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The effects of temperature, salinity and sinter growth rate on microbial diversity in Icelandic hot springs

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Extreme environments and the organisms that inhabit them i.e., extremophiles have been widely studied due to their importance in the search for extinct and extant life in the ancient Earth as well as on other planets. Amongst terrestrial extreme environments, geothermal hot springs and the associated silica sinters are well known analogues for early Earth conditions and the phylogenetic characterization of microbial communities in such systems has thus been the focus of extensive research. However, the parameters controlling the abundance and diversity of microbial communities as well as the links between community diversity and geochemical/ hydrodynamic regime prevalent in hot springs are still poorly understood.

Here we present results from *in-situ* sinter growth studies along with phylogenetic analyses of the microbial communities in five geochemically diverse (T, pH, salinity, nutrients, sinter growth rate) Icelandic hot springs where silica precipitation leads to the preservation/fossilization of microbial biomarkers. At each location, *in-situ* sinter growth was monitored using glass slides that acted as precipitation substrates along with T, pH, salinity and water chemistry and microbial diversity was evaluated using standard molecular techniques that targeted both bacterial and archaeal 16S rDNA.

Preliminary data show that the main factors controlling the microbial abundance and diversity are salinity, sinter growth rate and temperature. Where high-salt, high growth rates (300 kg silica $y^{-1}m^{-2}$) and high-T (75ºC) conditions dominate, neither bacterial nor archaeal strains were detected whereas in low-salt systems exhibiting low precipitation rates (1 $kgy^{-1}m^{-2}$) and lower T (66ºC), the microbial abundance and diversity

was characterized by the presence of both archaeal and bacterial strains BLAST search of sequenced bacterial clones indicated close relationship to the phyla Deinococcus-Thermus, Proteobacteria, Aquificae, Candidate division OP1, Nitrospirae and Firmicutes.