Host-Linked Soil Viral Ecology along a Permafrost Thaw Gradient

Joanne B. Emerson¹,²*, (jbemerson@ucdavis.edu), Simon Roux¹,³, Jennifer R. Brum¹,⁴, Benjamin Bolduc¹, Ben J. Woodcroft⁵, Ho Bin Jang¹, Caitlin M. Singleton⁵, Lindsey M. Solden¹, Adrian E. Naas⁶, Joel A. Boyd⁵, Suzanne B. Hodgkins⁷, Rachel M. Wilson⁷, Gareth Trubl¹, Changsheng Li⁸, Steve Frolking⁹, Philip B. Pope⁶, Kelly C. Wrighton¹, Patrick M. Crill¹⁰, Jeffrey P. Chanton⁷, Scott R. Saleska¹¹, Gene W. Tyson⁵, Virginia I. Rich¹, and Matthew B. Sullivan¹

¹The Ohio State University, Columbus; ²Current affiliation: University of California, Davis; ³Current affiliation: Department of Energy Joint Genome Institute, Lawrence Berkeley National Laboratory, Walnut Creek; ⁴Current affiliation: Louisiana State University, Baton Rouge; ⁵University of Queensland, Australia; ⁶Norwegian University of Life Sciences, Norway; ⁷Florida State University, Tallahassee; ⁸Deceased, formerly University of New Hampshire, Durham; ⁹University of New Hampshire, Durham; ¹⁰Stockholm University, Sweden; and ¹¹University of Arizona, Tucson

http://isogenie.osu.edu

Project Goals: Our objective is to discover how microbial communities mediate the fate of carbon in thawing permafrost landscapes under climate change. Our team is engaged in a systems approach integrating molecular microbial and viral ecology, organic chemistry and stable and radiocarbon isotopes, and state-of-the-art modeling along an interconnected chronosequence of thawing permafrost and post-glacial lakes in subarctic Sweden.

Abstract: Climate change threatens to release large amounts of carbon sequestered at high latitudes, but constraints on the microbial metabolisms that mediate the release of greenhouse gases, such as methane and carbon dioxide, are poorly understood. While viral ecology is largely unexplored in soils, viral contributions to ecosystem processes in other systems (e.g., viral impacts on microbial dynamics, metabolism, and biogeochemistry in the oceans) suggest that viruses are likely to be an important component of these microbially-mediated feedbacks to climate. Here, we investigated how viruses influence microbial ecology and carbon metabolism in peatland soils along a permafrost thaw gradient in northern Sweden. We recovered 1,907 viral populations (including genomes and genome fragments) from 197 bulk soil and size-fractionated metagenomes, approximately doubling known prokaryotic viral genera. 58% of these viruses were detected in metatranscriptomes and presumed to be active. In silico predictions linked 35% of the viruses to microbial host populations, highlighting likely viral predators of key carbon-cycling microorganisms, including methanogens and methanotrophs. Lineage-specific virus:host ratios varied with thaw, suggesting that viral infection dynamics may differentially impact microbial responses to a changing climate. Virus-encoded glycoside hydrolases (including an endo-mannanase with confirmed functional activity) indicated that viruses influence complex carbon degradation, while regression analyses revealed viral abundances—alone and together with host abundances—as significant predictors of methane dynamics. These findings suggest that viruses impact ecosystem function in terrestrial habitats undergoing climate change and identify multiple viral contributions to carbon cycling in thawing permafrost.
Funding statement. This research was funded by the U.S. Department of Energy Office of Biological and Environmental Research under the Genomic Science program, Awards DE-SC0004632, DE-SC0010580, and DE-SC0016440, with partial support from the Gordon and Betty Moore Foundation (GBMF#3305, 3790) and U.S. National Science Foundation (OCE#1536989).