

**DRIVERS OF SPATIAL AND TEMPORAL VARIATION IN LOCAL POPULATIONS OF THERMOPHILIC ARCHAEA (*Sulfolobus islandicus*) IN YELLOWSTONE NATIONAL PARK, WYOMING.**  
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**Introduction:** The geothermal hot springs of Yellowstone National Park (WY, USA) are a dynamic and extreme place for microorganisms to live. The thermoacidophilic crenarchaeon, *Sulfolobus islandicus*, was used as a model organism to identify evolutionary processes in natural microbial populations in hot springs. *S. islandicus* inhabits acidic geothermal hot springs, optimally 80°C and pH 3, and can be cultured in the laboratory. Selection pressures that change diversity within a sub-species level population can depend upon a variety of mechanisms. By combining genetics and geochemistry, the objective of this work is to measure spatial and temporal variation in local populations of *S. islandicus* and to evaluate the role of geochemical and biotic drivers of the observed population variation.

**Methods:** Hot springs were chosen to represent a range of temporal and spatial hydrogeochemical conditions in acid-sulfate springs including water with hot gas discharge mixing seasonally with shallow groundwater or surface water, water with hot gas discharge with relatively constant meteoric water mixing, and hot gas discharge mixing with deep hydrothermal water. Over two years, water and DNA samples were collected in five distinct regions within Yellowstone National Park from hot springs that showed viable cultured populations of *S. islandicus*. Environmental DNA was extracted and amplified for two *S. islandicus*-specific neutral loci and sequenced using 454-pyrosequencing. After removal of sequencing error and potential PCR error, unique alleles for each loci were identified. Water samples were analyzed in the field for pH, T, Eh, and specific conductance, and splits returned to the laboratory for analysis of a suite of major and trace elements, isotopes, and redox-sensitive species, described in detail in McCleskey et al [1]. Comparative data analysis was performed using Fst, Bray-Curtis, principle coordinate analysis (PCA), and Mantel statistical tests.

**Results:** Allelic abundance and composition are primarily controlled by the location of the spring, and the geochemistry of each region is unique enough to generally cluster the regional samples into distinct groups in PCA analysis. Geochemical composition has a general influence on allelic abundance at a regional scale, but it is not the only important controlling factor. Several springs exhibit temporally variable geochemi-

cal composition, but the allelic composition does not reflect the geochemical changes. Conversely, variable allelic composition was observed in springs that exhibited similar chemistry at the time of sampling. Even at different temporal scales (weeks vs. years), regional variations are stronger than temporal changes in geochemistry, although spring surface runoff in certain areas has a large effect on both allele abundance and geochemical composition.

Multiple processes besides geochemistry control the diversity of the *S. islandicus* populations. Spring size, geomorphology, and spring position in the landscape may influence the extent of surface effects (e.g., runoff), geochemical variation, and other spring events on allelic abundance. The size of the habitat and/or population may also be key factors in determining temporal stability, as springs with a small population may be more prone to other microbial interactions and extinction events.

#### References:

[1] McCleskey R.B., Chiu R.B., Nordstrom D.K., Campbell K.M., Roth D.A., Ball J.W., and Plowman T.I., (2014) Water-Chemistry Data for Selected Springs, Geysers, and Streams in Yellowstone National Park, Wyoming, Beginning 2009: doi:10.5066/F7M043FS.