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PROKARYOTES

Complete Genome Sequence of Multidrug-Resistant *Edwardsiella ictaluri* Strain MS-17-156

Hossam Abdelhamed,[a] Hasan C. Tekedar,[a] Ozan Ozdemir,[a] Chuan-Yu Hsu,[b] Mark A. Arick II,[b] Attila Karsi,[a] Mark L. Lawrence[a]

[a]College of Veterinary Medicine, Mississippi State University, Mississippi State, Mississippi, USA

[b]Institute for Genomics, Biocomputing and Biotechnology, Mississippi State University, Mississippi State, Mississippi, USA

ABSTRACT *Edwardsiella ictaluri* is a significant pathogen of cultured fish, particularly channel catfish. Here, we present the complete genome sequence of a multidrug-resistant *E. ictaluri* strain, MS-17-156, isolated from diseased channel catfish. The genome sequence of this multidrug-resistant strain is expected to help us understand the molecular mechanism of antibiotic resistance in this important pathogen.

Edwardsiella ictaluri, a Gram-negative bacillus in the order *Enterobacteriales*, is the etiological agent of enteric septicemia of catfish (ESC), which is one of the most significant diseases of the commercial catfish industry in the United States (1, 2). Although *E. ictaluri* is well adapted to channel catfish, it has been linked to mortalities in other fish species, including tilapia, zebrafish, and ayu (3–5). *Edwardsiella ictaluri* strain MS-17-156 was isolated from a diseased channel catfish in 2017 from the Aquatic Diagnostic Laboratory at the College of Veterinary Medicine, Mississippi State University. *E. ictaluri* strain MS-17-156 is resistant to tetracycline, oxytetracycline, doxycycline, florfenicol, erythromycin, chloramphenicol, streptomycin, penicillin, novobiocin, azithromycin, and spectinomycin.

Genome sequencing was conducted using HiSeq X Ten (Illumina, San Diego, CA, USA) and MinION (Oxford Nanopore Technologies, Oxford, UK) instruments, producing approximately 441-fold and 36-fold genome coverages, respectively. Illumina reads were trimmed and filtered with Trimmomatic (6), and Nanopore reads were corrected with Canu version 1.6 (7). Contig errors were corrected using Pilon version 1.21 (7). Assembly was performed using MaSuRCA version 3.2.4 (8). The circular physical structure of the chromosome and plasmids was confirmed by PCR. Proteins and noncoding RNAs (ncRNAs) were predicted with the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (9).

The complete genome sequence of *E. ictaluri* strain MS-17-156 consists of one circular chromosome (3,837,027 bp, with an average GC content of 57%) and two circular plasmids named pEI-MS-17-156-1 (135,268 bp, with an average GC content of 52%) and pEI-MS-17-156-2 (4,807 bp, with an average GC content of 51%). The complete genome of *E. ictaluri* strain MS-17-188 has 99.94% average nucleotide identity (ANI) (10) with the *E. ictaluri* isolate 93-146 genome (11), and it has 99.41% ANI with the *E. ictaluri* RUSVM-1 genome (12). A total of 3,837 genes, 3,709 protein-coding sequences (CDS), 273 pseudogenes, and 128 RNA genes (25 rRNAs [9, 8, and 8 for 5S, 16S, and 23S, respectively], 98 tRNAs, and 5 ncRNAs) were predicted in the genome.

pEI-MS-17-156-1 contains resistance genes *floR*, *sul2*, and *tetD*, and this plasmid is nearly identical (almost 100% ANI) to previously sequenced plasmids isolated from a wide variety of Gram-negative bacteria, including *Vibrio alginolyticus* strain Vb0506 (pVb0506) (13), *Klebsiella pneumoniae* strain K-109-R plasmid (14), *Photobacterium damselae* subsp. *piscicida* (pP91278) (15), *Vibrio cholerae* strain ICDC-1447 (pVC1447) (16), *Salmonella enterica* subsp. *enterica* serovar Senftenberg strain SRC119 (pSRC119-

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Address correspondence to Hossam Abdelhamed, abdelhamed@cvm.msstate.edu.

A/C) (17), and *Escherichia coli* strain PG010208 (pPG010208) (18). An *E. ictaluri* strain carrying the pEI-MS-17-156-1 plasmid would be potentially resistant to the three antimicrobial drugs (florfenicol, ormetoprim-sulfadimethoxine, and oxytetracycline) that are presently approved for use in aquaculture in the United States. In-depth analysis of this genome is expected to increase our understanding of the mechanisms of antibiotic resistance in *E. ictaluri*, which would facilitate combating antibiotic resistance and promote antibiotic stewardship programs.

Accession number(s). The complete genome sequences of *E. ictaluri* strain MS-17-156 and its two plasmids have been deposited in GenBank under the accession numbers CP028813 (chromosome), CP028814 (pEI-MS-17-156-1), and CP028815 (pEI-MS-17-156-2).

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