

Insights into *Sphagnum* physiology and the associated microbiome at SPRUCE

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The SPRUCE experiment is a large-scale peatland manipulation with multiple levels of warming at ambient or elevated CO₂ in a *Picea mariana*–*Sphagnum* peat bog in northern Minnesota. *Sphagnum* species are a dominant component of the SPRUCE community profile and boreal peatlands in general. At the SPRUCE site, The *Sphagnum* dominated moss layer is estimated to contribute to approximately 47 – 49% of net primary production (NPP) and is considered a critical component for maintaining low bog pH and N inputs through its associated microbiome. We installed eight clear-top automated gas exchange chambers (Li-COR 8100s) in hollows to assess *Sphagnum* net ecosystem exchange of C (NEE). Daily integrated values of chambers showed a slight trend in net CO₂ uptake in the beginning of the season that quickly transitions to a peak in CO₂ release during the middle of the season and gradually increases to near neutral or compensation values from September to November. Both gross primary productivity and peat/*Sphagnum* respiration peaked in mid-August and followed a near asymmetric distribution with the time from spring thaw to peak values. Insight from modeling activities suggests that considerable nitrogen (N) must be fixed and transferred to *Sphagnum* plants to support the observed production rates. To gain insight into the composition of the *Sphagnum* associated microbiome and possible role in N fixation, 16S rRNA profiling was performed within the experimental enclosures of the warming treatments. We found all samples to be dominated by *Alphaproteobacteria* (45-51%) followed by *Acidobacteria* (11-16%) and *Gammaproteobacteria* (8-9%). The functional member abundance varied by warming treatment: diazotroph abundance decreased with increased temperature (6% in ambient control, 3% in ambient +6C) while methanotroph abundance increased with temperature (0.14% in ambient control, 1.3% in ambient +6C respectively). The consequence of this functional community member shift is not clear and merits further exploration. A current collaboration with the DOE Joint Genome Institute has now expanded the genomic resources for this project by providing two draft genomes for *S. fallax* and *S. magellanicum* and the resequencing of a 200 individual *S. fallax* pedigree. Together with isolated fungal and bacterial strains, this represents a tremendous resource to the biological community interested in plant – microbe interactions, evolutionary and ecological genomics, and peatland ecology.