Geochemical Controls on the Phylogenetic Structure and Composition of NifH in Yellowstone National Park

T. L. Hamilton, E. S. Boyd, J. W. Peters.
Montana State University (thamilton@chemisty.montana.edu)

Abstract.

The origin and evolution of life on Earth was without question impacted by the availability of fixed nitrogen. The advent of biological nitrogen fixation represents a key step in the evolution of life on Earth facilitating the proliferation of life as abiotic sources of fixed nitrogen presumably dwindled. The ability to fix nitrogen is distributed throughout a small number of phylogenetically diverse bacteria and some methanogenic archaea. The phylogenetic distribution of nitrogen fixing organisms therefore provides little insight into the key physiological and environmental underpinnings that define the limits and diversity of diazotrophic organisms on Earth. The role of physical and chemical parameters in structuring the diversity of nitrogen-fixing organisms in the geothermal springs of Yellowstone National Park (YNP), Wyoming was investigated using a phylogenetic framework. Degenerate primers targeting the known diversity of the nitrogenase iron protein were developed and applied in PCRs using DNA extracted from sixty four geochemically-distinct springs from four geographic locations in YNP. A novel phylogenetic approach was employed to examine environmental factors that underpin the distribution, composition, and phylogenetic structure of *nifH* in YNP. The distribution of *nifH* in YNP springs was widespread and did not appear to be constrained by pH or temperature alone. Phylogenetic analysis of NifH from YNP indicated that the phylogenetic structure and composition could not be explained by single variable controls. Rather, the overall phylogenetic structure and composition of NifH in YNP were strongly correlated with the availablility of phosphate and nitrate. Individual clades of NifH are often comprised of sequences from geochemically-disparate environments. However subsets of environmental parameters were strong predictors of the abundance of sequences within the clades, indicating that geochemistry plays an important role in structuring the diversity of diazotrophic populations.