



ABSTRACT

Southern California salt marshes are an essential part of our coastline providing key ecosystem services. An important component of ecosystem services are microbes that are involved in cycling Nitrogen, Carbon, and Sulfur which promote vegetation growth and contribute to overall marsh health. Sea level rise caused by climate change is a threat to these habitats resulting in the need for restoration practices such as sediment amendments. The Seal Beach Wildlife refuge contains a salt marsh where a sediment amendment has been executed to restore marsh elevation. In addition, Spartina foliosa are being planted to revegetate the amended land. Not much is known about how these amendments will affect the natural ecology of the wetland. We hypothesize The microbiome associated with planted Spartina foliosa roots will diverge over time from sediments without plants in an amended salt marsh. This study will look at the bacterial diversity of sand amended areas with Spartina foliosa and compare it to areas lacking vegetation to provide a better understanding of the interactions of microbial communities with plants on amended marsh land. This project will provide important information about the impact of marsh amendments on plant and microbial communities.

INTRODUCTION

- Salt marshes provide a variety of ecosystem services like wildlife habitats.
- Seal Beach Wildlife Refuge has undergone a sediment amendment elevate marsh land to fight against the effects of sea level rise (1).
- To do this a slurry mixture of sediment and water is piped and spread evenly onto the marsh As little as 2-3 cm can promote plant productivity.
- Further restoration is being done by planting Spartina foliosa (cordgrass). This variety of plant can withstand high sulfur content in the soil which is a common characteristic of a salt marsh.
- Planting of Spartina can have vast effects on the soil microbial community (2).

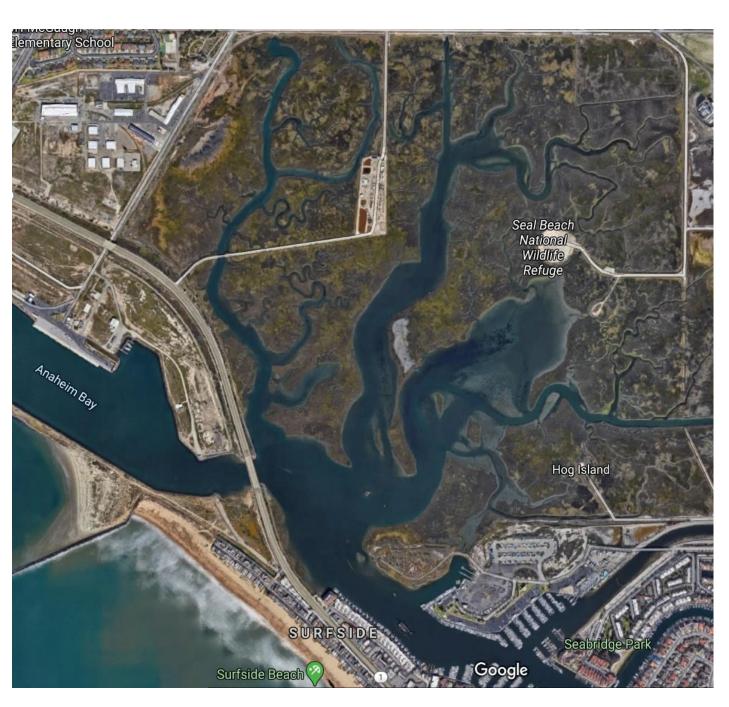


Figure 1. Salt Marsh at Seal Beach Wildlife Refuge

QUESTION

Does *Spartina foliosa* planting effect the sediment microbial communities in an amended salt marsh?

HYPOTHESIS

The microbiome associated with planted *Spartina foliosa* roots will diverge over time from sediments without plants in an amended salt marsh.

Effects of Plant Restoration on Microbial Soil Communities in a Sediment Amended Southern California Salt Marsh

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PROPOSED METHODS

Sample Collection and Physicochemical Measurements

Soil sample cores (10 cm deep x 1 cm diameter) will be collected over a one-year period following transplantation

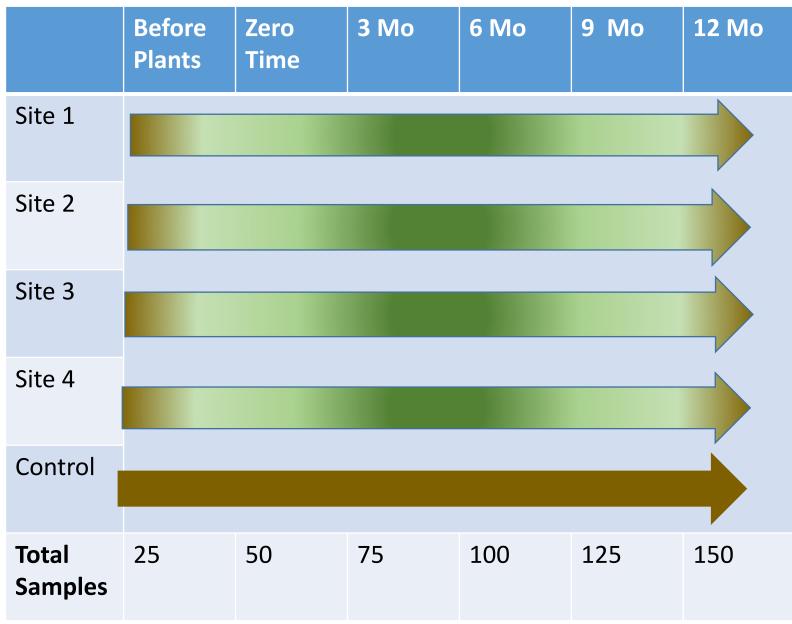


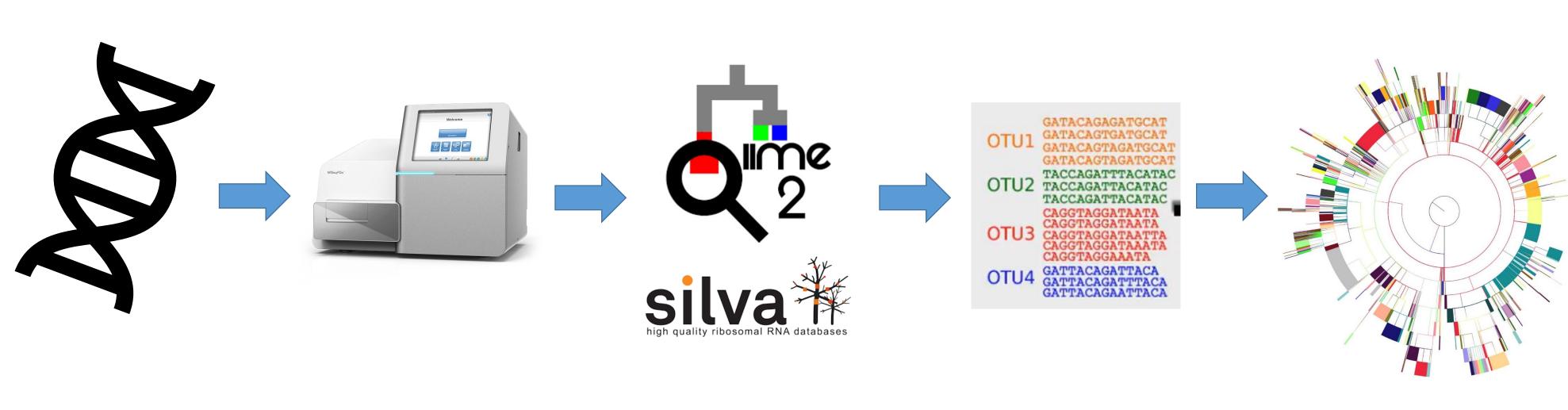


Figure 2. Spartina foliosa http://www.foundsf.org/index.php?title=File:Spartina foliosa upper newportbay.jpg

- Determine tidal height of each site.
- Other measurements taken include temperature, pH, sulfide quantities, rainfall

Nucleic Acid Extraction & Amplification

- DNA extraction via Fast DNA spin kit for soil
- Amplification and sequencing of 16S rRNA genes via Illumina MiSeq Next Generation Sequencing



Statistical Analysis

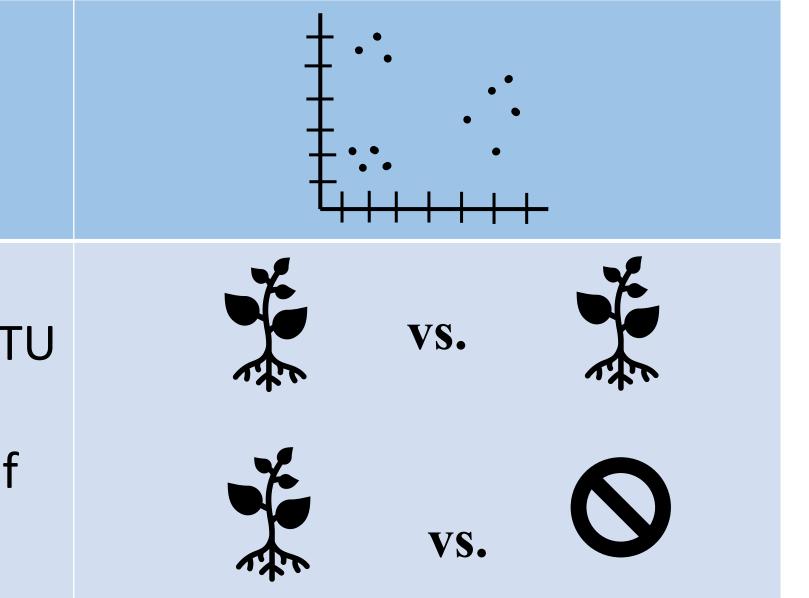
- Ordination analysis will allow us to visualize **community** differences
- Statistical analysis of alpha diversity using Shannon's Diversity Index will reveal how OTU diversity varies from sample to sample
- Beta diversity analysis will reveal diversity of species between site locations over time

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Bioinformatics

- Diversity analysis using QIIME2 software
- Taxonomy assigned using naïve Baysian taxonomy classifier against SILVA 97% database



EXPECTED RESULTS

Bacterial communities are expected to shift with the addition of Spartina plants. Three outcomes can be expected

Convergence: Bac communities ma at the beginning become similar c time

Divergence: Bact communities sta similar but chan time

Random: No similarities in bacterial commu can be seen

SIGNIFICANCE

The effects of sea level rise are endangering some of our most crucial wetlands. Sediment amendments and revegetation strategies will help combat this issue. Microbes are key players in biogeochemical cycling. This research will help us better understand how these microbial communities will respond to these strategies.

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ACKNOWLEDGEMENTS

This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Numbers; UL1GM118979; TL4GM118980; RL5GM118978. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health

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	Site 2						
	Site 3						
	Site 4						
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