Cold Spring Harbor Laboratory
DNA Learning Center

URBAN BARCODE RESEARCH PROGRAM

BIOTECH without borders

DNA Barcodes of Algae in Nutrient-Rich vs Nutrient-Poor NYC Waters

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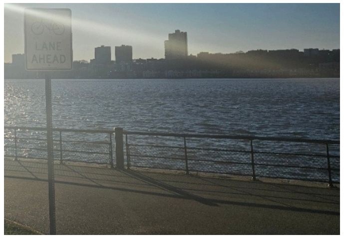
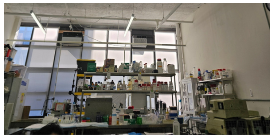
Abstract

New York City's coastal waters vary from nutrient-rich urban environments to more ocean-flushed conditions, providing an opportunity to study differences in algal diversity. This study compared algal communities from **Rockaway Beach, Sunset Cove, and the Hudson River** using **DNA metabarcoding** of the **chloroplast rbcL gene**. Six samples were collected, including both **surface water** and **rock biofilm brush-scrape samples**. Results showed that **brush-scraped biofilms contained significantly greater diversity than bulk-water samples**, recovering a wider range of diatoms and microalgae. In contrast, water samples were largely dominated by a single macroalgal taxon such as **Ulva or Fucus**. Overall, the findings suggest that **sampling method had a stronger effect on detected diversity than nutrient status**, emphasizing the importance of including substrate biofilms in environmental DNA biodiversity surveys.

Introduction



- NYC coastal waters range from:
  - **Nutrient-rich urban estuaries**
  - To **ocean-influenced oligotrophic environments**
- Example:
  - **Jamaica Bay receives high nitrogen input**
  - **Rockaway Beach experiences strong tidal flushing**
- Traditional algal surveys:
  - Chlorophyll measurements
  - Microscopy
  - Often fail to identify species accurately
- **DNA metabarcoding** enables identification of multiple taxa from environmental DNA
- Study used the **chloroplast rbcL barcode gene**
- Research Question:
  - Do nutrient-rich and nutrient-poor waters show distinct algal diversity patterns?
- Initial Hypothesis:
  - Nutrient-rich waters would show:
    - Lower diversity
    - Pollution-tolerant algae dominance
- Nutrient-poor waters would show:
  - Higher species richness



Materials & Methods

Sample Collection

- Sites sampled:
  - **Rockaway Beach**
  - **Sunset Cove**
  - **Hudson River**
- Two sample types collected:
  - **Bulk-water samples**
  - **Brush-scrape biofilm samples**
- Biofilms scraped from rocks using a **sterile toothbrush**
- Water filtered through a **0.45 µm filter**

DNA Extraction

- DNA extracted using:
  - **Zymo Quick-DNA Fungal/Bacterial Microprep Kit**
- DNA concentration measured using:
  - **Qubit fluorometry**

PCR Amplification

- Target gene:
  - **chloroplast rbcL**
- Used:
  - **Diatom-specific rbcL primers**
- PCR products verified with:
  - **1% agarose gel electrophoresis**

Sequencing & Analysis

- Sequenced using:
  - **Illumina paired-end 250 bp**
- Reads:
  - **Quality filtered**
  - **Clustered into OTUs**
- Taxonomic identification performed using:
  - **BLASTn against GenBank**

Results

We obtained 5 usable samples (A1, A2, A4, A5, A6); A3 (Hudson brush) produced no amplifiable DNA. After filtering, A1, A2, A4, and A5 each had ~5,000 reads, A6 had ~2,727, and A3 had ~1,017.

A1 (Rockaway-water): dominated by Ulva lactuca; 9 clusters.
A2 (Hudson-water): dominated by Fucus spiralis; 14 clusters.
A3 (Hudson-brush): no PCR product.
A4 (Rockaway-brush): most diverse sample (29 clusters), including Ulva smaragdina and many diatoms (Navicula, Licmophora, Amphora).
A5 (Sunset-water): dominated by Strombidium and Monostroma; 11 clusters.
A6 (Sunset-brush): contained diatoms (Navicula, Amphora) and other microalgae; 11 clusters.
Brush samples showed greater OTU diversity than water samples (e.g., A4: 29 clusters vs. A1: 9), while water samples were dominated by a single macroalga (Ulva or Fucus).

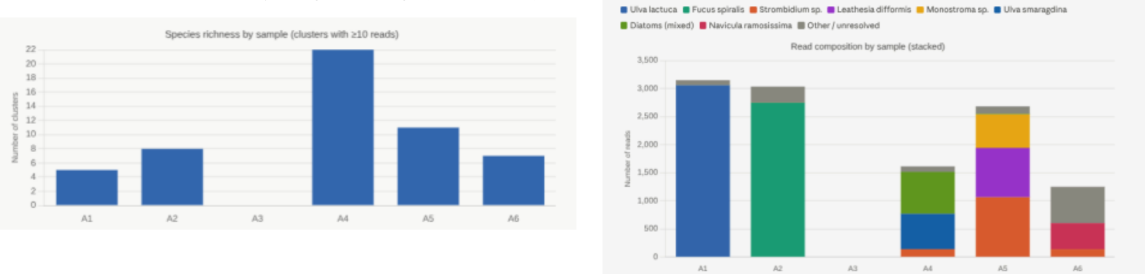


Table 1 and 2 (left to right) Summary of sequencing results by sample. Total reads = reads after quality filtering. Clusters (≥10 reads) = number of OTUs meeting the ≥10-read threshold. "Dominant taxa" are those with the highest read counts. Samples A1–A6 correspond to: A1=Rockaway-water, A2=Hudson-water, A3=Hudson-brush, A4=Rockaway-brush, A5=Sunset-water, A6=Sunset-brush.

Discussion

- Water samples were mainly dominated by:
  - Ulva
  - Fucus
- Brush-scraped samples contained:
  - More diatoms
  - Green algae
  - Other microalgae
- Sampling method affected diversity results more than nutrient level
- Rock biofilms contained taxa not found in surface water
- Findings support previous eDNA metabarcoding studies
- Shows importance of using:
  - Multiple sampling method

Limitations

- Only one sample collected per site and method
- Hudson brush sample failed
- Sequencing depth varied between samples
- Possible:
  - PCR bias
  - Database limitations
- Some low-abundance taxa may not have been detecte

Future Directions

- Use diversity analyses:
  - Alpha diversity
  - Beta diversity
- Improve: Replication, Taxonomic databases,
  - DNA purification methods

References (Scan Me!)

Acknowledgements

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