

METAGENOMIC INVESTIGATIONS OF SERPENTINIZATION-POWERED MICROBIAL ECOSYSTEMS.

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Ultramafic rocks in the Earth's mantle represent a tremendous reservoir of carbon and reducing power. Upon tectonic uplift and exposure to fluid flow, serpentinization of these materials generates copious energy, sustains abiogenic synthesis of organic molecules, and releases hydrogen gas. Microbial communities hosted within serpentinites may be important mediators of carbon and energy exchange between the deep Earth and the surface biosphere. During the past few years of our studies at several marine and continental sites of serpentinization, we have generated large sequence datasets including 16S rRNA amplicons, metagenomes, and metatranscriptomes. Our initial results have revealed that genes involved in lithotrophy, fermentation, and hydrogen oxidation are enriched in heavily serpentinized habitats. Interestingly, we see the same dominant taxa at each of our serpentinite-hosted sites. These similarities raise fundamental questions of microbial biogeography: How frequently do cells and genes disperse among these globally-dispersed and isolated locations? Does the geological history of these rock-hosted habitats correlate with their history of isolation and exchange? The interdisciplinary data required to address these questions are now available, so the next stage of the project is to develop techniques of interrogating the data that are amenable to tests of specific hypotheses regarding microbial biogeography.

We are currently testing the hypothesis that some genes are dispersed more rapidly among isolated sub-surface sites than are whole cellular organisms by comparing the environmental distributions of 16S rRNA sequences (obtained from deep sequencing of amplicons) with the distributions of a variety of core and accessory genes (obtained from shotgun metagenomic sequencing of representative sites). The inferred relative rates of genetic exchange (including lateral gene transfer) among subsurface locations will indicate the degree to which serpentinization-driven subsurface ecosystems are ecologically and evolutionarily isolated. If geographic barriers to dispersal of genes or organisms are evident in this dataset, it will allow a rare window into the processes of microbial dispersal, colonization, ecological succession, and speciation.

Astrobiology is fundamentally concerned with the distribution and dispersal of life in the universe, and making progress on that front will require techniques

that are capable of measuring the distribution and dispersal history of genes on Earth. The problem of detecting 'contamination' when evaluating potentially extraterrestrial life forms can be considered as one subset of the more general problem of determining the origin and recent past of a given gene by analyzing its current sequence. This is the same challenge currently being addressed by microbial ecologists who are testing hypotheses of microbial dispersal and genetic exchange on Earth. In this presentation, I will provide an overview of how we are employing these metagenomic approaches to explore our particular serpentinization-powered ecosystems on Earth and the associated challenges of applying these approaches to inform interpretations of molecular signatures of life from extraterrestrial sources.