

GENOME ANNOUNCEMENT

Complete Genome Sequence of *Erythrobacter litoralis* HTCC2594[∇]

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***Erythrobacter litoralis* has been known as a bacteriochlorophyll *a*-containing, aerobic, anoxygenic, phototrophic bacterium. Here we announce the complete genome sequence of *E. litoralis* HTCC2594, which is devoid of phototrophic potential. *E. litoralis* HTCC2594, isolated by dilution-to-extinction culturing from seawater, could not carry out aerobic anoxygenic phototrophy and lacked genes for bacteriochlorophyll *a* biosynthesis and photosynthetic reaction center proteins.**

The genus *Erythrobacter* (15) was originally created to accommodate red/orange-pigmented, bacteriochlorophyll *a* (Bchl *a*)-containing, and obligate aerobic marine bacteria that have been known as aerobic, anoxygenic phototrophs (21). Bchl *a*-containing marine *Alphaproteobacteria*, including *Erythrobacter longus* (15) and *E. litoralis* (15, 20), and *Gammaproteobacteria* such as the OM60 clade (5) have been regarded as major players in aerobic anoxygenic phototrophy in the ocean (21). Among the *Erythrobacter* species, however, the recently reported six species (8, 11, 17–19) lack Bchl *a*, and thus only two species, *E. longus* and *E. litoralis*, are considered to be aerobic, anoxygenic, phototrophic bacteria. Here we report the complete annotated genome sequence of *E. litoralis* HTCC2594, which is devoid of phototrophic potential.

E. litoralis strain HTCC2594 was isolated from a depth of 10 m in the Sargasso Sea, Atlantic Ocean, by dilution-to-extinction culturing using a low-nutrient heterotrophic medium as described previously (4). The whole genome of strain HTCC2594 was sequenced by the J. Craig Venter Institute as a part of the Moore Foundation Microbial Genome Sequencing Project (<http://www.moore.org/microgenome>), and the finished genome contig was analyzed by the genome annotation system built into GenDB (13) at the Center for Genome Research and Biocomputing at Oregon State University or the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (6). The *E. litoralis* HTCC2594 genome contains one circular chromosome of 3,052,398 bp and 63.07% G+C content. No plasmids were found in the genome. The number of protein coding genes was 3,011. There was one copy of 16S-23S-5S rRNA and 45 tRNA genes encoding 19 aminoacyl-tRNA sequences. Two prophage sequences were found in the genome

(9), a large prophage region (157,555 to 185,998 bp) and a medium prophage region (2,812,472 to 2,826,784 bp). The HTCC2594 chromosome encoded a normal complement of genes for metabolic enzymes involved in carbon respiration and biosynthesis of amino acids/fatty acids, as well as essential genes for nucleotide metabolism, transcription, replication, and protein synthesis. However, strain HTCC2594 lacked reaction center genes for phototrophic metabolism and genes for CO₂ fixation, such as ribulose-1,5-bisphosphate carboxylase/oxygenase and components of the reverse trichloroacetic acid cycle.

Since *E. litoralis* HTCC2594 was shown to form colonies with a characteristic pink pigment, the PCR assays for *pufLM* genes (2, 14) and spectroscopy measurements for Bchl *a* were carried out in parallel with the genome sequencing, yielding negative results. So far, two other draft genomes from the genus *Erythrobacter* have been published, *Erythrobacter* sp. strain SD-21 and *Erythrobacter* sp. strain NAP1. *Erythrobacter* sp. strain SD-21 is a nonphotosynthetic, manganese(II)-oxidizing bacterium (10), whereas *Erythrobacter* sp. strain NAP1 augments heterotrophic growth with light harvesting encoded by the *puf* operon and ribulose-1,5-bisphosphate carboxylase/oxygenase-independent CO₂ fixation (12). Comparisons using the Mummer (7) or Artemis (1, 3) tool, as well as the NCBI genomic comparison tool (gMap), showed that the HTCC2594 genome was more similar to the draft genome assembly of *Erythrobacter* sp. strain NAP1 (GenBank accession no. AAMW00000000 [genome] and AAMW01000000 [locus tag]) than to the contigs of *Erythrobacter* sp. strain SD-21 (ABCG00000000). This finding may support the scenario of lateral transfer and polyphyly of anoxygenic phototrophy-related genes proposed for the *Alphaproteobacteria* (14) and *Gammaproteobacteria* of the OM60 clade (5).

The HTCC2594 genomic sequence confirmed that photosynthetic gene clusters are missing from the genome of HTCC2594, although otherwise the genome is similar to that of *Erythrobacter* sp. strain NAP1, which is an aerobic, anoxygenic, phototrophic bacterium. Moreover, strain HTCC2594 may be exploited for biotechnological purposes as it encodes

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three distinct epoxide hydrolases with enantioselectivity toward styrene oxides (16).

Nucleotide sequence accession numbers. The complete genome sequence of *E. litoralis* HTCC2594 was deposited in GenBank under accession number CP000157. The GenDB-generated data were also processed to be accessed at Marine Microbial Genomics at Oregon State University (<http://bioinfo.cgrb.oregonstate.edu/microbes/>).

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