

Soil viral ecology along a permafrost thaw gradient

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Project Goals: The objective of the IsoGenie2 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, along an interconnected chronosequence of permafrost thaw and post-glacial lakes in subarctic Sweden.

Abstract: High-latitude environments are disproportionately impacted by climate change with decadal declines now known in sea ice extent and thickness and permafrost thaw, concomitant with increases in greenhouse gas emissions. Numerous efforts to evaluate the role of microbes in high-latitude soils have revealed that they significantly alter these ecosystem features. However, in spite of large viral impacts on microbial dynamics and metabolic outputs in other environments (e.g., oceans), virtually no knowledge exists for how viruses impact soil microbes and ecosystems. Here we analyzed 201 bulk soil metagenomes along an Arctic permafrost thaw gradient to identify viral genomes and large genome fragments as a basis for developing a population-based ecological understanding of viruses in these systems. A total of 1,907 viral genomes were recovered and taxonomically classified, which nearly triples known genera of prokaryotic soil viruses. Metatranscriptomic analyses of a subset (n=26) of these samples revealed that genes from approximately two-thirds (61%) of these viruses were expressed, suggesting that active infections were captured. Both active and overall viral community composition differed along the thaw gradient, concomitant with shifts in host community composition and biogeochemistry. *In silico* host prediction linked 35% of the viruses to co-occurring host populations, including biogeochemically relevant microbes such as methanogens and methanotrophs. Further, they enabled unprecedented field-based, lineage-specific virus:host abundance estimates, which revealed dynamic infections across the permafrost thaw gradient for select microbial lineages. Together, these data suggest that viruses are integral to modulating climate-critical peatland soil biogeochemistry.

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