

Microbial Diversity and the Corresponding Environmental Variables in Acidic Hot Springs Using Next Generation Sequencing

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Due to the unique conditions (e.g., high temperature, low pH and oxygen), acidic hot springs are considered as extreme environments, yet they contain abundant thermoacidophilic microorganisms capable of surviving and functioning under such conditions. This work was aimed to study the impact of environmental variables on microbial diversity, including temperature, pH, geochemistry, as well as mineralogy composition. Microbial communities in acidic hot springs from two different areas (Tengchong in China and the Philippines) were investigated and compared using an integrated approach that included geochemistry and next-generation sequencing. Regardless of large geographic distance, the archaeal communities in these hot springs were both dominated by phyla *Crenarchaeota*, *Euryarchaeota*, and unclassified Archaea; while Bacteria were mainly composed of phyla *Aquificae*, *Firmicutes*, and *Proteobacteria*. In acidic hot springs of the Philippines (Temperature: 60–92°C, pH 3.72–6.58), microbial communities were predominated by those related to sulfur metabolism, which are different from those in acidic springs of Tengchong (Temperature: 44–91°C, pH 2.34–6.86). The results of this study improve our understanding of microbial diversity and community composition in extreme environments, and provide information for further investigation of early life evolution on earth.