

The Impacts of Redox Periodicity on Microbial Community Structure and Carbon Transformations in a Wet Tropical Forest Soil

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Project Goals: This Early Career research examines the genomic potential and expression of tropical soil microorganisms as they experience shifts in soil temperature, moisture, depth and oxygen availability. Associated fluctuations in redox potential are proximal controls of mineral-organic matter interactions in humid, tropical soils. By tracking the degradation and fate of organic ¹³C labeled compounds during shifts in soil redox status, this work will improve our understanding of microbial metabolic flexibility, and how microbial processes affect the fate of organic carbon in wet tropical systems. The mechanistic understanding produced by this research will also improve the predictive capacity of mathematical models that forecast future tropical soil carbon balance.

Wet tropical soils can alternate frequently between fully oxygenated and anaerobic conditions, constraining both the metabolism of tropical soil microorganisms, and the mineral-organic matter relationships that regulate many aspects of soil C cycling. Using a 44 day redox manipulation experiment with soils from the Luquillo Experimental Forest, Puerto Rico, we examined patterns of tropical soil microorganisms and metabolites when soils were exposed to different redox regimes - static oxic, static anoxic, high frequency redox fluctuation (4 days oxic, 4 days anoxic), or low frequency redox fluctuation (8 days oxic, 4 days anoxic). Replicate microcosms were harvested throughout the incubation to measure the impact of redox condition on microbial community structure and activity, organic matter turnover, and soil chemistry. An addition of ¹³C enriched plant biomass allowed us to distinguish decomposition of fresh litter vs native organic matter, and conduct Stable Isotope Probing (SIP) to identify the responsible microorganisms. Recently we finished sequencing 16S rRNA libraries for 1127 SIP fractions, and metagenomic DNA from 88 SIP fractions, yielding over 22 billion reads and over 3.3 trillion base pairs. Individual metagenome assemblies produced over 6,000 genome bins (MAGs), and co-assemblies are under way to produce more high-quality MAGs. Virus-specific informatics recovered >30,000 viruses clustering into 6,123 viral populations (vOTUs), with ~1.82 vOTUs/Gbp of metagenome, and 466 vOTUs ≥10 kb. Viral richness was highest in the oxic samples and decreased by oxic dynamics (oxic>low frequency>high frequency>anoxic).

Our bulk 16S data shows the bacterial and fungal community composition in the two fluctuating redox treatments was indistinguishable from the native soil community, while those from the static redox conditions were distinct, suggesting communities in these soils are highly adapted to fluctuating redox conditions. Using differential abundance analysis, we found that fluctuating

redox enriched for relatively more bacterial and fungal taxa as compared to the static redox conditions. However, the anoxic treatment exhibited a distinct iron-cycling microbial structure compared to the other treatments. While gross soil respiration was slightly higher in static oxic soils, respiration derived from added litter was highest in static anoxic soils, suggesting that decomposition of preexisting SOM was limited by O₂ availability in the anoxic treatment. This is supported by distinct molecular composition of soil metabolites for each treatment (measured by FTICR-MS). Together, these results suggest that dynamic environmental conditions influence microbial community assembly and biogeochemistry in ways that could not be predicted based on extrapolation from static systems. Our results also point toward a microbial community that is highly resilient to dynamic redox conditions and show that distinct C compounds are differentially processed under varying redox conditions, likely because of their varying bioavailability (driven by mineral-OM dynamics) and/or shifted microbial metabolic capacity.

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