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Microbial life in collapsing permafrost in NE Greenland

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In recent years, permafrost-affected soils have been shown to be gradually subject of thawing (IPCC, 2019). Formerly frozen soil organic carbon stocks hence become increasingly susceptible to microbial decomposition and transformation into greenhouse gases (Schuur *et al.*, 2015). An estimated 20% of Arctic permafrost areas are subject of melting of belowground ice and consequent collapse (Olefeldt *et al.* 2016), but these thermokarst landscapes are often difficult to assess.

In 2018, a thermokarst developed into a thermal erosion gully in close vicinity to the Zackenberg Research Station. As one of the main stations of the Greenland Ecosystem Monitoring (GEM) program, the monitoring of various ecosystem parameters at this site during the past 25 years, including hydrology, soil temperature and active layer depth, enables a spatiotemporally precise description of the thermokarst's physical progression.

In order to characterize the development of a thermokarst soil microbial community and understand its spatial distribution and taxonomic biodiversity, soil cores of 30 cm above and below an ice lens were extracted in August 2018, as well as after a dry and warm summer season in September 2019, until 90 cm depth to also sample still frozen permafrost soils. Soil characterization included loss on ignition, radiocarbon dating and microbial viability assays for both years. Bacterial 16S rDNA V3-V4 and fungal ITS1 gene region amplicons of extracted DNA were sequenced and analyzed. With the microbiome involved in biochemical processes such as nitrogen fixation, methane production and oxidation as well as CO₂ respiration, knowledge about abundance, genetic and adaptation potential of bacteria, archaea and microeukaryotes in fast changing permafrost soils affects several ecosystem carbon fluxes significantly.

This work is part of a project, describing both the taxonomic and functional composition of this thermokarst microbiome, including the use of multi-omics to reveal the carbon cycling gene potential and expression in combination with in situ and laboratory incubation gas fluxes of CO₂, N₂O and CH₄. These biological and biogeochemical insights from this event are put into perspective with long-term, maintained data supplied by the GEM.