Viral Diversity and Potential Carbon Cycling Impacts Across a Soil Climate Gradient

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Project Goals: Microorganisms play key roles in soil carbon turnover and stabilization of persistent organic matter via their metabolic activities, cellular biochemistry, and extracellular products. Microbial residues are the primary ingredients in soil organic matter (SOM), a pool critical to Earth's soil health and climate. We hypothesize that microbial cellular-chemistry, functional potential, and ecophysiology fundamentally shape soil carbon persistence, and we are characterizing this via stable isotope probing (SIP) of genome-resolved metagenomes and viromes. We focus on soil moisture as a 'master controller' of microbial activity and mortality, since altered precipitation regimes are predicted across the temperate U.S. *Our SFA's ultimate goal is to determine how microbial soil ecophysiology, population dynamics, and microbe-mineral-organic matter interactions regulate the persistence of microbial residues under changing moisture regimes.*

Microorganisms play many important roles in carbon (C) cycling in soils, and though viruses are known to modulate these roles in other systems (via lysis, gene flow and metabolic reprogramming) little is known about the impact of soil viruses due to technical challenges. Here, we examined viruses in well-characterized soil environments using data from purified viral particles, sequencing, and viral ecogenomic analyses. The soils were sampled from four sites, UC Hopland Research and Extension Center, Angelo Coast Range Reserve, Sedgwick Natural Reserve, and Luquillo Experimental Forest in Puerto Rico, which represent a gradient of soil moisture regimes.

This revealed 28,608 unique viral populations (≥ 10kb contigs dereplicated at 95% average nucleotide identity and 80% coverage) that sorted into nearly three thousand viral genera via gene-sharing networks. This dataset increases known soil virus populations by ~15-fold and soil viral genera 9-fold. Viral communities were strongly and statistically separated based on location, with few (0% - 8%) viral populations shared between sampling sites, suggesting that the heterogenous environmental conditions in soil give rise to very distinct communities. To assess potential viral roles in carbon cycling, we *in silico* predicted hosts, which, buoyed by metagenome-assembled-genomes (MAGs) from co-sampled bulk soil metagenomes, revealed putative hosts for 5% of the ~28K viruses, including 47 MAGs that are key C cyclers, including multiple *Actinobacteria* and *Gammaproteobacteria*. Further, we explored whether these soil viruses directly encoded key C cycling enzymes by identifying carbohydrate active enzymes (CAZymes), which catalyze the biosynthesis or breakdown of complex carbohydrates. This revealed 273 viral populations containing plant polysaccharide degrading CAZymes: 49% (GH28, PL1, PL22) targeted pectin, whereas 27% targeted beta-mannin (GH130 and GH113), 15% many polysaccharide bonds (GH140), and 4% beta xylan (GH19 and GH120), with the remaining CAZymes detected only once or a few times.

Together these results add to our baseline understanding of soil viral ecology and implicate viruses in C cycling via infection and directly encoded auxiliary metabolic genes. This knowledge provides a path for soil viruses be incorporated terrestrial ecosystem models to better understand terrestrial C cycling.

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