

Characterization of permafrost microbiome

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1. Project description

The permafrost environment provides living space for numerous microorganisms from prehistoric era. Alpine permafrost compared to arctic permafrost is a new and underexplored niche for microbes although they have recently become a focus of attention. Thawing of permafrost due to global warming not only promotes microbial carbon turnover with direct feedback on greenhouse gases, but also unlocks unknown microbial diversity of potentially novel metabolic capacity residing in the permanent soils. Despite the great interest in this topic, the knowledge of microbial ecology and biodiversity in permafrost environments, especially alpine permafrost, is still lacking.

Our pioneering study at 'Muot da Barba Peider' in the Swiss Alps revealed a high taxonomic diversity of microbial taxa found in alpine permafrost soils (Frey et al. 2016). The occurrence of many undercharacterized candidate phyla with no cultured representatives in the permafrost soils at 'Muot da Barba Peider' is unprecedented and highlights our poor understanding of the biology in these habitats and the microbial metabolisms required to adapt to such extreme conditions. This study opened a new and exciting microbial resource which should further be explored. Many of the microorganisms isolated from permafrost represent

potentially novel microbial genera with unprecedented gene discovery. They may possess enzymes and bioactive compounds of significance to health applications (novel antimicrobials, anti-aging compounds) or engineering that may be specific to environmental characteristics (e.g. temperature and cold-adapted genes), potentially bringing new industrial and biotechnological applications. Permafrost, therefore, may serve as novel sources of biomolecules which can now be further explored.

With the research at Jungfraujoch we extend our high-altitude mountain sites for exploring the permafrost microbiome in the European Alps. In summer 2018 we have sampled active layer and permafrost at Jungfraujoch (see Figures 1 and 2) and have analysed the permafrost microbiome in these soil samples. From the 12 samples analysed we found a highly diverse soil microbiome with 3423 bacterial and 650 eukaryotic taxa. There was a variation in the microbial communities and clear differences between the sites (see Figures 3 and 4). Interestingly, we found many unknown taxa and in general the Jungfraujoch microbiome is poorly explored. In the near future we try to better characterize some of the unknown taxa by trying to isolate and genetically and biochemically identify them.

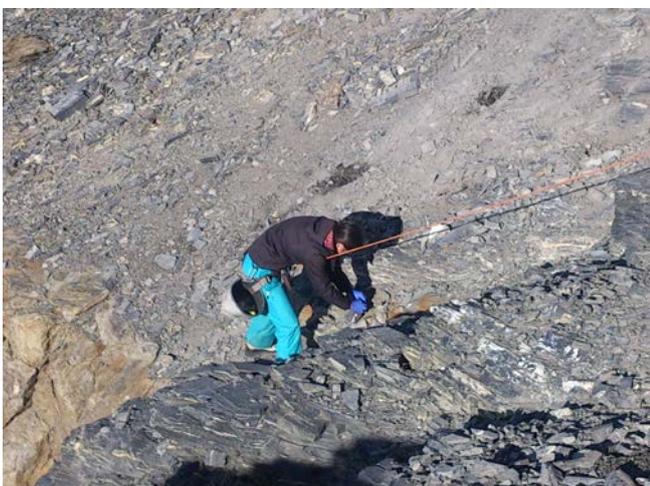


Figure 1. Sampling of permafrost soils at Jungfraujoch station.



Figure 2. Permafrost soil sampled at 3445 m.

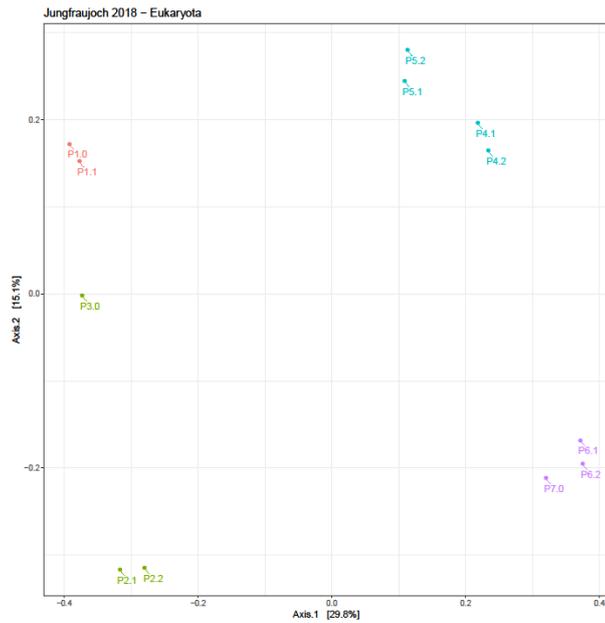


Figure 3. Eukaryotic community structures of the 12 sites.

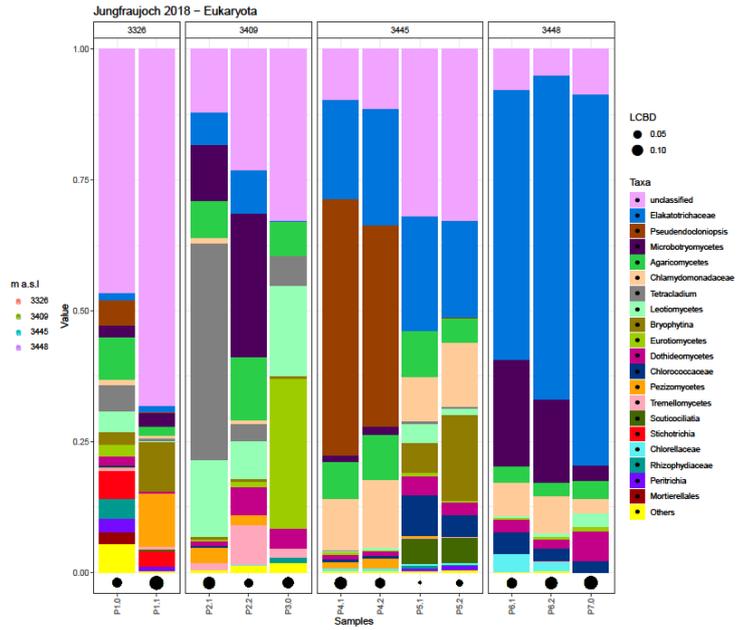


Figure 4. Eukaryotic classes at the 12 sampled sites.

References

Frey B., Rime T., Phillips M., Stierli B., Hajdas I., Hartmann M. (2016). Microbial diversity in European alpine permafrost and active layers. FEMS Microbiolog and Ecology 92, fiw018, doi: 10.1093/femsec/fiw018

Collaborating partners / networks

Swiss Permafrost Monitoring Network (PERMOS)
 Microarctic: Microorganisms in a warming Arctic (EU Horizon 2020)
 CLIMARCTIC - SNF: Climate change impacts on Arctic soil and lake microbiomes
 CRYOLINK - SNF: Influence of climate change on permafrost microbiome
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