

Do constructed habitats promote biodiversity in a recovering ecosystem? Analysis of biodiversity in the Newtown Creek living dock.



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Abstract

The Comprehensive Environmental Response, Compensation, and Liability Act of 1980 (CERCLA), otherwise known as Superfund, is a United States government program that is designed to clean up waste sites that are contaminated with hazardous substances. In September 2010, the U.S. Environmental Protection Agency (EPA) placed Newtown Creek on the CERCLA National Priorities list. Recent installations of living docks at Newtown Creek were made to foster biodiversity in the recovering ecosystem as a result. However, the efficacy of these structures remains mostly unstudied. This study aimed to compare the biodiversity of the living dock to other sites along the Creek. Though the results were inconclusive, this study confirmed that structures like the living dock help foster biodiversity in this recovering NYC ecosystem.

Introduction

- To assist in the restoration of biodiversity, the Newtown Creek Alliance installed two living docks with the aim of providing habitats for creek organisms.
- There are no studies that study the efficacy of these structures in fostering biodiversity.
- Samples were collected from the living dock and the bulkhead on Kingsland Avenue, which served as the control site. Using the samples that were identified, the biodiversity of both the living dock and bulkhead were calculated and compared.
- It was hypothesized that the living dock would have greater diversity than the control site.

Materials and Methods

Sampling: At the living dock and our control sites we used existing structures to collect our samples. At the living dock, removable inserts (milk crates) formed microhabitats for fish and invertebrates. At the the bulkhead, an existing lobster cage seeded with oyster shells as well as plankton troughs formed our sampling methods. Samples were preserved in ethanol and documented in advance of processing. **DNA isolation:** We isolated DNA from each collected sample according to the DNALC protocol and amplified DNA using the PCR primers LCO1490 and HC02198, confirming amplification by gel electrophoresis and subsequent Sanger sequencing (Genewiz). **Sequence Analysis:** The DNA sequences were analyzed using DNASubway (Blue Line) and verified using NCBI-BLAST. Some species calls were verified and extended by staff experts of the NCA. The biodiversity of the identified samples was calculated using the Shannon Index.

Results

Though not all of our sequences were of good quality, we were able to analyze a subset of samples from our three collection days. The species we identified through barcoding from our second day of collections were *Platorchestia platensis*, *Monocorophium insidiosum*, and *Melita nitida*. The species identified through barcoding from our third and final occasion of collections were *Monocorophium insidiosum* and *Sarsia tubulosa*. After using the Shannon-Wiener Index to calculate biodiversity, the living dock was observed to have greater biodiversity on all sampling dates.

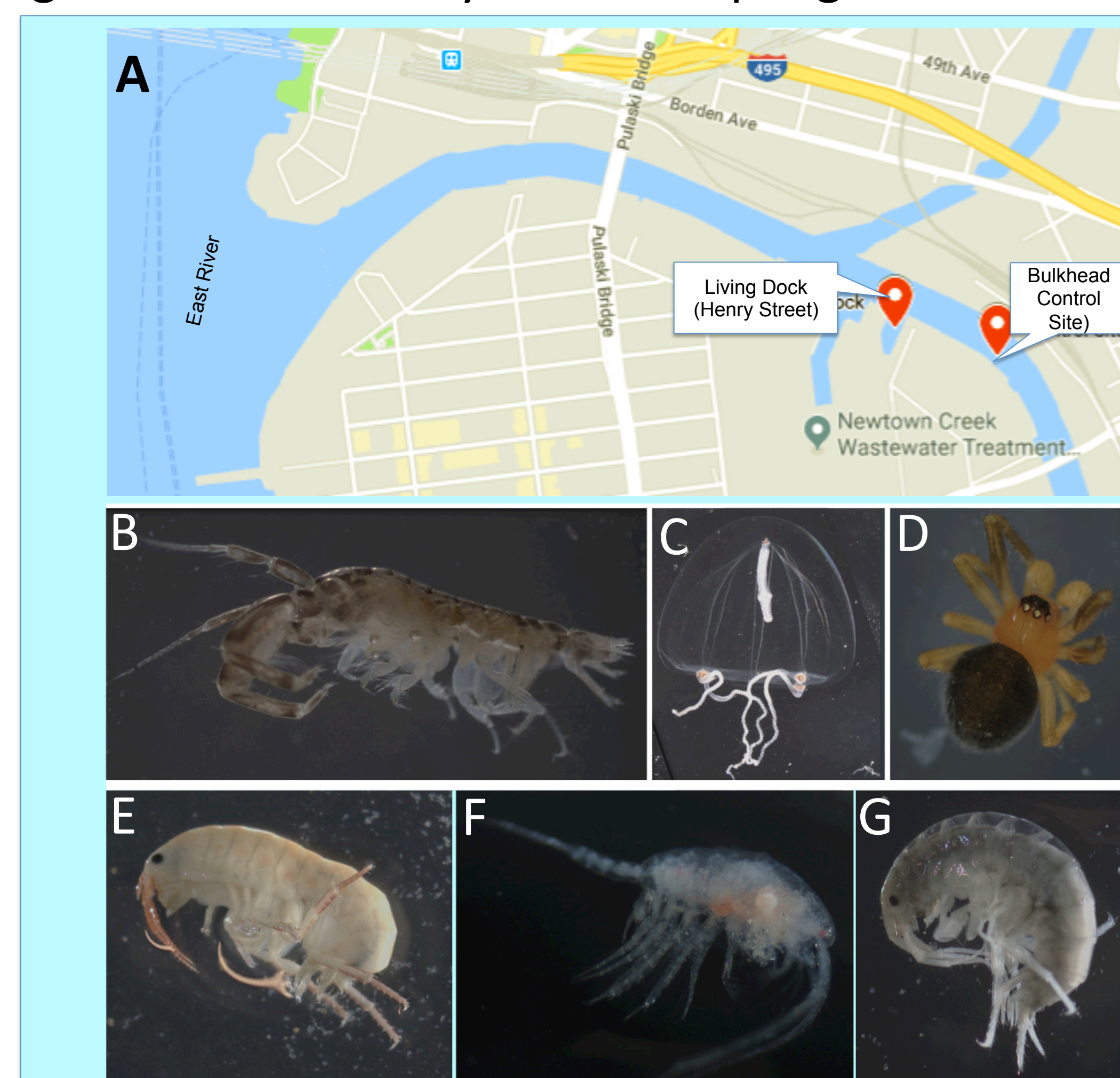


Figure 1. Sample Collection:

A. Sampling occurred on three consecutive weeks at two locations: the living dock on North Henry Street and the bulkhead near Kingsland Avenue. The sites are marked and labeled, showing their location and proximity to one another.

B. Representative invertebrates sampled at Newtown Creek including: *Monocorophium insidiosum* (B) *Sarsia tubulosa* (C) *Platorchestia platensis* (E), *Melita nitida* (G) as well as unidentified amphipod and arachnid organisms (D, F)

Sample #	Picture # (magnification)	Location	DNA Blast
A2	00145 (x0.63)	Living Dock	<i>Platorchestia platensis</i>
A4	00147 (x1.6)	Living Dock	<i>Monocorophium insidiosum</i>
A6	00148, 00149 (x2.5)	Living Dock	<i>Melita nitida</i>

Sample #	Picture # (magnification)	Location	DNA Blast
B3	n/a	Living Dock	n/a
B4	n/a	Living Dock	n/a
B5	n/a	Living Dock	<i>Monocorophium insidiosum</i>
B9	n/a	Living Dock	n/a
B14	00158, 00159 (x2.0)	Bulkhead	<i>Sarsia tubulosa</i>

Figure 2. Sequence-based identification for a limited number of samples :

A,B Few samples from the second (A) and third (B) collections had good quality sequences and were identified at the species level.

Figure 3. Invasive species may predominate at Newtown Creek:

The pie chart (far left) shows the percentages of invasive and native species identified along the creek

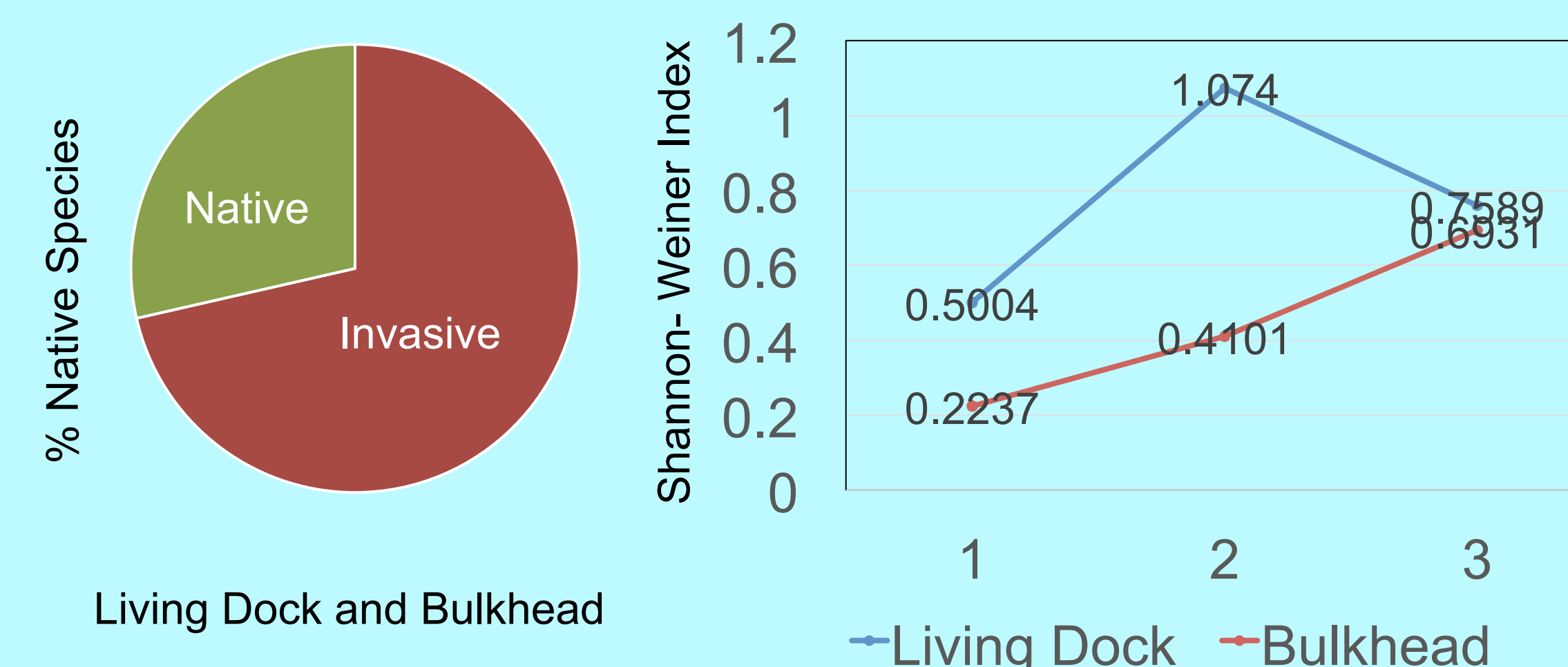


Figure 4. Shannon-Wiener Index: The line graph shows the calculated biodiversity from the different sampling sites for each collection.

Discussion

While we were able to successfully barcode a subset of our samples, and perform a limited analysis based on these results, our results are inconclusive due to small sample size and experimental setbacks. Previous studies have shown invertebrate diversity to be low during the winter months. For this reason, sampling did not begin until late March, presenting a challenging timeline for project completion as we had a short window for collection time and no time to re-sequence poor quality samples. We also were forced to use different collection methods at the control site than at the living dock as the steep drop from the bulkhead made it impossible to sample directly. It was difficult to use the plankton trough at the living dock due to the lack of depth in the water at times and lack of space. These sampling differences make it impossible to draw a quantitative conclusion about biodiversity from our study. Additionally, due to experimental error in final collection and the DNA extraction of those samples, many of our samples were badly degraded and unidentifiable, resulting in the dip in biodiversity reflected for the third collection, though biodiversity should increase as the weather gets warmer. Further studies will need to assess the effects of structures like the living dock on biodiversity in stressed and recovering ecosystems.

Acknowledgements

We would like to thank the Newtown Creek Alliance, especially Lisa Bloodgood, for helping us with our collections by providing us with information and equipment for our study; our families for supporting us along this journey; UBRP for providing us with this opportunity; and, most of all, Dr. Alison Dell for walking through each step of the way with us.

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