

Complete Genome Sequence of the Proteorhodopsin-Containing Marine Bacterium *Sediminicola* sp. YIK13

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***Sediminicola* sp. YIK13 is a marine flavobacterium, isolated from tidal flat sediment. Here, we present the first complete genome sequence of this genus, which consists of 3,569,807 bp with 39.4% GC content. This strain contains proteorhodopsin, as well as retinal biosynthesis genes, allowing it to utilize sunlight as an energy source.**

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Proteorhodopsin (PR) is a retinal-binding membrane protein belonging to the largest family of microbial rhodopsins, which function as light-driven proton pumps (1). PR genes are abundant in various ecosystems, particularly within the open ocean and are widely distributed among numerous bacterial groups, including *Gammaproteobacteria*, *Alphaproteobacteria*, and *Flavobacteria* (2–11). However, PR-containing sediment bacteria have not yet been studied. Here, we report the first complete genome for *Sediminicola* sp. YIK13, which was isolated from tidal flat sediment. The light-driven pumping activity of PR in this strain was directly measured using native cell suspensions and reported previously (12).

The strain YIK13 was isolated from a sample of tidal flat sediment collected at Yeongheung Island, Korea (E126°26', N37°16') in January 2009. Analysis of the 16S rRNA gene sequence indicates that the strain is a member of the family *Flavobacteriaceae* and shows the highest similarity to *Sediminicola luteus* CNI-3^T (99.5%).

Genomic sequencing was performed using PacBio RS II single-molecule real-time (SMRT) sequencing technology (Pacific Biosciences, USA). A 10-kb insert library was constructed and sequenced, yielding >189.9× average genome coverage. *De novo* assembly of the 131,118 reads (677,903,501-bp total) was conducted using the hierarchical genome-assembly process (HGAP) pipeline in SMRT Analysis version 2.2.0 (Pacific Biosciences). Open reading frames were predicted by NCBI Prokaryotic Genomes Annotation Pipeline (PGAAP) version 2.6 (http://www.ncbi.nlm.nih.gov/genome/annotation_prok). The complete genome of *Sediminicola* sp. YIK13 consists of 3,569,807 bp with 39.4% GC content as a circular chromosome without any plasmid DNA. The genome contained 3,113 protein-coding sequences, 9 rRNAs (5S, 16S, and 23S), and 41 tRNAs with a single rRNA operon.

Genomic analysis of YIK13 revealed the presence of a green light-absorbing PR, 242 amino acids in length, with features typical of proton-pumping rhodopsins, including the DTE (corresponding positions of D85, T89, and D96 positions in bacterio-

rhodopsin) motif, which acts as proton acceptor and donor (2, 13, 14). The *blh* gene encoding a 15,15'- β -carotene dioxygenase was located adjacent to the PR gene, as seen in other PR-containing genomes of *Bacteriodetes* (7). The genome also contains the genes required for β -carotene biosynthesis, including those encoding *crtB* (phytoene synthase), *crtI* (phytoene desaturase), *crtY* (lycopene cyclase), and *crtA* (spheroidene monooxygenase) (15). Furthermore, it also contained a putative transcriptional regulator (MerR family) in front of the *crtI*, *dxs* (1-deoxy-d-xylulose-5-phosphate synthase), and *idi* (isopentenyl pyrophosphate D-isomerase) genes involved in FPP (farnesyl diphosphate) and IPP (isopentenyl diphosphate) precursor synthesis. Similar to other PR-containing genomes of *Bacteriodetes* (7), this genome also contained the *crtZ* (β -carotene hydroxylase) gene involved in the synthesis of zeaxanthin (a carotenoid pigment). This sequence may provide further information necessary to understand the physiological and ecological functions of PR-mediated light utilization in sediment-dwelling microorganisms.

Nucleotide sequence accession numbers. The complete genome sequence of *Sediminicola* sp. YIK13 has been deposited at DDBJ/EMBL/GenBank under the accession number **CP010535**. The partial sequence of the 16S rRNA gene of *Sediminicola* sp. YIK13 has been deposited into the GenBank database under the accession number **JX312334**.

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