

Case Study Methane-Cycling Microbiome in Permafrost



Project Topic: Analysis of methane-cycling microbiome in permafrost

Project Partner: GFZ Potsdam, UiT, NIEER, Radboud University

Location: Lena Delta Siberia, Svalbard, Qinghai-Tibet Plateau

Sample type: Permafrost soils

Target Molecule: genomic DNA

Laboratory Analysis:

16S rRNA gene, metagenomic sequencing (Illumina) of genomic DNA retrieved from the active layer and frozen permafrost, as well as thermokarst lakes and lagoons which are subject to rapid thawing.

Bioinformatic Analysis:

Quality control, demultiplexing, taxonomic classification, metagenome assembly and binning, genome quality assessment, functional annotation, metabolic pathway reconstruction, downstream analysis including network analysis, LEfSe, ordination, SEM and multiple other numeric analyses.

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.

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>, <https://doi.org/10.1111/gcb.16649>
<https://doi.org/10.1007/s10482-022-01767-z>

