

## O45.4

### Development of greenhouse gas emissions and the microbial community of a brackish water rewetted coastal peatland

Cordula Gutekunst<sup>1</sup>, Anna K. Jenner<sup>2</sup>, Daniel Pönisch<sup>2</sup>, Anne Breznikar<sup>2</sup>, Michael E. Böttcher<sup>2,3,1</sup>, Manon Jansen<sup>1</sup>, Jens Kallmeyer<sup>4</sup>, Klaus-Holger Knorr<sup>5</sup>, Susanne Liebner<sup>4</sup>, Gerald Jurasinski<sup>1</sup>

<sup>1</sup>University of Rostock, Germany. <sup>2</sup>Leibniz Institute for Baltic Sea Research (IOW), Germany. <sup>3</sup>University of Greifswald, Germany. <sup>4</sup>GFZ German Research Centre for Geosciences, Germany. <sup>5</sup>University of Münster, Germany

#### Abstract

More than 5 % of global greenhouse gas (GHG) emissions derive from drained peatlands. However, when degraded peatlands are rewetted, high methane (CH<sub>4</sub>) emissions are frequently observed, offsetting reductions in carbon dioxide (CO<sub>2</sub>) emissions. The promotion of microorganisms that oxidize CH<sub>4</sub> (methanotrophs) or sulfate-reducing bacteria that outcompete methane-producing archaea (methanogens) can lower CH<sub>4</sub> emissions. Therefore, rewetting coastal peatlands with sulfate-containing brackish water possibly keeps methane production at a low level. We measured CO<sub>2</sub> and CH<sub>4</sub> fluxes with transparent and opaque manual-closed chambers before and after brackish water rewetting of a coastal fen, which was formerly used as agricultural grassland. We took soil cores for microbial analysis at seven stations along a water-level gradient before and after rewetting and used quantitative polymerase chain reaction (qPCR) on 16S *rRNA*, *mcrA*, *pmoA* and *dsrB* genes to quantify the abundances of methanogens, methanotrophs and sulfate-reducing bacteria. First results imply lower amplitudes of CO<sub>2</sub> fluxes and remaining low CH<sub>4</sub> emissions even after significant increase of water levels. Once GHG fluxes are modelled to provide annual budgets and microorganisms are quantified, we will determine if the observed patterns are consistent over time and whether they can be explained by the microbial community composition. We expect an increase of methanogenic and methanotrophic archaea under newly created anaerobic conditions in addition to an increase in the amount of sulfate-reducing bacteria in previously dry sampling plots. The microbial community at sampling locations that were wet before (e.g. inside or close to a drainage ditch) should shift from rather methanogens-dominated towards organisms more associated with sulfur cycling. Overall, after rewetting, microbial functional gene abundances should show higher homogeneity along the sampling transect due to more equally distributed water tables compared to the drained state. With this study, we test the hypothesis that coastal peatland rewetting with brackish waters will reduce potential methane emissions.

#### Keywords

Coastal peatland restoration, Carbon storage, Greenhouse gas emissions, Microbial communities