

## Genome Sequence of *Oceanicaulis* sp. Strain HTCC2633, Isolated from the Western Sargasso Sea<sup>∇</sup>

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**The genus *Oceanicaulis* represents dimorphic rods that were originally isolated from a marine dinoflagellate. Here, we announce the genome sequence of *Oceanicaulis* sp. strain HTCC2633, isolated by dilution-to-extinction culturing from the Sargasso Sea. The genome information of strain HTCC2633 indicates a chemoorganotrophic way of life of this strain.**

The order *Caulobacterales* is divided into two families designated *Caulobacteraceae* and *Hyphomonadaceae* based on 16S rRNA gene phylogeny (7). The family *Hyphomonadaceae* is currently comprised of 9 bacterial genera: *Hellea* (3), *Henriciella* (12), *Hirschia* (13), *Hyphomonas* (11), *Maricaulis* (1), *Oceanicaulis* (14), *Ponticaulis* (6), *Robiginotomaculum* (8), and *Woodsholea* (2). The family accommodates Gram-negative and prostheated bacteria that have been isolated mainly from various marine environments (7). *Oceanicaulis alexandrii* in the family *Hyphomonadaceae* was isolated from a nontoxicogenic culture of the dinoflagellate *Alexandrium tamarense* and described as dimorphic rods with either a nonmotile, stalked morphology or a motile, nonstalked morphology (14). Using the high-throughput culturing method based on dilution-to-extinction culturing (5), strain HTCC2633 was cultivated from a seawater sample collected at a depth of 10 m from the western Sargasso Sea in the Atlantic Ocean. Strain HTCC2633 was further identified as a member of the genus *Oceanicaulis* based on a 16S rRNA gene sequence that showed 98.8% sequence similarity to *Oceanicaulis alexandrii* C116-18<sup>T</sup>.

The genomic DNA of strain HTCC2633 was extracted from colonies grown on marine agar 2216 (BD Difco) at Oregon State University, and the genome was shotgun sequenced by the J. Craig Venter Institute as part of the Moore Foundation Microbial Genome Sequencing Project (<http://www.moore.org/microgenome>). The draft genome of HTCC2633, consisting of 15 contigs (AAMQ01000001 to AAMQ01000015), was analyzed by using the Joint Genome Institute IMG system (9), the GenDB annotation program (10), and the NCBI Prokaryotic Genomes Automatic Annotation Pipeline. Open reading frames (ORFs) were predicted and searched by using KEGG, SwissProt, Clusters of Orthologous Groups (COG), Pfam, and InterPro protein databases according to automated GenDB annotation schemes. The draft genome sequence was also uploaded into the RAST (Rapid Annotation using Sub-

system Technology) server (4) to check the annotated sequences and screen for noncoding rRNAs and tRNAs.

The draft genome of strain HTCC2633 was 3,166,372 bp in length with a coding density of 90% and had a 63.0 mol percent DNA G+C content. The genome contained 3,029 protein-coding genes, two copies of the 16S-23S-5S rRNA gene operon, and 44 tRNA genes. Strain HTCC2633 has a typical chemoorganotrophic way of life, as indicated by its complete metabolic pathways, including glycolysis, the pentose phosphate pathway, and the tricarboxylic acid cycle. Four copies of arsenate reductases and five copies of ferredoxin reductases are predicted to function as anaerobic respiratory enzymes. The genome is further predicted to contain iron transporters, high-affinity phosphate transporters with the *pho* regulon, multiple genes for general secretion pathways, 24 TonB genes, flagellar proteins, and a type IV secretion/conjugative transfer system. Fifteen genes for beta-lactamases and a bicyclomycin resistance protein in the genome are predicted. Additionally, there are several predicted isoprenoid biosynthesis genes as well as candidate genes encoding epoxide hydrolase, cyclohexanone monooxygenase, 6-hexanolactone hydrolase, and phytase, which are important candidates for biotechnology applications.

**Nucleotide sequence accession number.** The genome sequence of HTCC2633 was deposited under GenBank accession number AAMQ00000000. The GenDB-generated data are accessible at the Marine Microbial Genomics website at Oregon State University (<http://bioinfo.cgrb.oregonstate.edu/microbes/>).

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