Goldschmidt 2025 Abstract
https://doi.org/10.7185/gold2025.32293

Investigating soil microbiome responses to hydroclimate volatility with SIP-enabled multi-omics

TRISTAN A CARO, ALEX L. SESSIONS AND SMRUTHI KARTHIKEYAN

California Institute of Technology

The hydroclimates of California and other Mediterranean-type ecosystems are characterized by periods of drought followed by extreme precipitation (e.g., 'atmospheric rivers'). Climate change is expected to exacerbate the differential between these two end-members, increasing both the intensity of drought and the potency of winter precipitation events. Soil water availability modulates microbial activity, which in turn controls the balance of carbon flow in soils via growth (carbon assimilating) and respiration (carbon emitting). While recent progress has been made to understand microbial physiological and ecological responses to drought, little work to date has addressed the combination of increased drought intensity coupled with high-intensity precipitation events. It is currently unclear how a drought-stressed soil microbiome will respond to high intensity precipitation and what effects this response may have on soil carbon stocks. To bridge this knowledge gap, our work aims to understand the responses of soil microbiota to increased hydroclimate volatility, the mechanisms that underly these responses, and their landscape-level effects. At three distinct field stations in Southern California, we have deployed rainfall occlusion shelters, followed by high-intensity precipitation treatments, to experimentally alter the effective hydroclimate that soils experience. We deploy an array of stable-isotope probing and 'omics tools to characterize the soil microbial response to high-intensity precipitation after drought. We build upon recent advances in lipidomic stable isotope probing to sensitively quantify microbial growth rates in soil using a combination of traditional- and vapor-SIP approaches. We couple estimates microbial growth rates to in-situ flux measurements of CO_2 and CH_4 to quantify soil carbon flow. Metagenomic and metabolomic approaches are applied to determine the specific strategies and metabolites responsible for C transformation. Combined, these SIP-enabled 'omics approaches yield a multi-faceted, quantitative understanding of soil responses to future climate conditions.