

From Microbes to Zooplankton: What Defines A Beneficial Wetland?

Study Period
2021 – 2025

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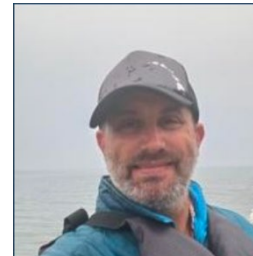
About this Project

How do wetlands provide food and shelter for juvenile fish, and how do these resources change with different wetland conditions? To better understand the variety of wetland species while focusing on food available for fish, this study investigated zooplankton and larval fish diets from wetlands in the Suisun Marsh and northern San Pablo Bay using a novel method called community environmental DNA (eDNA) metabarcoding.

Lead Investigators



Michelle Jungbluth, SF State University



Jason Hassrick, ICF International Inc.

What is eDNA Metabarcoding?

Collecting and analyzing environmental DNA (eDNA) is a novel sampling approach that allows scientists to assess the types of organisms present in different environments from which DNA can be extracted, including water, sediment, and air. All organisms regularly shed tiny amounts of DNA, so eDNA metabarcoding can detect the presence of rare species without needing to capture those organisms directly. Metabarcoding uses target-specific amplification and sequencing of DNA to

simultaneously identify multiple organisms. In other words, eDNA metabarcoding allows scientists to quickly grab a water sample, separate the small pieces of DNA floating in the water, and identify which species are present. In this project, scientists used eDNA metabarcoding to quickly and efficiently characterize fish communities in the San Francisco estuary, hoping to link the DNA in fish diets to species from nearby wetlands.

The species richness discovered by the research team using eDNA metabarcoding will be used to describe wetland conditions in different stages of restoration (early, intermediate, and mature). They will identify connections between those conditions and the food web resources provided to larval fishes, including longfin smelt, a threatened species.



Abundant larval fishes (mostly Pacific herring pictured) collected with a 500 μ m net and preserved in ethyl alcohol for the study, to be used for dietary DNA analysis.

(Credit, Max Chesser, ICF)

Project Objectives

- Collect eDNA samples at wetland restoration sites to identify the species present, from microbes to fish.
- Define a set of species that represents the stage of a restoration site and can be applied to future monitoring efforts.
- Identify food web resources provided by wetlands in different stages of restoration and compare them to standard ecological indicators.

Why this Research Matters

This study establishes cost-effective and non-invasive methods for the regional wetland management community to monitor, assess, and understand how tidal wetland restoration projects are progressing and contributing to the overall ecological health of the Sacramento-San Joaquin Delta. The research team is producing an unmatched baseline eDNA dataset for multiple levels of organisms in wetland restoration food webs from Suisun Marsh to northern San Pablo Bay.

Management Application

Surveying eDNA in each wetland will provide a list of biological indicator species that researchers and resource managers can use to prioritize sites and regions with the most beneficial food web resources.

Connections to the 2017-2021 Science Action Agenda

- 3: Develop Tools and Methods to Support and Evaluate Habitat Restoration
- 4: Improve Understandings of Interactions Between Stressors, Managed Species, and Communities
- 5: Modernize Monitoring, Data Management and Modeling