



Editorial

## Introduction to Special Issue: Study of Microbiological Safety in the Food Chain

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Ensuring microbiological safety in the food (of animal origin) chain is a challenging task due to the complex interactions among animals, humans and the environment. However, technological and analytical advances in recent years have provided a broader insight into microbiological hazards in the food chain and risk assessment. The objective of the proposed Special Issue "Study of Microbiological Safety in the Food Chain" was therefore to obtain scientific papers addressing microbiological hazards in the food chain, such as bacterial antimicrobial resistance, bacterial or fungal spoilage of foods, the antimicrobial potential of the indigenous microbiota, and the aminogenic or amine-reducing capacity of the microbiota, and papers that apply novel methods to study the food microbiome to discover potential, previously unknown microbial hazards. The Special Issue of the journal Processes entitled "Study of Microbiological Safety in the Food Chain" consists of nine research papers and one review paper. Four papers focus on microbiological aspects of milk and dairy products, three on meat and meat products, two on eggs and one on various market foods. The microorganisms of interest were species of lactobacilli, enterococci and molds, *Yersinia enterocolitica, Bacillus cereus* and the general microbiota in certain foods.

Antimicrobial resistance has been one of the most important public health problems in recent years, and its transmission through the food chain is being investigated in many studies. In addition to foodborne pathogens, transmissible resistance genes are also found in the indigenous food microbiota such as lactobacilli or enterococci. Výrostková et al. [1] reported in their work that strains of Lactobacillus johnsonii from raw milk showed the highest resistance to erythromycin (34.8%), similar to Lactobacillus zeae (33.3%). Of the 41 isolates, the presence of an erythromycin-encoding transmissible gene was confirmed in five strains of Lactobacillus johnsonii and in two strains of Lactobacillus zeae, demonstrating the potential risk of spreading antimicrobial resistance through the food chain. Enterococci are often carriers of resistance genes that can also be transferred to other bacteria in food. A study by Lauková et al. [2] showed that enterococci in goat milk have moderate resistance to antibiotics but also low pathogenic potential, which could be used for the selection of potential probiotic strains. In addition, Hu et al. [3] stipulated that antimicrobial resistance of Bacillus spp. could be widespread in the food chain. It was reported that 57.9%, 26.3% and 21.5% of Bacillus strains (B. cereus, B. licheniformis, B. pumilus and B. subtilis) carried fosfomycin resistance gene fosB, tetracycline resistance gene tet and erythromycin resistance gene *erm*, respectively. The authors found a high rate of resistance of foodborne pathogen B. cereus from dairy products, including vancomycin-resistant strains carrying van genes detected by whole-genome sequencing.

Recently, great efforts have been made to study molds in food processing, food spoilage and food safety (mycotoxins). Molecular methods are being developed for their identification and better characterization in the food chain. Demjanová et al. [4] detected the mold species *Penicillium verrucosum*, *P. commune* and *P. crustosum* on the shell surfaces of table eggs using conventional polymerase chain reaction (PCR) and polymerase chain reaction-internal transcribed spacer restriction fragment length polymorphism method



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(PCR-ITS-RFLP), confirming the presence of mycotoxin-producing strains and their importance for public health. Molecular identification of molds was performed in the study by Lešić et al. [5] focusing on the sensory properties of traditional fermented meat products. In the context of potential microbiological hazards, the authors reported that mycobiota were represented by a small proportion of mycotoxic mold species (12 and 14% in two types of dry-cured ham), identified as *Penicillium citrinum*, *Penicillium polonicum* and *Aspergillus niger*. In the work of Jevinová et al. [6], the effect of egg storage conditions on mold multiplication was studied. The authors reported that *Penicillium* and *Fusarium* species showed more intense growth with larger colony diameters on the eggshell surface at high relative humidity values, increasing the risk to consumers due to possible contamination of egg contents with mycotoxins. Interesting interactions among mold species were found in vitro, indicating the antifungal capacity of *Cladosporium cladoporioides* against *Penicillium chrysogenum*, *P. Crustosum* and *P. griseofulvum*.

The safety and quality characteristics of food can also be predicted by evaluating bacterial composition and growth during processing or storage. An example of this is the study by Kim et al. [7], in which metagenomic tools were used to correlate rancidity and microflora in dry-aged beef. Using analysis and quantification of microflora by qRT-PCR, the authors demonstrated that increases in the number of Pantoea spp. and decreases in the number of Streptococcus spp. could be used to determine rancidity of dry-aged beef and correlate with levels of reactive thiobarbituric acid (TBARS) and volatile basic nitrogen (VBN). In different cheese types, Zdolec et al. [8] demonstrated the effect of microbiota on biogenic amine content, focusing on applied bacterial or mold dairy cultures. The study showed that higher levels of biogenic amines, mainly tyramine, in cheeses were associated with the presence of Enterococcus durans, while negligible concentrations of amines were found in cheeses ripened with Lacticaseibacillus rhamnosus, Lactococcus lactis or Lacticaseibacillus paracasei cultures. The composition of the indigenous cheese microbiota was also investigated in the work of Lauková et al. [9] using next-generation sequencing. The results clearly confirmed the reliability of the method, revealing bacterial genera and their proportion in the population in a way that is not possible with traditional culturable methods.

The final review article in this Special Issue [10] presents a risk-based approach to ensuring meat safety from farm to slaughterhouse. It discusses the main biological hazards (bacteria, parasites) in the meat chain, focusing on under-controlled pathogens. On-farm food safety measures appear to be critical to reducing meatborne hazards and risk to consumers. Practical improvements in the control of biological hazards in the meat chain are still needed, and further developments can be expected in coming years.

As guest editor of the Special Issue "Study of Microbiological Safety in the Food Chain", I would like to thank all the authors, reviewers and supporting editors of the journal. I hope that this Special Issue will provide relevant new insights to scientists and professionals working in the field of food microbiology and public health.

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