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Genome Sequence of the Marine Bacterium *Vibrio campbellii* DS40M4, Isolated from Open Ocean Water

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***Vibrio* sp. strain DS40M4 is a marine bacterium that was isolated from open ocean water. In this work, using genomic taxonomy, we were able to classify this bacterium as *V. campbellii*. Our genomic analysis revealed that *V. campbellii* DS40M4 harbors genes related to iron transport, virulence, and environmental fitness, such as those encoding anguibactin and vanchrobactin biosynthesis proteins, type II, III, IV, and VI secretion systems, and proteorhodopsin.**

The marine bacterium *Vibrio* sp. strain DS40M4 was isolated from an open ocean water sample collected over the continental slope of the West Coast of Africa between Cape Verde and the Canary Islands. It was determined that this strain produces the siderophores anguibactin and vanchrobactin, which have previously been found only in *V. anguillarum* strains (1, 4, 6, 7). In addition, this strain produces other unique siderophores, such as di- and tri-vanchrobactin (6). Although DS40M4 was clustered with the Harveyi clade by 16S rRNA gene sequence analysis, its exact taxonomic position is still unknown (6). In this work, we assessed the whole genome sequence of *Vibrio* sp. strain DS40M4 and utilized whole-genome-based taxonomic analysis to determine its exact taxonomic position. In addition, genes related to iron transport, virulence, and fitness were identified.

The *Vibrio* sp. strain DSM40M4 genomic DNA was extracted using the Gentra Puregene Yeast/Bact kit (Qiagen, Valencia, CA) and sequenced by the Roche-454 pyrosequencing system. The reads were assembled by the Newbler program, which generated 121 contigs. The annotation and genomic analysis were performed by RAST (Rapid Annotation Subsystem Technology) (2). The genome consists of 5,126,655 bp. The number of coding sequences (CDS) is 4,779. The number of ribosomal genes is 87, of which 83 are tRNAs and 4 are rRNAs. The GC content of this genome is 45%.

The following set of genomic tools was used to determine the exact taxonomic position of the *Vibrio* sp. strain DS40M4: multilocus sequence analysis (MLSA), Karlin genomic signature, and average amino acid identity (AAI) (8). Our analysis revealed that this strain shared $>$97% DNA identity in MLSA, $<$6 in Karlin signature, and $>$96% AAI with two strains of *V. campbellii* BAA-1116 and HY01. It is our conclusion that strain DS40M4 should be allocated into this species according to the delineation for vibrios carried out by Thompson et al. (8). A variety of genes related to iron transport, virulence, and environmental fitness were identified in this genome, such as those encoding anguibactin and vanchrobactin biosynthesis as well as some iron transport genes (1, 4, 6, 7). The *plcA* gene, which is related to pathogenicity in *Listeria* and which plays an important role in signal transduction processes, was also identified in *V. campbellii* DS40M4 (9). The genome sequence also revealed the presence of type II, III, IV, and VI secretion systems and proteorhodopsin genes. The latter are globally abundant photoproteins found in bacteria in the photic zone of the ocean. Both types of genes are involved with pathogenicity and confer a fitness advantage to marine bacteria, increasing long-term survival in the ocean (3, 5). The genome sequence analysis also revealed genes associated with stress response. Some of these genes are related to osmotic and oxidative stress, cold and heat shock, and detoxification.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited in DDBJ/EMBL/GenBank under accession no. AGIE00000000. The version described in this paper is the first version, with accession no. AGIE01000000.

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