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PROKARYOTES

Complete Genome Sequence of *Pseudoalteromonas piscicida* Strain DE2-B, a Bacterium with Broad Inhibitory Activity toward Human and Fish Pathogens

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ABSTRACT *Pseudoalteromonas piscicida* strain DE2-B is a halophilic bacterium which has broad inhibitory activity toward vibrios and other human and fish pathogens. We report the first closed genome sequence for this species, which consists of two chromosomes (4,128,210 and 1,188,838 bp). Annotation revealed multiple genes encoding proteases with potential antibacterial properties.

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Pseudoalteromonas piscicida strain DE2-B is a naturally occurring, Gram-negative, motile, rod-shaped, and pigmented (orange) marine gammaproteobacterium that was isolated from seawater along the Delaware (United States) coast (1). This strain produces antibacterial compounds that kill human and fish pathogens, including *Aeromonas hydrophila*, *Listonella anguillarum*, *Photobacterium damselae*, *Shewanella algae*, *Shigella soneii*, *Staphylococcus aureus*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, and *Vibrio vulnificus* (1). The death of these pathogens has been associated with the secretion of proteolytic enzymes and other compounds by *P. piscicida* strain DE2-B, as well as the direct transfer to competing bacteria of surface vesicles containing lytic enzymes (1). Other compounds reported to have antimicrobial properties in various *Pseudoalteromonas* spp. include alkaloids, polyketides, and peptides (reviewed in reference 2) and a host of acids (3) and compounds associated with pigmented forms of *Pseudoalteromonas* spp. (4). *P. piscicida* has also been shown to be predatory toward *V. parahaemolyticus* in the marine environment (1). From a practical standpoint, *Pseudoalteromonas* spp. have been used as probiotics to reduce pathogens in aquaculture (5–8) and as aids to reduce biofilm formation (9, 10). The identification of *P. piscicida* has typically been through 16S rRNA gene sequencing, but this practice has led to questionable identifications because of considerable similarity with other species.

The genome was sequenced by the Genomics Core Facility, Clinical and Translational Research Institute, Drexel College of Medicine, Philadelphia, PA, using a PacBio RS II system (Pacific Biosciences, Menlo Park, CA) on single-molecule real-time (SMRT) cells using PacBio P6-C4 chemistry. *De novo* assembly was achieved using the Hierarchical Genome Assembly Process (HGAP) version 2.3 and assembly polishing with Quiver (11). Poorly supported contigs were removed using a custom Python script. The remaining contigs were circularized using Circlator 1.0.2 (12), and finally, the genomes were resequenced using RS_Modification_and_Motif_Analysis version 2.3 (Pacific Biosciences). For the analyses, Prokka version 1.11 (13) and Taxator version 1.2 (14) were used. Quality control files were generated using custom Python scripts. Coverage was 94×. The fully assembled genome contained 5,317,048 bp consisting of two chromosomes of 4,128,210 and 1,188,838 bp with a GC content of 43.44%. This is the first closed genome sequence reported for *P. piscicida* in GenBank.

Genome annotation was obtained from the NCBI Prokaryotic Genome Annotation Pipeline (Bethesda, MD). The genome contains 4,722 genes, 322 pseudogenes, 4,258 predicted protein genes, 31 rRNAs (5S, 16S, and 23S), and 107 tRNAs. Chromosome 1 contains 3,722 genes, 3,355 protein coding sequences, 27 rRNAs, and 106 tRNAs compared with the smaller chromosome 2, which contains 1,000 genes, 903 protein coding sequences, 4 rRNAs, and only 1 tRNA. Annotation also revealed the presence of coding regions for putative proteases, some of which may have antibacterial properties, as recently reported (1), including 11 serine proteases and 7 metalloproteases; however, no cysteine or aspartic protease genes were identified.

Accession number(s). This whole-genome sequencing project has been deposited at DDBJ/EMBL/GenBank under the accession numbers CP021646 (chromosome 1) and CP021647 (chromosome 2). The versions described in this paper are the first versions, CP021646.1 and CP021647.1, respectively.

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We declare no conflicts of interest.

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