One of the central functions of wetlands is to transform and remove nutrients from rivers prior to their entry into coastal waters. Globally, at least half of the world’s wetlands have been altered or lost due to diking and draining, while nutrient pollution of coastal zones continues to increase. In the Columbia River estuary, hydrologic connections to estuarine waters have been lost in >75% of tidal wetlands (~14,560 ha) in order to support shipping, fishing, logging, tourism, and agriculture. Over the last six decades, coastal communities have begun to breach some of the dikes to increase wetland habitat acreage, provide flood reduction, sequester carbon, and remove excess river borne nutrients.

A diverse assemblage of microorganisms carries out transformations and removal of excess nutrients in wetlands. While broad-scale differences in microbial communities have accompanied land use change, studies that demonstrate changes in microbial metabolism of particular nutrient elements such as nitrogen, phosphorus, and carbon are lacking. Since microorganisms often have a very narrow threshold of conditions for their growth, the presence of particular species provides important clues about environmental conditions. For example, β-Proteobacteria are more abundant in eutrophic systems while γ-Proteobacteria are more abundant in oligotrophic conditions. Thus, changes in habitat characteristics should result in altered microbial communities, with implications for ecological function.

I proposed to characterize the diversity (targeted metagenomic analysis) of microorganisms at sites that represent a chronologically aged gradient of times since restoration (2, 6, 24, 55 years), along with two reference sites (untouched natural wetland and agricultural site) in Youngs Bay, a lateral bay in the Columbia River estuary. The chronological age gradient provides an exceptional natural experimental system to investigate how microbial communities change in response to restoration actions. I hypothesized that sites >20 years since restoration would have similar microbial community structures to those observed in natural wetlands due to the observed recovery of hydrology and vegetation. I used the taxonomic marker 16S rRNA gene to provide a microbial community profile using the Illumina MiSeq sequencing platform. I collected sediments for DNA sequencing for two field seasons (2014, 2015) in triplicates from the top 5-10cm of wetland soils near the major hydrological features and along 50m transects from each site.

Funding provided by the Alan E. Leviton Student Research Award allowed for purchase of the specific primers and reagents to perform initial polymerase chain reactions (PCR) with environmental DNA and subsequent data from MiSeq analysis. Approximately 20Mb of data were obtained from MiSeq analysis in 42,000 sequences (~300 base pair median length) across the six sites. I used the python program QIIME to perform the 16S rRNA gene sequence analysis. I am currently performing alpha and beta diversity comparisons within and across restoration, natural and pasture wetland sites. Preliminary results indicate all sites undergoing restoration (2 – 55 years) and the wetland currently being used for pastures are similar to each other and vastly different from the natural wetland site.