

Genome Sequences of the *Listeria ivanovii* subsp. *ivanovii* Type Strain and Two *Listeria ivanovii* subsp. *londoniensis* Strains

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We present the complete genomes of *Listeria ivanovii* subsp. *ivanovii* WSLC 3010 (ATCC 19119^T), *Listeria ivanovii* subsp. *londoniensis* WSLC 30151 (SLCC 8854), and *Listeria ivanovii* subsp. *londoniensis* WSLC 30167 (SLCC 6032), representing the type strain of the species and two strains of the same serovar but different properties, respectively.

Received 4 December 2014 Accepted 9 December 2014 Published 22 January 2015

Citation Hupfeld M, Fouts DE, Loessner MJ, Klumpp J. 2015. Genome sequences of the *Listeria ivanovii* subsp. *ivanovii* type strain and two *Listeria ivanovii* subsp. *londoniensis* strains. *Genome Announc* 3(1):e01440-14. doi:10.1128/genomeA.01440-14.

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Listeria are Gram-positive rod-shaped *Firmicutes* bacteria, currently split into nine species. *L. ivanovii* is an animal pathogen and primarily infects ruminants (1). We report the complete genome sequence of three *L. ivanovii* strains. One of them is the type strain of *L. ivanovii* subsp. *ivanovii*, which is very sensitive to infection by bacteriophages. In contrast, members of the subspecies *londoniensis*, such as WSLC 30151 and 30167, generally seem resistant to phage infection, except for the large virulent A511-like viruses.

L. ivanovii WSLC 3010 is a widely used serovar 5 isolate that is quite similar to the recently sequenced WSLC 3009 strain (2). While strains WSLC 30151 and WSLC 30167 also belong to the serovar 5 group, they have been designated *L. ivanovii* subsp. *londoniensis*, based on their inability to utilize certain sugars, such as ribose, and the degradation of *N*-acetyl- β -D-mannosamine (3).

Strains were grown at 30°C in BHI medium under aerobic conditions. Genomic DNA was prepared using the Sigma Genomic DNA Kit. DNA was subjected to single-molecule real-time sequencing on a Pacific Biosciences RS2 device (10-kb insert library, P4/C2 chemistry). Sequencing resulted in 135,255 reads with a 6,358-kb average length for WSLC 3010; 106,607 reads with a 6,780-bp average length for WSLC 30151; and 141,048 reads with a 6,244-bp average length for WSLC 30167. Genomes were assembled *de novo*, using SMRTAnalysis version 2.1.1 and the HGAP3 algorithm, into single contigs of 2,919,538 bp (WSLC 3010), 3,045,017 bp (WSLC 30151), and 2,993,492 bp (WSLC 30167), with 207-, 184-, and 229-fold average coverages. Genomes were annotated by the NCBI Prokaryotic Genomes Automatic Annotation Pipeline.

The WSLC 3010 genome contains 2,876 genes, 107 pseudogenes, and 67 tRNAs; the WSLC 30151 genome encodes 3,015 genes, 104 pseudogenes, and 67 tRNAs; and the WSLC 30167 genome features 2,930 genes, 90 pseudogenes, and also 67 tRNAs. The CRISPRFinder algorithm (4) was used to identify putative CRISPR loci within these strains. WSLC 3010 harbors three CRISPR regions, which are identical to those reported for WSLC 3009 (2). Two and three CRISPR regions were identified in WSLC 30151 and WSLC 30167, respectively. However, these CRISPR

regions are significantly larger than those of related strains. Homologies of CRISPR spacers to different *Listeria* phages (e.g. B025, B054, PSA, and A500) were found in all three strains, and play a putative role in inactivation of invading phage DNA (5).

Phage_Finder (6) was used to screen the genomes for the presence of intact and cryptic phages. As previously reported for *L. ivanovii* WSLC 3009 (2), both *L. ivanovii* subsp. *londoniensis* WSLC 30167 and *L. ivanovii* subsp. *ivanovii* WSLC 3010 do not seem to harbor prophage sequences. One putative prophage region could be identified in *L. ivanovii* subsp. *londoniensis* WSLC 30151 at position 756388 to 792505 which is apparently inserted into a tRNA_{Ser} sequence. The prophage region features a mosaic structure, with homology to prophages of *L. innocua* Clip11262 (prophage Φ 11262.6 [7]), *L. welshimeri*, and *L. monocytogenes*. Only strain WSLC 30151 featured a predicted monicin locus (8) of 15,297 bp, located at position 198267 to 213563.

Nucleotide sequence accession numbers. The complete genome sequences have been deposited in GenBank under the accession numbers CP009575, CP009576, and CP009577.

ACKNOWLEDGMENT

This work was not supported by third-party funding. We declare no conflict of interest.

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