

Role of Viruses in Carbon Processing Along a Permafrost Thaw Gradient

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Project Goals: The objective of the IsoGenie3 Project is to discover how microbial communities mediate the fate of carbon in thawing permafrost landscapes under climate change. We are engaged in a systems approach integrating (a) molecular microbial and viral ecology, (b) molecular organic chemistry and stable and radiocarbon isotopes, and (c) state-of-the-art modeling, across an interconnected system of thawing permafrost and post-glacial lakes in Arctic Sweden.

Permafrost accounts for roughly 30%-50% of global soil carbon (C). Due to elevated temperatures resulting from climate change, permafrost is thawing. It is not fully understood how thawing permafrost will impact carbon dioxide or methane release, which in turn could accelerate climate change. Our prior work has demonstrated that microbial communities play a critical role the C cycle in these permafrost soils^{1,2,3} as has also been revealed in other permafrost systems⁴. Less well-studied is the role that viruses infecting these microbes might play in C cycling, though viruses are abundant across diverse soils, including permafrost⁵. If marine systems are a guide, then these abundant viruses are likely to impact carbon cycling by controlling microbial communities via predation, transferring genes from one host to another, and metabolically reprogramming their host cells via regulatory take-over and directly encoding auxiliary metabolic genes (AMGs). While relatively well-studied in marine systems, information about viruses in soils like permafrost is only now emerging.

We previously employed two approaches to explore viral roles along a permafrost thaw gradient in northern Sweden. First, we optimized viral capture methods to be able to directly study quantitatively-amplified metagenomes derived from the viral particles that could be resuspended from soils. These efforts have led to increasingly efficient viral capture methods⁵ and sequence datasets that revealed ~50 viral populations from 7 viral metagenomes, which were predominantly novel (species and genera), distinctly distributed along the thaw gradient, and contained 30 AMGs that likely directly impact C metabolism and soil organic matter degradation⁶. Second, we optimized identification of viral contigs from >200 bulk soil metagenomes along the permafrost thaw gradient collected in 2010-2012⁷. Whole genomes and large genome fragments from nearly 2,000 viral populations were identified, of which ~60% of were determined to be active, and also placed into ecological context to reveal soil-type preferences, variations in lineage-specific virus-host pressures, and that most key C cyclers in the system are infected by viruses. Functional analyses of one of the detected virus-encoded glycoside hydrolase genes further

demonstrated that these AMG are functional, and offer a clear example of how viruses can directly impact C degradation, here converting complex C to simpler C forms.

Building upon these prior successes, we are now analyzing the viral populations present in an expanded bulk soil metagenomic dataset that extends the permafrost thaw time series out to include the years 2013-2017. The resulting sequencing reads were assembled into contigs using an updated assembly algorithm (metaSPADES), and viruses were identified using an updated suite of approaches (VirSorter and DeepVirFinder) optimized from our work with marine metagenomes. These efforts alone have already revealed thousands of viral populations, though co-assemblies and genome binning are also being evaluated to increase viral population detection. These viral populations, combined with already-available reference genomes, will be used to further our understanding of the role and impact of viruses in permafrost.

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