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Genome Sequence of Strain HTCC2083, a Novel Member of the Marine Clade *Roseobacter*[▽]

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Strain HTCC2083 was isolated from Oregon seawater using dilution-to-extinction culturing and represents a novel member of the *Roseobacter* clade. The draft genome sequence of HTCC2083 is presented here. The genome is predicted to contain genes for aerobic anoxygenic phototrophy, sulfite-oxidizing chemolithotrophy, anapleurotic CO_2 fixation, carbon monoxide oxidation, and dimethylsulfoniopropionate (DMSP) utilization.

The marine clade *Roseobacter* (2, 5) is comprised of metabolically diverse members of bacterioplankton that represent chemoheterotrophic or mixotrophic lifestyles and thus are characterized as ecological generalists (9, 11). Many members of this clade have been analyzed by physiological and genomic approaches and have been shown to possess diverse metabolic suites, including aerobic anoxygenic phototrophy (AAnP), anapleurotic CO_2 fixation, inorganic sulfur compound oxidation, demethylation or cleavage of dimethylsulfoniopropionate (DMSP), denitrification, carbon monoxide oxidation, and both C_1 and aromatic compound utilization (6, 9, 10, 12, 13).

Three strains from the high-throughput culture collection (3, 4) (HTCC2083, HTCC2212, HTCC2035) were found to form a distinct group in the *Roseobacter* clade based on 16S rRNA gene phylogeny. These strains are most closely related to coastal bacterioplankton clones, such as EB080-L84F03 and NH10-29, retrieved from the Monterey Bay and Oregon coast, respectively, but showed less than 97% similarity to any validly published species, indicating that they represent a novel genus in the *Roseobacter* clade. Among these strains, HTCC2083 was chosen for genome sequencing. Strain HTCC2083 was isolated from a seawater sample collected at the southern jetty in Newport, OR, using the high-throughput culturing based on the dilution-to-extinction method (3, 4). The strain did not form colonies upon initial isolation but subsequently produced tiny colonies on diluted R2A agar after several passages in filtered (0.2 μm-pore-size filter) and autoclaved seawater medium (low-nutrient heterotrophic medium [LNHM]). Genomic DNA was extracted from liquid cultures grown in LNHM and purified for genome sequencing.

In this report, we present the draft genome sequence of strain HTCC2083 consisting of 20 contigs (ABXE01000001 to ABXE01000020) and 5 scaffolds (DS995276 to DS995280). Whole-genomic-DNA shotgun sequencing was performed by J. Craig Venter Institute and analyzed by using the Joint Genome Institute IMG system (7), the RAST (Rapid Annotation using Subsystem Technology) server (1), the GenDB annotation program (8) at the Center for Genome Research and Biocomputing at Oregon State University, and the NCBI Prokaryotic Genomes Automatic Annotation Pipeline. The predicted protein set and major metabolic pathways of HTCC2083 were searched by using the KEGG, SwissProt, Clusters of Orthologous Groups (COG), Pfam, and InterPro protein databases implemented in the IMG and GenDB systems.

The draft genome of HTCC2083 is 4,015,544 bp in length with a DNA G+C content of 53.3 mol percent and a coding density of 87.6%. The genome contains 4,179 predicted protein-coding genes, 41 tRNA genes, and 2 copies of the 5S, 16S, and 23S rRNA genes. The genome is predicted to have a complete citric acid cycle and an Entner-Doudoroff pathway but appears to lack a complete pentose phosphate pathway. The genome analysis of HTCC2083 suggests diverse metabolic potential for carbon and energy acquisition of the strain, including AAnP (*bchFNBHL lhaA puhABC acsF puhE hemA bchG pucC bchP pufXMLABQ bchZYXC crtFDC tspO crtBIA bchDO hemE*), sulfite-oxidizing chemolithotrophy (*soxRSWXYZ ABCDEF*), anapleurotic CO_2 fixation (predicted phosphoenolpyruvate carboxylase and pyruvate carboxylase genes), carbon monoxide oxidation (*coxMLS*), DMSP demethylation (*dmdA*) and cleavage (*dddD*, *dddP*), C_1 compound utilization, aromatic compound degradation, and secondary metabolite production.

Nucleotide sequence accession number. The draft genome sequence of HTCC2083 was deposited in GenBank under the accession number ABXE00000000.

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