Deep microbialites from Pavilion Lake, British Columbia, viewed through metagenomics

JENNIFER F. BIDDLE[1], GLENN CHRISTMAN[1] AND JOSEPH RUSSELL[1]

[1]School of Marine Science and Policy, University of Delaware, Lewes DE USA
joeruss@udel.edu glennchr@mac.com jfbiddle@udel.edu

Pavilion Lake in British Columbia, Canada, is home to actively growing microbialites that span the depths of the oligotrophic lake. The origin and evolution of this microbialite system is still unknown, particularly for structures deep in the lake. These "deep mounds" may be large rocks with microbialite growth, or large microbialites. A survey of microbialite bacteria suggested that deep structures may be inhabited by a large number of photoheterotrophs, including Chloroacidobacterium, which may allow for continued phototrophy in low light. To continue the investigation of these deep mound microbialites, we prepared two metagenomic libraries, one sequenced by Illumina short-read sequencing and another by PacBio long read sequencing. A total of 20Gb of sequence was seen by Illumina technology and 120Mb by PacBio. A combination of these datasets show that many carbon fixation pathways were found. Phylogenetically, many Proteobacteria sequences were identified, yet on the longer reads many genes did not share a common ancestor. We examine the community precipiating carbonate in these structures in comparison to other microbialite communities.