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Genome-resolved Metagenomics Enables Fine-Resolution Assessments of SPRUCE Peatland Microbial Communities

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Through both the direct and indirect effects of perturbation, the SPRUCE experiment is expected to lead to various alterations in peatland microbial communities and their biogeochemical processes. However, assessments of belowground communities are often challenging due to their high compositional diversity and complex functional attributes. In this effort, peat communities representing 2015 and 2016 sample collections (approx. 1 and 2 years after onset of warming respectively) were assessed with shotgun metagenomic sequencing resulting in ~1 Tbp of DNA sequence information. Through a combination of sequence assembly and binning techniques, a large proportion of the microbial community was recovered as metagenome-assembled genomes (MAGs). Our findings demonstrate that ~400 unique microbial genomes represent 70-90% of all DNA sequences recovered from intermediate and deep peat layers, and that individual MAGs are shown to exhibit strong depth-dependent abundance and gene content profiles, consistent with past studies and known physical and chemical gradients in the peat profiles. While 2015-2016 samples indicate little effect of warming on whole communities or MAG-level abundances, recent changes observed for various ecosystem properties (e.g., increased CH_4 flux, increased resin-available nutrients, and changes in plant productivity) suggest that the recently-collected microbial samples (e.g., 2017 and 2018, for which sequencing is pending) are likely to show response to experimental warming. We expect that analyses involving genome-resolved communities will enable a powerful evaluation of treatment effects on microbial composition and resulting functions. Future efforts will be able to leverage these microbial community data to track changes in MAG abundance with treatments and also in collaboration with other SPRUCE site investigators employing other ‘omics methods and detailed biochemical analyses in order to model microbial physiological responses in situ.