

Listeriosis: Bridging the Gap with Integrated Surveillance Among Livestock and Humans

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ABSTRACT

Listeria monocytogenes, a Gram-positive bacillus, remains a critical public health challenge due to its zoonotic potential and environmental ubiquity. This pathogen causes listeriosis, a severe foodborne disease with high mortality rates, particularly in immunocompromised individuals, neonates, and pregnant women. This article examines the epidemiology of listeriosis and emphasizes the necessity of integrated surveillance frameworks that address its transmission across livestock, humans, and the environment. By adopting the One Health approach, integrated surveillance leverages molecular epidemiology, whole-genome sequencing (WGS), and environmental monitoring to track outbreaks and elucidate transmission dynamics. Livestock surveillance, encompassing routine sampling and genomic characterization, serves as a foundation for early detection, while human surveillance integrates clinical diagnostics and outbreak investigations through real-time data sharing networks. Environmental surveillance further complements these efforts by identifying ecological niches that sustain the pathogen. Despite significant advancements, challenges such as resource constraints and antimicrobial resistance underscore the need for enhanced laboratory infrastructure and interdisciplinary collaboration. This article underscores the importance of integrated surveillance in mitigating the public health impact of *Listeria* outbreaks and advancing global health security.

Keywords: *Listeria monocytogenes*, integrated surveillance, One Health, zoonotic diseases, molecular epidemiology, environmental monitoring

INTRODUCTION

Listeria monocytogenes, a facultative intracellular pathogen, occupies a formidable niche in the pantheon of foodborne pathogens due to its remarkable adaptability and capacity to traverse interspecies barriers. This Gram-positive bacillus is ubiquitously distributed in the environment, colonizing soil, water, decaying vegetation, and animal reservoirs, thereby establishing a persistent risk for zoonotic transmission. Listeriosis, the clinical manifestation of *Listeria* infection, is characterized by a spectrum of presentations ranging from self-limiting febrile gastroenteritis to invasive diseases such as meningitis, encephalitis, septicemia, and adverse pregnancy outcomes, including spontaneous abortion and neonatal sepsis. The disproportionately high mortality rate associated with invasive listeriosis—estimated at 20% to 30%—renders it a critical public health concern.



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Epidemiology

The epidemiological landscape of Listeriosis underscores its global relevance. The disease has been linked to sporadic cases and outbreaks, often associated with contaminated ready-to-eat foods, unpasteurized dairy products, and improperly processed meats. Developed nations have reported an incidence rate of approximately 0.1 to 10 cases per million annually, with higher susceptibility observed in immunocompromised individuals, pregnant women, neonates, and the elderly. In developing countries, the true burden remains obscured by underreporting and limited diagnostic capabilities, despite substantial risk factors such as unhygienic food processing practices and close human-animal interaction. [1,2,3] The pathogen's ability to thrive at refrigeration temperatures and resist various environmental stressors further complicates control measures, amplifying the urgency for comprehensive surveillance systems. [4]

Integrated Surveillance: A One Health Approach

Integrated surveillance for *Listeria* outbreaks constitutes a pivotal strategy in bridging the epidemiological gap between livestock and human populations. Given its zoonotic potential, surveillance systems must encompass veterinary, food safety, and public health domains to facilitate early detection, source attribution, and outbreak containment. Such integrated approaches align with the One Health framework, recognizing the interconnectedness of human, animal, and environmental health. In this context, molecular epidemiology has emerged as an indispensable tool, enabling the identification of genetic clusters and transmission pathways through whole-genome sequencing [WGS] and multilocus sequence typing [MLST]. WGS, in particular, has revolutionized *Listeria* surveillance, offering unparalleled resolution in tracking outbreaks and delineating genetic relationships among strains isolated from disparate sources. [5,6]

Surveillance in Livestock

The cornerstone of integrated surveillance lies in the systematic monitoring of livestock populations, which serve as asymptomatic carriers and potential reservoirs of *Listeria monocytogenes*. Livestock surveillance involves regular sampling of milk, feces, and feed, complemented by robust laboratory diagnostics, including culture isolation and polymerase chain reaction [PCR]-based methods. High-throughput sequencing platforms further augment these efforts by characterizing the genetic diversity of *Listeria* strains, thereby enhancing the predictive capacity of risk assessment models. Concurrently, sentinel surveillance in abattoirs and dairy farms facilitates the identification of critical control points, guiding interventions to mitigate contamination along the food production continuum. [7]

Human Surveillance

Human surveillance, on the other hand, necessitates a multidisciplinary approach integrating clinical diagnostics, foodborne illness reporting, and epidemiological investigations. The implementation of standardized diagnostic protocols encompassing cerebrospinal fluid culture, blood culture, and histopathological examination is imperative for accurate case identification. Moreover, coordinated efforts to link human cases with food and environmental isolates via molecular subtyping techniques, such as pulsed-field gel electrophoresis [PFGE] and WGS, provide actionable insights into outbreak dynamics. Real-time data sharing through national and international surveillance networks, such as PulseNet and the European Surveillance System [TESSy], exemplifies the potential of collaborative platforms in combating *Listeria* outbreaks. [8,9]

Environmental Surveillance

The role of environmental surveillance in integrated frameworks cannot be overstated. Environmental sampling targeting soil, water sources, and food processing environments serves as a sentinel system for the early detection of *Listeria* contamination. The integration of environmental data with livestock and human

surveillance enables a holistic understanding of transmission dynamics, uncovering the ecological niches that sustain the pathogen. Predictive modeling based on environmental parameters, such as temperature, humidity, and soil composition, further enhances outbreak preparedness by identifying high-risk areas and temporal patterns of *Listeria* proliferation. [10,11]

Challenges and Future Directions

Despite significant advancements, integrated surveillance for *Listeria* faces formidable challenges. Resource constraints, particularly in low- and middle-income countries, limit the scalability and sustainability of surveillance programs. The lack of standardized methodologies across sectors and regions hinders data comparability, complicating global efforts to combat the pathogen. Additionally, the emergence of antimicrobial-resistant *Listeria* strains poses an insidious threat, necessitating the inclusion of antimicrobial susceptibility testing in routine surveillance protocols. Strengthening laboratory infrastructure, fostering interdisciplinary collaboration, and leveraging technological innovations are imperative to address these challenges effectively. [12]

Policy Implications and Community Engagement

The utility of integrated surveillance extends beyond outbreak detection and response, encompassing risk communication, policy formulation, and capacity building. By elucidating the interplay between livestock management practices, food safety protocols, and human health outcomes, surveillance data can inform evidence-based interventions to reduce the burden of listeriosis. Moreover, the inclusion of socio-behavioral research in surveillance frameworks can shed light on the determinants of risk perception and compliance with preventive measures, fostering community engagement in disease control efforts. [13]

CONCLUSION

In conclusion, Listeriosis represents a paradigmatic example of a zoonotic disease necessitating a coordinated response across multiple domains. Integrated surveillance, rooted in the One Health approach, offers a robust framework for addressing the multifaceted challenges posed by *Listeria* monocytogenes. By harnessing the synergistic potential of molecular epidemiology, environmental monitoring, and interdisciplinary collaboration, it is possible to mitigate the public health impact of *Listeria* outbreaks. As global interconnectedness intensifies, the imperative for resilient surveillance systems-capable of transcending traditional boundaries-becomes ever more pressing.

BIBLIOGRAPHY

- Farber JM, Peterkin PI. *Listeria monocytogenes*, a food-borne pathogen. *Microbiol Rev.* 1991;55(3):476-511. DOI: <https://doi.org/10.1128/mr.55.3.476-511.1991> PMID:1943998 PMCID:PMC372831
- Swaminathan B, Gerner-Smidt P. The epidemiology of human listeriosis. *Microbes Infect.* 2007;9(10):1236-43. DOI: <https://doi.org/10.1016/j.micinf.2007.05.011> PMID:17720602
- Ramaswamy V, Cresence VM, Rejitha JS, Lekshmi MU, Dharsana KS, Prasad SP, et al. *Listeria*-review of epidemiology and pathogenesis. *J Microbiol Immunol Infect.* 2007;40(1):4-13.
- Huss HH, Jorgensen LV, Vogel BF. Control options for *Listeria monocytogenes* in seafood. *Int J Food Microbiol.* 2000;62(3):267-74. DOI: [https://doi.org/10.1016/S0168-1605\(00\)00347-0](https://doi.org/10.1016/S0168-1605(00)00347-0) PMID:11156271
- Moura A, Tourdjman M, Leclercq A, Hamelin E, Laurent E, Fredriksen N, et al. Real-time whole-genome sequencing for surveillance of *Listeria monocytogenes*, France. *Emerg Infect Dis.* 2017;23(9):1462-70. DOI: <https://doi.org/10.3201/eid2309.170336> PMID:28643628 PMCID:PMC5572858
- Schlech WF. Epidemiology and clinical manifestations of *Listeria monocytogenes* infection. *Microbiol Spectr.* 2019;7(3):1-20. DOI: <https://doi.org/10.1128/microbiolspec.GPP3-0012-2018> PMID:31373270 PMCID:PMC6684298
- Carpentier B, Cerf O. Review-Persistence of *Listeria monocytogenes* in food industry equipment and premises. *Int J Food Microbiol.* 2011;145(1):1-8. DOI: <https://doi.org/10.1016/j.ijfoodmicro.2011.01.017> PMID:21315469
- Jackson BR, Salter M, Tarr C, Conrad A, Harvey E, Steinbock L, et al. Notes from the field: Listeriosis associated with stone fruit-United States, 2014. *MMWR Morb Mortal Wkly Rep.* 2015;64(10):282-83.

9. Buchanan RL, Gorris LG, Hayman MM, Jackson TC, Whiting RC. A review of *Listeria monocytogenes*: An update on outbreaks, virulence, dose-response, ecology, and risk assessments. *Food Control*. 2017;75:1-13. DOI: <https://doi.org/10.1016/j.foodcont.2016.12.016>
10. Weller D, Andrus A, Wiedmann M, den Bakker HC. *Listeria monocytogenes* lineages: Genomics, evolution, ecology, and phenotypic characteristics. *Int J Med Microbiol*. 2015;305(2):223-34. DOI: <https://doi.org/10.1016/j.ijmm.2014.12.015> PMID:25601631
11. Cartwright EJ, Jackson KA, Johnson SD, Graves LM, Silk BJ, Mahon BE. Listeriosis outbreaks and associated food vehicles, United States, 1998-2008. *Emerg Infect Dis*. 2013;19(1):1-9. DOI: <https://doi.org/10.3201/eid1901.120393> PMID:23260661 PMCid:PMC3557980
12. Alcock BP, Raphenya AR, Lau TT, Tsang KK, Bouchard M, Edalatmand A, et al. CARD 2020: Antibiotic resistance surveillance with the comprehensive antibiotic resistance database. *Nucleic Acids Res*. 2020;48(D1):D517-525. DOI: <https://doi.org/10.1093/nar/gkz935> PMID:31665441 PMCid:PMC7145624
13. Grindle M, Karanfil O, Liang T, Smith G, Wang Y, Zhang Y. Socioeconomic determinants of *Listeria* infection risk: A spatial analysis. *Epidemiol Infect*. 2021;149:e106. doi:10.1017/S095026882100068X.