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Using eDNA to assess impacts of oyster restoration on ecosystem biodiversity at a heavily impacted coastal lagoon

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Using eDNA to assess impacts of oyster restoration on ecosystem biodiversity at a heavily impacted coastal lagoon

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Introduction & Background

The Great South Bay (GSB; Fig. 1), a bar-built, temperate, coastal lagoon on the south shore of Long Island, New York, USA, is a highly modified estuary due to heavy urbanization in the last century. GSB historically provided up to 50% of the nation's hard clam (*Mercenaria mercenaria*) harvest, and is the legal home of the "Blue Point" oyster (eastern oyster; *Crassostrea virginica*). However, overexploitation and persistent stress from ongoing nitrogen pollution and harmful algal blooms, shellfish populations are fractions of their original abundances.

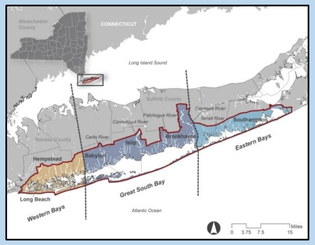


Figure 1: Map of New York and the location of the South Shore Estuary Reserve (SSER), which includes the Great South Bay (GSB; watershed in dark purple). Map produced by NY Department of State.

Figure 2: GSB stations from this study. Green points are open-water stations. Red are coastal. Orange are oyster habitat. Yellow is the new inlet station. Purple shaded areas are new or recent oyster aquaculture plots or designated no-take restoration sites.

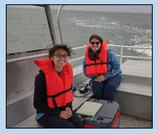
In the last century, GSB has gone through boom-bust periods with respect to the dominant filter-feeders. Various shellfish sanctuaries such as the Bay Bottom Program and Friends of Bellport Bay are working to build back the GSB's resiliency. Restoration of the eastern oyster is a focus as they are seen as ecosystem engineers and keystone species in this lagoon due to their significant capacity to filter water.

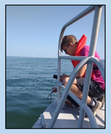
In summer 2023, we collected samples from 16 stations (Fig. 2) to isolate environmental DNA (eDNA) and implement next-generation sequencing to determine how new oyster habitat impact biodiversity. This is the first year of an ongoing project that will determine the impacts of oyster restoration on resiliency of GSB, as determined from eDNA-based biodiversity estimates. A secondary objective is to determine the impacts on biodiversity after the closing of an inlet between 2023 and 2024.

Methodology

- Sample Collection:
  - Sixteen total stations
  - Sampled 2-3 times a week from May to September 2023
  - Additionally collected water quality data (temperature, salinity, pH, dissolved oxygen)

- Water Quality Data collection:
  - Instruments: YSI ProDSS Multiparameter Water Quality Meter (Xylem), and horizontal water sampler
  - After water samples were collected, transported on ice to a Molloy field station (near station 10; Fig. 2) for processing.





- Sample Processing
  - 0.5- 1.0L of water filtered onto 0.22µm Sterivex Pressure filters (Millipore) using a peristaltic pump, preserved with lysis buffer (50 mM Tris-HCL, 40 mM EDTA, 0.73 M sucrose) and stored frozen.
  - DNA extracted according Suter et al. (2018), purified with the Genomic DNA Clean and Concentrator-25 kit (Zymo).

- Amplification and Sequencing:
  - Hypervariable region of the 12S rRNA gene from fishes (teleosts) was amplified using the universal primers designed by Miya et al. (2015) and modified by Stoeckle et al. (2022; MiFish-U-F/ MiFish-U-R2)
  - PCR products were cleaned by gel extraction (Zymo) and indexing and sequencing were performed at Michigan State University's RTSF Genomics Core on Illumina MiSeq 2 x 250bp using the Nano Kit v2.

Results

Station	Average DNA Concentration (ng/ µL)	Commonly Detected Species
2 (Open- Water)	39.7	Seq 1 (Summer Flounder) Seq 5 (Northern Kingfish) Seq 13 (Striped Burfish)
13 (Open- Water)	35.8	Seq 1 (Summer Flounder) Seq 46 (Summer Flounder) Seq 3 (Bay Anchovy) Seq 41 (Summer Flounder)
14 (Oyster Habitat)	70.2	Seq 1 (Summer Flounder) Seq 6 (Tidewater Silverside) Seq 40 (Tidewater Silverside)
Billie's Marina (Coastal)	70.7	Seq 1 (Summer Flounder) Seq 2 (Menhaden) Seq 3 (Bay Anchovy) Seq 4 (Tidewater Silverside)

Figure 3: Marine species variation based on various station locations around the GSB. Along with the corresponding DNA concentration averages from the samples sequenced from each of the stations.

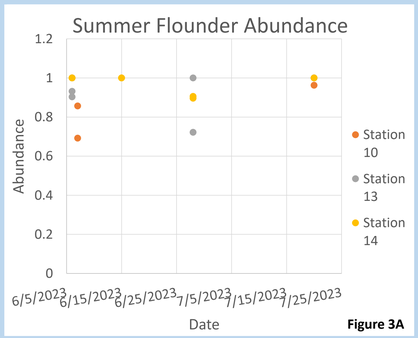


Figure 3A

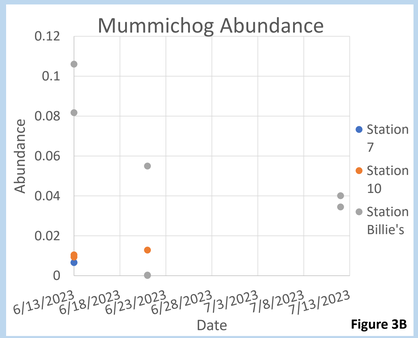


Figure 3B

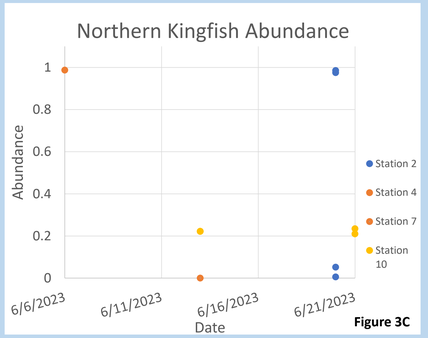


Figure 3C

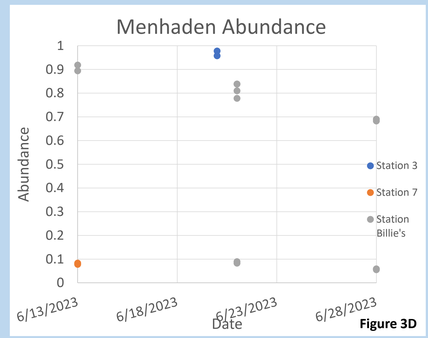


Figure 3D

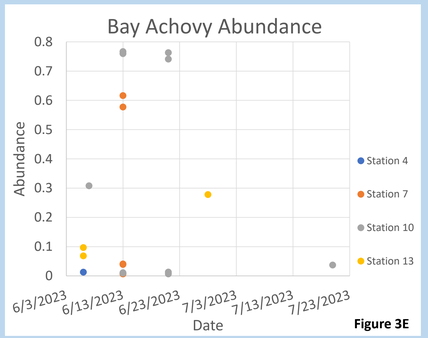


Figure 3E

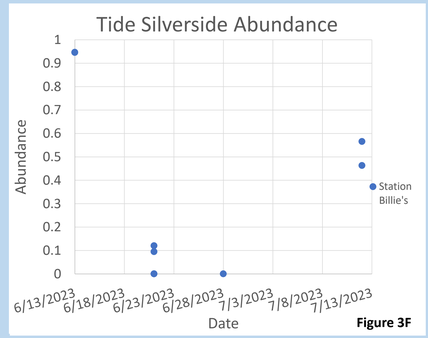


Figure 3F

Figures 3A- 3F: These figures show the abundance and distribution of a variety of native fish species over time. The distribution of the fish species is an additional indicator of the health of the ecosystem and the health of the fish population.

Conclusion

In this pilot study of the GSB, careful eDNA sampling and sequencing provided evidence that the GSB is home to a wide variety of commercially important fish. Longer term analyses will help us to determine if this is due to the extensive cooperation of the multiple shellfish restoration projects.

Future goals of this project include continuing to collect seasonal water samples for water quality and eDNA to see any potential changes to the type, distribution, or frequency of teleosts in order to gather a more comprehensive and complete view on how shellfish reintroduction to the GSB has benefitted the local marine ecosystem.

Acknowledgements

We especially thank Steven, Deborah, and the rest of Macchio family for their commitment to this and other projects dedicated to sustainability in Gino's name. We also thank the Foundation's executive director, Ken Daly, and boat Captain Steven Rafalko for their logistical support and invaluable input in the project, the Molloy BCES department for their assistance in facilitating this work, and CSTEP for support of DD during her thesis work.

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