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Genome Sequence of the Marine Photoheterotrophic Bacterium *Erythrobacter* sp. Strain NAP1

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Here we report the full genome sequence of marine phototrophic bacterium *Erythrobacter* sp. strain NAP1. The 3.3-Mb genome contains a full set of photosynthetic genes organized in one 38.9-kb cluster; however, it does not contain genes for CO_2 or N_2 fixation, thereby confirming that the organism is a photoheterotroph.

Aerobic anoxygenic phototrophic (AAP) bacteria were discovered in the late 1970s in Tokyo Bay, Japan (2, 9). The AAP bacteria contain bacteriochlorophyll *a* as the main light-harvesting pigment and photochemically functional reaction centers; however, in contrast to purple nonsulfur photosynthetic bacteria, they are obligate aerobes. They perform photoheterotrophic metabolism based on an obligatory supply of organic substrates for growth but derive a significant portion of their energy requirements from light (4, 5, 11). One of the first isolates (OCh 101) was later classified as *Erythrobacter longus* (10), establishing the first genus of marine AAP bacteria. However, the importance of AAP bacteria in the marine environment was fully recognized only later, after Kolber et al. reported their widespread occurrence in the euphotic zone of the oceans (6, 7).

Erythrobacter sp. strain NAP1 (order *Sphingomonadales*, family *Alphaproteobacteria*) was isolated by plating on minimal medium from a water sample collected in the Northwest Atlantic on 16 April 2000 (3, 7). The genome was sequenced using the whole-genome random shotgun method (1) by the J. Craig Venter Institute. The automatic annotation was done with NCBI Prokaryotic Genomes Automatic Annotation Pipeline, which combines hidden Markov model (HMM)-based gene prediction methods with a sequence similarity-based approach.

The complete genome of *Erythrobacter* sp. NAP1 consists of a single circular chromosome of 3,264,238 bp with an average G+C content of 61%. The predicted 3,177 putative genes cover 92% of the genome. The average gene size is 974.67 bp. There is one copy for each of the rRNA genes and 45 genes for tRNAs. The genome contains one continuous 38.9-kb-long photosynthetic gene cluster. The organization of the genes in the cluster is *bchIDO-crtCDF-bchCXYZ-pufBALM-tspO-bchP*-ORF-*bchG-ppsR-ppaA-bchFNBHLM-lhaA-puhABC-acsF-puhE-hemA-cycA*. While the photosynthetic gene cluster contains a complete set of genes for bacteriochlorophyll biosynthesis and reaction center proteins, most of the carotenoid biosynthesis genes are located outside the cluster. The gene cluster also contains homologues of regulatory genes *ppaA* (cobalamin binding) and *ppsR* (*crtJ* homologue).

Erythrobacter sp. NAP1 lacks the genes of any autotrophic CO_2 fixation pathway. The catabolic pathway contains genes encoding enzymes for glycolysis and the tricarboxylic acid cycle. The genome does not contain nitrogenase or nitrate reductase, which is consistent with its inability to grow on nitrate. There is a full set of genes for heme biosynthesis; δ-aminolevulinic acid is synthesized through the Shemin (C_4) pathway. There is a complete set of genes for the siroheme biosynthesis pathway, but the final enzymes of cobalamin (vitamin B_{12}) biosynthesis are missing.

The presence of photosynthetic genes but the absence of autotrophic fixation pathways in *Erythrobacter* sp. NAP1 is consistent with its photoheterotrophic metabolism in culture. The provided genome offers a valuable source of information for further studies focused on AAP metabolism and physiological nature. This valuable insight could also provide a comparison with the published genome of the closely related but heterotrophic strain *Erythrobacter litoralis* HTCC2594 (8).

Nucleotide sequence accession number. The genome is available in NCBI GenBank under accession number NZ_AAMW00000000.

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