

Wetland Microbial Community Response to Restoration

Susanna Theroux^{1*}, Wyatt Hartman¹, **Susannah Tringe**^{1*} (sgtringe@lbl.gov)

¹DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, Walnut Creek, California

Project goals: This project aims to identify the geochemical and biological controls on greenhouse gas (GHG) production in coastal wetlands. Current projections of wetland response to global climate change are poorly constrained due to a limited understanding of the microbial mediators of carbon cycling in wetland soils. Using large-scale environmental genome sequencing, we aim to identify the microbial sentinels of GHG production and consumption in historic and restored wetlands of the San Francisco Bay-Delta. An enhanced comprehension of microbial metabolic arsenals will allow us to recommend management practices for future wetland restoration projects to maximize carbon sequestration and minimize microbial production of greenhouse gases.

Wetland environments play a critical role in the global carbon cycle, storing up to 35% of all terrestrial carbon and producing up to 75% of all non-anthropogenic methane. However, estimates of wetland GHG budgets are difficult to constrain given large variations in salinity, tidal regimes, soil saturation, organic carbon content, restoration status, and other geochemical and biological variables. Belowground microbial communities are the main drivers of greenhouse gases (GHG) cycling and their response to climate change will dictate whether a wetland serves as a net carbon sink or source. Wetland restoration has been proposed as a potential long-term carbon sequestration strategy, however wetland site selection and management practices are critical for ensuring restored wetlands sequester more GHG than they emit.

In an effort to better understand the underlying factors that shape the balance of carbon flux in wetland soils, we targeted the microbial communities along a salinity gradient ranging from freshwater tidal marshes to hypersaline ponds in the San Francisco Bay-Delta region. Using 16S rRNA gene sequencing and shotgun metagenomics, coupled with greenhouse gas monitoring and soil biogeochemical characterization, we sampled sixteen sites capturing a range of salinities and restoration status. As expected, freshwater wetland soils produced more methane than brackish and saline sites, since sulfate in seawater encourages sulfate reduction and discourages methane production. Restoration status also significantly affected GHG cycling: notably, restored freshwater and brackish wetlands produced orders of magnitude more methane than their historic counterparts, possibly due to differences in trace metal and organic carbon content in younger wetlands. However, unrestored former industrial salt ponds produced methane at rates rivaling those of brackish restored wetlands, and reconnection to the Bay resulted in a decrease in methane production.

The results of our microbial diversity survey showed that sampling location, plant type, and salinity were the primary drivers of both methane production and belowground microbial community composition. While overall methanogen abundance was only weakly correlated with methane production, both 16S and metagenome sequencing allowed for the identification of hallmark species whose relative abundance trended consistently with methane production. In unrestored salt ponds, the primary methane producers were methylotrophic methanogens utilizing substrates not accessible to sulfate reducers. Our study links belowground microbial communities with their aboveground greenhouse gas production and provides a benchmark for predicting wetland soil microbial response in the face of both natural and unnatural disturbances.

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