

Driving the methane cycle – microbial communities and vascular plants in alpine fens

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Methane (CH_4) is an important greenhouse gas, and its atmospheric concentration has risen over the past decades to about 1.8 ppm. Biogenic CH_4 production is mediated by methanogens, a group of microorganisms involved in the decomposition of organic matter under anoxic conditions. A substantial fraction of this CH_4 can be used as energy and carbon source by methanotrophic microorganisms, thereby mitigating CH_4 emissions. An estimated 20-30% of global CH_4 emissions originate from natural wetland areas. In these environments emissions are influenced by various environmental factors, including the presence of vascular plants, as CH_4 can be released into the atmosphere through their aerenchyma. The present study focused on the CH_4 cycle in selected Swiss alpine fens (1900 - 2300 m a.s.l.), combining field measurements with microbiological analyses. The sites were dominated by two different vascular plants, (namely *Carex* spp. and *Eriophorum* spp) and showed variation in CH_4 emissions and pore water concentrations (down to 25 cm below the water table) in relation to location and dominating plant species. Active methanotrophs and methanogens were identified by transcripts of the metabolic genes *pmoA* and *mcrA*, respectively, which were detected throughout the depth profiles independently of O_2 and CH_4 pore water concentrations. The expected separation of oxic methanotrophic and anoxic methanogenic zones could not be clearly demarcated, indicating the presence of microniches. Detailed community profiling of the active methanotrophs and methanogens at different depths is currently being carried out. Our results will further elucidate the processes driving CH_4 emissions in alpine fens and increase our understanding of their contribution to global greenhouse gas emissions.