Microbial diversity and carbon cycling in San Francisco Bay wetlands

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Wetland restoration efforts in San Francisco Bay aim to rebuild habitat for endangered species and provide an effective carbon storage solution, reversing land subsidence caused by a century of industrial and agricultural development. However, the benefits of carbon sequestration may be negated by increased methane production in newly constructed wetlands, making these wetlands net greenhouse gas (GHG) sources to the atmosphere. We investigated the effects of wetland restoration on belowground microbial communities responsible for GHG cycling in a suite of historic and restored wetlands in SF Bay. Using DNA and RNA sequencing, coupled with real-time GHG monitoring, we profiled microbial communities clustered according to sampling site (Figure 3a) and sample type (Figure 3b), although sampling site was a stronger predictor of community composition than sample type (ANOSIM 0.38 vs. ANOSIM 0.22, respectively).

Increasing methane production rates were observed at Twitchell wetland along the transect from site A→C→L (Figure 1). Methane emissions were highest at the Twitchell wetland site C which was furthest from the water inlet (Figure 3a). These higher CH₄ emissions corresponded lower oxygen, nitrate, and sulfate availability (He et al., in review). Microbial communities varied along the gradient of sampling location (Figure 3a) and sample type (Figure 3b), with sampling site being a stronger predictor of community composition than sample type (ANOSIM 0.38 vs. ANOSIM 0.22, respectively).

Link microbial diversity to carbon flux measurements from wetland soils

Methane production rates clustered along salinity and plant type gradients (Figure 7a). Tule (Schoenoplectus acutus) and cattail (Typha spp.) were associated with the highest rates of methane production. Net methane consumption was measured at the oligotrophic, historic wetland Sandmound Slough in the tube and three-square bulrush soils. The influence of sampling location (76±4), salinity, and plant type on methane production were all statistically significant (ANOVA, p<0.0001), although these factors co-vary. Site was a stronger predictor of methane flux (R²=0.62) than salinity (R²=0.144) or plant type (R²=0.03), although only methane flux from freshwater restored wetlands was significantly greater than the mean.

In Phase II of the project, we sampled a suite of wetlands in San Pablo Bay, Suisun Bay, and the Delta region of San Francisco Bay (Figure 2). These wetlands encompassed a salinity gradient ranging from 0 ppt (Sandmound Slough) to 40 ppt (China Camp). Five wetland samples were sampled in historical wetland sites (blue markers, Figure 2) and six wetland samples were sampled in restored wetlands (red markers, Figure 2).