The role of viruses in the carbon cycle along a permafrost thaw gradient

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Project goals: *The activity of microbes in soil profoundly affects global energy and nutrient cycles. In consequence, whatever shapes soil microbial activity shapes the world. Substantial recent work in environmental microbiology has taught us that viruses are a key driver of microbial ecology in other systems, and we expect the same to hold true in soil. But soil is a complex milieu – highly structured, chemically and physically heterogenous, and resistant to extrapolation. Thus, even as new methods have revolutionized our understanding of microbial and viral ecology in other systems, our understanding of soil microbial ecology has lagged, and our understanding of soil viral ecology is still further behind. **Our objective is to develop paradigms for understanding the role of viruses in soil ecology, and to build the tools – scalable new methods, new databases, and new model systems – to test these paradigms.***

Permafrost accounts for approximately 30%-50% of global soil carbon (C). Unfortunately, permafrost is thawing due to elevated temperatures resulting from climate change. It is not entirely understood how thawing permafrost will impact the release of greenhouse gasses, which could in turn accelerate climate change. Microbial communities play a critical role the C cycle but viruses are less well studied in permafrost systems. If marine systems are a guide, then viruses are likely to impact C 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). Here, we examined viruses along a permafrost thaw gradient over eight years (2010-2017) using data from bulk metagenomic sequencing and viral eco-genomic analyses.

Samples were collected from a palsa (dry permafrost), a bog (intermediate thaw), and a fen (wet, fully thawed) in Stordalen Mire, Sweden. In total, we identified 4,132 unique viral populations ($\geq$ 10kb contigs dereplicated at 95% average nucleotide identity and 80% coverage) that clustered into nearly 614 novel viral genera via gene-sharing networks. This dataset increases both known permafrost viral populations and viral genera by 2-fold. Viral populations were site specific, with only 16 viral populations (0.2%) shared across all sites and 336 viral populations (4%) shared across any two sites. To evaluate how viruses might be playing a role C cycling, we *in silico* predicted hosts for our viruses, using metagenome-assembled-genomes (MAGs) that were generated from the same samples. Preliminarily, we found 26 MAGs that serve as hosts for 42 viruses, using CRISPR spacer matching. Of the MAGs identified as hosts, the majority (77%) are putative key C cyclers, implicating viruses in C cycling via infection. Building upon this work, we are optimizing virus-host prediction by using a combination of different computational methods in order to assign hosts to more permafrost viruses. In addition, high throughput methods are being used to detect directly encoded AMGs in viral sequences. Together, these viruses will be used to further our understanding of the role and impact of viruses in permafrost.