FISH PRODUCT

A. Outbreaks and Recalls

According to the U.S. Centers for Disease Control and Prevention (CDC), fish was the most common food category involved in foodborne outbreaks from 2009 to 2018, with 937 outbreaks causing 5,011 illnesses, 364 hospitalizations, and four deaths (CDC, 2018). While the number of outbreaks decreased from 62 in 1998 to 17 in 2010, the frequency rose again after 2011, averaging 37 per year. The most common causes were scombroid toxin (histamine), responsible for 377 outbreaks from fish spoilage (e.g., tuna, mahi-mahi); ciguatoxin, linked to 268 outbreaks from barracuda or jackfish; *Salmonella* spp., responsible for 15 outbreaks from raw tuna; and *Clostridium botulinum*, involved in 14 outbreaks with two fatalities. Tuna (34%), mahi-mahi, barracuda, and salmon were the leading species implicated, with *Salmonella* and histamine particularly prevalent in tuna-related outbreaks.

B. Prevalence of Common and Emerging Human Pathogens

Salmonella, *Listeria monocytogenes*, *Vibrio spp.*, *Aeromonas spp.*, and *Clostridium botulinum* are the most frequently identified pathogens in fish and fish products (Amagliani et al., 2012). *Salmonella* is the leading cause of fish-related outbreaks, while *Listeria monocytogenes* is associated with numerous recalls due to its persistence in processing environments and ability to grow at refrigeration temperatures. Emerging pathogens like *Aeromonas hydrophila* are increasingly recognized for their role in fish diseases and histamine production (Bermejo et al., 2003). In the U.S., *Listeria monocytogenes* has been isolated from up to 78.7% of fish processing environments, underscoring the need for strict processing controls (Daskalov, 2006). *Aeromonas hydrophila* is also a concern in catfish, with prevalence rates reaching up to 36% in U.S. studies.

VII CONTAMINATION SOURCES

The main sources of contamination in fish and fish products include: Aquatic environments, where microorganisms from water and sediment colonize fish, influenced by environmental factors; Processing plants, where equipment, utensils, and personnel contribute to contamination, with some bacteria exhibiting multidrug resistance (MDR) (Skowron et al., 2019); Cross-contamination at the consumer level, where improper food handling and temperature abuse increase microbial growth and pathogen spread. In processing plants, antibiotic-resistant bacteria (ARB) and antimicrobial resistance genes (ARGs) are found in high concentrations, spreading resistance through the food supply chain (Divyashree et al., 2019). Pathogens like *Listeria* and *Aeromonas* can survive and proliferate under suboptimal storage and handling conditions, highlighting the need for proper hygiene and temperature control.

VIII TEMPERATURE ABUSE AND CONTROL:

Temperature fluctuations during transportation and storage significantly impact the growth of harmful microorganisms. Surveys have shown temperature abuse during fish transport, with home storage often exceeding safe temperatures (Godwin et al., 2007; Baptista et al., 2020). Proper storage is crucial, with frozen fish requiring temperatures of −18°C or lower, and chilled fish at 0°C or lower. In conclusion, the microbiological safety of fish and fish products is influenced by multiple factors across the production and supply chain. The rise in antimicrobial resistance and growing fish demand necessitate improved monitoring, stricter controls, and innovative decontamination methods to ensure future safety.

IX. CONCLUSION

Contamination and spoilage of meat and fish products are significant food safety challenges. These perishable items are prone to microbial contamination at various stages, with pathogens like *Salmonella*, *E. coli*, *Listeria*, and *Vibrio* posing serious health risks. Spoilage microorganisms cause undesirable sensory changes. Effective interventions, such as refrigeration, hygiene protocols, and advanced packaging, are essential for maintaining

safety and quality. Stringent food safety regulations, antimicrobial measures, and innovative preservation technologies are key to reducing contamination risks and extending shelf life. As demand grows, addressing spoilage mechanisms is crucial to minimizing foodborne illness, reducing food waste, and ensuring the sustainable production of safe, high-quality meat and fish.

X. ACKNOWLEDGMENT

REFERENCES

[1] Elmadfa, I., & Meyer, A. L. (2017). Importance of food composition data to nutrition and public health. European Journal of Clinical Nutrition, 64(4), 503–510.

[2] Geiker, N. R. W., Astrup, A., Hjorth, M. F., Sjödin, A., Pijls, L., & Markus, C. R. (2021). Meat and human health—Current knowledge and research gaps. Foods, 10(7), 1556.

[3] Godfray, H. C. J., Aveyard, P., Garnett, T., Hall, J. W., Key, T. J., Lorimer, J., ... & Jebb, S. A. (2018). Meat consumption, health, and the environment. Science, 361(6399),5324.

[4] Karwowska, M., Łaba, S., & Szczepański, M. (2021). Environmental impacts of meat waste management—Review. Sustainability, 13(5), 2603.

[5] Sofos, J. N., Flick, G., Nychas, G. J. E., Ockerman, H. W., Pateras, I. M., & Untermann, F. (2013). Meat and meat products. In B. Caballero (Ed.), Encyclopedia of Food Sciences and Nutrition (2nd ed., pp. 3755–3764). Academic Press.

[6] Wyness, L. (2016). The role of red meat in the diet: Nutrition and health benefits. Proceedings of the Nutrition Society, 75(3), 227–232.

[7] Beumer, R.R. and E. Brinkman, 1989. Detection of Listeria spp. with monoclonal antibody based enzyme linked immunosorbent assay (ELISA). Food Microbiol., 6: 177-177.

[8] Gill, C.O., 1998. Microbiological Contamination of Meat During Slaughter and Butchering of Cattle, Sheep and Pigs. In: The Microbiology of Meat and Poultry, Davies A. and R. Board (Eds.). Blackie Academic and Professional, New York, pp: 118-157.

[9] Ziauddin, S.K., D.N. Rao and B.L. Amla, 1994. A study of microbial profiles of buffalo carcasses processed in local slaughter units. Ind. J. Comp. Microbiol. Immunol. Infect. Dis., 15: 61-62.

[10] Roberts, T.A., W.R. Hudson, O.P. Whelehan, B. Simonsen and K. Olgaard et al., 1984. Number and distribution of bacteria on some beef carcasses at selected abattoirs in some member states of the European Communities. Meat Sci., 11: 191-205.

[11] McNamara, A.M., 1995. Establishment of baseline data on the microbiota of meats. J. Food Safety, 15: 113-119.

[12] Scanga, J.A., A.D. Grona, K.E. Belk, J.N. Sofos, G.R. Bellinger and G.C. Smith, 2000. Microbiological contamination of raw beef trimmings and ground beef. Meat Sci., 56: 145-152.

[13] Farber, J.M. and P.I. Peterkin, 1991. Listeria monocytogenes, a foodborne pathogen. Microbiol. Rev., 55: 476-511.

[14] Chaudhari, S.P., 2001. Immunodiagnostic potential of PI-PLC virulence marker of L. Monocytogenes in listeric infection in buffaloes. Ph.D. Thesis, Indian Veterinary Research Institute, Izatnagar, India.

[15] Abouzeed, Y.M., H. Hariharan, C. Poppe and F.S.B. Kibenge, 2000. Characterization of Salmonella isolates from beef cattle, broiler chicken and human sources on Prince Edward Island. Comp. Immunol. Microbiol. Infect. Dis., 23: 253-266.

[16] Bachhil, V.N. and T.N. Jaiswal, 1988. Occurrence of Salmonella in meats. J. Food Sci. Technol., 25: 310-312.

[17] Hazarika, R.A., D.K. Singh, K.N. Kapoor, R.K. Agarwal, A.B. Pandey and D.N. Rajkumar, 2005. Detection and characterization of verotoxin producing E. coli (VTEC) isolated from buffalo meat. J. Food Safety, 24: 281-290.

[18] Acheson, D.W.K., L.L. Lincicome, S. De-Breucker and G.T. Keusch, 1996. Detection of shiga-like toxin producing Escherichia coli in ground beef and milk by commercial enzyme immunoassay. J. Food Prot., 59: 344 349.

[19] Gustavsson J, Cederberg C, Sonesson U, Van Otterdijk R, Meybeck A. Global Food Losses and Food Waste. Rome: Food and Agriculture Organization of the United Nations. (2011).

[20] Paludetti LF, Kelly AL, O'Brien B, Jordan K. Gleeson, D. The effect of different precooling rates and cold storage on milk microbiological quality and composition. J Dairy Sci. (2018) 101:1921–9. doi: 10.3168/jds.2017-13668

[21] Wambui J, Lamuka P, Karuri E, Matofari J, Njage PMK. Microbial contamination level profiles attributed to contamination of beef carcasses, personnel, and equipment: case of small and medium enterprise slaughterhouses. J Food Prot. (2018) 81:684–91.

[22] Fletcher B, Mullane K, Platts P, Todd E, Power A, Roberts J, et al. Advances in meat spoilage detection: a short focus on rapid methods and technologies. Cyta J Food. (2018) 16:1037–44.

[23] Wang GY, Ma F, Zeng LY, Bai Y, Wang HH, Xu XL, et al. Modified atmosphere packaging decreased Pseudomonas fragi cell metabolism and extracellular proteolytic activities on meat. Food Microbiol. (2018) 76:443– 9.

[24] Fu LL, Wang C, Liu NN, Ma AJ, Wang YB. Quorum sensing system-regulated genes affect the spoilage potential of Shewanella baltica. Food Res Int. (2018) 107:1–9.

[25] Chen YF, Bassey AP, Bai Y, Teng S, Zhou GH, Ye KP. Synergistic effect of static magnetic field and modified atmosphere packaging in controlling blown pack spoilage in meatballs. Foods. (2022) 11:10.

[26] Wang XH, Deng YH, Sun JS, Ding Y, Liu Y, Tian T. Unraveling characterizations of bacterial community and spoilage profiles shift in chilled pork during refrigerated storage. Food Sci Technol. (2022) 42:e80321

[27] Liao RY, Xia Q, Zhou CY, Geng F, Wang Y, Sun YY, et al. LCMS/MS-based metabolomics and sensory evaluation characterize metabolites and texture of normal and spoiled dry-cured hams. Food Chem. (2022) 371:131156. doi: 10.1016/j.foodchem.2021.131156

[28] Zhou CY, Xia Q, Du LH, He J, Sun YY, Dang YL, et al. Recent developments in off-odor formation mechanism and the potential regulation by starter cultures in dry-cured ham. Crit Rev Food Sci Nutr. (2022) 04:1– 15.

[29] Zhou CY, Pan DD, Cao JX, Zhou GH, A. comprehensive review on molecular mechanism of defective dry-cured ham with excessive pastiness, adhesiveness, and bitterness by proteomics insights. Compr Rev Food Sci Food Saf. (2021) 20:3838–57.

[30] Wang GY, Jia K, Xu XL, Zhou GH. Bacterial community and spoilage profiles shift in response to packaging in yellow-feather broiler, a highly popular meat in Asia. Front Microbiol. (2017) 8:2588.

[31] Rahkila R, Johansson P, Sade E, Bjorkroth J. Identification of enterococci from broiler products and a broiler processing plant and description of Enterococcus viikkiensis sp. nov Appl Environ Microbiol. (2011) 77:1196– 203.

[32] Harada T, Dang VC, Nguyen DP, Nguyen TAD, Sakamoto M, Ohkuma M, et al. Enterococcus saigonensis sp. nov, isolated from retail chicken meat and liver. Int J Syst Evol Microbiol. (2016) 66:3779–85.

[33] Montes, M., Perez, M.J., and Nieto, T.P. (1999) Numerical taxonomy of gram-negative, facultatively anaerobic bacteria isolated from the skin of turbot (Scophthalmus maximus) and surrounding water. Syst. Appl. Microbiol. 22, 604–618.

[34] Sakata, T., Sugita, H., Mitsuoka, T., Kakimoto, D., and Kadota, H. (1981) Microflora in the gastrointestinal tracts of fresh-water fish. 2. Characteristics of obligate anaerobic-bacteria in the intestines of fresh-water fish. Bull. Jpn. Soc. Sci. Fish. 47, 421–427.

[35] Lee, S. and Lee, Y. (1995) Identification of intestinal microflora in rainbow trout. J. Microbiol. 33, 273–277.

[36] Gonzalez, C.J., Lopez-Diaz, T.M., Garcia-Lopez, M.L., Prieto, M., and Otero, A. (1999) Bacterial microflora of wild brown trout (Salmo trutta), wild pike (Esox lucius), and aquacultured rainbow trout (Oncorhynchus mykiss). J. Food Protect. 62, 1270–1277.

[37] Ekman, E., Borjeson, H., and Johansson, N. (1999) Flavobacterium psychrophilum in Baltic salmon Salmo salar brood fish and their offspring. Dis. Aquat. Org. 37, 159–163.

[38] El-Shafai, S.A., Gijzen, H.J., Nasr, F.A., and El-Gohary, F.A. (2004) Microbial quality of tilapia reared in fecalcontaminated ponds. Environ. Res. 95, 231–238.

[39] Burr, G., Gatlin, S., and Ricke, S. (2005) Microbial ecology of the gastrointestinal tract of fish and the potential application of prebiotics and probiotics in finfish aquaculture. J. World Aquacult. Soc. 36, 425–436.

[40] Robertson, P.A.W., O-Dowd, C., Burrells, C., Williams, P., and Austin, B. (2000) Use of Carnobacterium sp. as a probiotic for Atlantic salmon (Salmo salar L.) and rainbow trout (Oncorhynchus mykiss, Walbaum). Aquaculture 185, 235–243.