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Should I grow or should I go? - Transcriptomic responses of permafrost soil microbiomes to sudden thaw and erosion

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Permafrost soils usually remain frozen in summer, often even for millennia. Due to low temperatures, decomposition rates are low and alone Arctic permafrost is estimated to store 1850 Gt carbon (C). This currently corresponds to about twice the amount of atmospheric CO₂. While microorganisms within their seasonally thawing surface (active) layer are adapted to enormous temperature fluctuations, the intact permafrost microbiome contains spore-formers and extremophiles at low metabolic states. With global warming, seasonal thaw depth increases, not only leading to loss of ancient communities, but also to a growing availability of soil carbon for decomposition. Much of permafrost microbial taxonomic and metabolic diversity is unknown still, but our most urgent gaps of knowledge exist in monitoring this vulnerable microbiome's ecological and metabolic adaptation in situ during permafrost thaw and erosion. Insights about microbial carbon sequestration in thawing soils is crucial - yet understudied, as permafrost environments are usually remote and modern sequencing techniques require elaborate sample storage and transport.

Here, we present our results of total RNA sequencing of abruptly eroding as well as intact 26200-year-old permafrost soils, from the high Arctic Northeast Greenland. Gene expression of samples describes the community composition (rRNA) and active metabolic pathways (mRNA) in zones of intensely degrading permafrost. The impact of changing physicochemical soil parameters with depth, such as pH, age, soil moisture and organic matter content was compared to determine possible metabolic and community-level responses. We revealed taxonomic composition and diversity, as well as metabolic pathways of microbial organic carbon remineralization especially at the crucial freshly thawed permafrost depths.