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Methanotroph populations and CH₄ oxidation potentials in High Arctic peat are altered by herbivory induced vegetation change

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Abstract:

Methane oxidizing bacteria (methanotrophs) within the genus *Methylobacter* constitute the biological filter for methane (CH₄) in many Arctic soils. Multiple *Methylobacter* strains have been identified in these environments but we seldom know the ecological significance of the different strains. High Arctic peatlands in Svalbard are heavily influenced by herbivory, leading to reduced vascular plant and root biomass. Here we have measured potential CH₄ oxidation rates and identified the active methanotrophs in grazed peat and peat protected from grazing by fencing (exclosures) for 18 years.

Grazed peat sustained a higher water table, higher CH₄ concentrations and lower oxygen (O₂) concentrations than exclosed peat. Correspondingly, the highest CH₄ oxidation potentials were closer to the O₂ rich surface in the grazed than in the protected peat. A comparison of 16S rRNA genes showed that the majority of methanotrophs in both sites belong to the genus *Methylobacter*. Further analyses of pmoA transcripts revealed that several *Methylobacter* OTUs were active in the peat but that different OTUs dominated the grazed peat than the exclosed peat.

We conclude that grazing influences soil conditions, the active CH₄ filter and that different *Methylobacter* populations are responsible for CH₄ oxidation depending on the environmental conditions.

Keywords: methane oxidation, *Methylobacter*, high-Arctic peatland soils, grazing pressure, active MOB community