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Genome Sequences of *Listeria monocytogenes* Serotype 4b Variant Strains Isolated from Clinical and Environmental Sources

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Listeria monocytogenes **strains that show a novel PCR serotyping profile (IVb-v1) have been reported recently. Here, we announce the draft genome sequences of five *L. monocytogenes* IVb-v1 strains isolated from the United States and Australia that harbor a 6.3-kb DNA cassette characteristic of serotype 1/2a strains.**

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Listeria monocytogenes is a Gram-positive food-borne pathogen that causes listeriosis, with 20 to 30% mortality and >95% hospitalization rates. The annual incidence of food-borne listeriosis in the United States is about 1,600 cases with 255 deaths (1). Based on somatic and flagellar antigens, *L. monocytogenes* strains can be grouped into 13 serotypes (2), of which serotypes 1/2a, 1/2b, and 4b represent the vast majority of the disease-causing strains (3–5). Due to the complexity involved in classical serotypic determination, a PCR-based method that targets four genes (*orf2110*, *orf2819*, *lmo01118*, and *lmo0737*) has been developed (6). Using this method, several 4b strains with an unusual PCR amplicon pattern, termed IVb-v1, have been reported (7–10). In addition, these IVb-v1 strains harbor a 6.3-kb DNA cassette that is characteristic of 1/2a strains (8).

To identify other genomic footprints of these IVb-v1 strains, we report the draft genome sequences of five *L. monocytogenes* serotype IVb-v1 strains isolated from two different continents. *L. monocytogenes* LS542 is an environmental isolate from a soft-cheese manufacturing facility in the United States, which was collected as part of monitoring of ready-to-eat food facilities by the FDA (9). Four clinical isolates were isolated from listeriosis patients in New South Wales (*L. monocytogenes* LS642, LS643, and LS644) and Victoria (*L. monocytogenes* LS645), Australia, in 2009. No epidemiological link has been established among the four Australian cases (10). Whole-genomic DNA was extracted using the Qiagen DNeasy blood and tissue kit (Qiagen, Valencia, CA), according to the manufacturer's protocol with a slight modification (11). The library was prepared from the extracted genomic DNA using a Nextera sample preparation kit (Illumina, San Diego, CA), and a 2 × 250 paired-end sequencing run was performed on an Illumina MiSeq platform (12). The reads were trimmed and *de novo* assembled using the CLC Genomics Workbench version 6.0.5 (CLC bio, Germantown, MD). The resulting assemblies have >50× coverage and generated 45, 24, 30, 32, and 24 contigs representing the genomes of *L. monocytogenes* strains LS542, LS642, LS643, LS644, and LS645, respectively. The estimated genome size is ~2.9 Mb with a G+C content of 37.9% for each strain. BLAST analysis of these contigs against the 6.3-kb gene cassette (*lmo0733* to *lmo0740*) of *L. monocytogenes* EGD-e confirmed the existence of the gene cassette in all five IVb-v1 strains. The genome annotation, performed on the Rapid Annotations using Subsystems Technology (RAST) server (13), revealed that the genomes contain 2,899, 2,927, 2,830, 2,826, and 2,827 protein-coding genes for strains LS542, LS642, LS643, LS644, and LS645, respectively. The availability of these *L. monocytogenes* IVb-v1 genome sequences will facilitate in-depth study of these strains that may lead to the discovery of previously unidentified genes and help in understanding the significance and evolution of this group of strains.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. AVQQ00000000, AVQM00000000, AVQN00000000, AVQO00000000, and AVQP00000000 for *L. monocytogenes* serotype IVb-v1 strains LS542, LS642, LS643, LS644, and LS645, respectively.

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