Draft Genome Sequence of a 94-Year-Old *Listeria monocytogenes* Isolate, SLCC208

Patrick Hyden,a,b Ariane Pietzka,b Franz Allerberger,b Burkhard Springer,b Christoph Sensen,a Werner Ruppitschb,c

Institute of Molecular Biotechnology, Graz University of Technology, Graz, Austriaa; Institute of Medical Microbiology and Hygiene, Austrian Agency for Health and Food Safety, Graz, Austriab; Department of Biotechnology, University of Natural Resources and Life Sciences, Vienna, Austriac

We report here the draft genome sequence of *Listeria monocytogenes* strain SLCC208 from Seeliger's historical Special *Listeria* Culture Collection, initially cultured from a human case in France in 1921. This is, to our knowledge, the oldest *L. monocytogenes* isolate available and may be useful for comparative genomic studies of *L. monocytogenes*.

Listeria monocytogenes, the causative agent of listeriosis, is a facultative intracellular, facultative anaerobic, Gram-positive, psychrophilic, and salt-tolerant pathogen of humans and animals. *L. monocytogenes* is spread widely in the environment. This bacterial species has the ability to survive and grow under extreme conditions (1). The characteristic symptoms of listeriosis comprise encephalitis, meningitis, gastroenteritis, and septicemia. With a high case-fatality rate of up to 30%, *L. monocytogenes* is a considerable human pathogen (2). Nearly all cases of listeriosis are caused by the consumption or use of contaminated food or feed. In listeriosis outbreaks and for epidemiological investigations, subtyping of *L. monocytogenes* is essential (3). *L. monocytogenes* strains can be categorized by serotyping into 12 serotypes (4), of which 4b, 1/2a, and 1/2 b isolates cause about 96% of all reported human listeriosis cases (5).

L. monocytogenes isolate SLCC208 was subcultured from the original agar slant of the Seeliger collection by adding Trypticase soy broth (bioMérieux, Marcy I'Etoile, France) and subculturing on Columbia blood agar plates (bioMérieux). After another subculture step using RAPID'L.Mono plates (Bio-Rad, Vienna, Austria) for species verification, overnight cultures grown on Columbia blood agar plates (bioMérieux) were used for isolation of genomic DNA using the MagAttract high-molecular-weight (HMW) DNA kit, according to the instructions of the manufacturer (Qiagen, Hilden, Germany). Serotype PCR was performed (6) for confirmation of the determined serotype 4b of isolate SLCC208. The fragment library was constructed with the Nextera XT kit, as recommended by the manufacturer (Illumina, Inc., San Diego, CA, USA), and 2 × 300-bp fragments were sequenced on a MiSeq (Illumina, Inc.), generating 1,121,712 reads from 281,542,985 unassembled nucleotides. Raw reads were preprocessed using Trimmomatic 0.32 (7) for adapter trimming, as recommended by the authors, and quality trimming for average Q30 in a window of 20 bp. The preprocessed reads were *de-novo* assembled into a draft genome using SPAdes version 3.5.0 (8). Contigs were filtered for a minimum coverage of 5× and minimum length of 200 bp, which resulted in 22 contigs with a total of 2,916,998

nucleotides at 56-fold coverage. A total of 2,930 genes, 2,842 coding sequences, 19 pseudogenes, 11 rRNA operons (6 complete and 5 partial), and 58 tRNA genes were identified by the NCBI Prokaryotic Genome Automatic Annotation Pipeline.

Extraction of the classical multilocus sequence type (MLST) from the draft genome assigned strain SLCC208 to sequence type 495 (ST495) and clonal complex 1 (CC1) (9).

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number LMXJ00000000. The version described in this paper is the first version, LMXJ01000000.

FUNDING INFORMATION

REFERENCES

1. **Allerberger F, Wagner M**. 2010. Listeriosis: a resurgent foodborne infection. Clin Microbiol Infect **16**:16–23. http://dx.doi.org/10.1111/j.1469-0691.2009.03109.x.
2. **Allerberger F, Huhulescu S**. 2015. Pregnancy related listeriosis: treatment and control. Expert Rev Anti Infect Ther **13**:395–403. http://dx.doi.org/10.1586/14787210.2015.1003809.
3. **Fretz R, Pichler J, Sagel U, Much P, Ruppitsch W, Pietzka AT, Stöger A, Huhulescu S, Heuberger S, Appl G, Werber D, Stark K, Prager R, Flieger A, Karpíšková R, Pfaff G, Allerberger F**. 2010. Update: multinational listeriosis outbreak due to "Quargel", a sour milk curd cheese, caused by two different *L. monocytogenes* serotype 1/2a strains, 2009–2010. Euro Surveill **15**:pii=19543. http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=19543.
4. **Allerberger F, Bagó Z, Huhulescu S, Pietzka A**. 2015. Listeriosis: the dark side of refrigeration and ensiling, p 249–286. *In* Sing A (ed), Zoonoses—infections affecting humans and animals. Focus on public health aspects. Springer Verlag, Heidelberg, Germany.
5. **Kasper S, Huhulescu S, Auer B, Heller I, Karner F, Würzner R, Wagner M, Allerberger F**. 2009. Epidemiology of listeriosis in Austria. Wien Klin Wochenschr **121**:113–119. http://dx.doi.org/10.1007/s00508-008-1130-2.
6. **Doumith M, Buchrieser C, Glaser P, Jacquet C, Martin P**. 2004. Differentiation of the major *Listeria monocytogenes* serovars by multiplex PCR. J Clin Microbiol **42**:3819–3822. http://dx.doi.org/10.1128/JCM.42.8.3819-3822.2004.

7. **Bolger AM, Lohse M, Usadel B**. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics **30:**2114–2120. http://dx.doi.org/10.1093/bioinformatics/btu170.

8. **Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA**. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol **19:**455–477. http://dx.doi.org/10.1089/cmb.2012.0021.

9. **Salcedo C, Arreaza L, Alcalá B, de la Fuente L, Vázquez JA**. 2003. Development of a multilocus sequence typing method for analysis of *Listeria monocytogenes* clones. J Clin Microbiol **41:**757–762. http://dx.doi.org/10.1128/JCM.41.2.757-762.2003.