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

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## **RESULTS & DISCUSSION** INTRODUCTION & AIM Pregnant (36%) – Fetal loss (33%) In vulnerable individuals, Listeria monocytogenes can cause invasive listeriosis, a severe foodborne infection Immunocompromised (16%) with 20-30% mortality. Case notification to the National Health Surveillance System (SNVS) combined with whole-60% 40% Transplant recipients (4%) genome sequencing (WGS) enhances surveillance and source identification. This study evaluated listeriosis Medical history cases and the genomic relationships of isolates in Isolation sites Argentina identified from 2023 to 2024. 56% **METHOD** 2024 ANLIS 2023 MALBRÁN n = 25**CSF** Blood Placenta Outcomes Unknown Demographic data Died - 16% Medical history Cured/improved- 24% Outcomes **7** 843-23 Reference Sequence types (STs) 58-23 823-24 Clonal complexes (CCs) Genomic 184-2. Relationship 617-23 **CC59** No food sources were identified SNPs analysis 1276-23 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.