

Genomic Surveillance of *Listeria monocytogenes* in Argentina: Analysis of Cases and Isolates, 2023-2024

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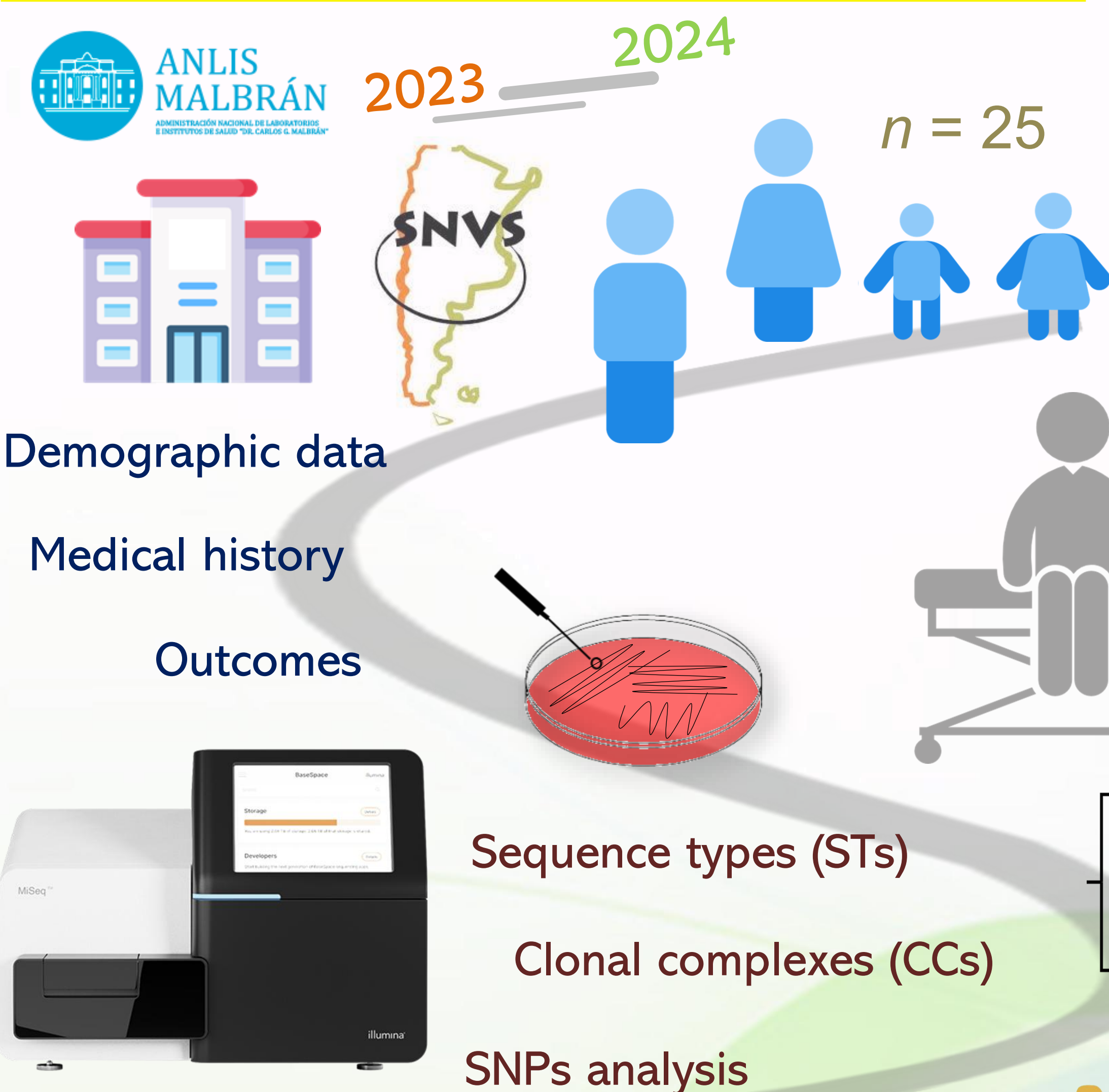
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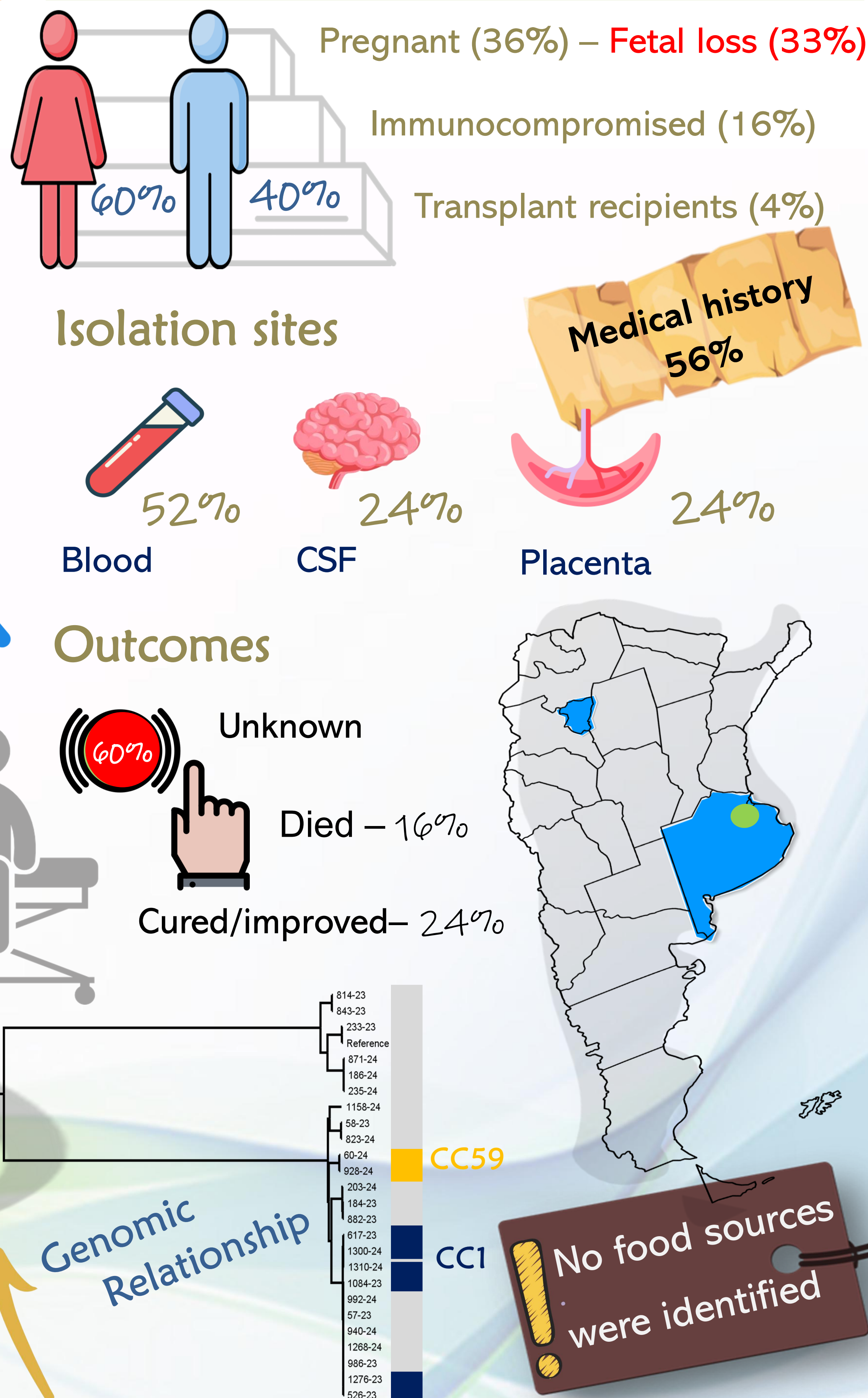
INTRODUCTION & AIM

In vulnerable individuals, *Listeria monocytogenes* can cause invasive listeriosis, a severe foodborne infection with 20-30% mortality. Case notification to the National Health Surveillance System (SNVS) combined with whole-genome sequencing (WGS) enhances surveillance and source identification. This study evaluated listeriosis cases and the genomic relationships of isolates in Argentina identified from 2023 to 2024.

METHOD



RESULTS & DISCUSSION



CONCLUSION

. The low amount of documented outcomes (40%) and missing medical history (44%) highlight the need for strengthened SNVS notification to better understand the disease burden and identify key populations at risk.

. Genomic clusters (CC1 and CC59) were detected without food source identification. Incorporating food surveys and systematic isolate referral will improve our consumption pattern knowledge and allow for epidemiological investigations for source identification.