



In situ permafrost thaw due to climate change drives holistic microbial community shifts with implications for methane cycling

Rhiannon Mondav (1,5), Carmody McCalley (2), Suzanne Hodgkins (3), Virginia Rich (2), Steve Frolking (4), Scott Saleska (2), Andrew Barnes (5), Jeff Chanton (3), and Patrick Crill (6)

(1) Uppsala University, Uppsala, Sweden (rhiannon.mondav@ebc.uu.se), (2) University of Arizona, Tucson, USA (cmccalley@email.arizona.edu), (3) Florida State University, Tallahassee, USA (sbh10c@fsu.edu), (4) University of New Hampshire, Durham, USA (steve.frolking@unh.edu), (6) Stockholm University, Stockholm, Sweden (patrick.crill@geo.su.se), (5) University of Queensland, Brisbane, Australia (r.mondav@uq.edu.au)

Thawing permafrost is a potentially significant source of radiative forcing feedback due to increased emissions of methane, a biogenic greenhouse gas (GHG). This study investigated changes in the microbial community along a permafrost thaw gradient at Stordalen Mire, Sweden using 16S rRNA gene amplicon and metagenomic methods. In situ measurements of geochemical parameters, including CH₄ and C isotopes, enabled linkage of community dynamics to significant shifts in C balance. The thaw gradient ranged from intact at a palsa (low productivity and GHG emissions), through partially thawed in a bog (high productivity, low GHG emissions) to a completely thawed fen (high productivity and GHG emissions).

Microbial assemblages in both the palsa and fen were highly diverse (in both richness and evenness), consistent with climax communities. The microbial community in the bog had distinctly lower diversity, characteristic of ecosystem disturbance. The palsa community was dominated by Acidobacteria and Proteobacteria, as is typical of a range of soils including permafrost. Methanogens dominated both the bog and fen and were most abundant within the zone of water table fluctuation. Inferring methanogens' production pathway from phylogeny showed a shift from mostly hydrogenotrophic methanogens in the bog towards acetotrophic methanogens in the fen. This corroborated porewater and flux emitted CH₄ and CO₂ carbon isotopic ¹³C signatures of CH₄ and CO₂. The fen, where the highest CH₄ flux was recorded, was significantly richer in methanogenic archaea. A novel archaea, *Candidatus Methanoflorens stordalenmirensis*, was present at up to 70% relative abundance in the bog, enabling recovery of a population genome. The genome (and associated metaproteome) of 'M. stordalenmirensis' indicates that hydrogenotrophic methane production is its main energy conservation pathway. 'Methanoflorens' may be an indicator species of permafrost thaw, it is globally ubiquitous, and appears a major contributor to global methane production. Our results revealed a distinct difference in the microbial community structure and membership at each site, which can be directly associated with increasing methane emission and thaw state.