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PROKARYOTES

Genome Sequences of *Listeria monocytogenes* Strains with Resistance to Arsenic

Vikrant Dutta,[a]* Sangmi Lee,[a]* Todd J. Ward,[d] Nathane Orwig,[d] Eric Altermann,[e,f] Dereje D. Jima,[b,c] Cameron Parsons,[a] Sophia Kathariou[a]

Department of Food, Bioprocessing and Nutrition Sciences, North Carolina State University, Raleigh, North Carolina, USA[a]; Center for Human Health and the Environment, North Carolina State University, Raleigh, North Carolina, USA[b]; Bioinformatics Research Center, North Carolina State University, Raleigh, North Carolina, USA[c]; USDA-ARS, Peoria, Illinois, USA[d]; Rumen Microbiology, AgResearch Grasslands, Palmerston North, New Zealand[e]; Riddet Institute, Massey University, Palmerston North, New Zealand[f]

ABSTRACT *Listeria monocytogenes* frequently exhibits resistance to arsenic. We report here the draft genome sequences of eight genetically diverse arsenic-resistant *L. monocytogenes* strains from human listeriosis and food-associated environments. The availability of these genomes will help elucidate the role of heavy-metal resistance in the ecology of *L. monocytogenes*.

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Address correspondence to Vikrant Dutta, vikrant.dutta@gmail.com.

* Present address: Vikrant Dutta, bioMérieux, Inc., Hazelwood, Missouri, USA; Sangmi Lee, National Institutes of Health, Bethesda, Maryland, USA.

The facultative intracellular foodborne bacterial pathogen *Listeria monocytogenes* is well known for its propensity for heavy-metal resistance, specifically to cadmium and arsenic. Cadmium resistance is frequently plasmid-associated and encountered among isolates of diverse serotypes, being especially common in serogroup 1/2 (1–4). Nonpathogenic *Listeria* spp. can conjugatively transfer such resistance to *L. monocytogenes* (5). In contrast, arsenic resistance is primarily encountered among *L. monocytogenes* strains of serotype 4b and is chromosomally mediated (2, 6, 7). Genome sequencing of strain Scott A revealed a 35-kb chromosomal island (*Listeria* genomic island 2 [LGI2]), which includes genes for arsenic and cadmium resistance (6, 7). However, mechanisms mediating arsenic resistance in *L. monocytogenes* strains of diverse sources and genotypes remain poorly understood. Here, we present the whole-genome sequences of eight arsenic-resistant *L. monocytogenes* strains, including 6 strains of serotype 4b and 1 strain each of serotypes 1/2a and 1/2c. Serotype 4b strains included 3 strains from food or food-processing environments, i.e., F8027 (celery; multilocus sequencing typing-based clonal complex 315 [CC315]), BS-26 (environment swab; CC1), and FDA 100 (environmental swab, 1986; CC2) and 3 CC1 human clinical isolates, J2213, J3422, and J4600 (from 2003, 2005, and 2007, respectively) (8). Thus, most serotype 4b strains were members of hypervirulent clonal complexes (9), specifically CC1 (BS-26, J2213, J3422, and J4600) and CC2 (FDA 100). The serotype 1/2a strain 2012-0070 (CC14) was from a food-processing environment in North Carolina, USA (2012), while 2008-911 (serotype 1/2c; CC9) was implicated in human listeriosis in North Carolina in 2008.

The genomic DNA extracted with the DNeasy blood and tissue kit (Qiagen, Valencia, CA) was used to prepare the sequencing libraries on a Zephyr next-generation sequencing (NGS) workstation (PerkinElmer, Waltham, MA) using the NEBNext Fast DNA library prep set (New England BioLabs, Ipswich, MA). The Ion Torrent Personal Genome Machine was used for sequencing with an Ion 318 Chip version 2 and the Ion PGM 400 sequencing kit (Life Technologies, Inc., Grand Island, NY). Overall, 6,175,875 single reads were produced, with a median read length of 282 nucleotides (nt). Barcode sequences attached during the library preparation were used for sorting the reads, and the CLC Genomics Workbench 7.5.1 (CLC bio, Boston, MA) software was used (with default parameters) for quality trimming and *de novo* assembly. Assembly size ranged between

ca. 2.6 and 2.8 Mbp, with an average coverage of 28.7 to 61.5×, and between 122 and 348 contigs were generated. Annotations were performed using the GAMOLA 2 and the NCBI Prokaryotic Genome Annotation Pipeline (10). Genome annotations identified 2,813 to 3,042 coding sequences, 5 to 10 rRNAs, and 59 to 65 tRNAs.

The availability of these genome sequences will further facilitate analysis of the roles of heavy-metal resistance in the ecology and adaptive physiology of *L. monocytogenes* from diverse sources and of diverse genotypes and serotypes.

Accession number(s). This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession numbers MPBE00000000, MLFL00000000, MNCA00000000, MNCB00000000, MNCC00000000, MNCD00000000, MNCE00000000, and MNCF00000000. The versions described in this paper are the first versions.

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