

Complete Genome Sequence of *Listeria monocytogenes* LL195, a Serotype 4b Strain from the 1983–1987 Listeriosis Epidemic in Switzerland

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The complete genome sequence of *Listeria monocytogenes* LL195, a serotype 4b clinical strain isolated during the 1983–1987 listeriosis epidemic in Switzerland, is presented.

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Listeria monocytogenes is a Gram-positive opportunistic food-borne bacterial pathogen. It causes listeriosis, an illness with serious consequences for immunocompromised people, such as pregnant women, neonates, and elderly people (1). Switzerland experienced a long-lasting listeriosis epidemic from 1983 to 1987, which was associated with the consumption of Vacherin Montd'or cheese and led to 122 clinical cases and 31 fatalities (2, 3). We determined the complete genome sequence of *L. monocytogenes* LL195, a serotype 4b strain recovered from a listeriosis case during this epidemic.

A paired-end library of the LL195 genome was created and sequenced using the Illumina Genome Analyzer (GA) II sequencer. In total, 107,606,904 reads of 50 bp were obtained from the sequencing (~1,700-fold genome coverage). The genome of *L. monocytogenes* F2365, a serotype 4b soft-cheese-derived isolate from the 1985 California Jalisco cheese listeriosis outbreak, was used as a reference (4, 5) for the comparative assembler AMOSmp (6). A total of 16 contigs were produced in the assembly. All gaps were closed using the Sanger sequencing method, resulting in one unambiguous scaffold. This single scaffold represents the complete circular LL195 chromosome, consisting of 2,904,662 bp with a G+C content of 38%.

The coding sequences (CDSs) were predicted based on a house-internal workflow that integrates *ab initio* predictions from Glimmer, GeneMark (7), Prodigal (8), and Critica (9) with homology information derived from a BLASTp search against the NCBI nonredundant (NR) database (10). Noncoding RNAs were identified using tRNAscanSE (11) and RNAmmer (12) and by searching against the Rfam database (13). Functional annotation of the CDSs was based on InterProScan (14) and the Swiss-Prot and trEMBL (15) databases.

The genome sequence of LL195 contains 2,838 protein-coding genes, six 16S-5S-23S operons, and 67 tRNA genes, and it harbors no plasmid or prophage genes. Although LL195 and F2365 genomes share high levels of similarity (99.9%), the LL195 genome has 197 single nucleotide polymorphisms (SNPs) and 37 insertions and deletions compared against the F2365 genome. Al-

though virulence genes are highly conserved between the two genomes, there are single SNPs in *hly* and *inlB* genes, as well as three SNPs and a single nucleotide deletion in the *inlJ* gene in LL195 compared against F2365. Notably, although the F2365 *inlB* is a pseudogene, due to a nonsense mutation that creates a premature stop codon (16), an SNP in the LL195 genome leads to an intact *inlB* gene in this strain.

Nucleotide sequence accession number. The sequence and annotation of the *L. monocytogenes* LL195 genome have been deposited in the EMBL database under the accession no. [HF558398](https://www.ebi.ac.uk/EMBL/nuccore/HF558398).

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REFERENCES

- Allerberger F, Wagner M. 2010. Listeriosis: a resurgent foodborne infection. *Clin. Microbiol. Infect.* 16:16–23.
- Bille J. 1990. Epidemiology of human listeriosis in Europe with special reference to the Swiss outbreak, p 71–74. In Miller AJ, Smith JL, Somkuti GA (ed), *Foodborne listeriosis*. Elsevier, New York, NY.
- Büla CJ, Bille J, Glauser MP. 1995. An epidemic of food-borne listeriosis in western Switzerland: description of 57 cases involving adults. *Clin. Infect. Dis.* 20:66–72.
- Mascola L, Lieb L, Chiu J, Fannin SL, Linnan MJ. 1988. Listeriosis: an uncommon opportunistic infection in patients with acquired immunodeficiency syndrome. A report of five cases and a review of the literature. *Am. J. Med.* 84:162–164.
- Nelson KE, Fouts DE, Mongodin EF, Ravel J, DeBoy RT, Kolonay JF, Rasko DA, Angiuoli SV, Gill SR, Paulsen IT, Peterson J, White O, Nelson WC, Nierman W, Beanan MJ, Brinkac LM, Daugherty SC, Dodson RJ, Durkin AS, Madupu R, Haft DH, Selengut J, Van Aken S, Khouri H, Fedorova N, Forberger H, Tran B, Kathariou S, Wonderling LD, Uhlich GA, Bayles DO, Luchansky JB, Fraser CM. 2004. Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen *Listeria monocytogenes* reveal new insights into the core genome components of this species. *Nucleic Acids Res.* 32:2386–2395.
- Pop M, Phillippy A, Delcher AL, Salzberg SL. 2004. Comparative genome assembly. *Brief. Bioinform.* 5:237–248.
- Borodovsky M, Mills R, Besemer J, Lomsadze A. 2003. Prokaryotic gene prediction using GeneMark and GeneMark.hmm. *Curr. Protoc. Bioinformatics* 4:4.5.
- Hyatt D, Chen GL, Locascio PF, Land ML, Larimer FW, Hauser LJ.

2010. Prodigal: prokaryotic gene recognition and translation initiation site identification. *BMC Bioinformatics* 11:119.
9. Badger JH, Olsen GJ. 1999. CRITICA: coding region identification tool invoking comparative analysis. *Mol. Biol. Evol.* 16:512–524.
 10. Sayers EW, Barrett T, Benson DA, Bolton E, Bryant SH, Canese K, Chetvernin V, Church DM, DiCuccio M, Federhen S, Feolo M, Fingerhman IM, Geer LY, Helmberg W, Kapustin Y, Landsman D, Lipman DJ, Lu Z, Madden TL, Madej T, Maglott DR, Marchler-Bauer A, Miller V, Mizrachi I, Ostell J, Panchenko A, Phan L, Pruitt KD, Schuler GD, Sequeira E, Sherry ST, Shumway M, Sirotkin K, Slotta D, Souvorov A, Starchenko G, Tatusova TA, Wagner L, Wang Y, Wilbur WJ, Yaschenko E, Ye J. 2011. Database resources of the National Center for Biotechnology Information. *Nucleic Acids Res.* 40:D38–D51.
 11. Lowe TM, Eddy SR. 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. *Nucleic Acids Res.* 25: 955–964.
 12. Lagesen K, Hallin P, Rødland EA, Staerfeldt HH, Rognes T, Ussery DW. 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. *Nucleic Acids Res.* 35:3100–3108.
 13. Griffiths-Jones S, Moxon S, Marshall M, Khanna A, Eddy SR, Bateman A. 2005. Rfam: annotating non-coding RNAs in complete genomes. *Nucleic Acids Res.* 33:D121–D124.
 14. Hunter S, Jones P, Mitchell A, Apweiler R, Attwood TK, Bateman A, Bernard T, Binns D, Bork P, Burge S, de Castro E, Coggill P, Corbett M, Das U, Daugherty L, Duquenne L, Finn RD, Fraser M, Gough J, Haft D, Hulo N, Kahn D, Kelly E, Letunic I, Lonsdale D, Lopez R, Madera M, Maslen J, McAnulla C, McDowall J, McMenamin C, Mi H, Mutowo-Muellenet P, Mulder N, Natale D, Orengo C, Pesseat S, Punta M, Quinn AF, Rivoire C, Sangrador-Vegas A, Selengut JD, Sigrist CJ, Scheremetjew M, Tate J, Thimmajananathan M, Thomas PD, Wu CH, Yeats C, Yong SY. 2012. Interpro in 2011: new developments in the family and domain prediction database. *Nucleic Acids Res.* 40:D306–D312.
 15. Magrane M, UniProt Consortium. 2011. UniProt Knowledgebase: a hub of integrated protein data. *Database (Oxford)* 2011:bar009.
 16. Nightingale KK, Milillo SR, Ivy RA, Ho AJ, Oliver HF, Wiedmann M. 2007. *Listeria monocytogenes* F2365 carries several authentic mutations potentially leading to truncated gene products, including *inlB*, and demonstrates atypical phenotypic characteristics. *J. Food Prot.* 70:482–488.