

Complete Genome Sequence of Strain HTCC2170, a Novel Member of the Genus *Maribacter* in the Family *Flavobacteriaceae*[∇]

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Strain HTCC2170 was isolated from surface waters off the Oregon coast using dilution-to-extinction culturing. Here, we present the finished genome sequence of a marine bacterium, *Maribacter* sp. strain HTCC2170. Strain sp. HTCC2170 is predicted to be a facultatively aerobic chemoorganotroph that, based on genomic sequence analysis, is capable of macromolecule degradation and anaerobic respiration.

In an attempt to cultivate novel marine bacterioplankton using dilution-to-extinction culturing (4, 6, 15), strain HTCC2170 was isolated from surface seawaters collected off the Oregon coast. Phylogenetic analyses based on 16S rRNA gene sequences assigned strain HTCC2170 to the genus *Maribacter* as a novel species. The most closely related uncultured clone was B78-51, retrieved from a Pacific Arctic sediment (97.9% sequence similarity) (8), while the closest validly published species is *Maribacter polysiphoniae* (97.0%), isolated from the red alga *Polysiphonia japonica* (13). The genus *Maribacter* (11) in the family *Flavobacteriaceae* (3) was created to accommodate aerobic marine bacteria that move by gliding motility. Since the designation of the genus *Maribacter*, many novel species have been described, and the genus now contains 10 validly published species (2, 5, 11–13, 16, 17). Environmental 16S rRNA gene clones affiliated with *Maribacter* spp. have been obtained from seawater, sea ice, and algae samples from the subantarctic region of Argentina, the Inland Sea of Japan, Pacific Arctic sediment, and the Northwestern Mediterranean Sea (1, 7, 8, 14). Some strains, such as *M. ulvicola*, *M. antarcticus*, *M. stanieri*, and *M. polysiphoniae*, have been cultivated from marine algae and, thus, are thought to be associated with coastal phytoplankton species (11–13, 17).

Here, we present the completed genome sequence of *Maribacter* sp. HTCC2170, which is the first genome report for the genus *Maribacter*. Whole-genome shotgun analysis was initiated by the J. Craig Venter Institute as a part of the Moore Foundation Microbial Genome Sequencing Project (<http://www.moore.org/microgenome>) and completed in the present study. Sequences in gaps between contigs were closed using direct sequencing of combinatorial PCR products by Macrogen, Inc. (Seoul, Republic of Korea). The completed genome was analyzed with the GenDB program (10) at the Center for Genome Research and Biocomputing at Oregon State University, by the NCBI Prokaryotic Genomes Automatic Annotation Pipeline, and through the Joint Genome Institute IMG system

(9). The completed HTCC2170 genome contains one circular chromosome of 3,868,304 bp with no predicted plasmids and a 37.0 mol% G+C content. Two copies of the 16S-23S-5S rRNA gene operon were predicted, along with 38 tRNA genes and two pseudo tRNA genes. A total of 3,411 open reading frames (ORFs) were predicted to cover all major metabolic pathways, including glycolysis, the tricarboxylic acid (TCA) cycle, the pentose phosphate pathway, amino acid biosynthesis, and the serine-glyoxylate cycle. While the genome of strain HTCC2170 is predicted to contain carotenoid biosynthesis genes, including a beta-carotene hydroxylase, the genome had no predicted photosynthetic genes or light-utilizing systems. Additionally, the genome contained genes for nitrate reductase, nitrous oxide reductase, and nitric oxide reductase for denitrification, as well as sulfate reductase genes and *pho* regulon genes. The genome is also predicted to contain several copies of genes for arylsulfatase, neuraminidase, and sialidase for galactosylceramide/sulfatide metabolism, and genes for mannose, chitin, and *N*-acetylglucosamine utilization.

The finished genome sequence confirmed that strain HTCC2170 is an obligate chemoheterotroph harboring a set of genes coding for enzymes required to degrade high-molecular-weight compounds, including peptidases, zinc/serine proteases, pectin-degrading protein, glucoamylase, and α -amylases, which coincides with the general physiological properties of members of the family *Flavobacteriaceae*.

Nucleotide sequence accession number. The complete genome sequence of *Maribacter* sp. HTCC2170 is available in GenBank under accession number CP002157. The GenDB-generated data were also processed to be accessible in the Marine Microbial Genomics database at Oregon State University (<http://bioinfo.cgrb.oregonstate.edu/microbes/>).

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