Introduction

New York Harbor’s Estuary is a unique habitat and community that is home to thousands of marine species (Nyman, 2012). It used to be full of thriving fish and plentiful estuary life (Juet, 1609). When Henry Hudson and Robert Juet came to New York in 1609, Juet described the incredible biodiversity of the estuary. When the Erie Canal was built in 1825, the waters became less about the marine life that lived there and more about shipping and transportation of goods (Finch, 1998). These waters are not only used by the marine species that live there, but the people as well. As of 2010, 86% of people in the United States rely on public supply water, which comes from city or county water departments (Petman, 2017). Not only do people rely on water, they heavily impact it as well, through nitrate infiltration (Re et al., 2017) and runoff. New York’s Estuary is and has been immensely important to the economy and social workings of New York. Between 1887 and 1996, the total produce from the New York Harbor Estuary’s most important commercial fish and fisheries decreased approximately 90%, attributed in large part to depleted dissolved oxygen (DO) levels caused by pollution (Tetra Tech and Stoddard, et al., 2000). Dissolved estuary salinity is another major factor that affects biodiversity (Narragansett Bay Commission, 2009). They can fluctuate based on natural occurrences or human induced climate change (Curry, 2003) (Ojaveer, et al., 2005). Although natural ocean currents and tides cause salt levels throughout the system to change daily, marine species can only live in specific salinity tolerances (Blair, 1972). Environmental factors can also influence phenotypic gene expression. If the salinity levels go below 10 ppt biodiversity can decrease in some macroinvertebrates (Ahmadi, et al., 2011). Little research has been done to compare salinity to biodiversity in the NY Harbor.

Goals

The goal of this project is to test the hypothesis that salinity affects biodiversity by determining the species richness, Shannon entropy, and percent cover of organisms on settling tiles at four sites in New York Harbor. After discovering different color morphologies of tunicates we sequenced mitochondrial DNA to determine if they were different species.

Methods

Field Sampling

Photographing

Data Collection

General Extraction

Analysis

Analysis

Results

Discussion

• Organisms were not using all the space available to them. This could mean that either, they die before they can spread out, or the substrate is not ideal for sessile organisms to settle on.
• The most common organisms were tunicates (both colonial and individuals), barnacles, byssocmous, and slipper snails.
• The species richness was fairly uniform across all sites, the highest being 6 and the lowest being 4, suggesting no relationship between salinity and biodiversity.
• The Shannon entropy was very similar, except in the case of the LIC site which had a SE of 0.425, much lower that the other sites. This suggests that even though there were the same number of species, the distribution in those numbers was different. This suggests no relationship between salinity and biodiversity.
• When we thought we were extracting individual tunicates we were actually extracting jellyfish polyps or byssocmous. This means that there is a missing piece of the biodiversity picture because we physically can not see microinvertebrates.
• Botryllus violaceus and Botryllus schlosseri would appear to be different species and that those different species have different morphological differences.

Final Words

Taking a look at cryptic biodiversity is important to get the whole picture of what is living in a community. Scientists should consider reevaluate how we look at biodiversity in general. Though there does not appear to be a correlation between salinity and biodiversity in this study, that doesn’t mean that there is not one on a larger scale.

Suggestions for Future Research

• Look at salinity as compared to biodiversity on a larger scale
• Use a bigger sample size
• Deploy tiles farther from shore
• Attach cameras on tiles to see if/how the organisms die

Acknowledgments/References

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Table 1: Table displaying average salinity, salinity range, species richness, Shannon entropy, and the inverse of Simpson dominance of all organisms.

<table>
<thead>
<tr>
<th>Site</th>
<th>Avg. Salinity (psu)</th>
<th>Salinity Range (psu)</th>
<th>Species Richness</th>
<th>Shannon Entropy</th>
<th>Inverse of Simpson Dominance</th>
</tr>
</thead>
<tbody>
<tr>
<td>UWS</td>
<td>13.5745</td>
<td>7 to 30</td>
<td>5</td>
<td>0.826</td>
<td>1.7</td>
</tr>
<tr>
<td>RH</td>
<td>22.3743</td>
<td>7 to 30</td>
<td>6</td>
<td>0.625</td>
<td>1.6</td>
</tr>
<tr>
<td>EW</td>
<td>21.5468</td>
<td>17 to 28</td>
<td>4</td>
<td>1.1</td>
<td>3.328</td>
</tr>
<tr>
<td>LIC</td>
<td>23.7425</td>
<td>17 to 30</td>
<td>4</td>
<td>0.904</td>
<td>3.664</td>
</tr>
</tbody>
</table>

Figure 01: Salinity gradient map of NY Harbor on July 20, 2018 as taken from Stevens Institute of Technology. Sampling sites are labeled with grey circles. Percent cover is shown as pie charts on the right.

Figure 02: The number of individuals over 1mm per cm² as compared to site. (upper left)

Figure 03: The number of individuals over 1mm per cm² as compared to site, excluding barnacles in order to take a closer look at the similarities and differences. (upper right)

Figure 04: The number of colonial tunicates per cm² as compared to site. (upper right)

Figure 05: Phylogenetic tree showing samples of Botryllus violaceus, Botryllus schlosseri, and Conopsia tenella.