

PHOTOSYNTHETIC MELAINABACTERIA AND THE EMERGENCE OF OXYGENIC PHOTOSYNTHESIS. D. Y. Sumner¹, K. Wall¹, C. L. Grettenberger¹, A. D. Jungblut², I. Hawes³, J. A. Eisen⁴, ¹Earth and Planetary Sciences, University of California, Davis, CA 95616, dysumner@ucdavis.edu ²Natural History Museum, London, UK, a.jungblut@nhm.ac.uk ³Waikato University, Tauranga, NZ, aquaticresearchsolutions@gmail.com, ⁴University of California, Davis, CA 95616, jaeisen@ucdavis.edu.

Introduction: Molecular oxygen is critical to complex life on Earth, with transitions increasing the availability of O₂ causing substantial changes in microbial ecosystems during Paleoproterozoic time and allowing increases in animal size during Ediacaran time. This O₂ is produced by oxygenic photosynthesis, which evolved within proto-cyanobacteria. However, the evolutionary paths and processes leading to oxygenic photosynthesis in cyanobacteria are poorly understood due to a paucity of analyzed genomic records that record its evolution. In recent years, organisms have been identified that are closely related to basal cyanobacteria that are not photosynthetic [1-3]. These organisms have been used to suggest that the lineage leading to cyanobacteria was not phototrophic and that protocyanobacteria obtained the genes required for phototrophic reaction centers and pigments through lateral gene transfer [see discussion in 4]. Once genes for both type 1 and type 2 photosynthesis were in protocyanobacteria, they became coupled and evolved to break H₂O into O₂. This process would have required a significant number of evolutionary changes, changes that might be preserved in the genomes of organisms closely related to oxygenic cyanobacteria.

Here, we report the identification of at least four organisms that are classified as basal to the oxygenic Cyanobacteria with 16S rRNA genes, but they also contain phototrophic genes. At least one organism contains both type 1 and type 2 photosynthetic genes, whereas at least three others contain only type 2 photosynthetic genes. We are in the process of evaluating these organisms and additional samples to gain insights into the evolutionary steps leading to oxygenic photosynthesis. Here, we describe our results to date.

Samples and Methods: In 2010 and 2013, under-ice divers collected a suite of microbial pinnacles from Lake Vanda, McMurdo Dry Valleys, Antarctica, as part of projects supported by NASA Astrobiology and the US Antarctic Program (2010) and Antarctica New Zealand (2013). Microbial pinnacles were dissected and frozen in Zymo Xpedition buffer in the field. DNA extraction and amplification were completed in the lab, and 16s rRNA was sequenced on an Illumina MiSeq. We identified 30 Melainabacteria and 11 ML635J-21 OTUs [5]. Samples contain up to 3% Melainabacteria 16S rRNA counts. The sample with the highest concentration of one Melainabacteria OTU was selected for metagenomic sequencing. We used BLAST to identify 7 Melainabacteria bins. Phototrophy-related genes were identified via KEGG, and marker genes were identified on the gene contigs containing phototrophic genes.

Results: Four metagenomic bins BLAST as Melainabacteria and contain phototrophy-related genes: Three contain genes coding for type 2 photoreaction centers, and one contains both type 1 and type 2 genes. These genes show low similarities to equivalent genes in Cyanobacteria, but key genes most closely related to Gloeobacter equivalents (Figure 1). These results demonstrate that some Melainabacteria have the metabolic potential for phototrophy. By exploring the evolutionary history of these genes and their phylogenetic distribution, we can place significant new constraints on the phototrophic capabilities of proto-cyanobacteria and the role(s) of lateral gene transfer in the origin of oxygenic photosynthesis.

Implications: Understanding the processes leading to origin of oxygenic photosynthesis will provide significant insights into the possibilities of complex life on other planets. If it arose solely from mutations in existing genes through lineal descent, its emergence required selection of numerous intermediate steps, each of which must have been favorable or neutral for the organisms. In contrast, if lateral gene transfer, gene homogenation, or other non-lineal genetic changes were important, alternative models of evolution and emergence of novelty need to be invoked and evaluated. The likelihood of the evolution of a metabolism providing enough energy for complex life depends on the nature and complexity of the required evolutionary processes.

References: [1] Di Rienzi SC, et al. (2013) *eLife* doi:10.7554/eLife.01102. [2] Soo RM, et al. (2014) *Genome Biol. Evol.* 6:1031-1045 [3] Soo RM, et al. (2015) *PeerJ* 3:e968. [4] Fischer WW, Hemp J, Johnson JE. (2016) *Ann Rev Earth & Planetary Sci* doi:10.1146/annurev-earth-060313-054810 [5] Wall K, Sumner DY, et al., (in prep).

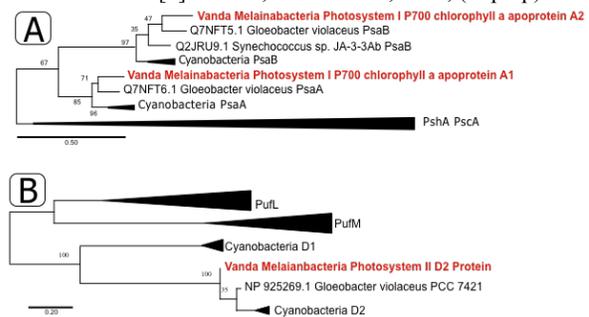


Figure 1: Phylogenetic trees for Melainabacteria genes in organisms with both type 1 and type 2 photosynthesis