

Viral ecogenomics across a permafrost thaw gradient

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Project goals: The overarching goal of this project is to establish ecological paradigms for how viruses alter soil microbiomes and nutrient cycles by developing foundational (eco)systems biology approaches for soil viruses. Within this overall project, we examined viruses from metagenomic datasets to investigate viral ecology across a nearly decadal time series. Such work is critical for establishing baseline ecological understanding of viruses in soils, as well as elucidating the role of viruses in terrestrial carbon and nutrient cycling.

Since permafrost accounts for 30% - 50% of global soil carbon (C), it is important to understand how thawing permafrost will impact the release of greenhouse gasses. Microorganisms are known to play critical roles in the terrestrial C cycle, but their viruses are less well-understood. In marine systems, viruses impact C cycling by controlling hosts via predation, transferring genes between hosts, and metabolically reprogramming hosts via encoding auxiliary metabolic genes (AMGs). Here we identify and examine viruses from a metagenomic dataset composed of peat samples collected between 2010 - 2017 across the active layer of a permafrost thaw gradient at a northern Sweden long-term ecological research site. This augmented known viruses at this already intensively studied site approximately 2-fold. The vast majority of viruses were novel, even when compared to other viruses from terrestrial ecosystems. Viral communities differentiated based on thaw stage (palsa, bog, and fen) and on depth, but not by time (year). Leveraging co-sampled metagenome-assembled genomes (MAGs) to *in silico* predict microbial hosts, we found that the majority of predicted hosts had genome-encoded functions involving the degradation of plant-derived C polysaccharide (such as cellulose, fructose, and xylose), which implicated viruses in soil C cycling. Further support for this came from identifying a myriad of virus-encoded AMGs, including those involved in central C metabolism and C degradation (e.g. glycoside hydrolases). Together, these results provide a growing baseline ecological understanding of soil viruses and increasingly implicate them in permafrost C cycling.

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