In situ Dynamics of Gene Expression in Hot Spring Microbial Mats: Implications Concerning Regulation and the Diel Cycling of Physiological Functions in Thermophilic Cyanobacteria.

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Microbial mats in effluent channels of the alkaline siliceous hot springs, Mushroom and Octopus Spring (Yellowstone National Park, USA), have been extensively studied for >40 years. The genomes of two ecologically relevant cyanobacteria from these mats (*Synechococcus* OS-B' and *Synechococcus* OS-A) have been sequenced, and these genomes, together with metagenomic data, provide a strong foundation for targeted *in situ* gene expression analysis.

In this study we investigated *in situ* dynamics of transcript abundance for genes of *Synechococcus* OS-B' (and cyanobacteria with highly similar genes) encoding proteins associated with: carbon concentrating mechanisms (CCM), protection against reactive oxygen species (ROS), respiration, fermentation metabolism and photosynthesis. Transcript abundances were quantified at different times of the diel cycle at a 60°C site. This data was coupled with *in situ* determination of irradiance and microenvironmental O_2 and pH levels.

Most investigated transcripts exhibited one of three abundance patterns: 1) A darkness to light increase that could be divided into: i) low light saturation and ii) low light induction followed by a high light increase: these changes in abundance are possibly associated with changes in light intensity, redox conditions, O_2 levels/ROS, or pH/inorganic carbon availability; 2) Afternoon decrease for some of the light induced genes; 3) Late afternoon/early evening increase with a decline as the evening progresses. Some genes associated with carboxysome biogenesis showed more complex expression patterns, with transcripts showing a predawn induction as well as a high light response. We discuss these gene expression patterns and the functions of the encoded genes with reference to the *in situ* physiology of the thermophilic cyanobacteria over the diel cycle and address factors likely to be regulating gene expression for each of the expression categories.