

39. Microbial Communities and Carbon Cycling in California Coastal Wetlands

Susannah G. Tringe^{1*} (sgtringe@lbl.gov), Shaomei He,¹ Susanna Theroux,¹ Lisamarie Windham-Myers² and Wyatt Hartman¹

¹DOE Joint Genome Institute, Walnut Creek, California; ²US Geological Survey, Menlo Park, California

Project goals: To understand the role of belowground microbial communities in plant growth and nutrient cycling in wetlands, particularly their potential to enhance or inhibit effective carbon retention. This includes characterizing the organisms, genes and pathways present and active in wetland soils via nucleic acid sequencing and correlating them with biogeochemical features and carbon cycling metrics.

Wetlands are an important global carbon reservoir and carbon sink. While wetland carbon uptake is largely due to plant primary productivity, the overall greenhouse gas budget is heavily dependent on microbial activities such as plant biomass degradation and methanogenesis.

Wetland restoration efforts on the deeply subsided peat islands in the Sacramento / San Joaquin river delta, currently used primarily for agriculture, have been demonstrated to increase land elevation and sequester atmospheric carbon. We are using DNA and RNA sequencing to study belowground microbial communities in these restored wetlands to assess their composition, functional potential and impact on carbon cycling. The wetland soils harbor diverse communities of bacteria, archaea and fungi whose membership varies with sampling location, proximity to plant roots, and sampling depth in patterns that closely correlate with gradients of electron acceptor availability and methane production. Shotgun metagenome sequencing revealed complementary patterns in functional gene distribution, including apparent competition between methanogens and other anaerobic guilds. Expanded studies throughout the San Francisco Bay/Delta region are enabling us to correlate microbial community composition and greenhouse gas cycling with key environmental variables including salinity, soil carbon and duration of flooding.

This project was funded by DOE Early Career Research Program, grant number KP/CH57/1, and was also supported by DOE JGI Community Sequencing Program. The work conducted by the U.S. Department of Energy Joint Genome Institute is supported by the Office of Science of the U.S. Department of Energy under Contract No. DE-AC02-05CH11231.