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Genome Sequence of *Fulvimarina pelagi* HTCC2506^T, a Mn(II)-Oxidizing Alphaproteobacterium Possessing an Aerobic Anoxygenic Photosynthetic Gene Cluster and Xanthorhodopsin$^\nabla$

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***Fulvimarina pelagi* is a Mn(II)-oxidizing marine heterotrophic bacterium in the order *Rhizobiales*. Here we announce the draft genome sequence of *F. pelagi* HTCC2506^T, which was isolated from the Sargasso Sea by using dilution-to-extinction culturing. The genome sequence contained a xanthorhodopsin gene as well as a photosynthetic gene cluster, which suggests the coexistence of two different phototrophic mechanisms in a single microorganism.**

Besides being mediated by the well-known process of aerobic oxygenic photosynthesis, utilization of light energy in the marine carbon and nutrient cycling processes is usually mediated by aerobic anoxygenic phototrophic bacteria (AAPB) or prokaryotes containing microbial rhodopsin family proteins (18). AAPB comprise about 10% of total microbial cells in the euphotic zone of diverse marine regimes, with alpha-, beta-, and gammaproteobacteria as major constituents (8, 10). Rhodopsin family proteins, including bacteriorhodopsin, proteorhodopsin, and xanthorhodopsin (XR), have been shown to exist in 7 to 70% of marine prokaryotes and contribute photoheterotrophy in diverse phylogenetic groups such as *Flavobacteria*, *Proteobacteria*, and *Archaea* (15, 19). However, no single microorganism has been reported to contain the genes for both aerobic anoxygenic phototrophy (AAnP) and rhodopsin family proteins.

F. pelagi HTCC2506^T was cultivated through a dilution-to-extinction approach (3) from the western Sargasso Sea and identified as a novel genus and species in the order *Rhizobiales* of the *Alphaproteobacteria* by polyphasic taxonomy (2). Later, three *F. pelagi* strains, including HTCC2506^T, were shown to have Mn(II)-oxidizing activity (1). The draft genome sequence of HTCC2506^T was determined by shotgun sequencing at the J. Craig Venter Institute as part of the Moore Foundation Microbial Genome Sequencing Project and analyzed by the GenDB annotation program (17) at the Center for Genome Research and Biocomputing at Oregon State University and the Joint Genome Institute IMG system (http://img.jgi.doe.gov) (14).

The draft genome was 3,802,689 bp in length, distributed in 20 contigs with 61.2% G+C content, and contained 3,754 protein-coding genes, three copies of 16S-23S-5S rRNA genes, and 54 tRNA genes. Remarkably, HTCC2506^T possessed XR and a complete gene set for AAnP together. A gene cluster encoding the AAnP apparatus was composed of *bchIDO-crtCDF-bchCXYZ-pufBALMC-puhE-acsF-puhCBA-lhaA-bchMLHBNF-aerR-ppsR-ubiA-pucC-bchP-hemT*. Mu-like prophage sequences were located closely adjacent to the AAnP gene cluster, which might imply the possibility of the lateral gene transfer of the AAnP gene cluster. The XR gene was followed by *blh*, a gene involved in retinal biosynthesis (16). To our knowledge, this is the first report of a microbe possessing both an AAnP apparatus and a rhodopsin family protein, although the two gene sets in HTCC2506^T had been separately reported to be present (5, 13). The HTCC2506^T genome also encoded a bacteriophytochrome (6, 7), a light-regulated signal transduction histidine kinase. Overall, the existence of a diverse repertoire of genes for sensing or harvesting of light energy implicates the importance of phototrophic metabolism for HTCC2506^T.

In addition to genes for phototrophy, the genome contained several genes with diverse metabolic potential. A lithotrophic mode of energy acquisition was predicted from the presence of the form II *coxSLM* genes, which encode aerobic-type carbon monoxide dehydrogenase (9). As expected from the Mn(II)-oxidizing activity of HTCC2506^T, the genome also encoded a multicopper oxidase (MCO) enzyme, suggesting a potential lithotrophy. In terms of carbon assimilation, genes encoding RuBisCO and phosphoribulokinase of the Calvin-Benson-Bassham cycle (11) were predicted, suggesting the possibility of autotrophic CO_2 fixation in HTCC2506^T. Serine transhydroxymethylase for formaldehyde assimilation (12) was predicted. A gene encoding dimethylsulfoniopropionate (DMSP) lyase, which conveys the production of dimethylsulfide from DMSP (4), was also found in the genome.

Although HTCC2506^T was originally isolated as a chemoheterotroph (2), the genome sequence clearly shows the phototrophic potential of this bacterium. This finding, combined

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with the prediction of many genes related to lithotrophy, carbon fixation, C_1 compound assimilation, and DMSP lysis, suggests that *F. pelagi* HTCC2506^T may use a wide range of potential metabolic functions to survive in the marine euphotic environment.

Nucleotide sequence accession number. The draft genome sequence of HTCC2506^T was deposited in GenBank under the accession number AATP00000000. The GenDB-generated data can be also accessed at Marine Microbial Genomics at Oregon State University (http://bioinfo.cgrb.oregonstate.edu/microbes/).

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