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Complete Genome Sequence of *Croceibacter atlanticus* HTCC2559$^{T\nabla}$

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Here we announce the complete genome sequence of *Croceibacter atlanticus* HTCC2559^T, which was isolated by high-throughput dilution-to-extinction culturing from the Bermuda Atlantic Time Series station in the Western Sargasso Sea. Strain HTCC2559^T contained genes for carotenoid biosynthesis, flavonoid biosynthesis, and several macromolecule-degrading enzymes. The genome confirmed physiological observations of cultivated *Croceibacter atlanticus* strain HTCC2559^T, which identified it as an obligate chemoheterotroph.

The phylum *Bacteroidetes* comprises 6 to ~30% of total bacterial communities in the ocean by fluorescence *in situ* hybridization (8–10). Most marine *Bacteroidetes* are in the family *Flavobacteriaceae*, most of which are aerobic respiratory heterotrophs that form a well-defined clade by 16S rRNA phylogenetic analyses (4). The members of this family are well known for degrading macromolecules, including chitin, DNA, cellulose, starch, and pectin (17), suggesting their environmental roles as detritus decomposers in the ocean (6). Marine *Polaribacter* and *Dokdonia* species in the *Flavobacteriaceae* have also shown to have photoheterotrophic metabolism mediated by proteorhodopsins (11, 12).

Several strains of the family *Flavobacteriaceae* were isolated from the Sargasso Sea and Oregon coast, using high-throughput culturing approaches (7). *Croceibacter atlanticus* HTCC2559^T was cultivated from seawater collected at a depth of 250 m from the Sargasso Sea and was identified as a new genus in the family *Flavobacteriaceae* based on its 16S rRNA gene sequence similarities (6). Strain HTCC2559^T met the minimal standards for genera of the family *Flavobacteriaceae* (3) on the basis of phenotypic characteristics (6).

Here we report the complete genome sequence of *Croceibacter atlanticus* HTCC2559^T. The genome sequencing was initiated by the J. Craig Venter Institute as a part of the Moore Foundation Microbial Genome Sequencing Project and completed in the current announcement. Gaps among contigs were closed by Genotech Co., Ltd. (Daejeon, Korea), using direct sequencing of combinatorial PCR products (16). The HTCC2559^T genome was analyzed with a genome annotation system based on GenDB (14) at Oregon State University and with the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (15, 16).

The HTCC2559^T genome is 2,952,962 bp long, with 33.9 mol% G+C content, and there was no evidence of plasmids. The number of protein-coding genes was 2,715; there were two copies of the 16S-23S-5S rRNA operon and 36 tRNA genes. The HTCC2559^T genome contained genes for a complete tricarboxylic acid cycle, glycolysis, and a pentose phosphate pathway. The genome also contained sets of genes for metabolic enzymes involved in carotenoid biosynthesis and also a serine/glycine hydroxymethyltransferase, which is often associated with the assimilatory serine cycle (13). The potential for HTCC2559^T to use bacterial type III polyketide synthase (PKS) needs to be confirmed because this organism had a naringenin-chalcone synthase (CHS) or chalcone synthase (EC 2.3.1.74), a key enzyme in flavonoid biosynthesis. CHS initiates the addition of three molecules of malonyl coenzyme A (malonyl-CoA) to a starter CoA ester (e.g., 4-coumaroyl-CoA) (1) and takes part in a few bacterial type III polyketide synthase systems (1, 2, 5, 18).

The complete genome sequence confirmed that strain HTCC2559^T is an obligate chemoheterotroph because no genes for phototrophy were found. As expected from physiological characteristics (6), the HTCC2559^T genome contained a set of genes coding for enzymes required to degrade high-molecular-weight compounds, including peptidases, metallo-/serine proteases, pectinase, alginate lyases, and α-amylase.

Nucleotide sequence accession number. The complete genome sequence of HTCC2559 was deposited under GenBank accession no. CP002046. The GenDB-generated data were also processed to be accessed at the Marine Microbial Genomics site at Oregon State University (http://bioinfo.cgrb.oregonstate.edu/microbes/).

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