

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

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ABSTRACT

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. 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 the WZ. Microbial diversity is highest in the OZ and GZ, while the WZ harbors a less diverse but functionally distinct community dominated by anaerobic processes. 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 nitrification appears absent based on functional predictions, though Nitrospirota, enriched in the WZ, may play a role. Denitrification is also enriched in the WZ, indicating active nitrogen cycling. 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.

Keywords: Metagenomics, Hot springs, Microbial mats

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