

Iron homeostasis in Yellowstone National Park hot spring microbial communities

I. Brown^{1*}, S. G. Tringe², H. Franklin⁵, D.A. Bryant³, C. G. Klatt⁴, S.A. Sarkisova¹, and M. Guevara⁵.

¹SARD/JSC, P. O. Box 58447, Houston, TX; ³DOE Joint Genome Institute, Walnut Creek, CA; ²PSU, University Park, PA 16802; ⁴Montana State University, Montana State University P.O. Box 173120, Bozeman, MT 59717; ⁵NASA USRP, NASA JSC, 2101 NASA Parkway, Houston, TX, 77058. USA.

It has been postulated that life may have originated on Earth, and possibly on Mars, in association with hydrothermal activity and high concentrations of ferrous iron. However, it is not clear how an iron-rich thermal hydrosphere could be hospitable to microbes, since reduced iron appears to stimulate oxidative stress in all domains of life and particularly in oxygenic phototrophs. Therefore, the study of microbial diversity in iron-depositing hot springs (IDHS) and the mechanisms of iron homeostasis and suppression of oxidative stress may help elucidate how Precambrian organisms could withstand the extremely high concentrations of reactive oxygen species (ROS) produced by interaction between environmental Fe²⁺ and O₂.

Proteins and clusters of orthologous groups (COGs) involved in the maintenance of Fe homeostasis found in cyanobacteria (CB) inhabiting environments with high and low [Fe] were main target of this analysis.

Preliminary results of the analysis suggest that the Chocolate Pots (CP) microbial community is heavily dominated by phototrophs from the cyanobacteria (CB), Chloroflexi and Chlorobi phyla, while the Mushroom Spring (MS) effluent channel harbors a more diverse community in which Chloroflexi are the dominant phototrophs. It is speculated that CB inhabiting IDHS have an increased tolerance to both high concentrations of Fe²⁺ and ROS produced in the Fenton reaction. This hypothesis was explored via a comparative analysis of the diversity of proteins and COGs involved in Fe and redox homeostasis in the CP and MS microbiomes.

To date, it has been found that the majority of COGs related to the maintenance of Fe homeostasis and suppression of oxidative stress in the CP bacterial community can be assigned to four main functional categories: V – defensive mechanisms; O - posttranslational modification, protein turnover, chaperones; E - amino acid transport and metabolism; and P - Inorganic ion transport and metabolism. The COGs related to the bacterioferritin comigratory protein and putative bacterioferritin comigratory protein functions were abundant in the CP microbiome. In the CP microbiome, roughly 50% of the COGs involved in Fe homeostasis and the suppression of oxidative stress fell into the bacterioferritin comigratory protein and putative bacterioferritin comigratory protein functions; in contrast, the fraction of proteins with the same functions comprised only about 30% of the hits in preliminary results for the MS microbiome. No significant differences in abundance of Fe, Fe²⁺, and Fe³⁺ transport system proteins were observed between CP and MS.

Results obtained so far may suggest that bacteria inhabiting IDHS have additional adaptive proteins that allow them to thrive in an iron rich environment. Further details and discussion will be presented during the meeting.