



**HAL**  
open science

## Genome Sequence of *Listeria innocua* Strain MEZLIS26, Isolated from a Goat in South Africa

Mohamed E El Zowalaty, Rachel A Hickman, Alexandra Moura, Marc S  
Lecuit, Oliver T Zishiri, Noelle Noyes, Josef D Järhult

### ► To cite this version:

Mohamed E El Zowalaty, Rachel A Hickman, Alexandra Moura, Marc S Lecuit, Oliver T Zishiri, et al.. Genome Sequence of *Listeria innocua* Strain MEZLIS26, Isolated from a Goat in South Africa. Microbiology Resource Announcements, 2019, 8 (44), 10.1128/MRA.00991-19 . pasteur-02395652

**HAL Id: pasteur-02395652**

**<https://pasteur.hal.science/pasteur-02395652>**

Submitted on 5 Dec 2019

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License



# Genome Sequence of *Listeria innocua* Strain MEZLIS26, Isolated from a Goat in South Africa

 Mohamed E. El Zowalaty,<sup>a,b,c</sup> Rachel A. Hickman,<sup>d</sup> Alexandra Moura,<sup>e,f,g</sup> Marc Lecuit,<sup>e,f,g,h</sup>  Oliver T. Zishiri,<sup>i</sup> Noelle Noyes,<sup>j</sup> Josef D. Järhult<sup>d</sup>

<sup>a</sup>Department of Infectious Diseases, St. Jude Children's Research Hospital, Memphis, Tennessee, USA

<sup>b</sup>Virology and Microbiology Research Group, School of Health Sciences, College of Health Sciences, University of KwaZulu-Natal, Westville Campus, Durban, South Africa

<sup>c</sup>Infectious Diseases and Anti-Infective Therapy Research Group, Sharjah Medical Research Institute and College of Pharmacy, University of Sharjah, Sharjah, United Arab Emirates

<sup>d</sup>Zoonosis Science Center, Department of Medical Sciences, Uppsala University, Uppsala, Sweden

<sup>e</sup>Institut Pasteur, National Reference Center & World Health Organization Collaborating Center for *Listeria*, Paris, France

<sup>f</sup>Institut Pasteur, Biology of Infection Unit, Paris, France

<sup>g</sup>Inserm U1117, Paris, France

<sup>h</sup>Université de Paris, Institut Imagine, Necker-Enfants Malades University Hospital, Division of Infectious Diseases and Tropical Medicine, APHP, Paris, France

<sup>i</sup>Discipline of Genetics, School of Life Sciences, College of Agriculture, Engineering and Science, University of KwaZulu-Natal, Durban, South Africa

<sup>j</sup>Department of Veterinary Population Medicine, College of Veterinary Medicine, University of Minnesota, St. Paul, Minnesota, USA

**ABSTRACT** Here, we report the draft genome sequence of *Listeria innocua* strain MEZLIS26, isolated from a healthy goat in Flagstaff, Eastern Cape Province, South Africa. The genome was sequenced using the Illumina MiSeq platform and had a length of 2,800,777 bp, with a G+C content of 37.4%, 2,755 coding DNA sequences (CDSs), 49 transfer RNAs (tRNAs), and 4 noncoding RNAs (ncRNAs).

*Listeria* spp. are small, motile, catalase-positive, non-spore-forming, rod-shaped, Gram-positive bacteria. The genus *Listeria* is currently known to consist of 20 species (1), of which *L. monocytogenes* is an important foodborne human pathogen causing serious epidemics and sporadic listeriosis (2, 3). *Listeria* spp. have been isolated from a wide variety of sources, and *L. innocua* is reported to be more commonly isolated than *L. monocytogenes* (4). *L. innocua* is a nonpathogenic surrogate species that is closely related to *L. monocytogenes*. Recently, atypical hemolytic *L. innocua* was reported to be virulent and can actively cross the intestinal epithelium and spread systemically to the liver and spleen, albeit to a lesser degree than *L. monocytogenes* (5). In addition to its clinical relevance (5–8) and similarity to *L. monocytogenes*, the genomes of *L. innocua* provide important information that helps understand the pathogenicity of *L. monocytogenes*. Limited data about the genome sequence of *L. innocua* are available. Here, we report the draft genome sequence of *L. innocua* strain MEZLIS26, isolated from a goat in Flagstaff, Eastern Cape, South Africa, in May 2018. The sample was collected in 10 ml of 0.1% buffered peptone water and incubated for 24 hours. Following enrichment in *Listeria* broth (Oxoid, England), the sample was streaked onto *Listeria* selective agar (Oxoid, England) and incubated at 37°C for 18 hours. A slant of the bacterial culture was shipped to North Carolina State University (NCSU) for further analysis as part of the GenomeTrakr project (9).

Colony PCR for the hemolysin (*hly*) gene was performed as previously described (10). An aliquot of overnight culture in brain heart infusion (BHI) broth was submitted to the Clinical Sciences Department at NCSU for matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) analysis for further confirmation. DNA isolation was performed using a MasterPure DNA isolation kit (Lucigen, WI) according to the manufacturer's protocol. Sequencing libraries were prepared using a Nextera XT library preparation kit (Illumina, CA). Sequencing

**Citation** El Zowalaty ME, Hickman RA, Moura A, Lecuit M, Zishiri OT, Noyes N, Järhult JD. 2019. Genome sequence of *Listeria innocua* strain MEZLIS26, isolated from a goat in South Africa. *Microbiol Resour Announc* 8:e00991-19. <https://doi.org/10.1128/MRA.00991-19>.

**Editor** Steven R. Gill, University of Rochester School of Medicine and Dentistry

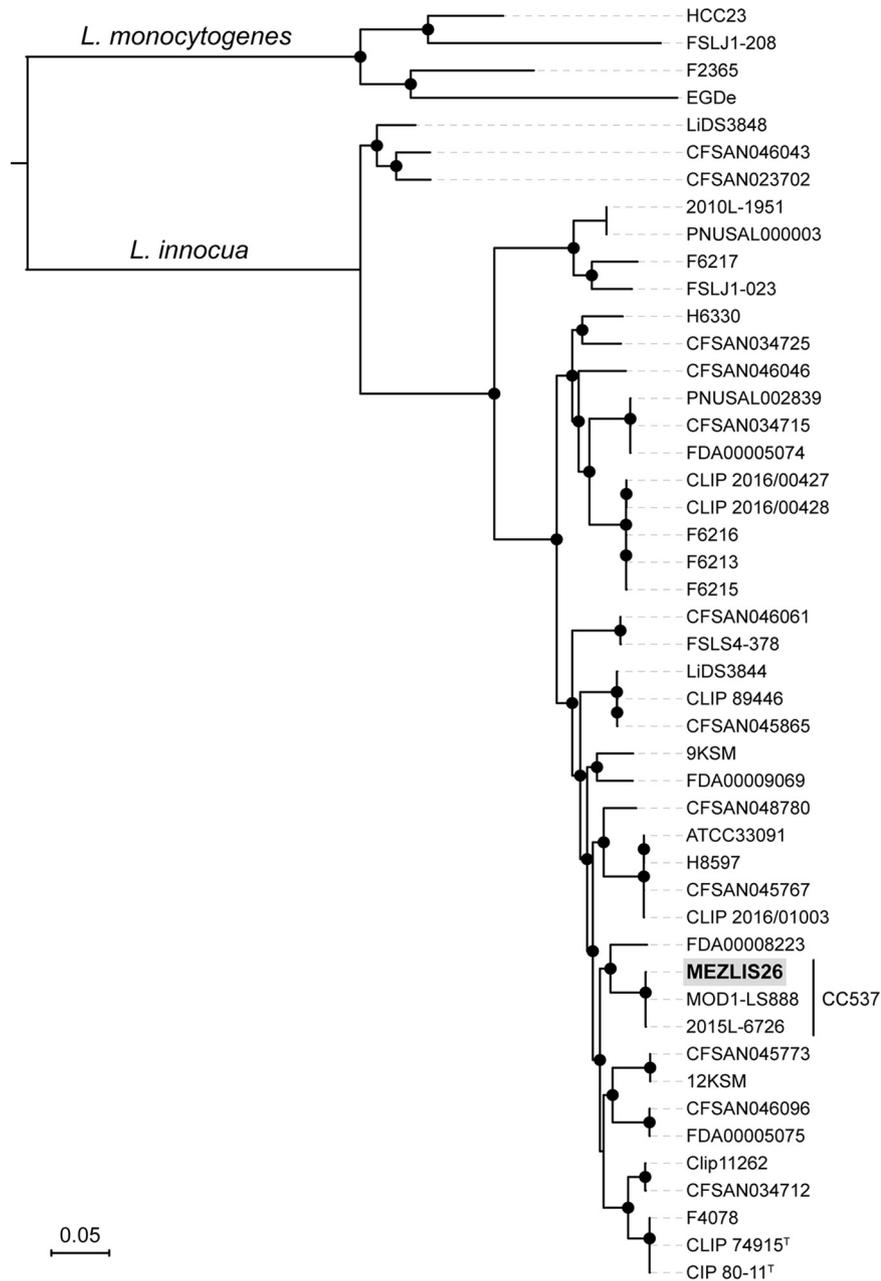
**Copyright** © 2019 El Zowalaty et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Mohamed E. El Zowalaty, [elzow005@gmail.com](mailto:elzow005@gmail.com).

**Received** 20 August 2019

**Accepted** 23 August 2019

**Published** 31 October 2019



**FIG 1** Phylogenetic positioning of isolate MEZLIS26 (highlighted in gray) within *L. innocua*. Representative genomes of *L. monocytogenes* were used as the outgroup. The maximum likelihood phylogeny was inferred from 642,408 core genome SNPs. Black circles represent bootstrap branch support values higher than 90% based on 1,000 replicates.

was performed on the Illumina MiSeq platform using the v2 reagent kit, which yielded 250-bp paired-end (PE) reads.

A total of 1,294 Mb (or ~1.3 Gb) raw data reads were generated, and a total of 1.191 Mb (or ~1.2 Gb) cleaned reads were obtained using Trim Galore, a Perl wrapper for Cutadapt (11), and FastQC (12) using the functions `-paired`, `-phred33`, `-clip_R1 11`, `-clip_R2 11`, `-three_prime_clip_R1 3`, and `-three_prime_clip_R2 3`. The  $N_{50}$  value of the cleaned sequence reads was 234 bp. Sequences were assembled using Unicycler version 0.4.7 (13) into 12 contigs of at least 200 nucleotides (nt) long, using default parameters with the addition of the `-min_fasta_length 200` parameter. Assembly quality was assessed using QUAST (13), yielding a total of 2,800,777 bp, with

a G+C content of 37.4%, an  $N_{50}$  value of 1,410,057 bp, and an  $L_{50}$  value of 1. Prokka version 1.13 (14) was used for annotation, indicating that the genome contained 2,755 coding DNA sequences (CDSs) and 49 tRNA, 1 transfer-messenger RNA (tmRNA), and 3 rRNA genes. The average nucleotide identity BLAST against *L. innocua* Clip11262 (GenBank accession number [NC\\_003212](https://ncbi.nlm.nih.gov/nuccore/NC_003212)) was of 98.73%, confirming species identity (15). To better understand the phylogenetic placement of isolate MEZLIS26, a maximum likelihood phylogeny was inferred from the core genome alignment of 42 *L. innocua* and 4 *L. monocytogenes* public genomes (5) using Parsnp, implemented in Harvest suite v.1.1.2 (16) and visualized with iTol v.4.2 (17). Isolate MEZLIS26 clustered within clonal complex CC537 (nonhemolytic *L. innocua*) together with isolates MOD1-LS888 and 2015L-6726 (SRA accession numbers [SRR1481929](https://ncbi.nlm.nih.gov/sra/SRR1481929) and [SRR2915359](https://ncbi.nlm.nih.gov/sra/SRR2915359), respectively), isolated from food in the United States (Fig. 1).

**Data availability.** This whole-genome sequencing project has been deposited at DDBJ/ENA/GenBank under the BioProject number [PRJNA514279](https://ncbi.nlm.nih.gov/bioproject/PRJNA514279) (BioSample accession number [SAMN11604718](https://ncbi.nlm.nih.gov/biosample/SAMN11604718) and GenBank accession number [AADHQU000000000](https://ncbi.nlm.nih.gov/nuccore/AADHQU000000000)). The version described in this paper is the first version, AADHQU010000000. The sequences have been submitted to the Sequence Read Archive (SRA) under the accession numbers [SRX5806851](https://ncbi.nlm.nih.gov/sra/SRX5806851) and [SRR9029426](https://ncbi.nlm.nih.gov/sra/SRR9029426). All isolates used in this study are also publicly available in <https://bigsd.bpasteur.fr/listeria/>.

## ACKNOWLEDGMENTS

The whole-genome sequencing work is supported by the National Institutes of Health/Food and Drug Administration under award number 1U18FD006780-01.

We thank the South African National Research Foundation for supporting this research through the Thuthuka Funding Instrument (grant number TTK170411226583) and the Swedish Research Council (VR) through grant number 2016-02606. We thank Lyndy Harden and Siddhartha Thakur from Population Health and Pathobiology, College of Veterinary Medicine, North Carolina State University (Raleigh, NC). We thank the Genome Trakr Network and the Whole Genome Sequencing Program for foodborne pathogen traceback and the Center for Food Safety and Applied Nutrition (CFSAN), U.S. Food and Drug Administration (FDA), for support in the whole-genome sequencing (WGS) of the strain MEZLIS26 as part of the US Food and Drug Administration's WGS surveillance effort.

M.E.E.Z. conceived, coordinated, and supervised the research project, isolated the strain, prepared and wrote the manuscript, and submitted the strain for WGS. R.A.H. and A.M. conducted the phylogenetic analysis. R.A.H. and A.M. contributed to manuscript writing. N.N., O.T.Z., M.L., and J.D.J. reviewed the manuscript. M.E.E.Z. critically revised the manuscript. All authors approved the final version of the manuscript.

## REFERENCES

- Leclercq A, Moura A, Vales G, Tessaud-Rita N, Aguilhon C, Lecuit M. 2019. *Listeria thailandensis* sp. nov. *Int J Syst Evol Microbiol* 69:74–81. <https://doi.org/10.1099/ijsem.0.003097>.
- Hoffman S, Macculloch B, Batz M. 2015. Economic burden of major foodborne illnesses acquired in the United States. United States Department of Agriculture, Economic Research Service, Washington, DC.
- Buchrieser C, Rusniok C, The *Listeria* Consortium, Kunst F, Cossart P, Glaser P. 2003. Comparison of the genome sequences of *Listeria monocytogenes* and *Listeria innocua*: clues for evolution and pathogenicity. *FEMS Immunol Med Microbiol* 35:207–213. [https://doi.org/10.1016/S0928-8244\(02\)00448-0](https://doi.org/10.1016/S0928-8244(02)00448-0).
- Petran RL, Swanson KM. 1993. Simultaneous growth of *Listeria monocytogenes* and *Listeria innocua*. *J Food Prot* 56:616–618. <https://doi.org/10.4315/0362-028X-56.7.616>.
- Moura A, Disson O, Lavina M, Thouvenot P, Huang L, Leclercq A, Fredriksson-Ahomaa M, Eshwar AK, Stephan R, Lecuit M. 2019. Atypical hemolytic *Listeria innocua* isolates are virulent, albeit less than *Listeria monocytogenes*. *Infect Immun* 87:e00758-18. <https://doi.org/10.1128/IAI.00758-18>.
- Favaro M, Sarmati L, Sancesario G, Fontana C. 2014. First case of *Listeria innocua* meningitis in a patient on steroids and etecept. *JMM Case Rep* 1. <https://doi.org/10.1099/jmmcr.0.003103>.
- Perrin M, Bemer M, Delamare C. 2003. Fatal case of *Listeria innocua* bacteremia. *J Clin Microbiol* 41:5308–5309. <https://doi.org/10.1128/jcm.41.11.5308-5309.2003>.
- Rocha P, Dalmasso A, Grattarola C, Casalone C, Del Piero F, Bottero MT, Capucchio MT. 2013. Atypical cerebral listeriosis associated with *Listeria innocua* in a beef bull. *Res Vet Sci* 94:111–114. <https://doi.org/10.1016/j.rvsc.2012.07.017>.
- Stevens EL, Timme R, Brown EW, Allard MW, Strain E, Bunning K, Musser S. 2017. The public health impact of a publically available, environmental database of microbial genomes. *Front Microbiol* 8:808. <https://doi.org/10.3389/fmicb.2017.00808>.
- Kumar A, Grover S, Batish VK. 2015. Exploring specific primers targeted against different genes for a multiplex PCR for detection of *Listeria monocytogenes*. *3 Biotech* 5:261–269. <https://doi.org/10.1007/s13205-014-0225-x>.
- Martin M. 2011. Cutadapt removes adapter sequences from high-throughput sequencing reads. *EMBnet J* 17:10–12. <https://doi.org/10.14806/ej.17.1.200>.
- Wingett SW, Andrews S. 2018. FastQ screen: a tool for multi-genome mapping and quality control. Version 2. *F1000Res* 7:1338. <https://doi.org/10.12688/f1000research.15931.2>.
- Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QUASt: quality assess-

- ment tool for genome assemblies. *Bioinformatics* 29:1072–1075. <https://doi.org/10.1093/bioinformatics/btt086>.
14. Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. *Bioinformatics* 30:2068–2069. <https://doi.org/10.1093/bioinformatics/btu153>.
  15. Goris J, Konstantinidis KT, Klappenbach JA, Coenye T, Vandamme P, Tiedje JM. 2007. DNA-DNA hybridization values and their relationship to whole-genome sequence similarities. *Int J Syst Evol Microbiol* 57:81–91. <https://doi.org/10.1099/ijs.0.64483-0>.
  16. Treangen TJ, Ondov BD, Koren S, Phillippy AM. 2014. The Harvest suite for rapid core-genome alignment and visualization of thousands of intraspecific microbial genomes. *Genome Biol* 15:524. <https://doi.org/10.1186/s13059-014-0524-x>.
  17. Letunic I, Bork P. 2016. Interactive tree of life (iTOL) v3: an online tool for the display and annotation of phylogenetic and other trees. *Nucleic Acids Res* 44:W242–W245. <https://doi.org/10.1093/nar/gkw290>.