



# Complete Genome Sequence of *Edwardsiella hoshinae* ATCC 35051

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**ABSTRACT** *Edwardsiella hoshinae* is a Gram-negative facultative anaerobe that has primarily been isolated from avians and reptiles. We report here the complete and annotated genome sequence of an isolate from a monitor lizard (*Varanus* sp.), which contains a chromosome of 3,811,650 bp and no plasmids.

The *Edwardsiella* genus was first recognized in the 1960s based on the new species *Edwardsiella tarda*, constituting a group of enteric Gram-negative bacteria (1). Shortly thereafter, a group of *Edwardsiella* strains demonstrating unique biochemical processes were isolated in Japan. These strains formed a cluster distinct from other *E. tarda* isolates based on biochemical, physiological, and morphological characters and were considered a biotype of *E. tarda* (2). Further investigations using biochemical and DNA relatedness methods identified this distinct clade as a novel species, designated *Edwardsiella hoshinae* (3). Relative to other *Edwardsiella* spp., there is limited information regarding *E. hoshinae*. This bacterium has been isolated from birds, reptiles, water, and human feces; however, its role as a human pathogen has not been established, and it is not considered a zoonotic agent (3–6). At present, strain ATCC 35051 is the only published complete genome sequence for *Edwardsiella hoshinae*.

Genomic DNA was sequenced using Pacific Biosciences (PacBio) technology to a depth of 25× genome coverage (96.5 Mb). Reads ≥8,000 bp were error corrected with shorter PacBio reads and assembled using Canu version 1.0 (7). Illumina sequences (109× coverage, minimum depth of 11) were mapped to the PacBio assembly using BWA version 0.7.10-r789 (8), and base errors and insertions/deletions were corrected iteratively using Pilon version 1.16 (9) until no further base corrections were made automatically. Overlapping sequence was identified, and the linear contig was circularized and relinearized at a position 1 million bases distant from the original position of circularization. Illumina and PacBio sequences were realigned and visualized using the Integrated Genome Viewer (10) for validation of contiguity and manual correction of assembly errors.

The circularized and completed genome sequence was submitted to the National Center for Biotechnology Information (NCBI) Prokaryotic Genome Annotation Pipeline (PGAP) for annotation and submission to GenBank. The genome sequence was also submitted for Rapid Annotations using Subsystems Technology (RAST) analysis (11, 12) employing the Glimmer option. Average nucleotide identities (ANI) (13) and digital DNA-DNA hybridization (dDDH) (14) estimations were determined using online calculators (ANI, <http://enve-omics.ce.gatech.edu/ani/>; dDDH, <http://ggdc.dsmz.de/distcalc2.php>).

This *E. hoshinae* genome consists of one circular chromosome with 3,811,650 bp (56.9% G+C content). PGAP annotation predicted 3,401 genes encoding 3,204 proteins and 101 tRNAs. RNAMmer (15) predicted nine rRNA operons. RAST analysis predicted 497 subsystems with 3,526 coding sequences and 128 RNAs. The complete genome of ATCC 35051 shares an ANI of 87.4% (dDDH, 35%) with *E. tarda* isolate FL95-01 (16);

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83.1% (dDDH, 25%) with *E. anguillarum* isolates LADL05-105 (17), EA181011 (18), and ET080813 (19, 20); 83.0% (dDDH, 25%) with *E. piscicida* isolates S11-285 (21) and C07-087 (22); and 82.6% (dDDH, 24%) with *E. ictaluri* isolate 93-146 (23). We detected no plasmids in ATCC 35051. The complete annotated genome of *Edwardsiella hoshinae* will be useful for the proper determination of taxonomic affiliation of future *Edwardsiella* species genomes, as well as investigations into host-pathogen interactions.

**Accession number(s).** The complete genome sequence for *Edwardsiella hoshinae* isolate ATCC 35051 has been deposited in GenBank under accession no. [CP016043](https://doi.org/10.1099/jps.0.64483-0).

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