No Significant Differences in Biodiversity of Aquatic Macroinvertebrates in Shu Swamp and its Interconnected Ponds Versus the Isolated Bailey Arboretum Pond

Bella Panossian, Dylan Schefter, Sofia Schwarz, and Taylor Price
Mentors: Jennifer Newitt, Vijay Suthar, Vedant Rawat, and Dr. Cristina Fernandez-Marco

Friends Academy

CSH Cold Spring Harbor Laboratory

Abstract

High nitrogen levels from septic systems, wastewater, and fertilizers contribute to hypoxia in the Long Island Sound (Save The Sound, 2022). This nitrogen influx drives eutrophication, where algal blooms block sunlight, reduce photosynthesis, and lower oxygen levels through decomposition (NOAA, 2024). As a result, aquatic biodiversity declines, especially among oxygen-sensitive species. Our study compares aquatic macroinvertebrate diversity between two Long Island sites: the semi-connected ponds at Shu Swamp, fed by Beaver Brook and Mill River, and the more isolated Bailey Arboretum Pond, which drains only into Mill Neck Creek. The semi-connected system is more exposed to nutrient-rich runoff, while Bailey Pond underwent recent restoration, including leaf litter removal and aeration, likely reducing nitrogen levels. We sampled macroinvertebrates using a D-net, preserved them in ethanol, and identified species through DNA barcoding. Water quality was tested at both sites using nitrate/nitrite test strips. We hypothesized that the semi-connected waters will have lower biodiversity due to higher nitrogen exposure, highlighting the ecological impact of nutrient pollution, although our findings did not exactly match this hypothesis.

Introduction

Aquatic invertebrates, small spineless organisms with diverse body structures, are widely used as bioindicators due to their sensitivity to environmental changes like nitrogen pollution (National Park Service, 2022). Excess nitrogen can lead to eutrophication, reducing oxygen and harming sensitive species (NOAA, 2024). This study compares aquatic macroinvertebrate biodiversity in two Long Island ecosystems: Shu Swamp, part of a semi-connected system exposed to nutrient-rich runoff, and the more isolated Bailey Arboretum Pond, which recently underwent restoration to reduce nitrogen levels. We hypothesized that biodiversity would be lower in the semi-connected waters due to greater nitrogen exposure.

Methods & Materials

40 samples, 20 from both, were collected from Shu Swamp and Bailey's Arboretum

↓

All 40 were uploaded to the Barcode Sample Database

↓

DNA was extracted using the Chelex extraction

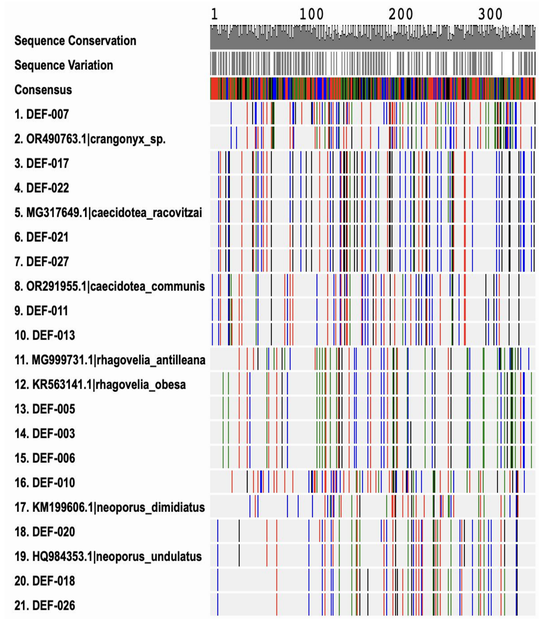
↓

DNA was amplified by PCR and confirmed using Gel Electrophoresis

↓

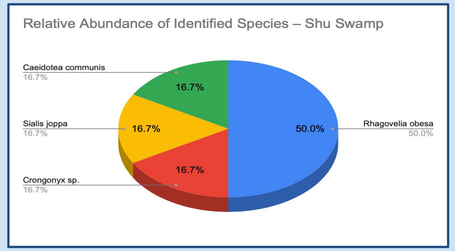
DNA was sequenced by DNA learning Center and analyzed with DNA Subway

MUSCLE DNA Sequence Alignment



Results

Thirty-eight samples were collected from Shu Swamp and Bailey's Arboretum. Fifteen were from Bailey's Arboretum, and twenty were from Shu Swamp. Twenty were sent out for sequencing. Nine were sequenced from Shu Swamp and four were sequenced from Bailey's Arboretum. In total, the aquatic invertebrates found from Shu Swamp include three *Rhagovelia obesa*, one *Sialis joppa*, one *Caecidotea racovitzai*, one *Caecidotea communis*, two *Neoporus undulatus*, and one *Crangonyx sp.* The Simpson's Diversity Index in Shu Swamp was 0.790. A smaller group was sequenced from Bailey's Arboretum, including three *Caecidotea racovitzai* and one *Neoporus undulatus* with an SDI of 0.375. Considering all specimens identified through field guides and barcoding, the SDI for Shu Swamp initially was 0.721, and for Bailey's Arboretum it was 0.75.



Figures 3 & 4. Taxonomic distribution of aquatic macroinvertebrates identified at Shu Swamp (3) and Bailey Arboretum (4), composition in semi-connected versus isolated freshwater habitats.

Figure 2. Map of Shu Swamp showing sampling sites for aquatic macroinvertebrates in semi-connected freshwater habitats for biodiversity comparison.

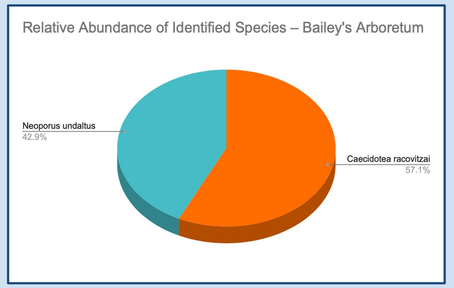


Figure 1. Map of Bailey Arboretum showing aquatic macroinvertebrate sampling sites used for biodiversity analysis in isolated freshwater habitats.

Discussion

At Shu Swamp, we identified *Rhagovelia obesa*, *Crangonyx* sp., *Neoporus dimidiatus*, and *Caecidotea communis*, while Bailey Arboretum yielded *Caecidotea racovitzae* and *Neoporus undulatus*. The distinct species at each site suggest differing ecological conditions. Notably, the *Crangonyx* sp. from Shu Swamp may represent a novel or understudied species, and one *Neoporus undulatus* showed high COI polymorphism, hinting at unexplored genetic diversity. Contrary to our hypothesis, nitrogen was undetectable at both sites, possibly due to recent renovations and isolation at Bailey's pond. The non-overlapping *Caecidotea* species point to potential habitat specificity. These findings highlight the need for further sampling and genetic analysis to better understand regional freshwater biodiversity.

Acknowledgements

We are so grateful for Jennifer Newitt, Vijay Suthar, and Vedant Rawat for their help and we would also like to thank Dr. Cristina Marco and the Cold Spring Harbor Laboratory DNA Learning Center for all of their support.

References: