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Complete Genome Sequence of *Robiginitalea biformata* HTCC2501▽

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***Robiginitalea biformata* HTCC2501, isolated from the Sargasso Sea by dilution-to-extinction culturing, has been known as an aerobic chemoheterotroph with carotenoid pigments and dimorphic growth phases. Here, we announce the complete sequence of the *R. biformata* HTCC2501 genome, which contains genes for carotenoid biosynthesis and several macromolecule-degrading enzymes.**

Members of the phylum *Bacteroidetes* constitute 6 to ~30% of total bacterial communities in the ocean, as shown by fluorescence in situ hybridization (4, 6, 8). The family *Flavobacteriaceae*, one of the major phylogenetic lineages in the phylum *Bacteroidetes*, forms a well-defined clade in the 16S rRNA gene phylogeny (2). Members of the family *Flavobacteriaceae* are gram negative, non-spore forming, and have low DNA G+C contents (27 to 44 mol%). They are short to moderately long rods that cannot degrade crystalline cellulose, according to the description of the family (1). They have been considered to be typical chemoheterotrophs that have the ability to degrade high-molecular-weight compounds. Some bacterial species from the genera *Polaribacter* and *Dokdonia* in the family *Flavobacteriaceae* have also been shown to have the light-dependent proton pump proteorhodopsin and display light-stimulated photoheterotrophic growth (9, 10).

Robiginitalea biformata HTCC2501 was originally isolated from the Sargasso Sea (Atlantic Ocean) by dilution-to-extinction culturing; based on the organism's low level of 16S rRNA gene sequence similarity to known members of the family *Flavobacteriaceae*, its distinctively high DNA G+C content, and carotenoid pigments, it was identified as a member of a new genus of *Flavobacteriaceae* (3). Recently, another member of the genus *Robiginitalea*, *R. myxolifaciens* (12), which exhibits ca. 8.5% DNA-DNA relatedness to strain HTCC2501, was reported to produce the monocyclic carotenoid (3*R*, 2′*S*)-myxol (12, 16). As the species name implies, the morphology of *R. biformata* varies from straight rods (in exponential phase) to coccoid cells (in stationary phase) (3), which is also observed for *R. myxolifaciens* (12).

Here, we report the genome sequence of *R. biformata* HTCC2501, which was initially determined 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. Gaps between contigs were closed using direct sequencing of combinatorial PCR products by Genotech Co., Ltd. (Republic of Korea). The finished genome contig was analyzed by a genome annotation system built on GenDB (13) at the Center for Genome Research and Biocomputing at Oregon State University or by the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (5). The *R. biformata* HTCC2501 genome contains one circular chromosome of 3,530,383 bp with no plasmid and a 55.29% G+C content. The number of protein coding genes is 3,211; there are two copies of 16S-23S-5S rRNA genes and 40 tRNA genes encoding 20 aminoacyl-tRNAs. No prophage sequences were found in the genome by the Phage_Finder program (7). The genome comprises a normal complement of genes for metabolic enzymes involved in aerobic respiration, morphogenesis (rod shape-determining protein), and the biosynthesis of 20 amino acids, fatty acids, menaquinone, and phylloquinone, as well as essential genes including those for nucleotide metabolism, transcription, replication, and protein synthesis.

R. biformata HTCC2501 forms colonies with a characteristic rusty red pigment (3). The complete genome contains genes for carotenoid biosynthesis but no genes for phototrophy, confirming the organism's obligately chemoheterotrophic metabolism. The genome of strain HTCC2501 has a set of genes for a putative carbon monoxide dehydrogenase and enzymes required to degrade high-molecular-weight compounds, including protease, sulfatase, pectinase, chitinase, α-amylases, and a predicted glycogen debranching enzyme. Aerobic carbon monoxide (CO) oxidation is an important biogeochemical process in marine environments (11, 14), and it is mediated by aerobic-type CO dehydrogenase (CODH), a molybdopterin protein (15). Although the genome contains genes (*coxL* and *coxS*) for a putative aerobic-type CODH, a complete pathway for CO utilization could not be reconstructed in strain HTCC2501 because the HTCC2501 genome lacks *coxM* and other genes that are thought to be required to produce a functional molybdopterin CODH.

Flavobacterial monocyclic carotenoids, such as saproxanthin and myxol, are rarely found in nature but were demonstrated previously to show significant antioxidative activities against lipid peroxidation and neuroprotective effects against L-glutamate toxicity (16). As Shindo et al. (16) suggested, members of the *Flavobacteriaceae* may be promising sources of diverse novel monocyclic carotenoids. Thus, the HTCC2501 genome

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may provide a model for studying the biosynthesis of carotenoid congeners produced by marine *Flavobacteriaceae* and related species.

Nucleotide sequence accession numbers. The complete genome sequence of *R. biformata* HTCC2501 was deposited in GenBank under accession number CP001712. 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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