## Genome Sequence of the Marine Alphaproteobacterium HTCC2150, Assigned to the *Roseobacter* Clade<sup>∇</sup>

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Here we announce the genome sequence of a marine bacterium, HTCC2150, that was isolated off the Oregon coast using dilution-to-extinction culturing and that is affiliated with the *Roseobacter* clade. The 16S rRNA phylogeny showed that the strain was closely related to members of the RCA clade. The genome sequence suggests that strain HTCC2150 is an organoheterotroph carrying diverse metabolic potential, including a close relationship with phytoplankton.

The Roseobacter clade in the order Rhodobacterales constitutes major alphaproteobacterial lineages in the pelagic ocean together with the SAR11 and SAR116 groups (2, 8). Owing to the well-developed polyphasic taxonomic approach, many novel genera, including Oceanicola, Maribius, and Maritimibacter, have recently been established, exceeding at least 50 genera in this clade (http://www.bacterio.cict.fr). Physiological and genomic analyses of these genera showed that members of the Roseobacter clade are phenotypically diverse and functionally heterogeneous, being associated with, e.g., aerobic anoxygenic photoheterotrophy, aerobic sulfite oxidation, methylotrophy, demethylation of dimethylsulfoniopropionate (DMSP), degradation of aromatic compounds, exopolysaccharide production, and rosette formation (9, 10, 13, 14). All of the validly published genera in this clade form colonies on nutrient agar media, such as marine agar 2216. In our continuing studies using dilution-toextinction culturing (4, 18), however, many novel isolates belonging to several subclades (OM42, NAC11-7, CHAB-I-V, etc.) in the Roseobacter clade did not produce colonies upon initial isolation, which made polyphasic characterization extremely difficult. Here we report the cultivation and draft genome sequence of strain HTCC2150, a new member of the Roseobacter clade that did not form colonies on nutrient agar medium.

Strain HTCC2150 was cultivated from surface seawaters off the Oregon coast using previously described dilution-to-extinction culturing with a pristine seawater-based medium (3). The initial extinction cultures did not form colonies on various solid agar plates even after prolonged incubation; thus, DNA extraction for genome sequencing was performed using cultures grown in a seawater-based low-nutrient heterotrophic medium (4). Phylogenetic analysis using 16S rRNA gene sequences showed that strain HTCC2150 was most closely related to members of the RCA clade (7, 17), a recently recognized abundant marine bacterial group, with 95 to 96% sequence similarity, but formed a distinct branch in the *Roseobacter* clade.

Genomic DNA was prepared at Oregon State University,

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sequenced and assembled at the J. Craig Venter Institute, and analyzed by using the Joint Genome Institute IMG system (11) and the GenDB annotation program (12) at the Center for Genome Research and Biocomputing at Oregon State University. A draft genome consisting of 25 contigs (AAXZ01000001 to AAXZ01000025) was 3,582,902 bp in length with a coding density of 92% and contained 40 tRNA genes, 2 copies of the 5S, 16S, and 23S rRNA genes, and 3,667 protein coding genes.

Analysis of the HTCC2150 genome suggests the overall organoheterotrophic mode of carbon and energy acquisition, although we cannot exclude the possibility of lithotrophic energy metabolism mediated by a sulfur oxidation (sox) gene cluster and carbon monoxide dehydrogenase (5, 15). The genome had a complete citric acid cycle, pentose phosphate pathway, and Entner-Doudoroff pathway. DMSP demethylase (encoded by *dmdA*) and DMSP lyase (encoded by *dddP*) encoded in the genome could be helpful for the survival of HTCC2150 in coastal environments (9, 16, 19), since members of the Roseobacter clade are well known for their association with organic compounds, such as DMSP, originating from phytoplankton (6). In addition, the predicted quorum-sensing-related genes might also be beneficial for HTCC2150 because the microzones surrounding phytoplankton cells could be densely populated with bacteria (1).

Nucleotide sequence accession number. The draft genome sequence of HTCC2150 was deposited in GenBank under the accession number AAXZ00000000. The GenDB-generated data can also be accessed at Marine Microbial Genomics at Oregon State University (http://bioinfo.cgrb.oregonstate.edu /microbes/).

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