Project acronym: DIVERSE

Project title: Microbial Genomics and Functional Diversity in Wetlands

Project leader: Joel White, Lund University, Sweden

Discipline: Earth Sciences & Environment: Ecosystems & Biodiversity

Station(s): Zackenberg Research Station (Greenland/Denmark)

Natural controllers of the carbon cycle in ecosystems are, e.g., the rate of CO2 uptake through primary production and the metabolic rate of heterotrophic microorganisms (Rh). Low temperatures and anoxic conditions limit Rh and C-sequestration often exceeds Rh in wetlands making them sinks for CO2 that is stored as peat. Anoxia often leads to microbial production of CH4 and wetlands are a considerable source of this greenhouse gas to the atmosphere.

We hypothesize that microbial metabolism and functional diversity play a key role in controlling the spatial variability in CH4 emission and is closely linked to the community composition of vascular plants. Where certain sedges may primarily fuel the metabolic activity of methanogens and result in higher CH4 while others may fuel methanotrophy and CH4 oxidation to CO2, due to their capacity to transport O2 to their root zone.

We will combine in-situ measurements of, e.g., CH4 and CO2 with capture metatranscriptomics, to target key genes related to microbial metabolism in complex metagenomes. Through this approach we will be able to determine the taxa of microorganism and identify the functional diversity of genes that regulate CH4 production and consumption and their level of gene expression. To determine the importance on a larger scale we aim to include three wetlands from temperate to arctic (Zackenberg), chosen explicitly to address current knowledge gaps. We believe that the results from this study will offer insight into how the functioning of wetland ecosystems may respond to future environmental change.