

## **16S rRNA metagenomics data on the bacterial communities in Poring Hot Spring, Sabah, Malaysia**

### **ABSTRACT**

Hot springs are known to harbor potentially unique microorganisms due to the extreme temperatures in which they thrive and their biotechnologically important enzymes that are active at high temperature, which are beneficial for various industries. Sabah, Malaysia, houses several hot springs, yet knowledge of their microbiological diversity remains limited. Here, the raw sequence data of bacterial communities in a hot spring through metagenomic analysis are revealed. The data were obtained by collecting water and sediment samples from Poring Hot Spring (PHS) in Ranau, Sabah, and their bacterial diversity was analyzed using 16S rRNA amplicon sequencing targeting the V3-V4 regions. The analysis identified bacterial diversity in both water and sediment samples, with 35 phyla, 76 families, and 90 genera in water, and 38 phyla, 114 families, and 128 genera in sediment. Proteobacteria dominated the water samples (87 %), while Cyanobacteria were most abundant in sediment samples (51 %). The most abundant genera in water were Tepidimonas, Hydrogenophilus and Methylothermus, whereas Geitlerinema, Calothrix and Nitrospira dominated the sediment. Sediment samples exhibited higher bacterial richness and diversity compared to water samples, as indicated by  $\alpha$ -diversity analysis. Sequences and sample data are deposited in the NCBI Sequence Read Archive under Bioproject ID PRJNA982554 (Accession number: SRX20671661 to SRX20671666) at [https://www.ncbi.nlm.nih.gov/Traces/study/?acc=PRJNA982554&o=acc\\_s%3Aa](https://www.ncbi.nlm.nih.gov/Traces/study/?acc=PRJNA982554&o=acc_s%3Aa)).