

Project report for a NENUN-funded research stay

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Identification of denitrifiers in Arctic palsa mires and their contribution to N₂O emissions

Background

Nitrous oxide (N₂O) is a major ozone depleting substance in the atmosphere and the third most important greenhouse gas on earth. The global warming potential of N₂O is about 12-fold and 300-fold higher than that of methane (CH₄) and carbon dioxide (CO₂), respectively. Palsa mires are subarctic mire complexes with permanently frozen peat hummocks. The degradation of these permafrost features has been accompanied by the release of CH₄ and CO₂ to the atmosphere, but their importance as sources of N₂O is just emerging (1, 4). It has recently been shown that N₂O emissions from bare peat surfaces in the subarctic European tundra are equivalent to those from tropical and agricultural soils. Bare surfaces lack competition for nitrogen between plants and microbes. Lack of vegetation, low C:N ratios and favourable moisture content were previously identified as key reasons for large N₂O emissions from bare peat surfaces (4). Denitrification is the main source of N₂O in water-logged soils such as peatlands (2, 3). Process rates and the product ratio of N₂O/N₂ are regulated by the denitrifying community and *in situ* soil parameters (e.g., pH, temperature, C:N ratio, substrate availability).

The **major objectives** of the research project were (1) to compare bacterial communities in vegetated and unvegetated surfaces from an Arctic palsa mire, using automated ribosomal intergenic spacer analysis (ARISA), (2) to describe the denitrifying community using functional genes (*napA*, *nirK/nirS*, *nosZ*), and (3) to determine if contrasting denitrifier communities occur in vegetated and unvegetated surfaces, and thereby identify the potential microbial key players of high N₂O emission from the palsa mire

Results and Outlook

- 1) Community-fingerprinting (ARISA) was successfully applied and preliminary data analysis revealed distinct bacterial communities in vegetated and unvegetated palsa mire samples.
- 2) Cloning and sequencing of bacterial SSU rRNA genes from two representative samples (vegetated versus unvegetated) revealed highly diverse communities and members of the *Proteobacteria* being the dominant phylum. Differences in species richness and phylogenetic diversity are currently under analysis.
- 3) Genes involved in nitrate reduction (*napA*) and denitrification (*nirK*, *nirS*) were successfully cloned and sequenced. A major fraction of *nirK* and *napA* sequences was found to be of alphaproteobacterial origin and further sequence analyses are currently carried out to assess differences in the nitrate reducer-/denitrifier communities.
- 4) Together with quantitative data about functional genes abundances, results from the research stay will be used in correlation analyses with soil parameters (pH, carbon and nitrogen content, moisture)

and N₂O emission patterns and eventually lead to a better understanding of the factors regulating N₂O emissions from palsa mires

References

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