



Genome Sequence of the Proteorhodopsin-Containing Bacterium *Flavobacterium* sp. Strain TH167, Isolated from Cyanobacterial Aggregates in a Eutrophic Lake

Haiyuan Cai,^a Feng Chen^b

^aState Key Laboratory of Lake Science and Environment, Nanjing Institute of Geography and Limnology, Chinese Academy of Sciences, Nanjing, China

^bThe Institute of Marine and Environmental Technology, University of Maryland Center for Environmental Science, Baltimore, Maryland, USA

ABSTRACT *Flavobacterium* is the most abundant group of bacteria within the cyanobacterial aggregates in Lake Taihu, China. Here, we present the genome sequence and annotation of *Flavobacterium* sp. strain TH167. Genome analysis revealed the presence of a proteorhodopsin-encoding sequence, together with its retinal-producing pathway, indicating a putative photoheterotrophic lifestyle that generates energy from light.

Lake Taihu is the third largest freshwater lake in China, located in the rapidly developing economically important Changjiang (Yangtze) River Delta. *Microcystis* spp. often form large mucilaginous blooms in the lake due to anthropogenic nutrient overenrichment. These bloom aggregates are composed of extracellular polymeric substances, mainly consisting of polysaccharides, proteins, lipids, and humic substances (1). It is known that many heterotrophic bacteria live in association with cyanobacteria (2, 3). *Flavobacterium* is the most abundant group of bacteria within the aggregates (3). Marine flavobacteria are a well-known reservoir of microbial rhodopsins (4, 5); however, proteorhodopsin (PR)-containing bacteria within cyanobacterial aggregates have not yet been studied. Here, we report the genome sequence of *Flavobacterium* sp. strain TH167, which was isolated from cyanobacterial aggregates during bloom in Lake Taihu, China.

Strain TH167 was isolated from cyanobacterial aggregates collected in the Meiliang Bay (31°30'N, 120°11'E) in Lake Taihu, China. The 16S rRNA sequence analysis revealed that strain TH167 belongs to the genus *Flavobacterium*.

Strain TH167 was cultivated in R2A broth at 28°C for 2 days. Genomic DNA was isolated using the Gentra Puregene Yeast/Bact. kit (Qiagen). Preparation of a paired-end sequencing library with the Nextera XT library preparation kit and sequencing of the library using the HiSeq PE150 system were performed as described by the manufacturer (Illumina, San Diego, CA, USA). *De novo* assembly of all trimmed reads with SOAPdenovo version 2.0 (6) resulted in 228 contigs. Open reading frames were predicted using the NCBI Prokaryotic Genomes Annotation Pipeline version 4.2 and the Rapid Annotations using Subsystems Technology (RAST) server (7). The genome of *Flavobacterium* sp. TH167 consists of 3.24 Mbp, with 40.4% GC content. The genome contained 2,954 protein-coding sequences, 3 rRNAs (5S, 16S, and 23S), and 38 tRNAs.

The genome of strain TH167 contained a full-length PR gene. The PR-encoding sequence codes for a green- and blue-light-absorbing PRopsin (8) of 243 amino acid residues. It shows sequence features suggestive of proton pump activity from the inside to the outside of the bacterial cell, leading to a proton motive force across the cell membrane (8, 9). A *blh* gene encoding a 15,15'- β -carotene dioxygenase, whose gene

Received 22 February 2018 Accepted 16 March 2018 Published 5 April 2018

Citation Cai H, Chen F. 2018. Genome sequence of the proteorhodopsin-containing bacterium *Flavobacterium* sp. strain TH167, isolated from cyanobacterial aggregates in a eutrophic lake. *Genome Announc* 6:e00217-18. <https://doi.org/10.1128/genomeA.00217-18>.

Copyright © 2018 Cai and Chen. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Feng Chen, chenf@umces.edu.

product is predicted to produce two molecules of retinal from β -carotene, was present immediately flanking the PR gene. The reading frames of the PR and *blh* genes were oriented in opposite directions, similar to other PR-containing *Bacteroidetes* (9). In addition, all genes required for β -carotene biosynthesis, including those for phytoene dehydrogenase (*crtI*), phytoene synthase (*crtB*), and β -carotene hydroxylase (*crtZ*), which located together in a cluster and under transcriptional control by a putative regulator (MerR family), geranylgeranyl diphosphate synthase (*crtE*), and lycopene β -cyclase (*crtY*), were located in the genome of strain TH167. In addition, cyanophycin granules were present in the cells, as indicated by the transmission electron microscopy study and genes coding for cyanophycin synthase in the genome of the strain. The genome of strain TH167 should provide further insight into the physiological and ecological functions of *Flavobacterium* spp. dominating within cyanobacterial aggregates.

Accession number(s). This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession no. [NOXX00000000](https://doi.org/10.1101/000000).

ACKNOWLEDGMENTS

This work was supported by National Natural Science Foundation of China (grant 31770129) and the Natural Science Foundation of Jiangsu Province of China (grant BK20151612).

REFERENCES

- Xu H, Cai H, Yu G, Jiang H. 2013. Insights into extracellular polymeric substances of cyanobacterium *Microcystis aeruginosa* using fractionation procedure and parallel factor analysis. *Water Res* 47:2005–2014. <https://doi.org/10.1016/j.watres.2013.01.019>.
- Cai H, Yan Z, Wang A, Krumholz LR, Jiang H. 2013. Analysis of the attached microbial community on mucilaginous cyanobacterial aggregates in the eutrophic Lake Taihu reveals the importance of *Planctomycetes*. *Microb Ecol* 66:73–83. <https://doi.org/10.1007/s00248-013-0224-1>.
- Cai H, Jiang H, Krumholz LR, Yang Z. 2014. Bacterial community composition of size-fractionated aggregates within the phycosphere of cyanobacterial blooms in a eutrophic freshwater lake. *PLoS One* 9:e102879. <https://doi.org/10.1371/journal.pone.0102879>.
- Atamna-Ismaeel N, Sabehi G, Sharon I, Witzel K-P, Labrenz M, Jürgens K, Barkay T, Stomp M, Huisman J, Beja O. 2008. Widespread distribution of proteorhodopsins in freshwater and brackish ecosystems. *ISME J* 2:656–662. <https://doi.org/10.1038/ismej.2008.27>.
- Riedel T, Gómez-Consarnau L, Tomasch J, Martin M, Jarek M, González JM, Spring S, Rohlf M, Brinkhoff T, Cypionka H, Göker M, Fiebig A, Klein J, Goemann A, Fuhrman JA, Wagner-Döbler I. 2013. Genomics and physiology of a marine flavobacterium encoding a proteorhodopsin and a xanthorhodopsin-like protein. *PLoS One* 8:e57487. <https://doi.org/10.1371/journal.pone.0057487>.
- Luo R, Liu B, Xie Y, Li Z, Huang W, Yuan J, He G, Chen Y, Pan Q, Liu Y, Tang J, Wu G, Zhang H, Shi Y, Liu Y, Yu C, Wang B, Lu Y, Han C, Cheung DW, Yiu SM, Peng S, Xiaoqian Z, Liu G, Liao X, Li Y, Yang H, Wang J, Lam TW, Wang J. 2012. SOAPdenovo2: an empirically improved memory-efficient short-read *de novo* assembler. *Gigascience* 1:18. <https://doi.org/10.1186/2047-217X-1-18>.
- Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. <https://doi.org/10.1186/1471-2164-9-75>.
- Fuhrman JA, Schwalbach MS, Stingl U. 2008. Proteorhodopsins: an array of physiological roles? *Nat Rev Microbiol* 6:488–494. <https://doi.org/10.1038/nrmicro1893>.
- Gómez-Consarnau L, González JM, Coll-Lladó M, Gourdon P, Pascher T, Neutze R, Pedrós-Alió C, Pinhassi J. 2007. Light stimulates growth of proteorhodopsin-containing marine flavobacteria. *Nature* 445:210–213. <https://doi.org/10.1038/nature05381>.