

# Microbial Community Structure and Functional Potential Across Stratified Mats in a Sankampaeng Hot Spring

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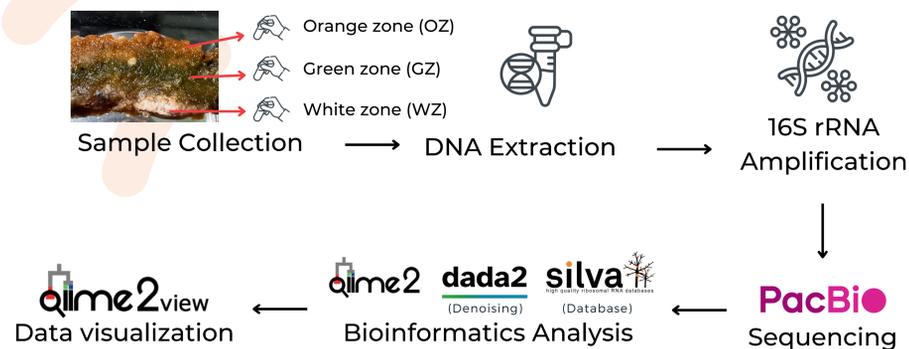
## BACKGROUND

Microbial mats in extreme environments serve as valuable models for understanding microbial ecology, biogeochemical cycling, and adaptation to harsh conditions. This study investigates the microbial community structure and functional potential across different layers of a microbial mat from the sulfidic hot spring of Sankampaeng, Thailand, using full-length amplicon sequencing. The stratified mat consists of three distinct layers: an orange zone (OZ), a green zone (GZ), and a white zone (WZ), from top to bottom.

A related study reported that the predominant Cyanobacterium, *Leptolyngbya*, accounted for over 60% of sequences in the upper layer of the microbial mat. Metabolic analysis further revealed the presence of complete carbon, sulfur, and nitrogen cycles within the community, highlighting the mat's role in biogeochemical cycling [1].

The integration of carbon and nitrogen cycles within the microbial mat underscores its role as a self-sustaining ecosystem in an extreme environment. This study enhances our understanding of microbial diversity, metabolic interactions, and biogeochemical processes in thermophilic microbial mats, contributing to the broader knowledge of life in extreme habitats.

## APPROACHES



## CONCLUSIONS

### 1. Alpha diversity

- From the evenness boxplot, OZ has the most even distribution, suggesting that microbial species are more uniformly distributed, GZ is not differently from OZ, and WZ has lowest even distribution.
- From the richness boxplot, WZ has highest microbial diversity, as indicated by the greater number of observed features, GZ demonstrate an intermediate level of richness, and OZ shows the lowest richness among all sample groups, suggesting a more selective or specialized microbial community.

### 2. Taxonomic identifications

- Across all layers, Alphaproteobacteria dominate, with Cyanobacteria from the order Leptolyngbiales being the predominant phototrophs in the OZ and GZ, while Planctomycetota, specifically class *Phycisphaerae*, dominate in the WZ.

### 3. Biogeochemical cycles

- Functional analysis suggests that the OZ and GZ primarily support oxygenic photoautotrophy, whereas the WZ exhibits the highest potential for chemoheterotrophy and photoheterotrophy. Nitrogen fixation is enriched in the OZ and GZ, carried out by Leptolyngbiales, while *Tistrellales*, enriched in the GZ and WZ, may play a role in sulfur oxidation. Nitrogen fixation is also enriched in the WZ, indicating active nitrogen cycling.

## REFERENCES

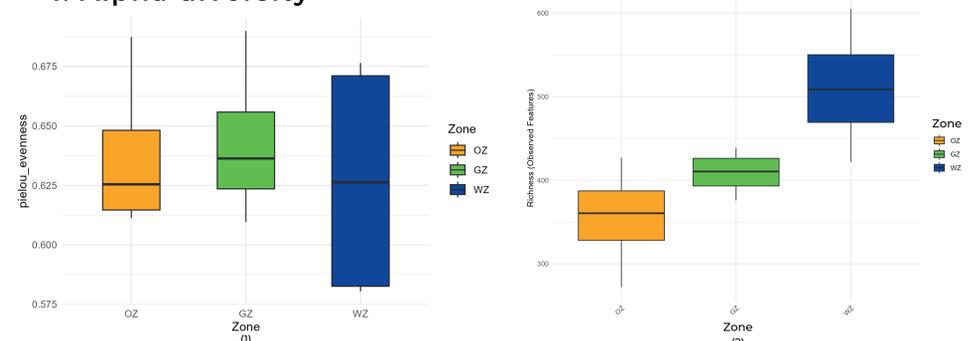
1. Rozanov AS, Bryanskaya AV, Peltek SE, et al. Biodiversity of the microbial mat of the Garga hot spring. BMC Evol Biol. 2017;17(Suppl 2):254. doi:10.1186/s12862-017-1106-9.

## OBJECTIVES

- To analyze microbial community structure and diversity in hot spring microbial mats using full-length 16S rRNA gene sequencing.
- To investigate the functional and ecological roles of dominant microbial groups in the hot spring environment.

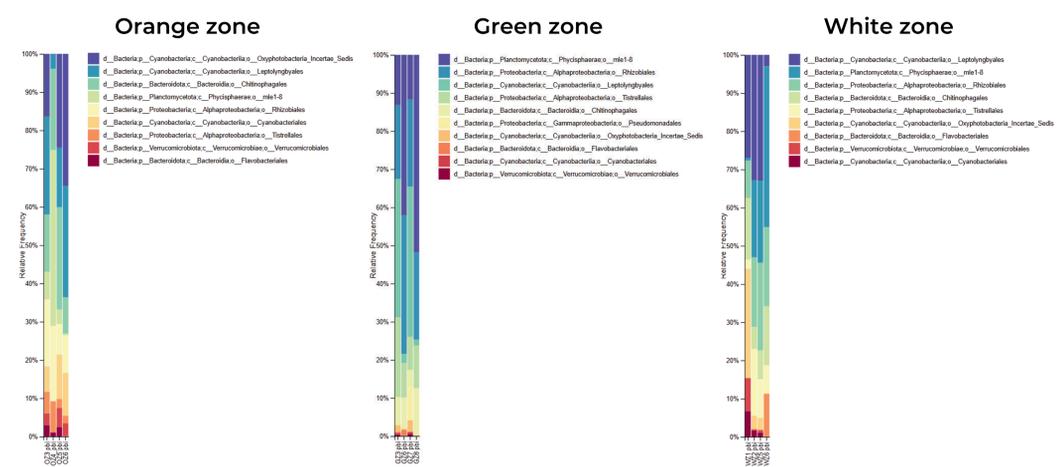
## RESULTS

### 1. Alpha diversity



**Figure 1. Alpha diversity boxplots.** (1) The distribution of evenness across sample groups. OZ and GZ exhibit similar evenness, while WZ shows the lowest evenness among the three zones. (2) The richness of observed features across sample groups. WZ demonstrates the highest richness, indicating the greatest number of observed bacterial features. GZ demonstrate an intermediate level of richness, and OZ shows the lowest richness among all groups.

### 2. Taxonomic identifications



**Figure 2. Main bacteria from orange zone samples.**

Main Phylum: Cyanobacteria, Bacteroidota, Planctomycetota, Proteobacteria, Verrucomicrobiota

**Figure 3. Main bacteria from green zone samples.**

Main Phylum: Planctomycetota, Proteobacteria, Cyanobacteria, Bacteroidota, Verrucomicrobiota

**Figure 4. Main bacteria from white zone samples.**

Main Phylum: Cyanobacteria, Planctomycetota, Proteobacteria, Bacteroidota, Verrucomicrobiota

### 3. Biogeochemical cycles model

