NEW YORK STATE WATER RESOURCES INSTITUTE
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Oyster Population Connectivity in Hudson River Estuary

Mapping Oyster Offspring and Testing for Restoration Contributions

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Matt Hare introducing this project to community scientists at the Hudson River Park Trust River Project facility at Pier 40. The goal of the work session was to find every oyster spat on shell that was deployed in the Hudson River Park for two months. Photo credit: Yuqing Chen

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This report was prepared for the New York State Water Resources Institute (NYSWRI) and the Hudson River Estuary Program of the New York State Department of Environmental Conservation with support from the NYS Environmental Protection Fund.

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Executive Summary

Hare Lab members from front to back: Yuqing Chen, Henry Hua, Harmony Borchardt-Wier. Photo: M. Hare

Keywords

Eastern oyster, restoration, biophysical model, genomic identification

Oyster restoration in Hudson/Raritan Estuary has seen recent successes in terms of growth, survival, and reproduction of installed oysters. However, the oyster life cycle begins with larvae in the plankton for 2-3 weeks. Settlement of larvae onto hard substrates has been minimal and sporadic through most of the estuary. When and where juvenile spat are found, it has been impossible to know whether they originated from restoration parents or the wild remnant Tappan Zee population. This is the usual 'blind spot' that all oyster restoration suffers from, making it nearly impossible to assess restoration impact in terms of a fundamental population metric (offspring re-supply), and leaving the black box of population connectivity shut tight. Here, we continue to use spatial spat monitoring to validate predictions of oyster larval dispersal (population connectivity) from a biophysical model. Genomic identification of parental source for each spat, either wild or restoration, further enhances our model validation as well as providing the first empirical estimates of restoration contributions to each annual spat cohort.

Policy Implications

Restoring a self-sufficient population of eastern oysters to Hudson River Estuary is not about success (growth, survivorship and reproduction) at any one restoration site. Planning and restoration site prioritization need to be at the system scale to build a set of demographically connected populations.

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Introduction

> **“What we know is a drop, what we don’t know is an ocean."**
>
> **-Sir Isaac Newton**

The native eastern oyster, *Crassostrea virginica*, was nearly extinguished from the Hudson/Raritan Estuary (HRE) over 100 years ago due to habitat degradation. Perhaps for this most urbanized of estuaries the denudement of oysters and most below-water biodiversity is not so surprising as the persistence of a remnant wild oyster population north of New York City (NYC). During the 20th century we gained the political will to improve HRE water quality. The Hudson River no longer stinks or contains large anoxic zones, welcoming back aquatic life. During the last few decades the science of oyster restoration has advanced, and in most places this requires introducing hatchery-produced oysters to jump-start restored habitat. Many organizations, Billion Oyster Project and Hudson River Park Trust prominent among them, have engaged thousands of citizens in the herculean task of bringing eastern oysters back to the lower HRE so that their natural ecosystem services (water filtration, nutrient cycling) further improve water quality and biodiversity. Growth and survival of the oysters is monitored for years, and yet it is very difficult to know whether the planted oysters can be self-sustaining because we are completely ignorant about the critical first stage of oyster life when dispersal happens.

Oysters start life near their parents as a tiny, neutrally buoyant larva – a tiny bivalve with swimming/feeding appendages for consuming microalgae. Eastern oyster larvae spend 2-3 weeks almost entirely at the mercy of the currents before instinctively diving to the bottom to find suitable attachment habitat (wisely, preferring to settle near living oysters). A restored reef of adult oysters may be a prolific generator of larvae, but in most cases scientists have no clue where they go. After 2-3 weeks of tidal currents, probability theory suggests that landing near parents is rare. If the home reef is isolated in a matrix of poor habitat, then chances are, most larvae will not find their way ‘home’ or to suitable habitat. However, if habitat restoration is achieved at multiple sites that are arranged spatially to be in the larval delivery path of average currents, then the exchange of oyster offspring between restoration sites can generate a self-sustaining population. Most restoration is not planned this way because it is nearly impossible to predict larval dispersal patterns accurately. Modeling 3D hydrodynamics and larval behavior can paint a picture, but larval behavior is a critical variable that scientists understand only vaguely. If some model predictions can be verified, then confidence increases that other model outcomes might also be accurate.

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The Hare Lab and collaborators are generating model predictions of larval dispersal in the HRE and verifying them with old-school spatial mapping of oyster juveniles (recently settled larvae metamorphosed into 'spat') and cutting-edge genomic discrimination of wild vs restoration oyster offspring. The NYHOPS hydrodynamic model for HRE was coupled with a larval behavior submodel by Sean Kramer at Norwich University. This biophysical model spatially tracks *in silico* tracers that behave like larvae, generating destination maps for tracers from any source. The genomic panel of DNA markers used in this study were previously determined to be genetically differentiated between wild oyster populations vs selectively bred aquaculture strains, i.e., domestication variants. HRE oyster restoration practitioners use aquaculture strains for restoration, so they are identifiable.

Methods

Starting in 2018 the Hare Lab and collaborators have annually deployed mesh bags of bivalve shell along the Hudson River shoreline to 'capture' settling oyster larvae. All bags go in the river and two months later get retrieved simultaneously so that spat numbers provide a snap-shot map of oyster offspring abundances. Cured shell is generously provided by the Billion Oyster Project and many cooperators help provide secure shoreline deployment sites.

Because Hudson River Park has planted millions of oysters in their park since 2021, and because the biophysical model predicts that offspring fromHRPTparents will rarely return home to settle within the park, sampling inHRPTwas a large focus of the 2024 field season with the help of River Project personnel. The biophysical model predicts that the majority ofHRPTlarvae settle on the NJ shore north of HRP, and to a lesser degree along the Manhattan shore. Thus, 2024 NY sampling included sites in Riverside Park, Dyckman Marina Park, the Baylander restaurant, Yonkers Science Barge, and the Irvington Boat Club. New Jersey sites were limited due to access constraints, but included Edgewater Marina in Edgewater and Chart House Restaurant in Weehawken. Table 1 lists all sites by name and the number of spat collected there from a deployment from ~July 19 to ~September 19.

Genomic analysis used a GTseq amplicon panel of 243 markers previously determined to be differentiated between wild and aquaculture oysters (domestication candidates identified by Zhao et al. 2024). DNA was extracted from spat gill and mantle (or whole spat if very small). The GTseq library (a pool of all individual spat and all loci, barcoded to allow recovery of individual data) was sequenced using an Illumina NextSeq 500 at the Cornell Institute of Biotechnology. Genotyping from sequence reads was done using software described in Campbell et al. 2015.

Spat genetic variation was compared with reference samples from the Tappan Zee wild population and from several aquaculture strains that have been used for restoration in Hudson River Park and elsewhere in the estuary. Genotypic assignments of spat to wild vs aquaculture population sources was done visually from principal component plots and quantitatively using the model-based Bayesian STRUCTURE program incorporating an admixture model.

Table 1: Deployment locations, number of mesh shell bags deployed, and spat numbers (both bags together) from the 2024 field season. Spat/shell is based on a count of every substrate shell larger than a quarter in the two bags combined. A subset of spat were ethanol preserved for genomic analysis.

Location	# bags	Shell count (both bags)	Spat count	spat/shell	ethanol count
Irvington Boat Club	2	575	1644	2.86	200
Science Barge, Yonkers	2	712	1130	1.59	362
Baylander, West Harlem	2	532	176	0.33	176
Dyckman Docks	2	496	256	0.52	256
Riverside Park, GW Bridge	2	602	253	0.42	253
Riverside Park, 97th st.	2	629	112	0.18	112
Riverside Park, RR Ruins	2	469	32	0.07	32
HRP Pier 96 mid-level	2	408	95	0.23	95
Pier 96 mid-level south	2	457	107	0.23	107
Pier 96 bottom-level	2	683	199	0.29	199
HRP Little Island - surface	2	474	50	0.11	50
Little Island mid-level	2	608	55	0.09	55
Little Island bottom-level	2	562	40	0.07	40
HRP Pier 40	2	461	57	0.12	57
HRP Pier 26	2	465	38	0.08	38
Gov. Island Pier 101	2	(1 bag) 282	0	0.00	0
Edgewater Marina	2	598	329	0.55	329
Chart House Restaurant	2	505	294	0.58	294
Fresh Kills, Staten Is, NY	2	587	83	0.14	83
Hackensack R, Laurel Hill	2	778	752	0.97	128
Hackensack CSX RR bridge	2	369 (holes in bags)	117	0.32	98
RCYC, Great Kills, Staten Is	2	777	3	0.004	3
Earle Navy base	2		50		15
			5944		3049

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Results and Discussion

Annual Hare Lab spat counts since 2018 provide spatially broad and systematically collected data to compare with model predictions. Table 1 provides the collection localities and spat numbers from 2024 mesh shell bag deployments. A total of 5944 spat were collected and 2660 spat were genotyped along with 46 reference aquaculture adults from the Gansevoort restoration planting (provided by Hudson River Park Trust).

Figure 1 shows the geographic distribution of 2024 spat counts throughout the Hudson/Raritan Estuary. Four out of seven years of spat monitoring have shown this pattern of diminishing spat abundance moving south from the remnant wild breeding population. Because the biophysical model shows this same spatial abundance gradient for tracers released from the remnant population, the upper estuary larval dispersal predictions seem reliable. Furthermore, in 2022, 2023 and 2024, thousands of spat from the upper estuary were genomically identified as offspring from wild parents, and the remnant population in the Tappan Zee/Haverstraw Bay area (TPZ/HB) is the only known wild, reproductive oyster population in the HRE. The model and empirical data agree that somehow, the river physics and larval behavior are keeping larvae in the north most years, where their settlement supports maintenance of this isolated population. This pattern may help explain why the TPZ/HB population has not spread south as water quality improved.

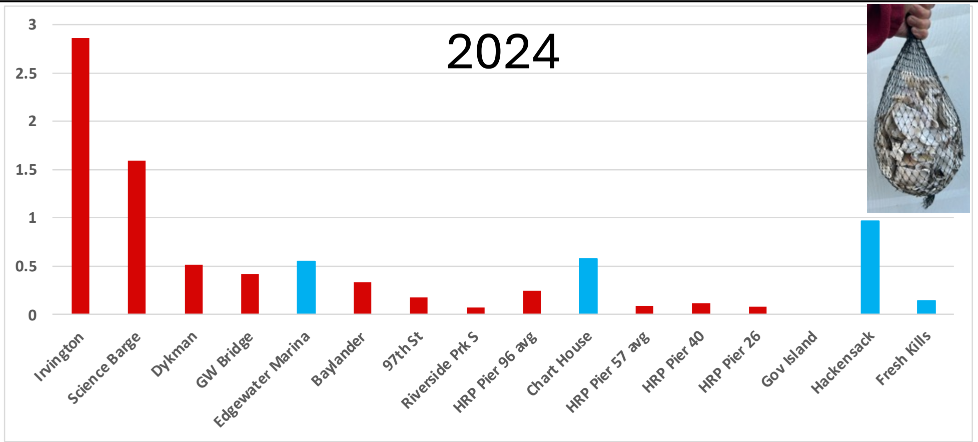

Fig. 1 – Number of spat per shell in 2024 after July-Sept deployment of shell bags, as shown in inset. Sites arranged North to South along Hudson Estuary, with west shore sites in blue and east shore sites in red.

One of the very consistent predictions made by the biophysical model is that the lower west side of Manhattan receives relatively few offspring from the TPZ/HB wild population in most years (as shown in Fig. 1). This is where Hudson River Park Trust (HRPT) has planted millions of oysters since 2021. Unfortunately, the model results also indicate that HRPT oyster offspring rarely return to settle in the Park. Instead, the majority of HRPT oyster offspring are predicted to settle near the NJ Palisades where heavy siltation may lower survivorship. This model prediction is tested here with thousands of spat collected in 2024, replicating a similar effort in 2023, both years when HRPT restoration oyster reproduction was documented. Figure 2a shows a principal component plot (PCA) of individual oysters (round colored symbols) from TPZ/HB

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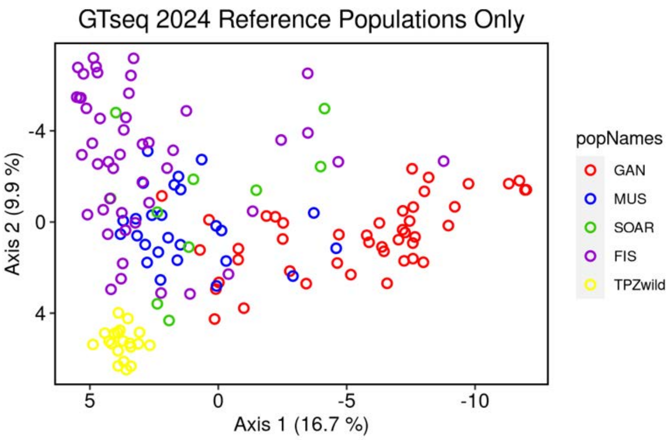

Fig. 2 – Principal component plot of oyster samples from 4 aquaculture strain and 1 wild reference populations. Axes 1 and 2 are shown because they are the two axes that explain the greatest genetic variance (in parentheses). Each colored symbol is an individual oyster, and its relative position depends on genetic similarity.

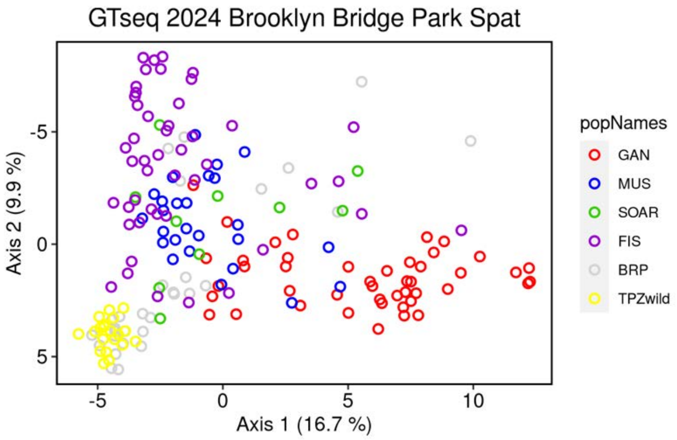

Fig. 3 – Principal component plot of oyster samples from 5 reference populations and one set of spat unknowns from Brooklyn Bridge Park (BRP; gray). Each colored symbol is an individual oyster, and its relative position depends on genetic similarity.

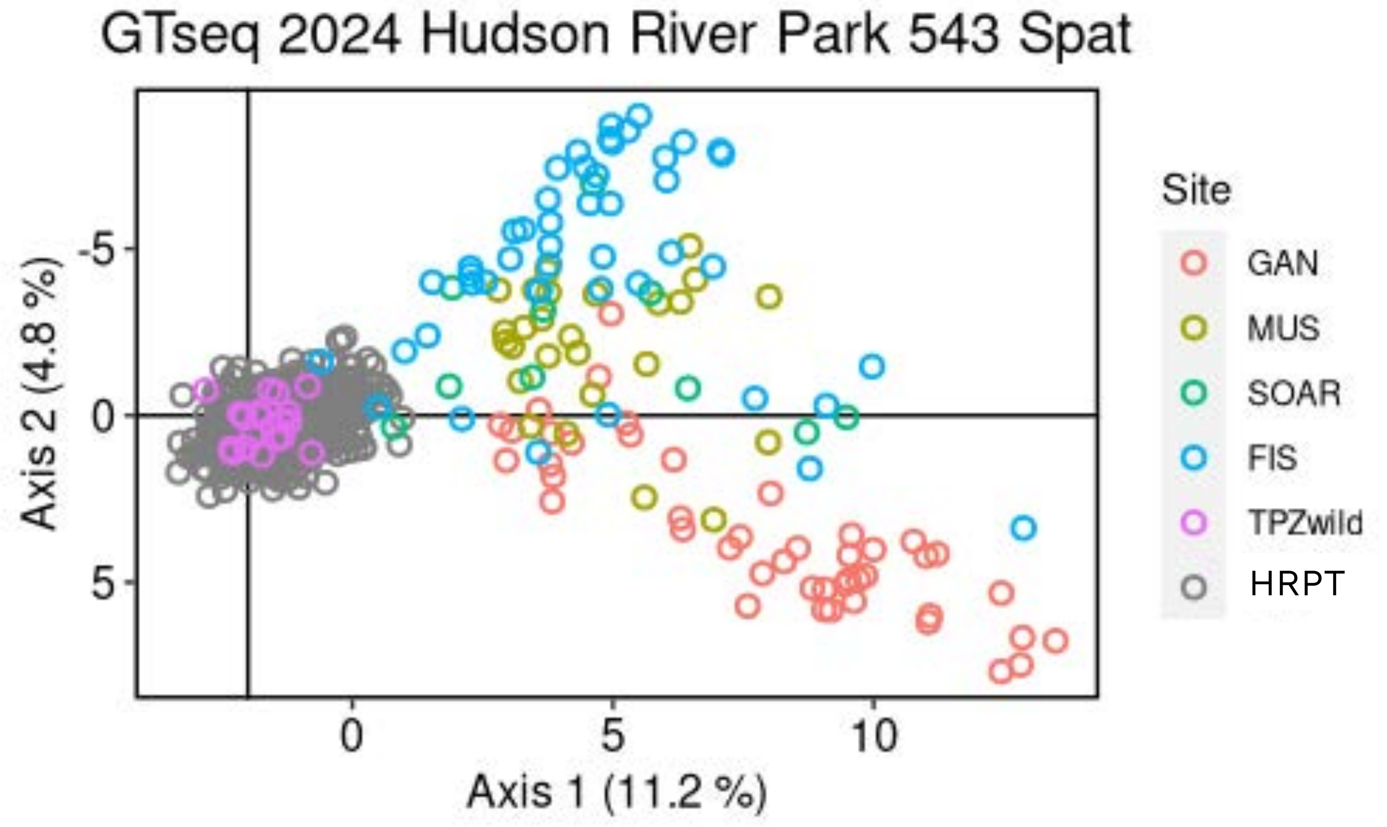

Fig. 4 – Principal component plot of oyster samples from 5 reference populations and one set of spat unknowns from Hudson River Park Trust (HRPT; gray individuals from 4 sites within HRPT). Each colored symbol is an individual oyster, and its relative position depends on genetic similarity. Note that legend colors have changed; the Tappan Zee wild reference is now fuchsia instead of yellow.

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(=TPZwild in legend) and several aquaculture strains planted in HRPT. A PCA describes genetic variance, and Fig. 2 shows that wild TPZ/HB oysters (yellow, lower left) can be distinguished from any of the aquaculture strains used for restoration. Based on Mendelian principles, the result in Fig. 2 using adult reference samples means their offspring also can be distinguished. Figure 3 is a PCA with the same reference populations and 31 gray spat unknowns collected by Billion Oyster Project near their Brooklyn Bridge restoration site. Half of these spat have genetic variation indicating wild parents, the other half are scattered in the 'genotypic space' proximate to aquaculture strains indicating they are likely restoration source population offspring. Finally, in Figure 4 we see that 543 spat collected from HRPT in 2024 (gray symbols) all show genetic similarity to the TPZ/HB wild population (fuchsia). Some HRPT spat overlap a few of the most 'wild-like' aquaculture reference individuals, but the tight clustering of gray spat circles is characteristic of wild genetic variation, and the spat are centered on TPZwild diversity. This provides robust evidence that oyster larvae settling in HRPT are largely coming from wild oyster reproduction. Given that this result validates the biophysical model prediction that it is rare for HRPT offspring to return to their source Park, are their HRPT oyster offspring found elsewhere?

All HRE restoration efforts use the same aquaculture strains so we cannot determine at this point whether the subset of Brooklyn Bridge Park spat, identified as restoration origin (Fig, 3), were born at a BOP or HRPT reef. An additional 2086 spat collected throughout the estuary, all outside of HRPT in 2024 (all sites in Fig. 1), were analyzed. All were determined to be offspring of wild oysters (Results not shown). This includes NJ samples across from Manhattan, Hackensack River samples (which probably have Hackensack wild parents), and southern Raritan Bay spat (Earle Naval Base) that may or may not reflect dispersal from TPZ/HB.

At this point our research demonstrates an incredibly informative combination of tools to understand potential oyster population connectivity in the HRE and measure restoration impact in terms of offspring contributed at any sampled site. Because our spat collection efforts to date have been spatially limited to sites we can access from shore, and have not included NJ palisades sites with the highest likelihood of receiving HRPT offspring (according to the model), there is further work needed to more fully test the biophysical model and understand HRPT restoration contributions to the HRE oyster population. In other words, we may not have been looking in the right places to find HRPT oyster offspring. Funding and a boat are being sought to make more targeted 2025 oyster spat collections.

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Student Training

This project did not financially support any students, but in 2024 our field work provided training for a PhD student in the Natural Resources graduate field.

Publications/ Presentations

1. "Recruitment mapping and multilocus genotyping helps validate biophysical model predictions about oyster connectivity" (publication in preparation with S. Kramer, P. Orton, Yuqing Chen, Henry Hua and Harmony Borchardt-Wier).

2. Hare, M.P., S. Kramer, H. Hua, Y. Chen, H. Borchardt-Wier. Advancing oyster restoration by studying connectivity with biophysical models and genomic assignment tests. University of New Hampshire, Nov. 2024

3. Hare, M.P., S. Kramer, H. Hua, Y. Chen, H. Borchardt-Wier. 2024 had the strongest oyster recruitment ever observed. Hudson River Estuary Program Annual Conference, Nov. 2024

4. Hare, M.P., S. Kramer, H. Hua, Y. Chen, H. Borchardt-Wier. Biophysical modeling and genomic dispersal estimates to map larval connectivity for oyster restoration planning in Hudson River, NY. International Conference on Shellfish Restoration, Jekyll Island GA, Sept. 2024

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