

Can Microbial Ecology and Mycorrhizal Functioning Inform Climate Change Models?

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Abstract

Our funded research focused on soil organic matter dynamics and plant-microbe interactions by examining the role of belowground processes and mechanisms across scales, including decomposition of organic molecules, microbial interactions, and plant-microbe interactions associated with a changing climate. Research foci included mycorrhizal mediated priming of soil carbon turnover, organic N use and depolymerization by free-living microbes and mycorrhizal fungi, and the use of isotopes as additional constraints for improved modeling of belowground processes. This work complemented the DOE's mandate to understand both the consequences of atmospheric and climatic change for key ecosystems and the feedbacks on C cycling.

Progress

As a initial study we estimated the source and quantify the use of organic N among ectomycorrhizal taxa by analyzing existing stable isotope data from the Duke Forest FACE experiment. Building off our experience at FACE, we extended our questions into the Spruce and Peatland Responses Under Changing Environments, or SPRUCE experiment, in the Marcell National Forest.

Our research was initiated prior to experimental infrastructure establishment. Our initial studies focused on establishing baseline understanding of the spatial and temporal variability in organic N cycling within the bog. This included assaying extracellular enzyme activity, microbial biomass, ergosterol concentration, fungal isotopes, and bacterial and fungal community composition. In addition to generating data on fresh peat cores, we sand-filled ingrowth bags to estimate EM production and both sand. We coupled this with peat ingrowth bags to identify the active, extraradical EM community. This system of ingrowth cores was deployed in the replicated SPRUCE rings to capture the ^{13}C signature from photosynthates to the EM fungi in response to climate manipulations (elevated CO_2 and temperature). The goal of this experiment is to estimate C allocation to EM hyphal growth. In conjunction with isotope data generated by ORLN and SPRUCE collaborators, we incorporated the isotopic signatures of fungal hyphae and fruiting bodies to assess the sources of C and N supporting fungal growth. We are using measurements of microbial activity, biomass, composition and isotopic signatures to understand how environmental change influences the structure and function of boreal forest microbial communities. By examining differences in $\delta^{13}\text{C}$ among bulk tissue, structural carbon, and protein extracts of sporocarps of three fungal types (saprotrophic fungi, fungi with hydrophobic ectomycorrhizae) or fungi with hydrophilic ectomycorrhizae, we were able to determine whether fungi received carbon from recent plant photosynthate, litter or soil-derived organic (C:N bonded) nitrogen. We successfully demonstrated that fungi with hydrophobic ectomycorrhizae used soil-derived organic nitrogen sources for protein carbon, fungi with hydrophilic ectomycorrhizae used recent plant photosynthates for protein carbon and both fungal groups used photosynthates for structural carbon. Further this approach allowed us to differentiate how specific fungal species are acquiring carbon and nitrogen under field conditions. Our research has demonstrated that natural abundance and isotopic

tracers are useful for tracking N from different depths into fungal taxa, generally corresponding to estimates of fungal activity within soil profiles, and providing new insights into interpreting natural abundance $\delta^{15}\text{N}$ patterns. This work was extended to a whole ecosystem isotopic analysis to evaluate past vegetation dynamics, climate and microbial processes in the Marcell bog, including mycorrhizal activity after tree colonization of the bog and upland-derived dissolved organic nitrogen inputs and accompanying shifts in nitrogen dynamics.

Education

At Iowa State University one postdoc and one undergrad contributed to this work. The undergrad continued to intern at PNNL. At UNH one graduate student contributed to this research.

Publications

Hobbie EA, Chen J, Hanson PJ, Iversen CM, McFarlane KJ, Thorp NR, Hofmockel KS. 2017 Long-term carbon and nitrogen dynamics at SPRUCE revealed through stable isotopes in peat profiles. *Biogeosciences*. May 17;14(9):2481-94.

Chen J, Hofmockel KS, Hobbie EA 2016. Isotopic analysis of sporocarp protein and structural material improves resolution of fungal carbon sources. *Frontiers Microbiology* 7:1994. doi: 10.3389/fmicb.2016.01994.

McCormack ML, Dickie IA, Eissenstat DM, Fahey TJ, Fernandez CW, Guo D, Helmisaari H-S, Hobbie EA, Iversen CM, Jackson RB, et al. 2015. Redefining fine roots improves understanding of root contributions to terrestrial biosphere processes. *New Phytologist* 207(3), 505-518.

Hobbie EA, Hofmockel KS, van Diepen LT, Lilleskov EA, Ouimette AP, Finzi AC 2014. Fungal carbon sources in a pine forest: evidence from a ^{13}C labeled global change experiment. *Fungal Ecology* 10: 91-100.

Hobbie EA, van Diepen LT, Lilleskov EA, Ouimette AP, Finzi AC, Hofmockel KS 2014 Fungal functioning in a pine forest: evidence from a ^{15}N -labeled global change experiment. *New Phytologist* 201:1431-1439.

van Diepen, L.T.A., Hobbie, E.A., Mohan, J.E. Fungi, ecosystems and global change. *Fungal Ecology*, April 2014.

Data

Iversen, C. M., Hanson, P. J., Brice, D. J., Phillips, J. R., McFarlane, K. J., Hobbie, E. A., and Kolka, R. K. 2014. SPRUCE peat physical and chemical characteristics from experimental plot cores, 2012, Carbon Dioxide Information Analysis Center, Oak Ridge National Laboratory, US Department of Energy, Oak Ridge, Tennessee, USA, doi:10.3334/CDIAC/spruce.005.

Hofmockel, K.S., Chen, J. and Hobbie, E.A. 2016. SPRUCE S1 Bog Pretreatment Fungal Hyphae Carbon and Nitrogen Concentrations and Stable Isotope Composition from In-growth Cores, 2013-2014. Carbon Dioxide Information Analysis Center, Oak Ridge National Laboratory, Oak Ridge, Tennessee, USA. <http://dx.doi.org/10.3334/CDIAC/spruce.025>

Presentations

ML Smith. Enzymatic potential in microbial communities shift with environmental change. Pacific Northwest National Laboratory. February 12, 2018

KS Hofmockel, EA Hobbie. Belowground N budget. SPRUCE All Hands Meeting. ORNL, January 30, 2018

SL Bell, ML Smith, EA Hobbie, KS Hofmockel. Ecological network analysis of peatland microbial communities. Ecological Society of America. August 2017.

KS Hofmockel, *SL Bell, *M Smith, *A Thompson and EA Hobbie, Bacteria, archaea and fungi respond to warming in SPRUCE peatland experiment. Ecological Society of America, August 10, 2017 Portland, OR, 2017.

KS Hofmockel, JGutknecht, L Kluber, C Schadt, J Pett Ridge, X Mayali, Microbial responses to deep peat heating, AGU, San Francisco, CA, December 14, 2016.

KS Hofmockel Photosynthetic allocation to mycorrhizae quantified by ecosystem tracer experiment. DOE SPRUCE Advisory Meeting, Minneapolis, MN, June 7, 2016.

KS Hofmockel, F Yang*, EA Hobbie. Organic N cycling at SPRUCE. TES/SBRJoint Investigators Meeting, Potomac, MD May 6, 2014.

KS Hofmockel. Linking molecular processes to terrestrial biogeochemistry. Environmental Molecular Sciences Laboratory; Pacific Northwest National Laboratory, Department of Energy. April 23, 2014.

KS Hofmockel, The value of northern peatlands as carbon sinks. Society of Wetland Scientists Annual Meeting, Duluth MN, June 3, 2014.

KS Hofmockel. New approaches to scaling microbial metabolism to ecosystem processes. Environmental Molecular Sciences Laboratory; Pacific Northwest National Laboratory, Department of Energy. October 2013.

EA Hobbie, KS Hofmockel, L van Diepen, EA Lilleskov, AP Ouimette, A Finzi. Stories a mushroom told me: 13C and 15N in a pine FACE study reveal fungal functioning. MassMyco Meeting, Clark University, Worcester, MA, October 2012.

Erik Hobbie was the lead organizer of a symposium on Fungi in a Changing World at the Mycological Society of America (MSA) meeting in July 2012 at Yale University. Eight articles and a lead editorial stemming from the symposium were published in a special issue of Fungal Ecology in April 2012.

Other presentations

Dr. Hobbie gave a talk to the microbial study group at Duke University in October 2012 and Dr. Hobbie and Dr. Hofmockel both presented results of their research to a biogeochemistry study group at Duke University in April 2013.

Posters

KS Hofmockel, SL Bell, ML Smith, A Thompson, EA Hobbie. Microbial responses to deep peat heating in SPRUCE peatland experiment. DOE Environmental System Sciences Meeting, 2017.

ML Smith, KS Hofmockel, SL Bell, A Thompson, EA Hobbie. Microbial enzymatic responses to elevated temperatures. Ecological Society of America, Portland OR, Aug 2017.

KS Hofmockel, SL Bell, ML Smith, A Thompson, L Bramer, J Brown, EA Hobbie. Microbial response to deep peat heating. Environmental System Sciences Meeting, Potomac, MD, May 2016.

ML Smith, AD Keiser, KS Hofmockel. Microbial functional response to low molecular weight carbon compounds, temperature, and moisture manipulation, Iowa State University, December 2015.

ML Smith, KS Hofmockel, F Yang, SL Bell. Assembly of the V4 region of 16S rRNA gene sequences for downstream analysis, Iowa State University, April 2015.

KS Hofmockel, F Yang, C Davis, AD Keiser, EA Hobbie. Peatland topography influences microbial function at SPRUCE. DOE Terrestrial Ecosystem Science Meeting, Potomac, MD May 2015.

C Davis, F Yang, KS Hofmockel. Microbial impacts on C-N cycle in northern peatlands during 2013 growing season. Iowa State University- Science with Practice, December 10, 2014.

F Yang, KS Hofmockel. The Genetic Potential for organic N decomposition at SPRUCE, TES/SBRJoint Investigators Meeting, Potomac, MD May 2014.

F Yang, KS Hofmockel The Genetic Potential of Microbial Depolymerization of SPRUCE Peatland in Marcell Experimental Forest, MN. Argonne Soil Metagenomics Meeting, Chicago, October 2013.

EA Hobbie, KS Hofmockel, L van Diepen. Fungal Functioning In A Pine Forest: Evidence From A15N-Labeled Global Change Experiment. American Geophysical Union, San Francisco, December 2012.