

Environmental conditions shape active viral community structure and virus-host dynamics in soil ecosystems

Gareth Trubl^{1*} (trubl.1@llnl.gov), Jeffrey A. Kimbrel¹, Ashley Campbell¹, Dariia Vyshenska², Simon Roux², Rex Malmstrom², Emiley Eloë-Fadrosh², Mark P. Waldrop³, **Steven J. Blazewicz¹, Jennifer Pett-Ridge¹**

¹Lawrence Livermore National Laboratory, Livermore, CA; ²Joint Genome Institute, Berkeley, CA; ³U.S. Geological Survey, Menlo Park, CA

Website: <https://sc-programs.llnl.gov/soil-microbiome>

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 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.*

Abstract: Soil viruses play a large but uncharacterized role as regulators of microbial growth dynamics and microbial biogeochemistry, largely by controlling microbial activity via cell lysis and redirection and modulation of host metabolism. Research on the diversity, functional capabilities, and host predictions of soil viruses is expanding near-exponentially, however, current methods are fragmented, limiting our ability to make connections important to soil ecology. We hypothesize that virus-microbe dynamics, and microbial cellular-chemistry and ecophysiology fundamentally shape soil carbon persistence. Our SFA team is characterizing these phenomena via stable isotope probing (SIP) combined with meta-omics approaches including metagenomics, viromics, metatranscriptomics, and eDNA. Here, we used stable isotope probing (SIP) targeted metagenomics to reveal the genomic potential of active microbial and viral communities using two different isotopically labelled substrates. We used heavy-water (¹⁸O) SIP in Arctic peat soils to identify and track active microbes and viruses over a year under subzero and anoxic conditions. We found that active bacterial populations represented only a small portion of the detected microbial community, were capable of fermentation and organic matter degradation, and were responsible for significant CO₂ production throughout the entire incubation. In contrast, the active viral populations in our arctic soil represented a large portion of the detected viral community and one-third were linked to active bacterial populations. In a second study, we incubated ¹³C-plant biomass in a tropical forest soil under four redox treatments to track viruses infecting microbes that degrade organic matter. Viral diversity was highest in the oxic samples and decreased in soils with lower O₂ exposure. More than a quarter of the soil viruses infected key active microbial organic matter degraders, and many of these were present only in anoxic samples. These findings highlight the impact temperature and soil redox conditions have on microbial and viral community structure and the fate of organic matter

in soils. Similar studies can help us: (1) learn more about how microorganisms grow and die in soil and how those factors mediate soil organic matter formation, (2) predict more accurately the impacts of shifting climate conditions on carbon cycling and biosequestration in ecosystems, and (3) examine potential means of biological sequestration of carbon.

This research is based upon work of the LLNL 'Microbes Persist' Soil Microbiome SFA, supported by the U.S. Department of Energy Office of Science, Office of Biological and Environmental Research Genomic Science program under Award Number SCW1632 to the Lawrence Livermore National Laboratory, and LLNL LDRDs 18-ERD-041 (S. Blazewicz) and 21-LW-060 (G. Trubl). Work at Lawrence Berkeley National Laboratory was performed under the auspices of the U.S. Department of Energy Contract No. DE-AC02-05CH11231. Work at Lawrence Livermore National Laboratory was performed under U.S. Department of Energy Contract DE-AC52-07NA27344.