Pelagic photoferrotrophy under a genomic lens

CROWE S A[1,2], HAHN A[1], LLIRÓS M[3], THOMPSON K[12], CANFIELD D E[4] AND HALLAM S[1]

[12]Microbiol. & Imm., and Earth, Ocean & Atmos. Sci. Dpts., Univeristy of British Columbia, Canada sean.crowe@ubc.ca, hahnaria@gmail.com, kjtomo14@gmail.com, shallam@mail.ubc.ca,

[3]Microbiol.& Im., Universitat Autònoma de Barcelona, Spain. marc.lliros@uab.cat

[4]NordCEE & Dpt. of Biology, University of Southern Denmark, Denmark. dec@biology.sdu.dk

Fe-based photosynthesis, photoferrotrophy, likely supported global biological production in the iron-rich (ferruginous) oceans of the Precambrian Eon(1). Photoferrotrophy may thus have played a pivotal role in ocean ecology driving the coevolution of life and Earth surface chemistry over billions of years. Knowledge on photoferrotrophic physiology and genetics relevant to Precambrian ocean ecology remains poor because the few photoferrotrophic organisms studied to date were isolated from ephemeral high-light, sedimentary environments—unlikely habitats for their pelagic Precambrian ancestors. We isolated into axenic culture a lowlight adapted photoferrotrophic green sulfur bacterium (GSB) from the water column of Kabuno Bay (KB), a ferruginous sub-basin of Lake Kivu in East Africa. The KB isolate is 99% similar to Chlorobium ferrooxidans str. KoFox, based on small subunit ribosomal RNA gene sequence similarity.

Unlike KoFox, which was enriched from sediments(2), the KB isolate grows without a co-culture partner, and is adapted to a pelagic habitat.

To gain insight into the genetic potential that supports pelagic photoferrotropy and infer its evolutionary history we have sequenced the genome of the KB isolate. A preliminaryanalysis of assembled contigs reveals that the KB isolate posseses an assimilatory sulfate reduction pathway, and components of an ABC-type sulfate transport system.

Assimilatory sulfate metabolims are absent from most GSB with the notable exception of Chl. Ferrooxidans str. KoFox and Chl. luteolum str. DSMZ 273(3). The KB strain, and possibly other photoferrotrophs, therefore appear adapted to growth under the low sulfur concentrations characteristic of ferruginous environments.

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