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Complete Genome Sequence of the Persistent *Listeria monocytogenes* Strain R479a

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The complete genome sequence of the persistent *Listeria monocytogenes* strain R479a isolated from smoked salmon in Denmark and belonging to lineage II, serovar 1/2a, and multilocus sequence type 8 (ST8) is presented here.

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The Gram-positive facultative intracellular pathogen *Listeria monocytogenes* is the causative agent of listeriosis, a rare but severe disease transmitted through the consumption of contaminated food (1). *L. monocytogenes* can survive and grow in a multitude of natural and man-made habitats (2). The long-term occurrence of genetically indistinguishable *L. monocytogenes* strains in the same food production plant over a long time period has been termed persistence. Some *L. monocytogenes* strains are able to persist for months or years in food production environments (2–4). Currently, two models are available to explain this persistence (2): either certain *L. monocytogenes* strains have unique phenotypic and genotypic characteristics facilitating long-term survival in food processing environments, or persistence is largely a random process and most *L. monocytogenes* strains can establish persistence if present in an appropriate niche at an appropriate time (2). Thus, persistent *L. monocytogenes* strains represent a big challenge for food safety; we therefore analyzed the genome sequence of the persistent *L. monocytogenes* isolate R479a (lineage II, serovar 1/2a, sequence type 8 [ST8]), which was isolated from smoked salmon from Denmark and persisted from November 1996 to January 1999 (5).

DNA was isolated using the Qiagen Genomic-tip columns and buffers, according to the recommendations of the manufacturer. Genome sequencing was performed using an Illumina GAII genome analyzer with paired-end sequencing technology and 100-bp read length, using Illumina standard protocols. A total of 3.057 million reads were used for a *de novo* assembly using Velvet, resulting in 33 contigs, with an average coverage of 140×. The remaining gaps were closed by PCR and Sanger sequencing (LGC Genomics, Berlin, Germany). Gene prediction and annotation were done using the MicroScope platform (https://www.genoscope.cns.fr/agc/microscope/home/ [6]). Multilocus sequence typing (MLST) was performed with the MLST tool available on the Center for Genomic Epidemiology website (https://cge.cbs.dtu.dk/services/MLST/ [7]).

The R479a genome consists of a single circular chromosome with a size of 2,944,998 bp and 2,995 predicted coding sequences, a G+C content of 37.9%, and a plasmid (pLMR479a) of 86,652 bp containing 92 predicted coding sequences and a G+C content of 37.0%. Interestingly, and in contrast to most other sequenced *Listeria* genomes, the R479a genome contains only 5 rRNA operons and 58 tRNA genes.

The *L. monocytogenes* R479a genome contains a typical *Listeria* pathogenicity island and a full-length internalin AB (*inlAB*) locus. R479a encodes 11 internalins and 17 internalin-like proteins. All virulence genes present in *L. monocytogenes* EGDe, except the homologues of *lmo0320* (*vip*) and *lmo2026*, are present in R479a.

pLMR479a is highly similar to other *Listeria* plasmids and carries many genes possibly involved in stress response or transporters for the export of heavy metals, such as a Tn*5422* copy. Interestingly, pLMR479a harbors a region of 14 genes (LMR479A_p0071 to LMR479A_p0083) of approximately 10 kbp, with a G+C content of 37.9%, in which all proteins show the highest similarity to proteins from *Firmicutes* other than *Listeria* species; this region had thus most likely recently been transferred into pLMR479a.

Nucleotide sequence accession numbers. The complete genome and plasmid genome sequences of strain R479a have been deposited in ENA/GenBank/DDBJ under the accession numbers HG813247 and HG813248, respectively. The versions described in this paper are the first versions.

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