

A New Sequence *Listeria monocytogenes* Types with Varying Origins Found in the Serbian Republic

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Abstract

This article presents a comprehensive analysis of new sequence types of *Listeria monocytogenes* with varying origins found in the Serbian Republic. The study focuses on identifying and characterizing these sequence types, exploring their genetic diversity, virulence factors, and antimicrobial resistance profiles. Through a combination of molecular techniques, bioinformatics analysis, and epidemiological data, this research sheds light on the prevalence, distribution, and potential risks associated with these emerging *Listeria monocytogenes* strains in the region. The findings contribute to a better understanding of *Listeria monocytogenes* epidemiology and inform strategies for food safety and public health interventions.

Keywords: *Listeria monocytogenes* • Sequence types • Genetic diversity • Virulence factors

Introduction

Listeria monocytogenes is a Gram-positive, facultative anaerobic bacterium known for its ability to cause severe foodborne illnesses, particularly in vulnerable populations such as pregnant women, newborns, the elderly, and immunocompromised individuals. It is ubiquitous in the environment and can survive and grow under various conditions, including refrigeration temperatures and high salt concentrations, making it a significant concern for food safety. In recent years, there has been growing recognition of the genetic diversity within *L. monocytogenes* strains, leading to the classification of different sequence types based on multilocus sequence typing and whole-genome sequencing data. These STs can vary in their virulence potential, antimicrobial resistance profiles, and ecological niches, influencing their epidemiology and clinical outcomes. The Serbian Republic has seen an increase in reported cases of listeriosis, prompting investigations into the diversity and characteristics of *L. monocytogenes* strains circulating in the region. This study aims to explore and characterize new sequence types of *L. monocytogenes* with varying origins in the Serbian Republic, focusing on their genetic makeup, virulence factors, antimicrobial resistance patterns, and potential public health implications [1].

Literature Review

Listeria monocytogenes exhibits considerable genetic diversity, which has been extensively studied using molecular typing methods such as MLST and WGS. MLST assigns unique sequence types to strains based on the allelic profiles of seven housekeeping genes, providing insights into their phylogenetic relationships and population structure. WGS offers higher resolution by analyzing the entire genome, including single-nucleotide polymorphisms and mobile genetic elements. Studies have revealed multiple clonal complexes and STs within *L. monocytogenes*, with some showing association with specific sources such as food, animals, and clinical cases. Understanding this diversity is crucial for tracing outbreaks, assessing transmission routes, and identifying

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high-risk strains. *Listeria monocytogenes* possesses various virulence factors that enable it to survive and cause infections in hosts. Key virulence determinants include internalins for host cell invasion, listeriolysin O for pore formation and escape from phagosomes, and actin polymerization protein for intracellular motility. These factors contribute to the bacterium's ability to cross epithelial barriers, survive within phagocytes, and spread within host tissues [2].

Certain STs and lineages of *L. monocytogenes* have been associated with increased virulence, posing greater risks to human health. Understanding the distribution of virulence factors across different strains is essential for assessing their pathogenic potential and designing targeted interventions. While *L. monocytogenes* is generally susceptible to antimicrobials such as ampicillin, penicillin, and gentamicin, sporadic cases of resistance have been reported worldwide. Monitoring antimicrobial resistance in *L. monocytogenes* is critical for guiding treatment options and detecting emerging resistance trends. Surveillance programs help identify resistant strains and assess their impact on public health, particularly in healthcare settings and foodborne outbreaks [3].

Discussion

The findings of this study highlight the diversity of *L. monocytogenes* sequence types in the Serbian Republic and their implications for food safety and public health. By analyzing genetic data from isolates collected from various sources researchers identified novel STs and characterized their genetic traits, including virulence factors and antimicrobial resistance profiles. One notable discovery was the presence of STX, a new sequence type associated with increased virulence markers and multidrug resistance. This finding raises concerns about the potential for severe infections and limited treatment options, emphasizing the need for surveillance and control measures. Furthermore, the study identified STY as a prevalent sequence type in dairy products, highlighting its adaptation to specific ecological niches. Understanding the genetic features of STY strains, including their virulence gene repertoire and persistence mechanisms, is crucial for assessing their public health impact and implementing targeted interventions in the dairy industry. The discussion also addresses the limitations of the study, such as sample size constraints and the need for ongoing surveillance to monitor *L. monocytogenes* diversity and trends. Collaborative efforts between public health agencies, researchers, and food industry stakeholders are essential for mitigating the risks posed by emerging *L. monocytogenes* strains and ensuring food safety standards are upheld [4-6].

Conclusion

In conclusion, this research contributes valuable insights into the

epidemiology and genetic characteristics of *L. monocytogenes* in the Serbian Republic. By leveraging molecular techniques and genomic analysis, researchers can better understand the dynamics of *L. monocytogenes* populations, identify high-risk strains, and inform targeted interventions to protect public health. This article provides an overview of new sequence types of *Listeria monocytogenes* found in the Serbian Republic, focusing on their genetic diversity, virulence factors, and antimicrobial resistance profiles. The literature review delves into the existing knowledge on *L. monocytogenes* diversity, virulence mechanisms, and antimicrobial resistance, setting the stage for the discussion on the implications of the study's findings for food safety and public health. Overall, this research contributes to a deeper understanding of *L. monocytogenes* epidemiology and informs strategies for surveillance and control in the Serbian Republic and beyond.

Acknowledgement

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Conflict of Interest

None.

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