

Case Study Methane-Cycling Microbiome in Permafrost

Project Topic: Analysis of methane-cycling microbiome in permafrost

Project Partner: GFZ Potsdam, UiT, CAREERI

Location: Siberia, Svalbard, Qinghai-Tibet Plateau

Sample type: Permafrost soils

Target Molecule: genomic DNA

Laboratory Analysis:

16S rRNA gene and metagenomic sequencing (Illumina) of genomic DNA retrieved from the active layer and frozen permafrost

Bioinformatic Analysis:

Quality control, demultiplexing, taxonomic classification, assembly and binning, genome quality assessment, functional annotation, metabolic pathway reconstruction

Summary:

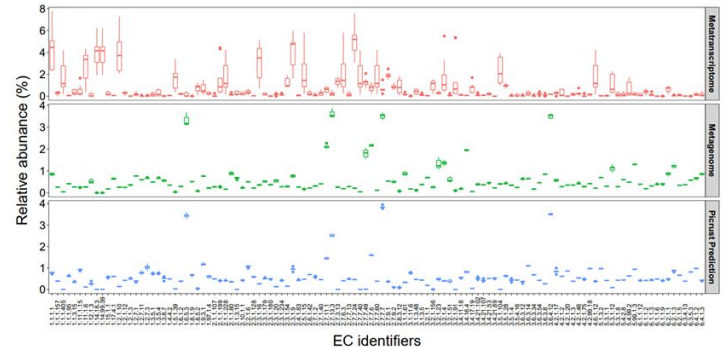
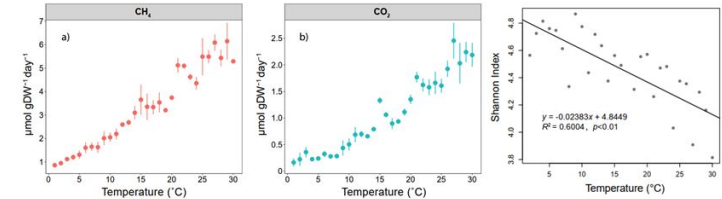
Taxonomic and functional profiling revealed high diversity of methane cycling microbiome residing in permafrost soil, with heterogeneous distribution patterns in active layer and permafrost. Diversity loss after excessive warming will lead to larger variability of production rate of greenhouse gas CH₄ and CO₂ from permafrost soils.

More details:

<https://doi.org/10.1111/mec.16118>

<https://doi.org/10.1002/ppp.2131>

<https://doi.org/10.1016/j.soilbio.2017.03.007>



EC identifiers