

Fungal, bacterial, and archaeal communities mediating C cycling and trace gas flux in peatland ecosystems subject to climate change

Erik Lilleskov, PI

Peatland ecosystems represent 3-5% of the land surface, but sequester 12-30% of soil organic carbon (C). However, this very large pool of C is vulnerable to oxidation as a function of climate change. Our goal is two-fold: to create a resource for understanding the large-scale patterns of microbial (here defined as bacterial, archaeal, and fungal) community structure and function in peatland ecosystems, and to understand how these communities regulate C cycling in response to environmental change.

Specifically, we are planning three activities:

First, we plan to carry out extensive microbial community profiling in a network of natural peatland ecosystems spanning large-scale climate gradients, as well as manipulated field and lab systems subject to climate change related treatments. The sites targeted are all subjects of existing research activities that include key C cycling measurements, so that C cycling and microbial community data can be directly linked.

Second, we will explore the drivers of microbial community composition via metagenomic and metatranscriptomic analysis of samples from a controlled experimental system (the PEATcosm Experiment) enabling independent examination of the effects of vegetation and water table changes. One of the key open questions in understanding peatland C cycles is the role of plants in mediating microbial processing of soil C. We hypothesize that peatland vegetation, including Ericaceae (heather family) and sedges, are key ecosystem engineers that influence microbial community structure both via symbiotic associations that have strong extracellular enzyme activity (Ericaceae; heath plants), and by transport of oxygen and labile C into the peat (Cyperaceae; sedges). Sedge roots also act as conduits for methane efflux. Thus Ericaceae and non-mycorrhizal sedge species are expected to generate fundamentally different carbon cycles and microbial communities in their rhizospheres, and to interact in fundamentally different ways with changing redox profiles. Therefore we will examine metagenomes and metatranscriptomes of rhizosphere communities of sedges and Ericaceae in shallower, more oxic and deeper less oxic conditions.

Third, we will investigate particular microbial guilds of interest, such as methanogens and sulfate reducers, via single cell sequencing. Targets will be chosen based on ribosomal tag and metagenome/metatranscriptome results, and will enable more in-depth examination of these critical players as well as an improved reference set for interpreting metatranscriptome data.