

FINAL TECHNICAL REPORT

AWARD # DE-SC0007144

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**TITLE: THE RESPONSE OF SOIL CARBON STORAGE AND MICROBially MEDIATED CARBON
TURNOVER TO SIMULATED CLIMATIC DISTURBANCE IN A NORTHERN PEATLAND FOREST:
REVISITING THE CONCEPT OF SOIL ORGANIC MATTER RECALCITRANCE**

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I. Executive Summary

The goal of this project was to investigate changes in the structure of dissolved and solid phase organic matter, the production of CO₂ and CH₄, and the composition of decomposer microbial communities in response to the climatic forcing of environmental processes that determine the balance between carbon gas production versus storage and sequestration in peatlands. Cutting-edge analytical chemistry and next generation sequencing of microbial genes were been applied to habitats at the Marcell Experimental Forest (MEF), where the US DOE's Oak Ridge National Laboratory and the USDA Forest Service are constructing a large-scale ecosystem study entitled, "Spruce and Peatland Responses Under Climatic and Environmental Change"(SPRUCES). Our study represented a comprehensive characterization of the sources, transformation, and decomposition of organic matter in the S1 bog at MEF. Multiple lines of evidence point to distinct, vertical zones of organic matter transformation: 1) the acrotelm consisting of living mosses, root material, and newly formed litter (0-30 cm), 2) the mesotelm, a mid-depth transition zone (30-75 cm) characterized by labile organic C compounds and intense decomposition, and 3) the underlying catotelm (below 75cm) characterized by refractory organic compounds as well as relatively low decomposition rates. These zones are in part defined by physical changes in hydraulic conductivity and water table depth. O-alkyl-C, which represents the carbohydrate fraction in the peat, was shown to be an excellent proxy for soil decomposition rates. The carbon cycle in deep peat was shown to be fueled by modern carbon sources further indicating that hydrology and surface vegetation play a role in belowground carbon cycling. We provide the first metagenomic study of an ombrotrophic peat bog, with novel insights into microbial specialization and functions in this unique terrestrial ecosystem. Vertical structuring of microbial communities closely paralleled the chemical evolution of peat, with large shifts in microbial populations occurring in the biogeochemical hotspot, the mesotelm, where the highest rates of decomposition were detected. Stable isotope geochemistry and potential rates of methane production paralleled vertical changes in methanogen community composition to indicate a predominance of acetoclastic methanogenesis mediated by the Methanosarcinales in the mesotelm, while hydrogen-utilizing methanogens dominated in the deeper catotelm. Evidence pointed to the availability of phosphorus as well as nitrogen limiting the microbially-mediated turnover of organic carbon at MEF. Prior to initiation of the experimental treatments, our study

provided key baseline data for the SPRUCE site on the vertical stratification of peat decomposition, key enzymatic pathways, and microbial taxa containing these pathways.

The sensitivity of soil carbon turnover to climate change is strongly linked to recalcitrant carbon stocks and the temperature sensitivity of decomposition is thought to increase with increasing molecular complexity of carbon substrates. This project delivered results on how climate change perturbations impact the microbially-mediated turnover of recalcitrant organic matter in peatland forest soils, both under controlled conditions in the laboratory and at the ecosystem-scale in the field. This project revisited the concept of “recalcitrance” in the regulation of soil carbon turnover using a combination of natural abundance radiocarbon and optical spectroscopic measurements on bulk DOM, and high resolution molecular characterization of DOM. The project elucidated how organic matter reactivity and decomposition will respond to climate change in a both a qualitative (organic matter lability) and quantitative (increased rates) manner. An Aromaticity Index was developed to represent a more direct and accurate parameter for modeling of DOM reactivity in peatlands. The abundance and community composition of soil microorganisms that mediate C cycling were interrogated with depth in the peat, with season, and in manipulated climate enclosures at unprecedented resolution. Therefore this project delivered strategic new insights on the functioning of peatland ecosystems that collectively store approximately one-third of the world's soil carbon. Furthermore, results from the detailed characterization of DOM lability and microbial community structure/ function will be employed to further develop biogeochemical models to include microbial respiration pathways as well as to track carbon flow with a term that incorporates relative reactivity based on aromaticity index. As it stands now, detailed soil organic matter structure and microbial parameters are not included in Earth system models.

II. Research Highlights

Goal: The overall goal of this project was to investigate the lability of soil organic matter and the composition of decomposer microbial communities in response to the climatic forcing of environmental processes that determine carbon storage and sequestration in peatlands.

This project was conducted at the Marcell Experimental Forest (MEF) where ORNL has established a Climate Change Response Scientific Focus Area known as Spruce and Peatland Response Under Climatic and Environmental Change (SPRUCE). Working hypotheses driving the proposed research were: 1) Soil environment (temperature, moisture content, O₂, pH, plant community composition and physiology) determines the functional diversity of heterotrophic bacteria and saprobic microfungi which in turn controls or regulates soil carbon storage, 2) Refractory or recalcitrant polyphenolic compounds (plant residues) such as lignin act as a “bottleneck” to organic matter decomposition in peatland forest soils because of their toxicity to microorganisms, 3) Dissolved organic matter (DOM) is the primary intermediate pool regulating carbon turnover in peatland soils, 4) The rate limiting step in peatland soil organic matter decomposition is the degradation of aromatic polymers that is catalyzed by a range of extracellular enzymes produced by a broad diversity of prokaryotic and eukaryotic (fungi) microorganisms, and 5) The presence and relative abundance of condensed aromatic and phenol-type compounds is a molecular signal of DOM lability, and that signal can be quantified using an Aromaticity Index (AI).

To address these hypotheses, our objectives were to:

1) conduct a comprehensive interrogation of organic matter recalcitrance and the functional diversity of keystone microbial guilds that are likely to control organic matter decomposition at the ecosystem scale in a boreal peatland forest.

- 2) validate the molecular-based Aromaticity Index (AI) as an indicator of DOM recalcitrance.
- 3) directly link the phylogenetic identity and metabolic function of keystone microbial guilds that mediate soil carbon turnover in response to perturbations in climate change variables (temperature, redox, pH) under controlled conditions in the laboratory.
- 4) determine the response of DOM recalcitrance, decomposition, and the functional diversity of keystone microbial decomposers to climate change manipulation in the field at the ecosystem scale.

The major findings/ advances of this project were:

A. Molecular characterization of organic matter reactivity and microbial community dynamics.

- A combination of advanced analytical chemistry and microbiology approaches revealed that organic matter reactivity and microbial community dynamics were closely coupled in an extensive field dataset compiled across seasons in transects at bog and fen sites established for the SPRUCE program, Marcell Experimental Forest (MEF).
- Strong vertical stratification was observed in organic matter composition, microbial community composition, respiration rates, and decomposition pathways, whereas smaller variations were observed between seasons and sites (Tfaily et al., 2014; Lin et al., 2014a&b).
- We developed a high throughput gene sequencing pipeline to interrogate peat microbial communities at an unprecedented whole ecosystem scale. All domains of microbial life (Bacteria, Archaea, Fungi/ Eukaryotes) were characterized using 454 pyrosequencing and Illumina platforms, with the dataset encompassing hundreds of field samples, > 1600 SSU rRNA gene sequences or > 1000 ITS sequences per sample (Lin et al., 2014a).
- Chemical and spectroscopic analyses of soil organic matter throughout the MEF identified three distinct zones, each with unique properties, within the peat column: (1) a poorly decomposed surface portion; (2) a more decomposed middle section, and (3) a homogeneous lower section that exhibited little change with depth (Tfaily et al., 2014).
- A decline in the aromaticity of pore water dissolved organic matter (DOM) was accompanied by an increase in microbially-produced DOM, consistent with the radiocarbon data. Solid phase peat, on the other hand, became more humified and highly aromatic with depth (Tfaily et al., 2014).
- Bacteria were nearly always more abundant than fungi in peat soils, as determined by quantitative PCR, and incubation experiments point to prokaryotic dominance over the carbon cycle, even in surface peats (Lin et al., 2014a).
- Microbial community composition is dominated by the Acidobacteria, Proteobacteria, and Verrucomicrobia. Multivariate modeling showed that their spatial turnover is governed by vegetation cover along with the quantity and quality of DOM (Lin et al., 2014a).
- Stable isotope geochemistry parallels with vertical changes in methanogen community composition to reveal a mid-depth maximum in acetoclastic methanogenesis, while hydrogenotrophic methanogenesis appears to dominate deeper peat layers (Lin et al., 2014a).

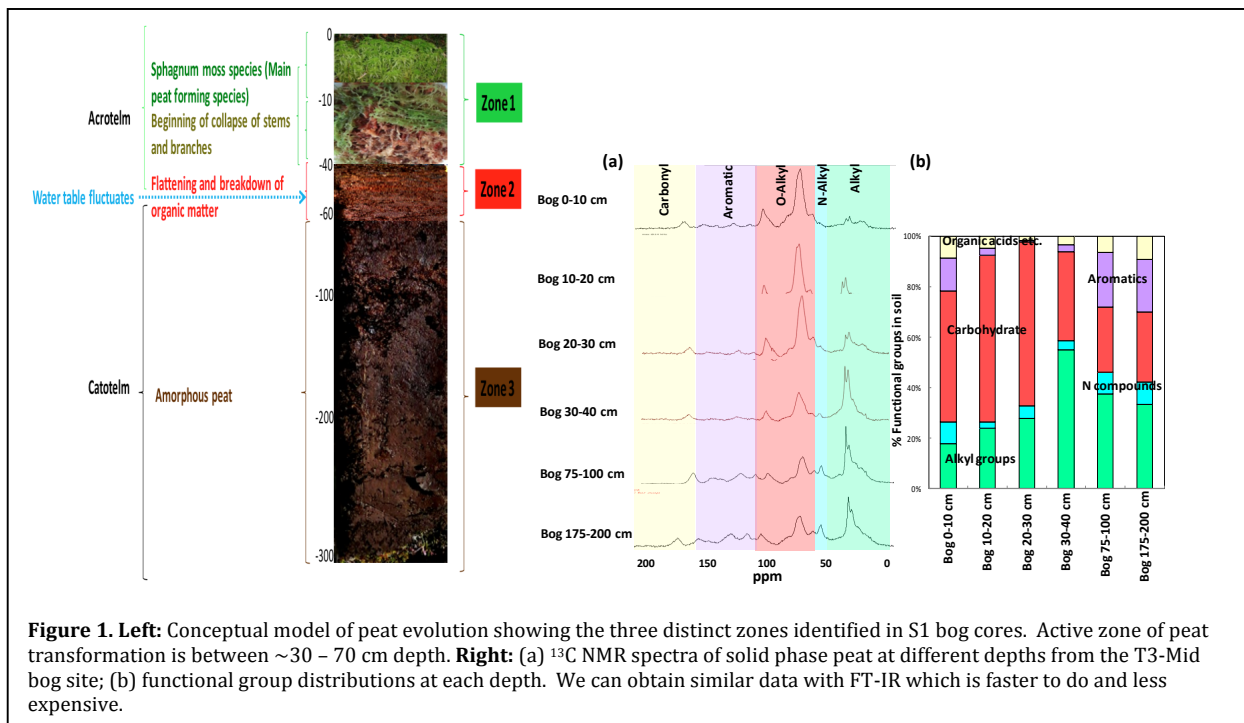
- Isotope mass balance indicates that processes other than methanogenesis (fermentation, anaerobic respiration) predominate in the deep peat leading to dominance of CO₂ production at depth.
- Radiocarbon signatures of microbial respiration products in peat porewaters more closely resemble that of dissolved organic matter (DOM) rather than solid peat, indicating that carbon from recent photosynthesis is fueling the majority of the decomposition, even in the subsurface.
- A combination of geochemical and microbiological evidence indicated P limitation of microbial communities in the subsurface peat. A decline in the abundance of organic orthophosphate monoesters was accompanied by an increase in phosphatase enzymes that hydrolyze orthophosphate monoesters to orthophosphate (Lin et al., 2014b).
- The Crenarchaeota, Archaea that are not known to produce methane, are suggested to play a critical role in the carbon cycle of deeper peat layers as they accounted for up to 60% of total microbial community (Lin et al., 2015).

B. Metabolic potential of peatland microbial communities.

- Rates of CO₂ and CH₄ production were quantified with depth in the peat column in samples collected from bog and fen sites of the MEF. Rates were comparable to those measured at other boreal peatland sites. The highest methane production rates were observed in the mid-depth reactive zone, in agreement with vertical stratification of organic compounds observed with analytical chemistry (Tfaily et al., 2014).
- Extensive modification, standardization, and calibration was performed on phenol oxidase and peroxidase enzyme assays. Substrates used for these assays were observed to be especially sensitive to the in situ pH of peat soil. Therefore, we have chosen the substrate, ABTS, as the appropriate substrate for the pH range observed at MEF.
- A large number of pure cultures was isolated with peat extract as the sole carbon and energy source under aerobic conditions. Isolates will serve as model organisms used to investigate the controls of oxidative enzyme activity.
- The metabolic potential of peat microorganisms was investigated using a metagenomic approach. Four shotgun metagenome libraries were generated for bog and fen sites using an Illumina platform, resulting in an average of 10 billion base-pairs of sequences per library (Lin et al., 2014b).
- Genes for the metabolism of amino acids, fatty acids, ABC transporters, and phenolic compound degradation were most abundant near the surface and decreased with depth, suggesting active degradation and utilization of organic matter near the surface peat. In contrast, genes for the metabolism of carbohydrates and methane production increased with depth (Lin et al., 2014b).
- The deep peat harbored a higher proportion of genes encoding debranching enzymes, endohemicellulases, and oligosaccharide degrading enzymes, suggesting microbes in deep peat have high potential for the degradation of these compound classes (Lin et al., 2014b).
- Enzymes for the degradation of cellulose, xylan, chitin, protein, and organic phosphate consistently showed decreasing activity with peat depth, with no apparent seasonal trends.
- The temperature response of polymer-degrading enzymes was determined in a specially designed temperature gradient block. Temperature response, calculated

as activation energy, was similar between seasons with no measurable difference between winter and summer. An increase in activation energy was observed with peat depth, indicating that enzymes of the deep peat may more responsive to increases in temperature,

- Ultra-deep amplicon sequencing of laccase genes revealed that sequences affiliated with Proteobacteria predominate in MEF peats, challenging the previous view that the laccase sequences of Acidobacteria are most important in acidic soil environments (Lin et al., 2014b).

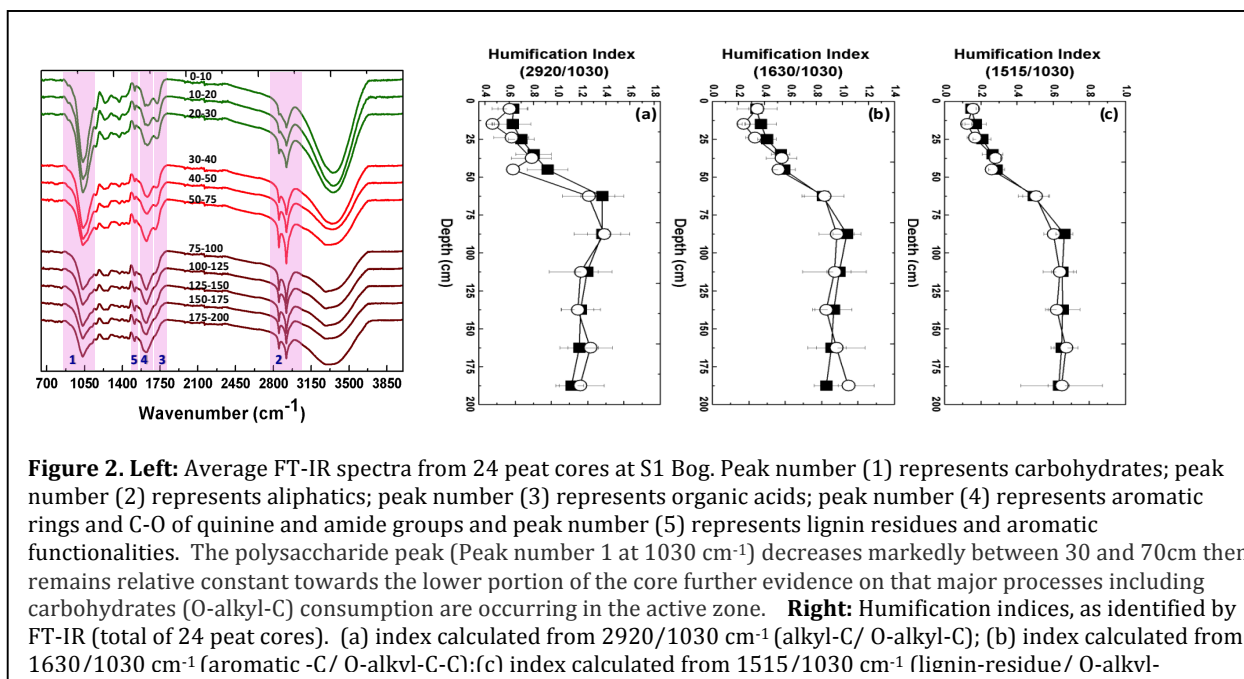


C. RESEARCH PROGRESS. A total of 12 personnel from GT, FSU, ORNL have participated in this project. A total of 6 publications and 40 seminars/ meeting presentations were completed from 2011 to 2015, and 3 publications are in preparation.

A combination of advanced analytical chemistry and microbiology approaches revealed that organic matter reactivity and microbial community dynamics are closely coupled in an extensive field dataset compiled across 2 seasons and 3 transects in the S1 bog. Multiple independent lines of evidence lead to the characterization of three distinct, vertical zones of organic matter transformation within the peat column: 1.) the acrotelm that consists of living mosses and their newly formed litter (0-30 cm), 2.) a mid-depth transition zone (30-75cm) characterized by labile organic C compounds and intense decomposition, and 3.) an underlying zone (below 75cm), the catotelm, characterized by refractory organic compounds as well as relatively low decomposition rates (Fig. 1; Tfaily et al., 2014).

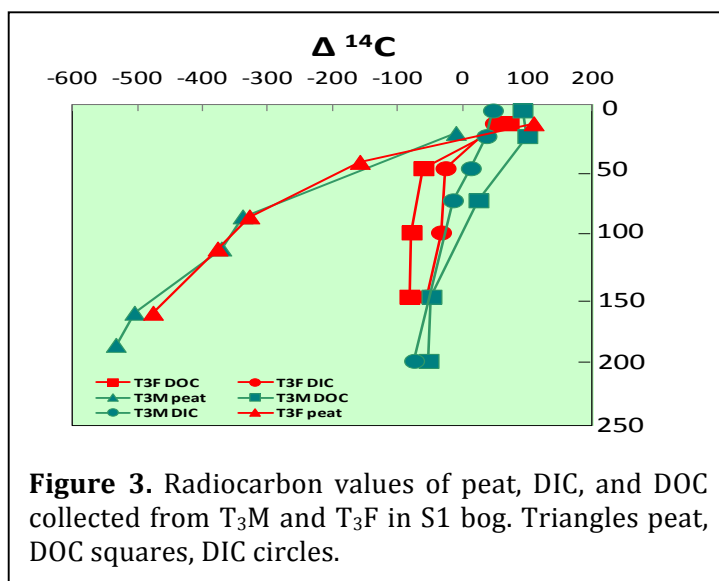
The mid-depth highly reactive zone was identified using a combination of bulk density, rate measurements, microbial investigations, and changes in organic matter composition determined by a variety of techniques including solid state ^{13}C NMR (Fig. 2) and FT-IR spectroscopy (Fig. 3). Soil organic matter (SOM) quality can be defined by spectroscopic

parameters provided by FT-IR and NMR that identify the nature and relative proportions of the functional groups present in organic phases. In particular, the relative abundance of O-alkyl-C carbon (polysaccharides) was as a strong predictor of SOM decomposition,



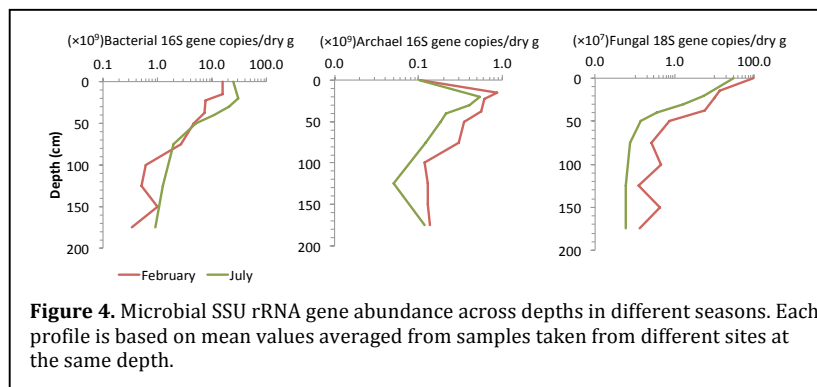
and methane production rates, in agreement with previous work (Tfaily et al., 2014). Mineralization of organic matter was quantified by gas production in a series of microcosm incubations (data not shown). The highest methane (CH_4) production rates and the highest ratio of CH_4/CO_2 production were observed in the mid-depth reactive zone, in agreement with corresponding shifts in organic compounds described in the paragraph above. Furthermore, the spectroscopic-based data on functional group distributions can be reduced to a series of "humification indices" that correlate strongly with peat lability. Moreover, our work has validated the utility of FT-IR (Fig. 2) as a high-throughput, high-resolution surrogate for the conventionally accepted but instrument-intensive ^{13}C NMR technique and allows estimates of decomposition potential over much wider areas.

Recent radiocarbon ($\Delta^{14}\text{C}\%$) measurements of the solid phase peat, dissolved inorganic carbon (DIC) and dissolved organic carbon (DOC) at two sites within the S1 bog indicate that the majority of the microbial respiration occurring in the deeper peat is currently driven by surface photosynthetic production rather than peat decomposition (Fig. 3). Negative values



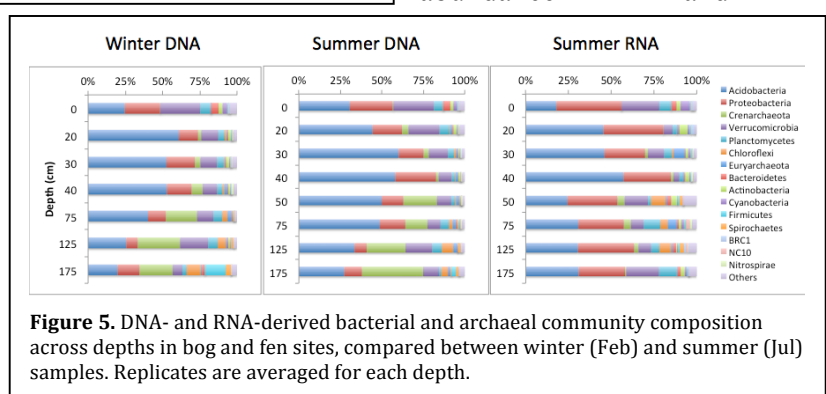
indicate older material at depth (triangles) where the peat approaches 6000 years old (-600‰). The DOC (squares), which represents the remnants of plant and microbial biomass, varies from 40 to 100‰ at the surface, reflecting the values of recent photosynthetic production influenced by bomb testing in the 1960-70s. DOC is thus modern relative to the solid peat to a depth of 2 meters, indicating that even at depth, DOC input is dominated by surface production rather than from the decomposition of peat at a particular horizon. DIC represents the signature of microbial respiration products. The $\Delta^{14}\text{C}$ values of DIC, representing the substrates utilized for microbial respiration, are more similar to the modern DOC values than they are to the peat, further reinforcing the relative stability of the catotelm peat under current climatic conditions. Similar findings have been reported for other peatlands. However, we hypothesize that the heating and enhanced CO_2 treatments will foster the decomposition of the catotelm peat, with microbial respiration products and DOC shifting to older carbon with more depleted ^{14}C values.

Microbial community dynamics showed a strong vertical stratification that paralleled organic matter composition. By comparison, lateral spatial and temporal variation in the organic geochemistry and microbiology were minimal. Microbial communities were characterized using a next generation sequencing platform (500 field samples, > 1600



SSU rRNA gene sequences or > 1000 ITS sequences per sample). Surface peat (0-20 cm depth), characterized by high C:N ratios, high enzyme activities, and low humification, harbored the highest abundance and

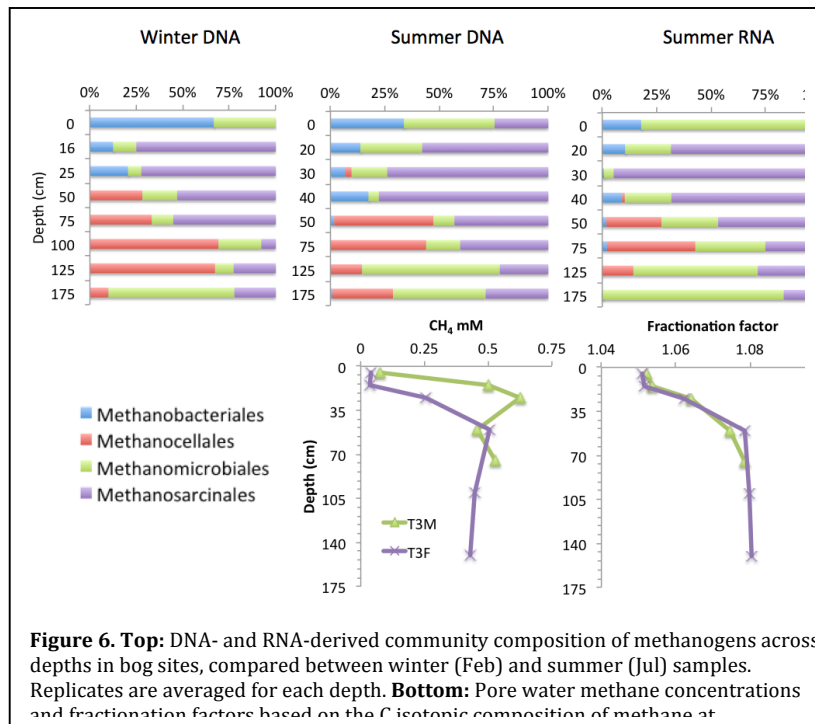
diversity of all forms of microbial life (Bacteria, Archaea, Fungi; Fig's 4, 5). Below the surface, microbial communities drastically differ in peatland soils in comparison to mineral soils of forests or grasslands (Lin et al., 2014a). Oxygen is depleted close to the water table, and prokaryotes appear to predominate over the



biomass and decomposition activity in peatlands. Archaea especially increase in relative abundance with depth, comprising up to 60 % of the microbial community in the deep peat below 75 cm depth. The Crenarchaeota, Archaea that are not known to produce methane, are suggested to play a critical role in the carbon cycle of deeper peat layers. This is corroborated by evidence from a C isotope mass balance, which indicates that

processes other than methanogenesis (fermentation, anaerobic respiration) predominate in the deep peat leading to dominance of CO₂ production at depth (data not shown).

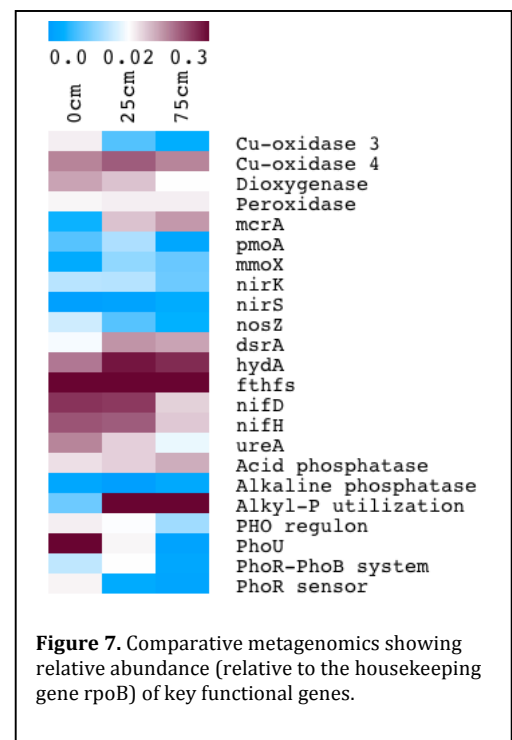
Bacterial communities were co-dominated by Acidobacteria (blue), Proteobacteria (red), and Verrucomicrobia (purple; Fig. 5). A substantial number of carbohydrate-



utilizing members of the Acidobacteria have been cultivated from acidic peatlands and many of these are well represented in our sequence dataset, particularly in the transition zone from 20 - 40 cm. These data correlate nicely with geochemical parameters such as humification index that suggest loss of carbohydrates from the solid phase in this zone. Fungal community composition is characterized by an increasing proportion of

yeasts and a reduction of the white-rot fungi observed with peat depth. At 30-75 cm depth, we observed a peak in the abundance of Syntrophobacteraceae that corresponded to the highest concentration of organic acids presumably released from peat degradation. The Syntrophobacteraceae are known for their fermentative C metabolism that supplies methanogenesis. Stable isotope geochemistry parallels with vertical changes in methanogen community composition to reveal a mid-depth maximum in acetate-utilizing methanogens (Methanosarcinales in purple), while hydrogen-utilizing methanogens (all other groups shown) appear to dominate the deeper peat layers (Fig. 6). An increase in fractionation factor points to the increasing significance of hydrogenotrophic methanogenesis with depth.

Although metabolic potential can be inferred from the microbial groups detected, DNA-based molecular approaches do not provide information on microbial function. Ribosome content is proportional to cellular metabolism and thus rRNA analysis can be used as a



proxy for the “metabolically-active” microbial community members. RNA-derived sequence libraries supported the conclusion that the Acidobacteria and Proteobacteria are active throughout the peat column and acetate-utilizing methanogens dominate the active community in the mid-depth zone where the highest rates of methane production are observed (Fig’s 5, 6).

The metabolic potential of peat microorganisms was further investigated using a metagenomic approach (Fig. 7). Three shotgun metagenome libraries were generated for the S1 bog site using an Illumina platform, resulting in an average of 10 billion base-pairs of sequences per library. Our analysis revealed vertical stratification in key enzymatic pathways, thereby supporting our conceptual model of organic matter decomposition in the peat column (Lin et al., 2014b). Short-read sequences assigned to phenol oxidases and central carbohydrate metabolism declined in relative abundance with depth, while metabolism of amino sugars and all four saccharide groups became increasingly important with depth. Most Cu-oxidases (associated with degradation of polyphenolic compounds) were hosted in Proteobacteria and Acidobacteria, and surprisingly, the type 4 laccase-like Cu-oxidase gene was >8 times more abundant than type 3, indicating an important but overlooked role for type 4 Cu-oxidase in phenolic compound degradation. Anaerobic respiration was dominated by sulfate reduction (dsr), with low detection of denitrification (nir, nos) and Fe(III) reduction genes. Both methanogenesis (mcrA) and fermentation (fthfs) genes increased with depth and were mainly affiliated with hydrogenotrophic methanogens and Syntrophobacter, respectively. Non-copper-dependent type II methanotrophs – Methylocystaceae outcompeted other methanotrophs in this nutrient-poor environment (pmoA, mmoX). Genes encoding N fixation (nif), P uptake (pho), and P regulons were significantly enriched in the surface peat and in comparison to other ecosystems, indicating N and P limitation in our ecosystem. ³¹P-NMR results supported the microbiological evidence for P limitation, as a decline in the abundance of organic orthophosphate monoesters was accompanied by an increase in phosphatase enzymes that hydrolyze orthophosphate monoesters to orthophosphate. The comparative metagenomic analysis revealed microbial functional specialization in this ombrotrophic peatland, and potential mechanisms controlling microbial C, N, P cycles.

Deliverables to Date:

III. Papers and Other Products Delivered.

Service/ Honors:

Kostka serves as editor of the journal *Applied and Environmental Microbiology*.

Kostka participated in the following visioning workshop and in writing of the report: U.S. Department of Energy Biological and Environmental Research Workshop on Molecular Science Challenges. May 27-29, 2014.

Kostka wrote for and received funding from the Joint Genome Institute for the Community Sequencing Program project entitled: “The role of the Sphagnum microbiome in carbon and nutrient cycling in peatlands.” This project involves field sampling and collaboration at the

SPRUCE and NGEE-Arctic sites. The project also links to ongoing Sphagnum genome sequencing and Global Peatland Microbiome efforts conducted at JGI. Kostka attended the JGI Users Meeting in Walnut Creek, CA, during the last week of April, 2015, to kick off the project.

Kostka received the 2014 College of Sciences Faculty Mentor Award at Georgia Tech. Kostka received this award for his mentorship of Dr. Jennifer Glass, a new faculty member in the School of Earth and Atmospheric Sciences at Georgia Tech. Kostka helped Dr. Glass to begin a research program on nutrient cycling and nitrogen fixation at the SPRUCE site. This collaborative research has substantially contributed to our understanding of the microbial nitrogen cycle and nutrient limitation in the S1 bog where the SPRUCE experiment is ongoing. This collaboration also resulted in a new proposal to the TES program.

The following 6 publications, 2 M.S. theses, and 40 seminars/ meeting presentations were completed. Three publications are in preparation.

Publications (printed, accepted or in review):

1. Lin, X., K. M. Handley, J. A. Gilbert, and J. E. Kostka. 2015. Metabolic potential of fatty acid oxidation and anaerobic respiration by abundant members of Thaumarchaeota and Thermoplasmata in deep anoxic peat. *ISME Journal*, doi: 10.1038/ismej.2015.77.
2. Tfaily, M. M., J. E. Corbett, R. Wilson, J. P. Chanton, P. H. Glaser, K. M. Cawley, R. Jaffé, and W. T. Cooper. 2015. Utilization of PARAFAC-Modeled Excitation-Emission Matrix 2 (EEM) Fluorescence Spectroscopy to Identify Biogeochemical Processing of Dissolved Organic Matter in a Northern Peatland. *Photochemistry & Photobiology*, 91: 684–695. doi:10.1111/php.12448
3. Tfaily, M.M. W. T. Cooper, J. Kostka, P. R. Chanton, C. W. Schadt, P. J. Hanson, C. M. Iversen, and J. P. Chanton. 2014. Organic matter transformation in the peat column at Marcell Experimental Forest: Humification and vertical stratification. *Journal of Geophysical Research Biogeochemistry*, 119, 661-675, doi:10.1002/2013jg002492.
4. Hodgkins, S. B., M. M. Tfaily, C. K. McCalley, T. A. Logan, P. M. Crill, S. R. Saleska, V. I. Rich, and J. P. Chanton. 2014. Changes in soil chemistry help drive higher greenhouse gas emissions from thawing permafrost. *PNAS*, www.pnas.org/cgi/doi/10.1073/pnas.1314641111 PNAS.
5. Lin, X., M. M. Tfaily, J. M. Steinweg, P. Chanton, J. P. Chanton, K. Esson, W. Cooper, C. Schadt, J. E. Kostka. 2014a. Microbial Community Stratification Linked to Utilization of Carbohydrates and Phosphorus Limitation in a Boreal Peatland at Marcell Experimental Forest, Minnesota, USA. *Applied Environmental Microbiology*, 80, 3518-3530.
6. Lin, X., M. M. Tfaily, S. Green, J. M. Steinweg, P. Chanton, J. P. Chanton, W. Cooper, C. Schadt, J. E. Kostka. 2014b. Microbial Metabolic Potential for Carbon Degradation and Nutrient (Nitrogen and Phosphorus) Acquisition in an Ombrotrophic Peatland. *Applied Environmental Microbiology*. 80, 3531-3540.

Two M.S. Theses have been produced:

Esson, K.C. 2014. Active Methane Oxidizing Bacteria In A Boreal Peat Bog Ecosystem. Georgia Institute of Technology, 40 pages.

Chanton, P.R. 2014. Calibration of a phenol oxidase assay for acidic wetland ecosystems, Georgia Institute of Technology, 42 pages.

Publications (in preparation):

7. Medvedeff, C.A., J. K. Keller, S. D. Bridgham, J. P. Chanton, J. E. Kostka, X. Lin, L. Pfeifer-Meister, and M. M. Tfaily. A bog by any other name: do all 'bogs' have similar anaerobic carbon dynamics.
8. Tfaily, M. M., W. T. Cooper, J. P. Chanton, W. Wilson, J. Kostka. Composition and transformation of dissolved organic matter in the peat column at Marcell Experimental forest.
9. Esson, K.C., X. Lin, D. Kumaresan, J. P. Chanton, J. C. Murrell, J. E. Kostka. 2015. Alpha and Gammaproteobacterial Methanotrophs Co-Dominate the Active Methane Oxidizing Communities in an Acidic Boreal Peat Bog.

Invited Talks and Sessions:

1. Kostka, J.E. 2015. Toward a predictive understanding of the response of belowground microbial carbon turnover to climate change drivers in a boreal peatland. 2015 Environmental Systems Science Principal Investigator Meeting, U.S. Department of Energy, Washington, DC, April.
2. Chanton, J.P. 2015. The Canary in the Climate Change Coal Mine, New Topics Lecture, New College, Sarasota Florida, March, 2015.
3. Chanton, J.P. 2014. Peatlands and controls on the CO₂/CH₄ ratio of decomposition. American Geophysical Union Fall Meeting, San Francisco.
4. Chanton, J.P. 2014. Peatlands and Climate Change. FSU student chapter American Meteorological Society
5. Chanton, J.P. 2014. Peatlands, Permafrost and Oil spills Department of Geography, Florida State University, September 12, 2014.
6. Chanton, J.P. 2014. Peatlands, Permafrost and Oil spills, Invited Speaker, University of Arizona, Soil and Environmental Science Department. Chanton, J.P. 2014. Peatlands and controls on the CO₂/CH₄ ratio of decomposition. Gordon Research Conference on Gas Hydrates, Galveston Texas, March 24-28, 2014.
7. Kostka, J.E. 2014. Microbial Interactions with Sphagnum. Scaling evolution from genomes to ecosystems in peatmosses (Sphagnum), Workshop at the National Evolutionary Synthesis Center, Durham, NC, October.
8. Kostka, J.E. 2014. Coupling peat decomposition and metagenomics to incorporate molecular scale processes into climate models. Terrestrial Ecosystem Science/ Subsurface Biogeochemical Research Principal Investigators Meeting, U.S. Department of Energy, Washington, DC, April.
9. Kostka co-chaired the following session: "Coupling between methane and nitrogen cycles revealed by geochemical and molecular approaches." Fall Meeting of the American Geophysical Union, December, 2014.
10. Kostka J.E., X. Lin, M. M. Tfaily, P. R. Chanton, K. Esson, J. M. Steinweg, J. P. Chanton, W. T. Cooper, C. W. Schadt. 2013. Toward a predictive understanding of microbial carbon

turnover in a northern peatland. Terrestrial Ecosystem Science/ Subsurface Biogeochemical Research Principal Investigators Meeting, U.S. Department of Energy, Washington, DC, May.

11. Kostka, J.E., X. Lin, M.M. Tfaily, P. Chanton, K. Esson, J.M. Steinweg, J.P. Chanton, W. Cooper, C. Schadt. 2013. Towards a predictive understanding of microbial carbon turnover in a northern peatland. Annual Meeting of the Society of Wetland Scientists, Duluth, June.
12. Chanton, J.P. 2012. "Permafrost and peatland carbon cycling in boreal and arctic soils". AGU fall meeting, San Francisco, December.
13. Chanton, J.P. 2012. Presentation on teaching of climate change. AGU fall meeting, San Francisco, December.
14. Cooper, W.T., Tfaily, M.M., Corbett, J.E., Chanton, J.P., Glaser, P.H. 2012. "Correlating Bulk Optical Spectroscopy and Ultrahigh Resolution Mass Spectrometry to Determine the Molecular Composition of Dissolved Organic Matter in Northern Peatlands", invited plenary lecture at the 16th Meeting of the International Humic Substance Society, Hangzhou, China, September.

Meeting presentations:

15. Hoppie, A., J. K. Keller, C. A. Medvedeff, L. Pfeifer-Meister, J. Chanton, J. E. Kostka, and R. Wilson, P.J. Hanson, and S. D. Bridgham. 2015. Initial Responses of Methane Cycling to Deep Peat Warming in a Minnesota Bog. Terrestrial Ecosystem Science/ Subsurface Biogeochemical Research Principal Investigators Meeting, U.S. Department of Energy, Washington, DC, April.
16. Warren, M.J., J. C. Gaby, C. B. Kretz, X. Lin, K. Esson, P. L. Morton, J. Pett-Ridge, S. J. Green, J. A. Gilbert, J. E. Kostka, J. B. Glass. 2015. Interactions between nitrogen fixation and methane cycling in boreal peat bogs. Terrestrial Ecosystem Science/ Subsurface Biogeochemical Research Principal Investigators Meeting, U.S. Department of Energy, Washington, DC, April.
17. Hodgkins, S., R. Wilson, J. Chanton, W. Cooper. 2015. A Comprehensive Analytical Approach for Characterizing the Impacts of Climate Change on Carbon Sequestration in Peatlands. 2015 Spring National Meeting, American Chemical Society, Denver, CO, March.
18. Kostka, J.E., M. Kolton, D. Weston, J. Shaw, J. Glass, and E. Lilleskov, S. Tringe. 2015. The role of the Sphagnum microbiome in carbon and nutrient cycling in peatlands. 10th Annual Users Meeting, Joint Genome Institute, Walnut Creek, CA, March.
19. Kolton, M., X. Lin, J.E. Kostka. 2015. Taxonomic and functional shifts in peatland microbial communities coupled to methane dynamics and peat decomposition. 2nd Annual Southeastern Biogeochemistry Symposium, Atlanta, April.
20. Tfaily, M., J. E. Corbett, R. Wilson, J. P. Chanton, P. H. Glaser, K. M. Cawley, R. Jaffé, and W. T. Cooper. 2015. Molecular composition and fluorescence properties of natural organic matter in a Northern peatland; implications for climate change. 2014 Fall National Meeting, American Chemical Society, San Francisco, CA, August.

21. Warren, M.J., J. C. Gaby, X. Lin, P. L. Morton, J. E. Kostka and J. B. Glass. 2014. Interactions between nitrogen fixation and methane cycling in Northern Minnesota peat bogs. Fall Meeting of the American Geophysical Union, San Francisco, December.
22. Hamdan, R., A. Mukherjee, A. R. Zimmerman, W. T. Cooper. 2014. Chemical Composition of Fresh and Aged Biochars. 2014 Fall National Meeting, American Geophysical Union, San Francisco, CA, December.
23. Warren, M.J., X. Lin, J.E. Kostka, Y. Oda, and J.B. Glass. 2014. Influence of temperature on alternative nitrogenase activity: implications for nitrogen cycling in high latitude peatlands. First Annual Southeastern Biogeochemistry Symposium, Atlanta, April.
24. Steinweg, J.M., M. S. Robeson, Z. K. Yang, P. J. Hanson, J. E. Kostka and C. W. Schadt. 2014. Scoping potential microbial responses to warming and drying in the SPRUCE peatland ecosystem. Terrestrial Ecosystem Science/ Subsurface Biogeochemical Research Principal Investigators Meeting, U.S. Department of Energy, Washington, DC, April.
25. Bridgham, S.D., J. P. Chanton, J. K. Keller, J. E. Kostka, X. Lin, C. A. Medvedeff, L. Pfeifer-Meister, and M. M. Tfaily. Do all 'bogs' have similar anaerobic carbon dynamics and microbial community structure? Putting the SPRUCE site in a regional perspective. Terrestrial Ecosystem Science/ Subsurface Biogeochemical Research Principal Investigators Meeting, U.S. Department of Energy, Washington, DC, April.
26. Gaby, J.C., and J. E. Kostka. 2014. High-Throughput Analysis of Diazotroph Diversity in Marine, Wetland, and Agricultural Systems. American Society for Microbiology Annual Meeting, Boston, MA, May.
27. Kostka, J.E., X. Lin, M.M. Tfaily, J.P. Chanton, W. Cooper, S. Bridgham, and J. Keller. 2014. The Abundance and Expression of Genes for Methanogenesis and Methanotrophy in Northern Peatlands. American Society for Microbiology Annual Meeting, Boston, MA, May.
28. Esson, K., X. Lin, D. Kumaresan, J. C. Murrell, S. Bridgham, J. Keller, J. Chanton, and J. E. Kostka. 2014. Microbial methane cycling in peatlands of northern Minnesota. Gordon Research Conference on C1 Metabolism, August.
29. Esson, K., D. Kumaresan, C. Murrell, X. Lin, and J.E. Kostka. 2014. DNA stable isotope probing reveals a prevalence of type I methanotrophs in an acidic boreal peatland. First Annual Southeastern Biogeochemistry Symposium, Atlanta, April.
30. Gaby, J.C., P. Steck, M. Blejwas, I.K. Jordan, and J.E. Kostka. 2014. A high-throughput sequencing pipeline for characterization of nitrogen-fixing communities. First Annual Southeastern Biogeochemistry Symposium, Atlanta, April.
31. Tfaily, M.M., J.P. Chanton, J.E. Kostka, X. Lin, J.M. Steinweg, C.W. Schadt W. T. Cooper, 2013. Identifying Dissolved Organic Matter Decomposition in Northern Peatlands using Complimentary Analytical Techniques. Terrestrial Ecosystem Science/ Subsurface Biogeochemical Research Principal Investigators Meeting, U.S. Department of Energy, Washington, DC, May.
32. Cooper, W.T., M.M. Tfaily, J.P. Chanton, A. Invittaya, J.E. Kostka, X. Lin, P. Chanton, J.M. Steinweg, C.W. Schadt. 2013. Linking Chemical Signatures and Microbial Communities that Affect Carbon Cycling in Northern Peatlands. Terrestrial Ecosystem Science/ Subsurface

Biogeochemical Research Principal Investigators Meeting, U.S. Department of Energy, Washington, DC, May.

33. Lin, X., M.M. Tfaily, P. Chanton, J.M. Steinweg, J.P. Chanton, W. Cooper, C. Schadt, J.E. Kostka. 2013. Environmental controls over the distribution of microorganisms and organic matter reactivity at the ecosystem scale in a northern peatland. American Society for Microbiology Annual Meeting, Denver, CO, May.
34. Kostka, J.E., X. Lin, P. R. Chanton, S. J. Green, M. M. Tfaily, O. Prakash, J. P. Chanton, W. Cooper, J. M. Steinweg, and C. W. Schadt. 2012. The response of soil carbon storage and microbially mediated carbon turnover to simulated climatic disturbance in a northern peatland forest: revisiting the concept of soil organic matter recalcitrance. Terrestrial Ecosystem Science Principal Investigators Meeting, Washington, DC, April.
35. Chanton, P.R., E. Aquadro, O. Prakash, J. Delgardio, X. Lin, J. M. Steinweg, C. Schadt, and J. E. Kostka. 2012. Determination of phenol oxidase activity and carbon storage in peatland of Marcell Experimental Forest in Northern Minnesota. Terrestrial Ecosystem Science Principal Investigators Meeting, Washington, DC, April.
36. Lin, X., S. Green, M.M. Tfaily, O. Prakash, K. Konstantinidis, J.E. Corbett, J.P. Chanton, W. Cooper, J.E. Kostka. 2012. Multi-domain Community Composition Linked to Contrasting Biogeochemical Conditions in Bog and Fen Environments of The Glacial Lake Agassiz Peatland. American Society for Microbiology General Meeting, New Orleans, LA, May
37. Choi, H., X. Lin, P.R. Chanton, and J.E. Kostka. 2012. Mesophilic Crenarcheota in the Marcell Experimental Forest. Research Experience for Undergraduates Symposium, Georgia Institute of Technology, Atlanta, GA, July.
38. Cooper, W.T., Hamdan, R., Zimmerman, A.W. 2012. "Characterization of Pyrogenic Black Carbon by Desorption Atmospheric Pressure Photoionization (DAPPI) coupled to Fourier-Transform Ion Cyclotron Resonance Mass Spectrometry", 242nd National Meeting of the American Chemical Society, Denver, CO, August.
39. Tfaily, M.M, Corbett, J. Elizabeth, Chanton, Jeffrey P., Cooper, William T., Burdige, David, and Glaser, Paul. 2012. "Understanding Anaerobic C Dynamics and Methane Production in Peatlands through Molecular Characterization of Porewater DOM Reactivity: Oxygen Shedding by DOM during Fermentation", International Wetland Conference, Orlando, FL, June 3-8.
40. Corbett, J. Elizabeth, Chanton, Jeffrey P., Tfaily, M.M, Cooper, William T., Burdige, D. and Glaser, P. 2012. "Partitioning Peat Respiration in the Catotelm" International Wetland Conference, Orlando, FL, June 3-8.