

The Metagenome in Action

METAGENOMIC STUDY OF IRON HOMEOSTASIS IN IRON DEPOSITING HOT SPRING CYANOBACTERIAL COMMUNITY

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Introduction: It is not clear how an iron-rich thermal hydrosphere could be hospitable to cyanobacteria, since reduced iron appears to stimulate oxidative stress in all domains of life and particularly in oxygenic phototrophs. Therefore, metagenomic study of cyanobacterial community in iron-depositing hot springs may help elucidate how oxygenic prokaryotes can withstand the extremely high concentrations of reactive oxygen species (ROS) produced by interaction between environmental Fe^{2+} and O_2 .

Method: Anchor proteins from various species of cyanobacteria and some anoxygenic phototrophs were selected on the basis of their hypothetical role in Fe homeostasis and the suppression of oxidative stress and were BLASTed against the metagenomes of iron-depositing Chocolate Pots and freshwater Mushroom hot springs.

Results: BLASTing proteins hypothesized to be involved in Fe homeostasis against the microbiomes from the two springs revealed that iron-depositing hot spring has a greater abundance of defensive proteins such as bacterioferritin comigratory protein (Bcp) and DNA-binding Ferritin like protein (Dps) than a fresh-water hot spring. One may speculate that the abundance of Bcp and Dps in an iron-depositing hot spring is connected to the need to suppress oxidative stress in bacteria inhabiting environments with high Fe^{2+} concentration. In both springs, Bcp and Dps are concentrated within the cyanobacterial fractions of the microbial community (regardless of abundance). Fe^{3+} siderophore transport (from the transport system permease protein query) may be less essential to the microbial community of CP because of the high [Fe].

Conclusion: Further research is needed to confirm that these proteins are unique to photoautotrophs such as those living in iron-depositing hot spring.