



Conference Abstract

The Geochemical Habitats that Favored the Origin of Thermophilic Lineages

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Abstract

Evidence in the fossil and isotopic records suggests that life inhabited hot springs by ~3.5 Ga. Further, phylogenetic evidence places Bacteria and Archaea from high temperature environments as among the earliest evolving lineages. Moreover, contemporary hot spring communities host an extensive level of biodiversity coinciding with extensive geochemical variation due to spatial and temporal heterogeneity in available oxidants and reductants generated by variable mixing of reduced volcanic and oxidized meteoric fluids. Thus, thermophilic archaeal and bacterial lineages have been co-evolving with their hydrothermal environments since early in the history of life and through dramatic changes in Earth's geologic history. Yet, little is known of the environmental characteristics that enabled the extensive diversification of microbial life and their metabolic functionalities in these environments. To begin developing a framework to understand the environmental characteristics that enabled expansive microbial taxonomic and functional innovation in thermophilic lineages - coordinated geochemical, metagenomic, and phylogenetic analyses were conducted on 37 high-temperature Yellowstone National Park (YNP) hot spring ecosystems that spanned the range of geochemistry (pH ~1.5-10) in YNP springs.

Considerable variation in dissolved solutes and gases were identified, consistent with spatial and temporal variation in the geological, geochemical, and hydrologic processes that influence the YNP hydrothermal system. Shotgun sequencing and bioinformatics

analyses yielded 1,154 archaeal and bacterial metagenome-assembled-genomes (MAGs) from the 37 springs. Genomic diversity and metabolic functions encoded by the MAGs were not uniformly distributed among spring types based on geochemistry, with moderately acidic springs (pH 5-7) harboring the greatest overall diversity, despite these spring types being relatively rare among continental hydrothermal systems. Phylogenomic analyses of MAGs indicated that their divergence times (estimated by distance to phylogenetic roots) were variable, but highly associated with spring geochemistry. Specifically, spring types hosting the highest genomic, taxonomic, and functional diversity also predominantly harbored microbial lineages with the oldest inferred divergence times. In addition, MAG-encoded metabolic functions related to carbon fixation, methane, sulfur, iron, arsenic, hydrogen, and nitrogen metabolism were discretely distributed across spring geochemical types. The distribution of metabolic functions coincided with variation in spring geochemical parameters related to those metabolisms. For example, iron metabolism was most prevalent in acidic springs exhibiting the highest iron concentrations, gas metabolism was most prominent in moderately acidic springs that exhibited the highest dissolved gas concentrations, and arsenic metabolism was prevalent among alkaline pH springs where arsenic concentrations were highest. Lastly, preliminary comparisons of microbial communities from YNP and other global continental hydrothermal systems suggest that geologic setting (e.g., bedrock type) significantly influences hot spring geochemistry and ultimately, microbial compositional and functional profiles that coincide with distinct evolutionary trajectories of hot spring taxa and functional genes. Results will be discussed in the context of the early evolution of life and the co-evolution of microbial lineages and their geologic settings in hydrothermal systems.

Keywords

Hot Springs, Yellowstone, Metagenome, Geochemistry, Evolution, Early Earth, Hydrothermal, Astrobiology, Geobiology, Archaea, Biodiversity

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Conflicts of interest

The authors have declared that no competing interests exist.