

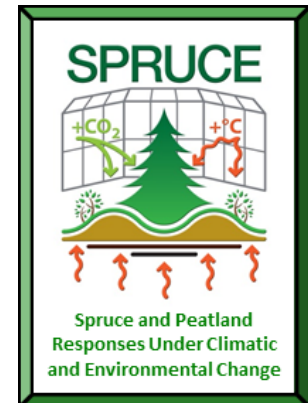
SPRUCE microbiology results -- links to microbial metagenomes

SPRUCE Publication:

Microbial Metabolic Potential for Carbon Degradation and Nutrient (Nitrogen and Phosphorus) Acquisition in an Ombrotrophic Peatland

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Appl. Environ. Microbiol. 2014, 80(11):3531. DOI: [10.1128/AEM.00206-14](https://doi.org/10.1128/AEM.00206-14).
Published Ahead of Print 28 March 2014.



Abstract:

This study integrated metagenomic and nuclear magnetic resonance (NMR) spectroscopic approaches to investigate microbial metabolic potential for organic matter decomposition and nitrogen (N) and phosphorus (P) acquisition in soils of an ombrotrophic peatland in the Marcell Experimental Forest (MEF), Minnesota, USA. This analysis revealed vertical stratification in key enzymatic pathways and taxa containing these pathways. Metagenomic analyses revealed that genes encoding laccases and dioxygenases, involved in aromatic compound degradation, declined in relative abundance with depth, while the relative abundance of genes encoding metabolism of amino sugars and all four saccharide groups increased with depth in parallel with a 50% reduction in carbohydrate content. Most Cu-oxidases were closely related to genes from *Proteobacteria* and *Acidobacteria*, and type 4 laccase-like Cu-oxidase genes were >8 times more abundant than type 3 genes, suggesting an important and overlooked role for type 4 Cu-oxidase in phenolic compound degradation. Genes associated with sulfate reduction and methanogenesis were the most abundant anaerobic respiration genes in these systems, with low levels of detection observed for genes of denitrification and Fe(III) reduction. Fermentation genes increased in relative abundance with depth and were largely affiliated with *Syntrophobacter*. *Methylocystaceae*-like small-subunit (SSU) rRNA genes, *pmoA*, and *mmoX* genes were more abundant among methanotrophs. Genes encoding N₂ fixation, P uptake, and P regulons were significantly enriched in the surface peat and in comparison to other ecosystems, indicating N and P limitation. Persistence of inorganic orthophosphate throughout the peat profile in this P-limiting environment indicates that P may be bound to recalcitrant organic compounds, thus limiting P bioavailability in the subsurface. Comparative metagenomic analysis revealed a high metabolic potential for P transport and starvation, N₂ fixation, and oligosaccharide degradation at MEF relative to other wetland and soil environments, consistent with the nutrient-poor and carbohydrate-rich conditions found in this *Sphagnum*-dominated boreal peatland.

Excerpt:

Properties of metagenomes. A total of 6 metagenomic libraries were obtained from the 3 distinct vertical zones (acrotelm, mesotelm, and catotelm; see reference 27) observed in the peat column at the Marcell Experimental Forest (MEF) and documented in companion studies (Table 1) (27, 38). The average coverage of each sequenced metagenome increased with depth and ranged from 42% to 86% (Table 1). The three zones differed in physical (e.g., bulk density) and chemical (e.g., organic matter composition) properties. A neighbor-network analysis showed that microbial community composition and functional potential had more pronounced change across depths than over space in either bog or fen sites (see Fig. S2 in the supplemental material). Thus, sequences from two surface bog metagenomes were combined into one data set for downstream analyses, and the same procedure was used for the two surface metagenomes from the fen sites.

After pooling, Illumina sequencing resulted in 4.6 to 10.4 Gb per library. On average, 33% and 50% of reads were annotated to known and unknown proteins, respectively (Table 1). Generally, our metagenomic results were

reproducible and consistent between samples from the same depth and site. For example, 76% of the total compared genes and pathways listed in [Table 2](#) showed less than 30% variation in relative abundance in pairwise comparisons among 4 surface metagenomes, relative to, on average, 77% and 88% variation from 0-cm to 25-cm and from 0-cm to 75-cm metagenomes, respectively. High reproducibility of metagenomic data has also been reported in other studies ([39](#), [40](#)), ensuring that the results reported here are robust and likely to be characteristic of peatland microbial communities.

Acknowledgments:

This work was supported by the Office of Biological and Environmental Research, Terrestrial Ecosystem Science Program, under U.S. DOE contract number DE-SC0007144, and the U.S. National Science Foundation (NSF-EAR-0628349).

Metagenomics Results:

Access SPRUCE microbial community metagenome:

National Center for Biotechnology Information (NCBI) BioProject Archive.

<http://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA221719>

[Note that there is not a SPRUCE data citation for the community metagenome.]

Chemical Content and Enzyme Assay Results:

Coming Soon. Likely in the typical data product format.