

IS1.3 - Microbial mats of Mushroom Spring, Yellowstone National Park, WY, USA: a panoply of chlorophototrophs and their friends

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The composition and ecophysiology of microbial mats associated with the effluent channels of Octopus and Mushroom Springs, thermal features in the Lower Geyser Basin in Yellowstone National Park, WY, have been studied as models of chlorophototroph communities for nearly 50 years. Although often described as “cyanobacterial mats,” in which thermophilic *Synechococcus* sp. are the predominant primary producers, the mats are in fact dominated by members of the *Chloroflexi*, principally members of the genus *Roseiflexus*. The mats can be divided vertically into two zones: an upper green-colored, euphotic layer that is ~1–2 mm in thickness, and an orange-colored undermat that is about 1.0–2.0 cm in thickness, although only the uppermost 0.5 cm of the undermat is biologically active. We have applied metagenomics, genomics, metatranscriptomics, metaproteomics, meta-metabolomics, and traditional enrichment and cultivation methods to study this mat community. The upper green layer is principally composed of chlorophototrophic members of four phyla (*Cyanobacteria*, *Chloroflexi*, *Chlorobi*, and *Acidobacteria*). The undermat is more complex—more than 300 operational taxonomic units are detected by iTag analysis. However, the undermat community is dominated by members of the *Chloroflexi* and is highly uneven in composition. We have detected 18 different chlorophototrophs, which include representatives from all seven phyla currently known to contain such organisms between ~50 to 65°C. The diel transcription patterns in the mats were studied in 2009 (principally the upper green layer) and again in 2014 (both the upper green layer and the orange undermat layer). The transcript abundance patterns observed for the major chlorophototroph populations were essentially identical for these two studies. Light does not appear to control transcriptional patterns in the undermat population, at least not to the same degree as in the upper mat layer. A novel non-chlorophototrophic member of the *Chlorobi* has been detected in the metagenome, and surprisingly it contains all of the genes required for sulfate reduction. These genes were identically regulated in the upper green layer and in the undermat, which suggests that their transcription is not regulated by light but instead is regulated by oxygen. Oxygen has been suggested to control gene expression for some other metabolic processes as well in other mat members (e.g., *nif* gene regulation in *Synechococcus* spp.). Enrichment and cultivation approaches to the study of this mat system will be discussed, using the example of *Chloracidobacterium thermophilum*, a novel chlorophototrophic member of the phylum *Acidobacteria*, which was first detected in the metagenome and eventually isolated as an axenic culture using –omics information as a guide. Progress towards the cultivation and isolation of axenic cultures of all of the chlorophototrophs will be discussed. (Supported by grants DE-FG02-94ER20137 from the U. S. Dept. of Energy, NNX16AJ62G from NASA-Exobiology, and MCB-1613022 from National Science Foundation to D. A. B.).