

Taxon-Specific Growth and Mortality Rates of Bacteria in Soil Following the Rewetting of a Seasonally Dried Grassland

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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. 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.

Microbial activity increases after rewetting dry soil, resulting in a pulse of carbon mineralization and nutrient availability. This phenomenon is of particular interest because predicted changes in precipitation patterns in Mediterranean ecosystems could profoundly change soil C dynamics and nutrient availability. While there has been much interest in the response of indigenous communities to wet-up of dry soil, to date no work has identified the microorganisms in semi-arid soils that grow in response to soil wet-up. We used heavy water (H₂¹⁸O) DNA quantitative stable isotope probing coupled with high throughput sequencing of bacterial 16S rRNA genes to characterize taxonomic and phylogenetic composition of bacteria following the rewetting of a seasonally dried California annual grassland soil. Bacterial growth and mortality were detected at all time points throughout the incubation (3, 24, 72, 168 h), with patterns of sequential growth observable at the phylum and order levels. Of the 37 phyla detected in the pre-wet community, growth was found in 18 phyla, while mortality was measured in 26 phyla. Rapid growth and mortality rates were measurable within 3 hours of wet-up but had contrasting characteristics; growth at 3 h was dominated by a select few taxa found in the Proteobacteria and Firmicutes phyla, whereas mortality was taxonomically widespread. Sequential growth patterns observed at the phylum and order level suggest that an ecologically coherent response occurred at a high taxonomic level with members of particular groups employing different life strategies in response to rewetting.

To determine the effect of reduced Spring rainfall on newly fixed plant C persistence, genome resolvable ecophysiological traits of growing microbes, and phage-driven bacterial mortality, we conducted a second wet-up experiment using soils from an ongoing field experiment at the Hopland Research and Extension Center (HREC) in Hopland, California. Precipitation on these

plots has been manipulated so that half the plots receive a 50% reduction of the 65-year rain fall average, and the other half receive the full average rainfall amount. A $^{13}\text{CO}_2$ plant-labeling event was conducted in the Spring of 2018 to trace the pathways and persistence of C as it was fixed by plants, delivered belowground in the form of exudates and fresh roots, consumed by the various residents of the soil during the growing season, and persisted after plant senescence and the hot dry summer. Isotopically labeled soils were collected at the end of summer, shortly before the first seasonal rainfall event. These soils were subjected to a simulated precipitation event using H_2^{18}O in the laboratory to quantify and characterize C efflux, microbial growth and mortality, and phage dynamics driven by the rapid change in water potential using a combination of SIP-targeted metagenomics, virome sequencing and imaging, and ^{13}C flux measurements.

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