Fish Monitoring at the Giant Marsh Living Shorelines Habitat Restoration Project
Evaluation of Fish Abundance, Biodiversity, and Habitat

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Introduction

Surveys compared the fish assemblage in two control sites (unvegetated mudflats, natural eel-grass beds) and two treatment sites (restored eelgrass beds, oyster reefs) in and around the The San Francisco Bay Living Shorelines Project (LSP) restoration project at Giant Marsh in the the Point Pinole Regional Shoreline. Fisheries data were collected using Adaptive Resolution Imaging Sonar (ARIS) technology (i.e., a sonar camera), two physical sampling gears (seine and hoop nets), and environmental DNA (eDNA) metabarcoding

Objectives

1) To provide information on diversity, relative abundance, distribution, size structure, and habitat use of the fish community in restored and unrestored habitats.
2) To assess how various sampling gears performed in each habitat.

Methods

Field Methods

Surveys were conducted at four different locations within and adjacent to the project area:
1) restored eelgrass beds (eelgrass treatment),
2) oyster reefs (reef treatment),
3) natural eelgrass beds located southwest of the Project site (vegetation control), and
4) in a nearby mudflat with similar depths but without eelgrass or oyster reefs (mud control).

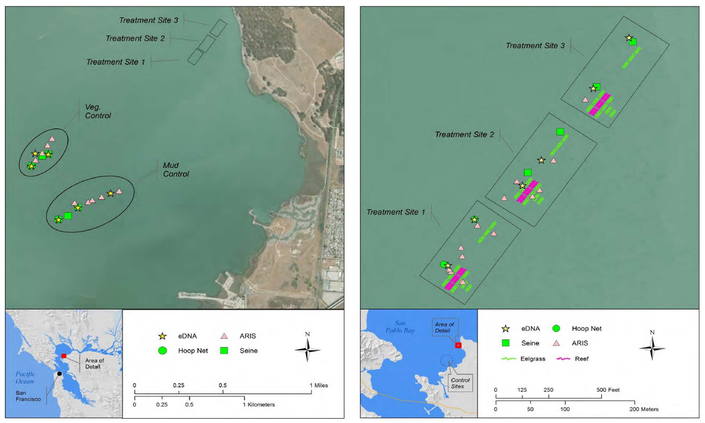
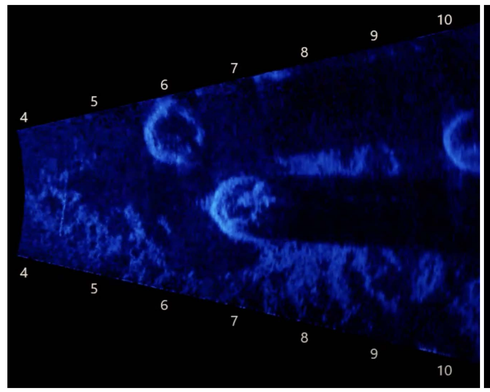
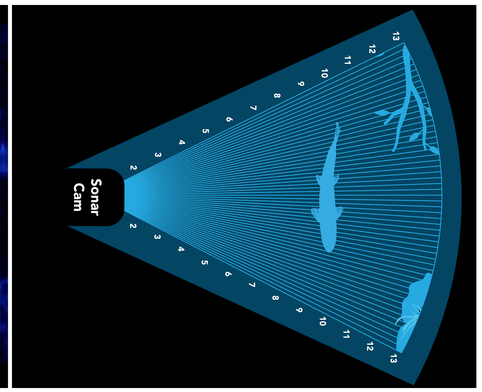


Figure 1. Maps depicting the sites where various sampling gears were deployed by the field team.

- Sonar surveys were conducted by boat, utilizing an ARIS camera to observe and enumerate fish. ARIS data were collected through transect and stationary surveys that were conducted at multiple locations in both the treatment and control sites.
  - o Individual sampling locations were selected to encompass the range of habitats at each site.
  - o Stationary surveys were replicated five times at the mud control site, six times at the vegetation control site, five times at the eelgrass treatment site, and nine times at the reef treatment site.
- Traditional, physical sampling surveys were conducted using both a winged hoop net and a seine net to sample fish at treatment and control sites
  - o Specific sampling locations were identified based on-site conditions, as determined during the preceding ARIS surveys, and the recommendations of the Project partners.
  - o All fish and crustaceans collected during physical sampling were identified to species and counted, and their fork and total lengths were measured in milli-meters. After processing, all fish were released at their location of capture.

Data Analyses





Species Diversity

- Shannon-Wiener Diversity Index (H') values, species richness values, and rarefied species richness values were calculated for each of the sample sites.
- All of these metrics of diversity were calculated both at the site level, and also for each type of fish sampling equipment or "gear" used at each site (i.e., seine nets and hoop nets).

Relative Abundance – Catch Per Unit Effort (CPUE)

- Catch-per-unit-effort (CPUE) was evaluated by gear type and location in order to assess relative fish abundance at each site.
- As with biodiversity data, all CPUE assessments were repeated by pooling treatment sites and control sites together to allow for comparison between restored and unrestored areas.
- This grouping was performed to allow for comparison of biodiversity metrics between areas where restoration activities have taken place and unrestored areas.

Fish Community Size Composition

- Average, minimum, and maximum total lengths of fish captured by each gear type in each location were analyzed in order to evaluate overlap in the fish being captured by each gear type.
- Large differences in standard lengths between gears may indicate that different age- and/or size-classes are more susceptible to capture by a particular gear.
- Assessing standard length data by site also provided additional insight into differences in fish community composition in each location.

eDNA Metabarcoding

- To supplement sampling of the fish community with traditional gears (seine nets and hoop nets), a total of 12 eDNA samples were collected across the sample sites.
- eDNA samples were collected with single-use sampling kits (Jonah Ventures) across a range of habitats corresponding to sample locations for both the ARIS and traditional gears.

Results

Species Diversity

- A total of 11 species of fish representing 11 distinct families were captured in the seine and hoop net sampling.
  - o Seven of these species were captured only in seine net samples
  - o Three were captured only in hoop net samples
  - o One was captured by both seine and hoop nets
- An additional five invertebrate taxa were captured by the seine net hauls.
- The H' value for each of the control sites was slightly higher than that of the two treatment sites (Figure 2).
  - o This pattern was paralleled by the rarefied species richness values for the control and treatment sites.
- Rarefied species richness values demonstrates that the higher diversity in the control sites was driven by a slightly higher species richness in the seine net catch in the mud control site (Figure 3).
  - o However, the minimal difference among all sites suggests that the actual diversity among the control and treatment sites was quite similar, and the difference in species richness and diversity index calculations may have simply been due to chance or sampling conditions.

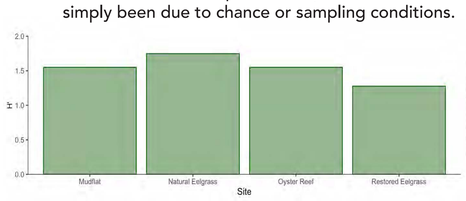


Figure 2. Shannon-Wiener Diversity Index (H') values based on the total fish diversity captured in seine net and hoop net sampling in the four habitat types sampled.

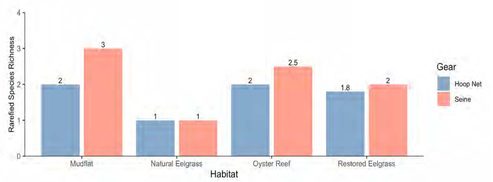


Figure 3. Rarefied species richness in the catch of each fishing gear used in the four habitat types sampled.

ARIS

- Significantly more fish were observed with the ARIS compared to traditional net sampling.
- However, mean CPUE for ARIS deployments showed a similar pattern to the seine nets, with slightly higher CPUE on average in the two control sites but wide standard deviation amongst individual habitats.
- The average, maximum, and minimum total lengths of fish observed in the ARIS footage also shows a pattern of similar fish sizes between the control and treatment sites.
- The detection of much larger individuals with the ARIS suggests that the hoop and seine sampling failed to capture fish at the upper end of the size distribution.

eDNA

- A total of 82 unique sequences belonging to 17 different fish taxa were observed across all 12 samples.
- Sequences identified to species include:
  - o three that were also captured by seine net,
  - o one that was captured by the hoop net sampling,
  - o and another six that were not represented in the seine and hoop net catch.
- Notable taxa that traditional sampling failed to capture but whose DNA was detected in the eDNA samples included sturgeon (either Acipenser medirostris or A. transmontanus), as well as invasive yellowfin goby (Acanthogobius flavimanus).

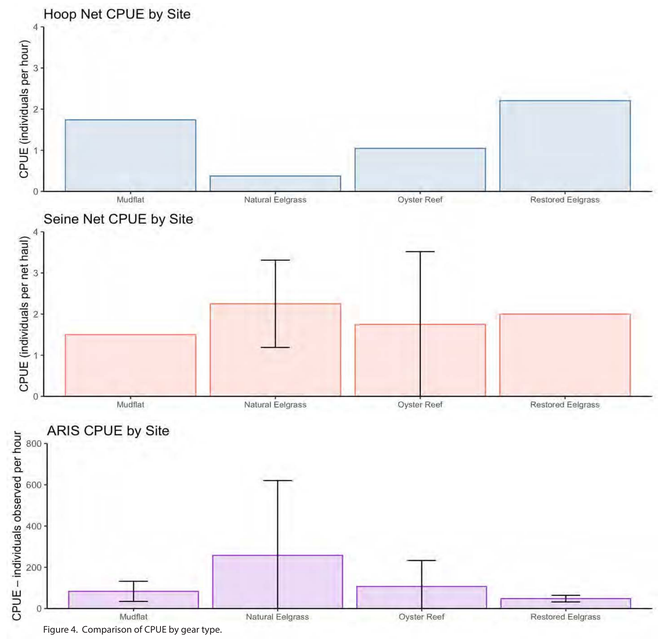


Figure 4. Comparison of CPUE by gear type.

Summary and Implications

- Multi-gear sampling of fish at Giant Marsh suggests that species composition, size composition, and relative abundance of the fish community is generally consistent across both the restored and existing habitats.
- The lack of significant differences in the fish community between treatment and control sites should be considered in the context of recent restoration activities, challenges associated with sampling of the project area, and the dynamic nature of the intertidal zone.
- Although it is not possible to definitively determine whether the species detected by eDNA occurred within or outside of the sample sites, gathering data on their presence in the marsh may help document important or imperiled species that would otherwise go undetected.
- To effectively and accurately capture the fish community within the region, fish community surveys should be conducted throughout the year. Repeated monitoring would improve confidence that the patterns (or lack thereof) observed in this study are ecologically meaningful.
- A mixed sampling approach is the most effective means of monitoring the fish community at the Giant Marsh LSP.

Acknowledgements

We would like to thank the staff at the San Francisco State University Estuary & Ocean Science Center who assisted with this study. In particular, Katharyn Boyer and Margot Buchbinder provided knowledge of onsite conditions and helped with planning and study design, and Margot Buchbinder, Jessica Bruno, Tessa Filipczyk, Shea Grady, and Taylor Jenks aided field surveys. Lastly, we would like to acknowledge the California Coastal Conservancy who provided funding for this study.

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