

Supplementary Appendix

This appendix has been provided by the authors to give readers additional information about their work.

Supplement to: Thomas J, Govender N, McCarthy KM, et al. Outbreak of listeriosis in South Africa associated with processed meat. *N Engl J Med* 2020;382:632-43. DOI: 10.1056/NEJMoa1907462

Supplementary Appendix

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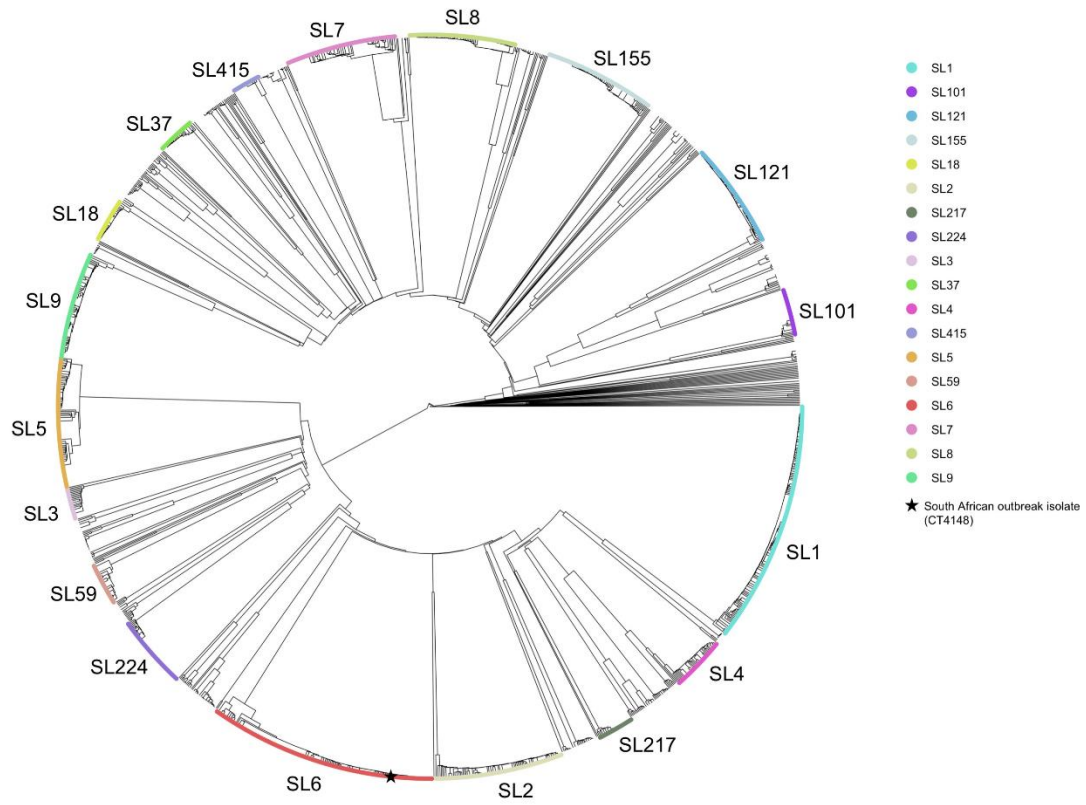


Figure S1. Global *Listeria monocytogenes* diversity based on cgMLST

Single-linkage clustering of 1697 *L. monocytogenes* isolates based on their cgMLST profiles, including the 1696 isolates of the global and international dataset published by Moura et al.,¹ and one isolate representative of the 2017-2018 South African outbreak (HM00108598, CT4148, food origin). Major cgMLST sublineages (SLs) are highlighted. The position of the South African outbreak isolate is indicated with a black star.

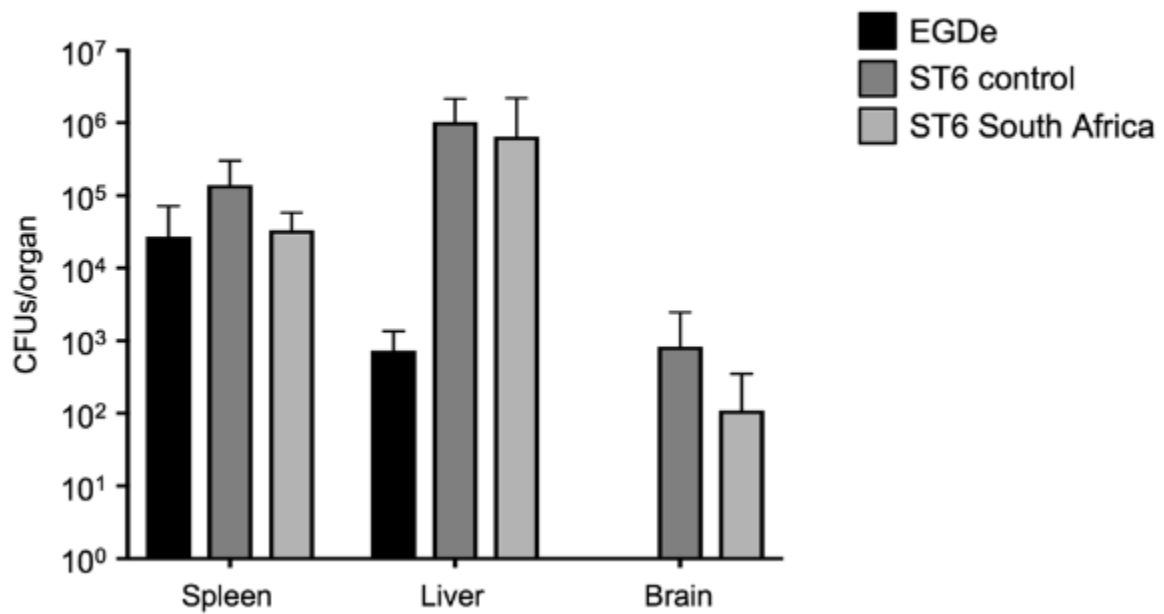


Figure S2. Virulence of the outbreak isolate

EGDe is a ST9 reference laboratory strain², “ST6 control” is an isolate representative of the hypervirulent clone CC6 (CLIP 2009/01092)³, which was isolated from a patient with neurolisteriosis. “ST6 South Africa” is a representative strain of the South African outbreak (YA00061615). K1E16P mice were orally inoculated with 2×10^8 CFUs/mouse, then euthanized 4 days after inoculation. Spleen, liver and brain bacterial load were estimated by CFU counts from ground tissue. Five mice were inoculated per group. Mean + SEM values are presented.

References

1. Moura A, Criscuolo A, Pouseele H, et al. Whole genome-based population biology and epidemiological surveillance of *Listeria monocytogenes*. *Nat Microbiol* 2016;2:16185.
2. Glaser P, Frangeul L, Buchrieser C, et al. Comparative genomics of *Listeria* species. *Science* 2001;294:849-52.
3. Maury MM, Tsai YH, Charlier C, et al. Uncovering *Listeria monocytogenes* hypervirulence by harnessing its biodiversity. *Nat Genet* 2016;48:308-13.