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Molecular characterization and genetic diversity of salmonella SPP

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Abstract

This study investigated the molecular characterization and genetic diversity of Salmonella spp. isolated from various food sources between April and June 2025. A total of 90 samples (chicken, cheese, and beef) were collected, of which 70 (77.8%) tested positive for Salmonella spp. Biochemical identification was performed using conventional tests and the API 20E system, followed by species-level confirmation via the VITEK® 2 COMPACT system. Chicken samples showed the highest contamination rates (85–100%), followed by cheese (70–90%) and beef (55–75%). S. Typhimurium was the most prevalent serotype (42.8%), followed by S. arizona (25.7%) and S. paratyphi (17.3%). Molecular detection using conventional PCR and real-time PCR targeting the 16S rRNA gene, combined with sequencing and phylogenetic analysis (MEGA-X), revealed high genetic similarity (84–96%) among isolates, suggesting a common evolutionary origin. These findings underscore the significant public health risk posed by Salmonella contamination in animal-derived foods and highlight the necessity for rigorous food safety monitoring and targeted interventions to reduce pathogen transmission along the food chain.

Keywords: Salmonella SPP, Molecular characterization, Genetic diversity, VITEK 2 compact, PCR, Food safety.

Introduction

Infectious and foodborne diseases caused by Salmonella spp. represent a major global public health and food safety concern. According to the World Health Organization, approximately 10% of diarrheal diseases worldwide each year are attributable to Salmonella infections (Besser, 2018). Salmonella is a Gram-negative, facultatively anaerobic bacterium and one of the most prevalent foodborne pathogens of animal origin. Recent epidemiological reports indicate that more than 72% of bacterial food poisoning cases are specifically linked to Salmonella, posing a significant threat to both consumer health and the food industry. Among its numerous serovars, Salmonella enterica serovar Typhimurium (S. Typhimurium) is particularly associated with foodborne outbreaks and gastroenteritis.

The widespread distribution of Salmonella across regions including the Middle East, Asia, Europe, and the United States has been facilitated by its ability to persist in the food cold chain. Notably, refrigeration and conventional food sterilization processes often fail to eliminate these bacteria, largely due to genetic adaptations that confer enhanced tolerance to adverse environmental conditions. In addition to gastroenteritis, Salmonella is implicated in severe systemic diseases such as typhoid and paratyphoid fevers, typically transmitted via contaminated food or water. This underlines the importance of investigating its molecular characteristics and genetic diversity to better understand its epidemiology, evolution, and pathogenicity.

Recent research has emphasized molecular epidemiology approaches for Salmonella characterization, often employing 16S rRNA gene sequencing for phylogenetic analyses. The invA virulence gene is also widely used as a molecular marker for detection and strain differentiation. Over the past few decades, novel Salmonella serotypes have emerged, including monophasic S. Typhimurium variants, which exhibit unique genetic structures and altered flagellar expression. These variants frequently lack second-phase flagellar antigens due to mutations or deletions in the fljB gene and related loci (Zamperini et al., 2007). Some harbor IncHI2 plasmids carrying extended-spectrum β-lactamase (ESBL) and virulence genes, contributing to multidrug resistance (MDR) profiles against sulfonamides, tetracyclines, ampicillin, and streptomycin. For instance, a study in China

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