


Draft Genome Sequence of *Listeria monocytogenes* LM201, Isolated from Foodstuff

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***Listeria monocytogenes* is a facultative intracellular foodborne pathogen that can cause listeriosis in humans and animals. *L. monocytogenes* LM201 was isolated from foodstuff. The draft genome sequence of strain LM201 provides the genetic basis for the application of this strain in biotechnological vaccine production.**

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Listeria monocytogenes is a Gram-positive, nonsporulating, aerobic and facultative anaerobic, rod-shaped, and facultative intracellular bacterium (1, 2). It is a foodborne pathogen (3) that can cause listeriosis (gastroenteritis, meningitis, encephalitis, septicemia, and abortion) in animals and humans, especially immunocompromised individuals (the old, neonates, and pregnant women), with a mean mortality rate of 20–30% or higher (4). *L. monocytogenes* LM201, a serovar 4b strain, was isolated from foodstuff in Hubei province (China). The LD₅₀ of strain LM201 was 6.3 × 10⁶ CFU for Kunming mice after i.p. infection. Strain LM201 was also assayed for other phenotypic characteristics and was determined to be a good candidate for developing a vaccine. Here we report the genome sequence of *L. monocytogenes* LM201, which provides the genetic basis for rationally designing and generating defined virulence-attenuated strains for biotechnological vaccine production.

Genomic DNA of the strain LM201 was sequenced with a whole-genome shotgun strategy using an Illumina HiSeq 2000 platform. Two different sequencing libraries (300-bp paired end and 5,000-bp mate pair) were prepared. In total, 43,930,390 paired-end reads of 100 bp and 20,921,890 mate-pair reads of 90 bp were obtained from the sequencing (1,910-fold genome coverage). *De novo* assembly was done using ABySS version 1.3.4 software (5), yielding 86 contigs with an *N*₅₀ size of 226,587 bp and a maximum contig size of 342,356 bp. A total of 66 scaffolds were produced, with a total size of 3,200,729 bp and a G+C content of 37.44%.

Genome annotation was accomplished using the RAST server (6). Gene prediction revealed 3,165 protein-coding genes (CDSs), 6 rRNA operons, and 35 tRNA genes. Among the protein-coding

genes, there were 2,736 genes with function prediction; 2,504 were identified in the COG database; and 2,674 were identified in the Pfam database.

Nucleotide sequence accession number. The *L. monocytogenes* LM201 draft genome sequence has been deposited in the GenBank database under the accession number [AYPT00000000](https://ncbi.nlm.nih.gov/nucl/AYPT00000000). The version described in this paper is the first version.

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