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Effects of saltwater intrusion on the methane-cycling microbial community of a freshwater rewetted coastal fen

Cordula Gutekunst¹, Anna-K. Jenner², Gerald Jurasinski¹, Michael E. Böttcher^{2,3,4}, Franziska Koebsch¹, Jens Kallmeyer⁵, Klaus-Holger Knorr⁶, Viktoria Unger¹, Sizhong Yang⁵, and Susanne Liebner^{5,7}

¹Institute of Agricultural and Environmental Sciences, University of Rostock, Rostock, Germany (cordula.gutekunst@uni-rostock.de)

²Leibnitz Institute for Baltic Sea Research Warnemünde, Rostock, Germany

³Marine Geochemistry, University of Greifswald, Greifswald, Germany

⁴Department of Maritime Systems, Interdisciplinary Faculty, University of Rostock, Rostock, Germany

⁵GFZ German Research Centre for Geosciences, Helmholtz Centre Potsdam, Potsdam, Germany

⁶Institute of Landscape Ecology, University of Münster, Münster, Germany

⁷Institute of Biochemistry and Biology, University of Potsdam, Potsdam, Germany

Drainage of peatlands for intensive and long-term agricultural use leads to higher mineralization rates of the organic material and thus, increased carbon dioxide (CO₂) emissions. However, when degraded peatlands are rewetted, high methane (CH₄) emissions are frequently observed, that may offset the reductions in CO₂ emissions. The created anaerobic conditions are favorable for methanogenic microorganisms and lead to the production of CH₄. The presence of sulfate in marine waters typically inhibits methanogenesis because methanogens are outcompeted by sulfate reducers. Therefore, the rewetting of coastal peatlands with marine waters is assumed to keep CH₄ emissions low. Flooding of coastal wetlands as a consequence of higher sea levels could strengthen the carbon sink function of these systems if the peatlands are able to grow their surface on par with the sea level. We used the January 2019 storm surge in the southern Baltic Sea to investigate the effects of brackish water intrusion on microbial abundance and community data along with CO₂ and CH₄ exchange data on a rewetted minerotrophic fen. Previous studies showed that despite the proximity to the Baltic Sea, the fen's marine sulfate pool was substantially exhausted, and the microbial community was dominated by acetotrophic methanogens and high CH₄ emission characteristic for freshwater environments. We took parallel soil cores to compare the microbial methane-cycling community to the former freshwater rewetted state from four locations along a brackish water gradient. We used high-throughput sequencing and quantitative polymerase chain reaction (qPCR) on pools of DNA and cDNA targeting total and putatively active bacteria and archaea (16S rRNA gene), methanogens (mcrA), methanotrophs (pmoA) and sulfate-reducing bacteria (dsrB). Greenhouse gas (GHG) fluxes along the salinity transect were measured locally with closed-chambers and in addition on the ecosystem level using the eddy covariance approach. Chamber measurements along the transect imply lower CH₄ emissions at plots with higher salinity post-intrusion. This coincides with a drop in ecosystem CH₄ fluxes and with shifts

from methane-cycling to sulfate-reducing microorganisms. We expect that organisms involved in anaerobic CH₄ oxidation with sulfate as terminal electron acceptor will be more prominent after the saltwater intrusion.

Moreover, the effect of rewetting with saltwater on GHG fluxes and microbial communities in degraded fens will be discussed relative to the effects of freshwater inundation and seasonal droughts which were assessed in the same location before.