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4 **The Complete Genome Sequence of *Erythrobacter litoralis* HTCC2594**

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## ABSTRACT

*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 that 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 and has been known as aerobic anoxygenic phototrophs (21). Bchl *a*-containing marine *Alphaproteobacteria* including *E. 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 that is devoid of phototrophic potential.

*E. litoralis* strain HTCC2594 was isolated from a depth of 10 m, 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

49 Moore Foundation Microbial Genome Sequencing Project  
50 (<http://www.moore.org/microgenome>) and the finished genome contig was  
51 analyzed by genome annotation system built on GenDB (13) at CGRB at  
52 Oregon State University or NCBI Prokaryotic Genomes Automatic Annotation  
53 Pipeline (6). The *E. litoralis* HTCC2594 genome contains one circular  
54 chromosome of 3,052,398 bp and 63.07% G+C content. No plasmids were  
55 found in the genome. The number of protein coding genes was 3,011. There  
56 was one copy of 16S-23S-5S rRNA, and 45 tRNA genes encoding 19  
57 aminoacyl-tRNA sequences. Two prophage sequences were found in the  
58 genome (9): a large prophage region (157,555-185,998 bp) and a medium  
59 prophage region (2,812,472-2,826,784 bp). The HTCC2594 chromosome  
60 encoded a normal complement of genes for metabolic enzymes involved in  
61 carbon respiration and biosynthesis of amino acids/fatty acids as well as  
62 essential genes including nucleotide metabolism, transcription, replication, and  
63 protein synthesis. However strain HTCC2594 lacked reaction center genes for  
64 phototrophic metabolism and genes for CO<sub>2</sub>-fixation, such as ribulose-1,5-  
65 biphosphate carboxylase/oxygenase (RuBisCO) and components of the  
66 reverse TCA cycle.

67         Since *Erythrobacter litoralis* HTCC2594 was shown to form colonies with  
68 a characteristic pink pigment, the PCR assays for *pufLM* genes (2, 14) and  
69 spectroscopy measurements for Bchl *a* were carried out in parallel with the  
70 genome sequencing, yielding negative results. So far two other draft genomes  
71 from the genus *Erythrobacter* have been published; *Erythrobacter* sp. SD-21  
72 and *Erythrobacter* sp. NAP1. *Erythrobacter* sp. SD-21 is a non-photosynthetic,

73 manganese (II) oxidizing bacterium (10), whereas *Erythrobacter* sp. NAP1  
74 augments heterotrophic growth with light-harvesting encoded by the *puf* operon  
75 and RuBisCO-independent CO<sub>2</sub> fixation (12). Comparisons using Mummer (7)  
76 or Artemis tools (1, 3) as well as the NCBI genomic comparison tool (gMap)  
77 showed that the HTCC2594 genome was more similar to the draft genome  
78 assembly of *Erythrobacter* sp. NAP1 (GenBank accession: AAMW000000000)  
79 than to the contigs of *Erythrobacter* sp. SD-21 (ABCG000000000). This finding  
80 may support the scenario of lateral transfer and polyphyly of anoxygenic  
81 phototrophy-related genes that were proposed for the *Alphaproteobacteria* (14)  
82 and *Gammaproteobacteria* of the OM60 clade (5).

83 The HTCC2594 genomic sequence confirmed that photosynthetic gene  
84 clusters are missing from the genome of HTCC2594, although otherwise the  
85 genome is similar to that of *Erythrobacter* sp. NAP1, which is an aerobic  
86 anoxygenic phototrophic bacterium. Moreover, strain HTCC2594 may be  
87 exploited for biotechnological purposes as it encodes three distinct epoxide  
88 hydrolases with enantioselectivity toward styrene oxides (16).

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#### 90 **Nucleotide sequence accession numbers**

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

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