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A Spatial and Temporal Analysis of Microbial Communities in Great Boiling Spring, Nevada, USA

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Introduction

GBS is a large, geothermal, long-residence-time geothermal spring located in the US Great Basin. It is remarkably monotonous, with analyses showing major shifts of Nut and C and an active nitrogen cycle [1,2].

Results and Conclusions

Water and sediment-borne microbial communities were distinct with very little overlap, regardless of the sampling location or temperature (Fig 2). Water-borne communities were extremely uneven and were dominated by a single phylotype (water). At the different sites through GBS, with only 19.77% of variation explained, this result is similar to the unweighted UniFrac analysis. This amounts to an explanation of 88.15% by P2, site type, resulting in a total variation explained of 35.57%, indicating that relative OTU abundance has a greater influence on the sample clusters in the weighted analysis, again suggesting that relative OTU abundance has a greater influence on the sample clusters in the weighted analysis.

Methods

Eight sediment samples were collected using sterile coring devices and four water samples were collected using sterile coring devices. Sediment samples were collected from four sites at the inlet of the hot spring, sampling in average temperatures from 81.3 - 82.0°C (Fig 1). Samples were stored on ice and transported to the lab, where DNA was extracted using a slightly modified version of the Joint Genome Institute (JGI) CTAB protocol [4]. Phylogenetic analyses were performed using the RDP4 [5] pipeline. The rRNA gene was performed using the RDP4 [5] pipeline. The results were visualized using the RDP4 pipeline [5].

References


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