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Draft Genome Sequence of Bowmanella denitrificans JL63, a Bacterium Isolated from Whiteleg Shrimp (Litopenaeus vannamei) That Can Inhibit the Growth of Vibrio Parahaemolyticus

Jason P. LaPorte
University of Rhode Island

Edward J. Spinard
University of Rhode Island

See next page for additional authors

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ABSTRACT  Bowmanella denitrificans strain JL63 was isolated from a whiteleg shrimp (Litopenaeus vannamei) and was determined to have antibacterial activity against an acute hepatopancreatic necrosis disease (AHPND) strain of Vibrio parahaemolyticus. Here, we report the draft genome sequence of this strain and identify genes that are potentially involved in its antibacterial activity.

Bowmanella, a genus in the family Alteromonadaceae within the Gammaproteobacteria, was first identified in 2006 (1). Currently, only three species belonging to this genus have been described, Bowmanella denitrificans, Bowmanella pacifica, and Bowmanella dokdonensis. B. denitrificans is a chemoorganotrophic bacterium capable of respiratory, but not fermentative, metabolism (1). B. denitrificans strain BD1T, the first strain of this species to be identified, is capable of anaerobic growth by carrying out denitrification, whereas B. denitrificans strain S088 has been shown to produce a potent heat-stable algicidal compound (1, 2). B. denitrificans JL63 was isolated from a whiteleg shrimp (Litopenaeus vannamei). A zone-of-inhibition assay (3) determined that B. denitrificans JL63 can inhibit the growth of an acute hepatopancreatic necrosis disease (AHPND) strain of Vibrio parahaemolyticus on an agar surface. The B. denitrificans JL63 genome sequence reported here is the first draft genome sequence of a Bowmanella species.

B. denitrificans JL63 was grown overnight in yeast-tryptone broth supplemented with 3% artificial sea salts (LB30IOS) at 27°C. Genomic DNA was isolated using the Promega Wizard genomic DNA purification kit, and DNA was resuspended in 2 mM Tris-HCl buffer (Bio Basic). Sequencing was performed at the Rhode Island Genomics and Sequencing Center using an Illumina MiSeq sequencer. Sequence trimming was performed using CLC Genomics Workbench (version 9.5.3), resulting in 2,641,396 paired-end reads averaging 180 bp in size. Contigs with a coverage of ≥34 X were assembled using the SPAdes genomic assembler (version 3.1.1) (4). The resulting contigs were processed using the CLC Microbial Genome Finishing module. The draft genome consists of 39 contigs, with a total sequence length of 5,479,914 bp and a G+C content of 50.4%. Gene annotation was performed using the Rapid Annotations using Subsystems Technology (RAST) server and resulted in 4,980 open reading frames (5–7).

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Address correspondence to David R. Nelson, dnelson@uri.edu.
those of B. denitrificans BD1T and 81.2% and 80.8% similar to those of B. pacifica W3-3A, respectively.

The genome of B. denitrificans JL63 encodes several gene clusters that are potentially involved in the production of the following antibacterial compounds: lanthionine, colicin V, a secreted hemolysin-type calcium-binding bacteriocin, and the broad-spectrum antibacterial protein marinocine (encoded by the lodAB operon). The genome also encodes an antibiotic biosynthesis monoxygenase, a type VI secretion system (T6SS), and two iron acquisition systems (hemin and TonB), including the full complement of proteins responsible for the formation of the TonB-ExbB-ExbD complex. Gene clusters for a type IV pilus and a mannosone-sensitive hemagglutinin type IV pilus system are also present. The genome contains gene clusters for denitrification and for nitrate/nitrite ammonification. Three secondary metabolic gene clusters in the JL63 genome were predicted using antiSMASH (8). Gene clusters predicted to synthesize a nonribosomal peptide and two bacteriocins, including lantipeptide, were identified.

Accession number(s). This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession no. PEBU00000000. The version described in this paper is the first version, PEBU01000000.

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REFERENCES