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PROKARYOTES

Complete Genome Sequences of Two Bioluminescent *Vibrio campbellii* Strains Isolated from Biofouling Communities in the Bay of Bengal

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ABSTRACT *Vibrio campbellii* is a pathogen of aquatic animals and has been proposed as a bacterial partner in the formation of bioluminescent milky seas. We present here the complete genome sequences assembled from Illumina and Oxford Nanopore data for two bioluminescent *Vibrio campbellii* strains (BoB-53 and BoB-90) isolated from biofouled moorings in the Bay of Bengal.

Vibrio campbellii is a central member of the Harveyi clade (1) and *Vibrio* core group (2, 3) that is primarily found in tropical and temperate marine environments, is increasingly recognized as an economically important pathogen of aquatic animals (4–6), and demonstrates a high level of intraspecies genomic diversity (5, 7, 8). Recently, *V. campbellii* has been proposed to be the bioluminescent bacterial partner (9) responsible for the luminescence associated with the large-scale environmental phenomenon known as bioluminescent milky seas (BMS) (10–12). Observations of BMS have most often been reported from equatorial waters and coastal environments in the northern Indian Ocean, yet there has been only one *in situ* characterization of a BMS (11).

Although BMS were not observed during a research expedition conducted from 3 to 16 August 2015 in the southern Bay of Bengal, *V. campbellii* strains were isolated from recovered subsurface moorings. A biofouling sample from mooring NRL3 (recovered 8 August 2015 at 8°0′00″N, 85°30′02″E from a depth of 20 to 100 m) was spread on a thiosulfate-citrate-bile salts-sucrose agar plate, and an isolated bioluminescent colony was designated strain BoB-53. Similarly, a biofouling sample from mooring NRL6 (recovered on 11 August 2015 at 6°30′00″N, 87°0′00″E from a depth of 20 to 100 m) was spread on a marine agar plate, and a bioluminescent colony was harvested and designated strain BoB-90. Both strains were identified as *V. campbellii* using previously described methods (8).

Genomic DNA was extracted using the Gentra Puregene yeast/bacteria kit (Qiagen) and prepared for sequencing using the Nextera XT sample preparation kit (Illumina). DNA libraries were sequenced using a version 2 300-cycle kit (2 × 150-bp paired-end reads) on an Illumina MiSeq platform. Genomic DNA was also processed using end repair and A-tailing reagents (New England BioLabs) and the 1D ligation sequencing kit MinION Mk1B with the SpotON flow cell R9.4 (Oxford Nanopore Technologies). Hybrid *de novo* assemblies were performed using Unicycler (13), subsequently aligned with Mauve 2.4.0 (14), and annotated using the NCBI Prokaryotic Genome Annotation Pipeline version 4.4.

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The *V. campbellii* BoB-53 genome (45.6% G+C content) contains two chromosomes totaling 5,425,575 bp, with 4,955 predicted coding sequences (CDSs) and relatively few mobile elements. In contrast, *V. campbellii* BoB-90 (45.3% G+C content) contains two chromosomes and four presumptive plasmids totaling 6,171,067 bp, with 5,734 CDSs and >200 mobile elements. The two genomes had an average nucleotide identity of 97.3% and between 96.0 and 97.8% with other *V. campbellii* genomes (15). Prophage prediction via PHASTER (16) indicates one and at least two complete prophages in BoB-53 and BoB-90, respectively. Both genomes contain 12 rRNA operons, 133 tRNAs, and genes encoding the type II, III, IV, and VI secretion systems and lateral and polar flagellar systems. These strains were isolated from previously unsampled geographic and environmental niches and will provide additional information on the potential ecology, genetic diversity, and metabolic capabilities of this species.

Accession number(s). These whole-genome sequencing projects have been deposited at DDBJ/EMBL/GenBank under the accession numbers CP026315 to CP026320 (BoB-90) and CP026321 and CP026322 (BoB-53). The versions described in this paper are versions CP026315.1 to CP026322.1.

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