



Linking carbon and nitrogen cycling: Environmental transcription of *mmoX*, *pmoA*, and *nifH* by methane oxidizing Proteobacteria in a Sub-Arctic palsa peatland

Susanne Liebner (1) and Mette M. Svenning (2)

(1) Helmholtz Centre Potsdam - German Research Centre for Geosciences (GFZ), Potsdam, Germany (sliebner@gfz-potsdam.de), (2) University of Tromsø, Department of Arctic and Marine Biology, Tromsø, Norway (mette.svenning@uit.no)

Sub-Arctic terrestrial ecosystems are currently affected by climate change which causes degradation of stored organic carbon and emissions of greenhouse gases from microbial processes. Methane oxidizing bacteria (MOB) mitigate methane emissions and perform an important function in the soil-atmosphere interaction. In this study we investigated presence and environmental transcription of functional genes of MOB along the degradation of permafrost in a Sub-Arctic palsa peatland using molecular approaches. The acidic and oligotrophic peatland hosts a small number of active MOB among a seemingly specialized community. The methanotrophic community displayed a broad functional potential by transcribing genes for key enzymes involved in both carbon and nitrogen metabolisms including particulate and soluble methane monooxygenase (pMMO and sMMO) as well as nitrogenase. Transcription of *mmoX* that encodes for a subunit of the sMMO suggests an ecological importance of sMMO with a broad substrate range in this peatland. In situ transcripts of *mmoX* were tracked mainly to Methylocella related Beijerinckiaceae, and to relatives of Methylomonas while Methylocystis constituting the dominant group which utilizes pMMO. These results address interesting questions concerning in-situ substrate preferences of MOB, and the general importance of species that lack a pMMO for mitigating methane emissions. The importance of MOB for the nitrogen budget in this low pH, nitrogen limited habitat was identified by *nifH* transcripts of native methanotrophs. Hence, methane oxidizing Proteobacteria show an extended functional repertoire and importance for the biogeochemical cycling in this dynamic ecosystem of degrading permafrost.