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Complete Genome Sequence of *Listeria monocytogenes* Strain MR310, Isolated from a Pastured-Flock Poultry Farm System

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ABSTRACT Investigation of *Listeria monocytogenes* transmission from environmental sources associated with pasture-raised chickens to poultry products is needed to determine ways to prevent potential foodborne illness. Here, we report the complete genome sequence of *Listeria monocytogenes* MR310, one of the isolates from a pastured-flock poultry management system.

Due to the increased demands for natural and organic poultry products by consumers, high-quality and safe poultry products without antibiotic treatments are now more commonly found in grocery markets. Foodborne pathogens from the environment, such as *Listeria monocytogenes*, may be associated with pasture-raised poultry and thus are potential threats (1–3). The goal of the study was to initiate an investigation of the presence, abundance, and diversity of *Listeria monocytogenes* in pastured-flock poultry management systems. In the overall study, *Listeria* organisms were isolated from live production (feces and soil), processing (ceca and whole-carcass rinses), and final products (whole-carcass rinses) to determine which *Listeria* species were present, the sites along the farm-to-fork continuum where they were present, and how the diversity of *Listeria* species varies based on the different farms and management stages investigated in the study. Achieving a better understanding of the ecology of *Listeria* species through their genotypes may elucidate potential intervention targets for future studies.

Pure genomic DNA from overnight-grown culture was extracted using a Qiagen DNeasy blood and tissue kit according to the manufacturer's protocol. DNA was subsequently diluted to 0.2 ng/μl for construction of tagmented DNA with a Nextera XT DNA library prep kit (Illumina). Libraries were loaded on a cartridge in the MiSeq reagent kit v2 and sequenced with an Illumina MiSeq instrument. In total, 1,003,393 reads of 250 bp were obtained from the MiSeq run. The reads were trimmed using the sickle tool to remove low-quality nucleotides that may have occurred in the 5′ or 3′ ends (https://github.com/najoshi/sickle). Reads with less than 50 nucleotides and Phred quality scores lower than 30 were discarded. The trimmed reads were assembled *de novo* using SPAdes 3.5.0 (4), with k-mer sizes set at 21, 33, 55, 77, 99, and 127. The resulting assembly showed 86× coverage in 20 contigs. The estimated genome size was 2.88 Mb, with a G+C content of 37.93%. There were 2,842 coding sequences (CDSs) and 52 tRNA and 7 rRNA sequences predicted by the Pathosystems Resource Integration Center (PATRIC) database (5). The multilocus sequence type (MLST) of the MR310 strain was ST-389 according to analysis by the Center for Genomic Epidemiology (CGE)

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(6). A total of 33 virulence factors were predicted by performing BLASTn analysis of the MR310 genome against the Virulence Factors Database (VFDB). The predicted virulence profiles included genes for immune modulation, intracellular growth, toxins, invasion, bile resistance, immune evasion, stress resistance, adherence, and actin-based motility. The predicted proteins were analyzed by BLASTp against the Comprehensive Antibiotic Resistance Database (CARD) (7) to predict potential antibiotic resistance. Two antimicrobial resistance genes were identified in the MR310 genome, an antibiotic target-modifying enzyme (*mprF*) that changes cell wall charge, and an antibiotic target-modifying enzyme (*fosX*) that is a determinant of fosfomycine resistance. The identification of antibiotic resistance gene prevalence in the genome will contribute to a better understanding of horizontal gene transmission from environmental sources to poultry.

Accession number(s). The sequence and annotation information of the *L. monocytogenes* strain MR310 genome has been deposited at DDBJ/EMBL/GenBank under the accession no. PPHC00000000.

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