Microbial Communities in Restored Wetland Sediments

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http://www.jgi.doe.gov/sequencing/why/CSP2011-tringe.html

Project Goals: In this project, we use high-throughput sequencing tools to characterize microbial communities in restored wetland sediments, aiming to understand how the biotic and abiotic environmental factors govern microbial community structure and how microbial communities influence carbon flux, and thus impact long-term biological carbon sequestration.

On peat islands previously drained for agriculture, aerobic decomposition of peat has led to substantial land surface subsidence, thereby increasing risk of levee failure. Restoration of wetlands has a great potential to reverse land subsidence by slowing down decomposition and favoring new peat accumulation. In addition, the high primary production and slow decomposition rates found in restored wetlands may result in a net atmospheric CO2 sequestration. However, one major concern is the emission of CH4 that could potentially offset the carbon captured due to primary production. In wetland ecosystems, microbial communities play key roles in governing greenhouse gas flux, yet they are poorly characterized due to their high complexity. By using powerful high-throughput sequencing tools, we aim to identify community patterns, indicator species, genes or pathways that are associated with peat accretion rates and CH4 flux, and these will providing vital information for better modeling of wetland carbon flux and management.

In this preliminary study, we collaborated with scientists at the U.S. Geological Survey (USGS), and collected belowground samples from a restored wetland from a USGS pilot-scale restoration project on Twitchell Island in the Sacramento/San Joaquin Delta, CA. The wetland is continuously fed by water from San Joaquin River, and is primarily vegetated with cattails (*Typha* spp.) and tules (*Schoenoplectus acutus*). We selected three sites that have varied proximity to the inflow, thus exhibiting gradients in physicochemical conditions and peat accretion rates. From each site, we collected three sample types, including the bulk decomposed material, cattail rhizomes and tule rhizomes. Pyrosequencing of amplified V8 regions of 16S rRNA genes was used to generate microbial community profiles. In parallel, mesocosm anaerobic incubation was conducted to evaluate CO2 and CH4 flux.

Our sequencing data indicate that wetland community composition is primarily governed by sampling site, and secondarily by sample type. Particularly, wetland communities from these three sites transited in a direction largely consistent with the physicochemical gradients along these sites. The mesocosm incubation experiment

showed that CO2 flux was significantly higher in the rhizome samples than in the bulk samples. By contrast, difference in CH4 flux was more related to sample sites. Low CH4 flux communities were associated with the site closest to the inflow, correlated to higher availabilities of electron acceptors, particularly sulfate and nitrate. Some of their more abundant microbial populations, as compared to high CH4 flux communities, are likely reducers of these electron acceptors, as suggested by their closest microbial isolates. High CH4 flux communities were associated with sites further from the wetland inflow, which have shown higher peat accretion rates. These sites harbored more abundant methanogenic archaeal populations, which likely contributed to the higher methane flux observed.

Currently, additional samples collected in a different season are being analyzed to identify seasonal effects, and comparative metagenomic analyses are being conducted to reveal differences in community functional profiles.

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