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GENOME SEQUENCES

Draft Genome Sequence of Multidrug-Resistant *Listeria innocua* Strain UAM003-1A, Isolated from a Wild Black Bear (*Ursus americanus*)

Cameron Parsons,[a] Yi Chen,[b] Jeffrey Niedermeyer,[a] Kevin Hernandez,[a] Sophia Kathariou[a]

[a]Department of Food, Bioprocessing, and Nutrition Sciences, North Carolina State University, Raleigh, North Carolina, USA
[b]Division of Microbiology, Center for Food Safety and Applied Nutrition, Food and Drug Administration, College Park, Maryland, USA

ABSTRACT There is currently limited knowledge of the genome sequences of nonpathogenic *Listeria* species, especially strains from wildlife. Here, we report the draft genome sequence and associated genome information of an antibiotic-resistant *Listeria innocua* strain, UAM003-1A, isolated from the feces of a black bear in California, USA.

The genus *Listeria* is distributed widely in nature (1, 2). *Listeria monocytogenes*, the only human pathogen in the genus, is a leading cause of death due to foodborne disease (listeriosis) in the United States and other industrialized nations (3, 4), with severe health outcomes including septicemia, meningitis, and stillbirths (5). *Listeria innocua* and other *Listeria* spp. are nonpathogenic but can serve as important reservoirs for resistance determinants that can transfer to *L. monocytogenes* (6). They can therefore be of particular concern if there is transmission of antibiotic resistance to a pathogen of major human health concern.

Here, we report the genome sequence and antimicrobial resistance (AMR) of *Listeria innocua* UAM003-1A, isolated in May 2017 using the previously described ISO method, which involved culturing the feces of a black bear (*Ursus americanus*) captured in California, first with primary enrichment (24 to 48 h) in Half Fraser broth, followed by transfer to Full Fraser broth for secondary enrichment for 24 to 48 h (7). The lack of hemolysis on blood agar indicated that this strain was likely a *Listeria* species other than *monocytogenes*.

The strain was grown aerobically overnight at 37°C in brain heart infusion broth (Becton, Dickinson and Company, Franklin Lakes, NJ, USA), and genomic DNA was extracted using a DNeasy blood and tissue kit (Qiagen, Valencia, CA); libraries were prepared using 1 ng of genomic DNA with the Nextera XT DNA library preparation kit (Illumina, San Diego, CA, USA), and the genome was sequenced using the NextSeq 500 desktop sequencer with the NextSeq 500/550 high-output v.2 kit (300 cycles) (Illumina) for 2 × 151 cycles according to the manufacturer's instructions. Sequencing resulted in 3,282,404 150-bp paired-end reads. Raw sequencing reads were quality-trimmed and *de novo*-assembled using Spades v.3.3.13 (8) with an average coverage of 141.406×. Assembly was quality-assessed using QUAST v.4.6.4 (9) and interrogated for AMR genes using the ResFinder database (10) in ABRicate (https://github.com/tseemann/abricate). Default parameters were used for all software.

The genome was assembled into 27 contigs with a total length of 2.89 Mb, an N_{50} value of 480,020 bp, and an average GC content of 37.45%. Whole-genome sequence analysis, including *in silico* multilocus sequence typing (MLST) via BIGSdb-*Lm* (https://bigsdb.pasteur.fr/listeria/), confirmed that this strain was *L. innocua* with the novel sequence type 1495 (ST1495) in clonal complex (CC) 140, which also includes the *L. innocua* reference strain CLIP11262 (11). ResFinder analysis revealed three putative

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Address correspondence to Cameron Parsons, ctparson@ncsu.edu.

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antibiotic resistance determinants, *tet*(M), *ant(6)-Ia_2*, and *mphB*, known to confer resistance to tetracycline, aminoglycosides, and macrolides, respectively. Interestingly, each determinant was harbored on a different mobile genetic element, with *tet*(M) and *ant(6)-Ia_2* on separate transposons, while *mphB* appeared to be harbored on a prophage. Testing for antimicrobial resistance was done as previously described (12) against a panel of antibiotics, the heavy metals cadmium and arsenic, and the quaternary ammonium disinfectant benzalkonium chloride. Testing confirmed that *L. innocua* UAM003-1A was resistant to tetracycline (MIC, >5 μg/ml) and streptomycin (MIC, >20 μg/ml) but not other aminoglycosides, such as kanamycin and gentamicin, while it lacked resistance to the macrolide erythromycin (MIC, >0.5 μg/ml). The sequence data will further elucidate AMR emergence and functionality/specificity of AMR genes in *Listeria* spp. The public and animal health relevance of *L. innocua* UAM003-1A is enhanced by current demographic trends that are enhancing the likelihood of human contact with black bears and other wildlife.

Data availability. The whole-genome sequence of *L. innocua* strain UAM003-1A was deposited at DDBJ/EMBL/GenBank under the accession number VNKM00000000. The version described in this paper is version VNKM01000000. The raw sequence reads were deposited in the SRA under accession number PRJNA556464.

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