

Genomic Surveillance of *Listeria monocytogenes* from Human sources and Food Products in Argentina

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INTRODUCTION & AIM

Listeria monocytogenes is an opportunistic pathogen that causes the infection listeriosis, primarily affecting immunocompromised patients and pregnant women. The invasive form of the disease is characterized by severe symptoms, with an estimated mortality rate of 20–30%. The transmission of the bacteria typically occurs through contaminated ready-to-eat foods, including unpasteurized dairy products and raw vegetables. Understanding the molecular epidemiology and genetic diversity of isolates collected from clinical and food sources is crucial for identifying clusters and common sites of infection. This study aimed to determine the population structure and genomic epidemiology of *L. monocytogenes* strains in Argentina.

METHOD



2018 - 2023

L. monocytogenes isolates

(n = 71)

41

30

Illumina MiSeq

Molecular typing

Lineage and serogroup

MLST Sequence type (ST)

MLST Clonal Complex (CC)

Phylogenetic analysis

Single nucleotide polymorphisms (SNPs)

SRST2

ARIBA

SNIPPY

Coverage ≥ 30X

RESULTS & DISCUSSION

The hypervirulent clone CC1, belonging to lineage I and serogroup IVb, was predominant in both clinical (36.6%, 15/41) and food samples (23.3%, 7/30).

Epidemiological relationship

0 - 9 SNPs
High

10 - 30 SNPs
Possible

Source
■ Food ■ Human

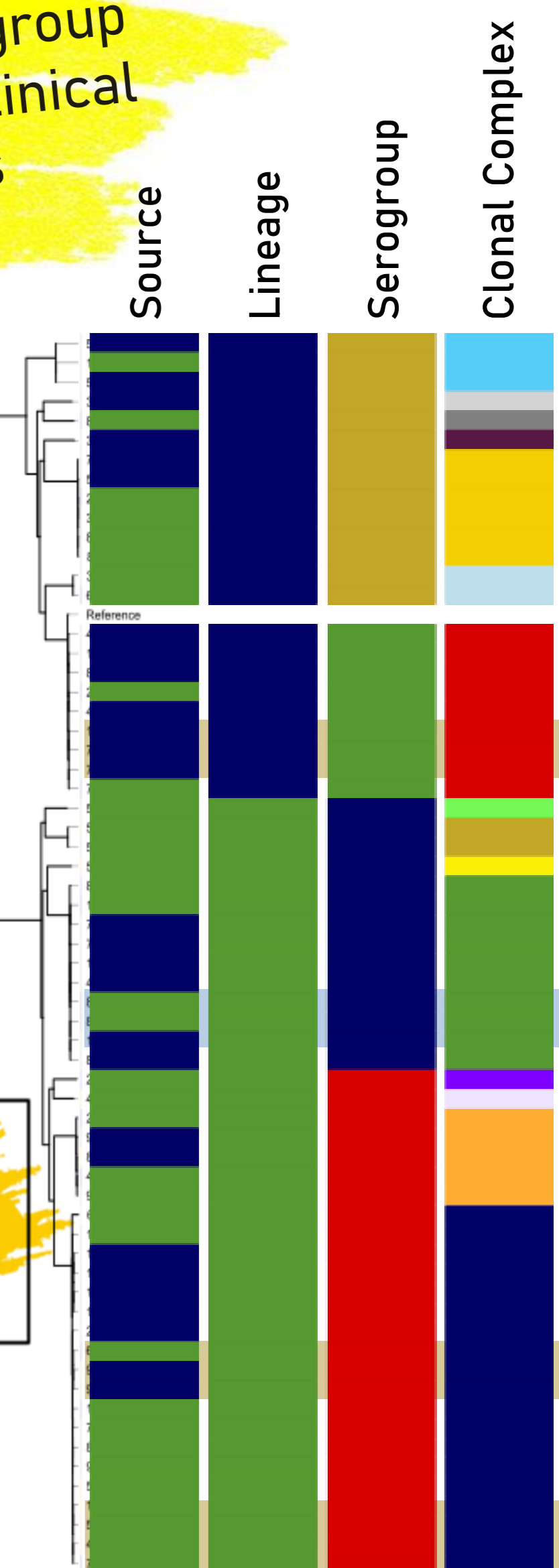
Lineage
■ I ■ II

Serogroup
■ IVb ■ IIb
■ IIa ■ IIc

Clonal Complex (CC)
■ CC1 ■ CC9
■ CC3 ■ CC59

17 MLST STs

15 MLST CCs



CONCLUSION

Integrating genomic data with metadata from food and environmental isolates, along with information from patient questionnaires—including medical details, travel history, and food consumption patterns—could help formulate more targeted public health intervention strategies for the control and prevention of listeriosis.

FUTURE / REFERENCES

- Jackson BR, *et al.* Implementation of nationwide real-time whole-genome sequencing to enhance listeriosis outbreak detection and investigation. *Clin Infect Dis.* 2016;63:380–6.
- Lakicevic B, *et al.* Wholegenome sequencing as the gold standard approach for control of *Listeria monocytogenes* in the food chain. *J Food Prot.* 2023;86:100003.