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GENOME ANNOUNCEMENT

Genome Sequence of the Bacterioplanktonic, Mixotrophic *Vibrio campbellii* Strain PEL22A, Isolated in the Abrolhos Bank

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***Vibrio campbellii* PEL22A was isolated from open ocean water in the Abrolhos Bank. The genome of PEL22A consists of 6,788,038 bp (the GC content is 45%). The number of coding sequences (CDS) is 6,359, as determined according to the Rapid Annotation using Subsystem Technology (RAST) server. The number of ribosomal genes is 80, of which 68 are tRNAs and 12 are rRNAs. *V. campbellii* PEL22A contains genes related to virulence and fitness, including a complete proteorhodopsin cluster, complete type II and III secretion systems, incomplete type I, IV, and VI secretion systems, a hemolysin, and CTXΦ.**

Vibrio campbellii is a *Gammaproteobacteria* species that is widely distributed in marine environments (8). This species has also been associated with disease of wild and reared marine organisms and is apparently an important pathogen (5). *V. campbellii* PEL22A was isolated from an aliquot of seawater by the use of thiosulfate-citrate-bile salts-sucrose (TCBS) culture medium in the South Atlantic Ocean (Abrolhos Bank, south of Bahia state in Brazil, 17°00′10′′S, 39°00′00′′W; 10-m depth). This work reports the draft genome sequence of *V. campbellii* PEL22A.

The genome sequence was obtained using PGM Ion-Torrent sequencing technology (7). The reads were assembled using the Newbler program. The annotation and genomic analyzes were performed by means of Rapid Annotation using Subsystem Technology (RAST) (1). The genome consists of 6,788,038 bp (the GC content is 45%). The coverage is approximately 140×, and the number of contigs generated is 319. The number of coding sequences (CDS) is 6,359. The numbers of tRNA and rRNA genes are 68 and 12, respectively. The following set of genomic tools was used to determine the exact taxonomic position of strain PEL22A: multilocus sequence analysis (MLSA), Karlin genomic signature characterization, and average amino acid identity (AAI) calculation (9). Our analysis revealed that this strain shared >97% DNA identity in MLSA, 6 in Karlin signature analysis, and >96% AAI with *V. campbellii* strain DS40M4 (3). We can conclude that strain PEL22A belongs to the species *V. campbellii* according to the delineation for vibrios carried out by Thompson et al. (9).

We identified a complete proteorhodopsin cluster in the genome of *V. campbellii* PEL22A. Proteorhodopsin is an important light-harvesting pigment, involved in proton translocation, which generates a chemiosmotic potential by translocating protons across an energy-transducing membrane (2, 4, 6). The protons can be used for production of energy in the form of ATP by an ATP synthase. However, this produced ATP is not used for autotrophic CO_2 fixation, which classifies this vibrio as photoheterotrophic or mixotrophic (4). Mixotrophy appears to be a rare phenotype among vibrios, and it may confer an adaptive advantage to planktonic cells living in oligotrophic oceanic areas.

We also identified virulence genes in this genome. We found an incomplete CTXΦ. The *ace* and *zot* genes belonging to the core region of the CTXΦ were identified, but the *ctxA* and *ctxB* genes (which encode the cholera toxin [CT]) were not. The complete CTXΦ plays an important role in the pathogenicity of *V. cholerae*, as it encodes the CT responsible for cholera. The *rstA* and *rstB* genes are also present in the PEL22A genome. These genes are implicated in the gene regulation of the CTXΦ. We found the *hlyA* gene that encodes a hemolysin, an important exotoxin related to pathogenicity in vibrios (10). We found complete sets of genes for the type II and III secretion systems and genes related to the type I, IV, and VI secretion systems. The presence of these genes may confer a fitness advantage to *V. campbellii* PEL22A by allowing intimate interactions with marine organism cells.

Nucleotide sequence accession numbers. The sequence determined in this whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under accession number AHYY00000000. The version described in this paper is the first version, with accession number AHYY01000000.

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