

Genome Sequence of the Oligotrophic Marine Gammaproteobacterium HTCC2143, Isolated from the Oregon Coast[∇]

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Strain HTCC2143 was isolated from Oregon Coast surface waters using dilution-to-extinction culturing. Here we present the genome of strain HTCC2143 from the BD1-7 clade of the oligotrophic marine *Gammaproteobacteria* group. The genome of HTCC2143 contains genes for carotenoid biosynthesis and proteorhodopsin and for proteins that have potential biotechnological significance: epoxide hydrolases, Baeyer-Villiger monoxygenases, and polyketide synthases.

Strain HTCC2143 was sampled and isolated from surface waters (depth, 10 m) off the Coastal Pacific Ocean, Newport, OR (44°36'0"N, 124°6'0"W). In the course of dilution-to-extinction culture studies on coastal microbial communities, strain HTCC2143 was isolated in a pristine seawater-based medium (2). Phylogenetic analysis of 16S rRNA gene sequences placed strain HTCC2143 in the BD1-7 clade of the oligotrophic marine *Gammaproteobacteria* (OMG) group (2) and indicated that it is related to *Dasania marina*, isolated from Arctic marine sediment (3, 8). The HTCC2143 16S rRNA gene sequence is 95.3% similar to that of *D. marina* (AY771747) and is 96.6% similar to that of environmental gene clone 20m-45 (GU061297), taken from intertidal beach seawater of the Yellow Sea, South Korea. Other closer relatives of HTCC2143 included uncultured gammaproteobacterial clones from seafloor lava (clone P0X3b5B06 from Hawaii South Point X3, EU491383; 96.3%) (9), deep-sea sediment (Ucp1554 from the South Atlantic Ocean, Cape Basin, AM997645; 95.9%) (10), Yellow Sea sediment (95.8%; D8S-33, EU652559), and Arctic sediment (from Kings Bay, Svalbard, Norway; clone SS1_B_07_55, EU050825; 95.7%).

Genomic DNA was prepared at Oregon State University and sequenced by the J. Craig Venter Institute. The finished contigs were automatically annotated with a system based on the program GenDB (5) and manually annotated as described in previous reports (7, 12). The annotation is available at <http://bioinfo.cgrb.oregonstate.edu/microbes/>. The draft genome of strain HTCC2143 comprises 3,925,629 bases and 3,662 predicted coding sequences with a G+C content of 47.0%. The genome of HTCC2143 was predicted to contain 40 tRNAs, 1 16S rRNA, 2 5S rRNAs, and 2 23S rRNA genes. Four genes for selenocysteine metabolism were found, including a selenophosphate-dependent tRNA 2-selenouridine synthase and an L-seryl-tRNA(Sec) selenium transferase (EC 2.9.1.1).

Strain HTCC2143 had genes for a complete tricarboxylic

acid cycle, glycolysis, a pentose phosphate pathway, and an Entner-Doudoroff pathway. Genes were present for a high-affinity phosphate transporter and a *pho* regulon for sensing of environmental inorganic phosphate availability, as well as genes from the NUDIX (nucleoside diphosphate linked to some other moiety X) hydrolase domain family (1) that reflects the metabolic complexity of prokaryotes (4). Genes for ammonium transporters, nitrate reductase, and sulfate reductase were also present in the HTCC2143 genome.

Carotenoid and proteorhodopsin genes were also found in the genome, as well as genes for polyketide synthase modules and related proteins. Carotenoid and proteorhodopsin genes were reported previously from another member of the OMG group, strain HTCC2207, a SAR92 clade isolate (11). HTCC2143 also encoded two epoxide hydrolases, two cyclohexanone monoxygenases (CHMOs) and a cyclododecanone monoxygenase (CDMO). CDMOs and CHMOs are members of the Baeyer-Villiger monoxygenase (BVMO) family. BVMOs are “green” alternatives to the chemically mediated Baeyer-Villiger reactions that allow the conversion of ketones into esters or of cyclic ketones into lactones (6).

This genome provides further evidence that dilution-to-extinction culturing methods that make use of low-nutrient media that are similar to the conditions of the natural environment can result in the isolation of novel, environmentally significant organisms with potential biotechnological value (13).

Nucleotide sequence accession number. The draft genome sequence of HTCC2143 was deposited in GenBank under accession number AAVT00000000. The GenDB-generated data can also be accessed at the Marine Microbial Genomics website at Oregon State University (<http://bioinfo.cgrb.oregonstate.edu/microbes/>).

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