Impact of water quality on bacterial diversity in the Long Island sound revealed by metagenomics

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Introduction

In all ecosystems including aquatic environments biodiversity is affected by environmental and biological factors, such as rapid climate change, pollution and invasive species, these effects on biodiversity are mainly due to differences in the ways organisms are able to adapt to those new conditions (Beaugrand, G. et al.,2015). For instance, pollution from industrial waste, particularly through combustion of hydrocarbons, increases the release of Carbon dioxide (CO_2) leading to increased dissolved CO_2 in water bodies, acidification, as well as increases in mean global sea surface and interior temperatures. All these changes cause the elimination of many species, reducing biodiversity (IPCC AR4 WG1,2007). Biodiversity conservation is the most important factor in the maintenance of a healthy ecosystem (Pinto et al., 2014), which is also required for sustaining economic and social benefits from the ecosystems (Elliott, 2011, 2013). Therefore, monitoring microbiota at different water bodies as well as identifying environmental stressors that affect changing bacterial diversity, is an important task. In this study we examined and compared bacterial diversity in terms of variety of taxa and relative abundance of each bacterial class in two bodies of water in Long Island sound, East river and Oyster Bay. ***We hypothesized decreased bacterial biodiversity in the East River side of Sound due to more industrial pollution and human activities, compared to the Oyster Bay side.*** To test our hypothesis, we performed metagenomic analysis, using 16S rRNA sequencing as well as physicochemical analysis of parameters which could be the result of climate change, in these areas. Our study gives new insights into correlations between the abundance and variety of bacterial populations to bacterial metabolic capabilities which are affected by particular contaminants found between water samples. Our study showed the importance of these data in monitoring water ecology and a healthy aquatic ecosystem.

Materials and Methods

DNA Extraction, Amplification of 16s rRNA Genes, Sequencing, and Identification:

Water Samples were filtered through a 22 µm Millipore filter. DNA was extracted using a PowerWater® DNA extraction kit (MoBio Laboratories, Carlsbad, CA, USA). 16S RNA was amplified using Polymerase Chain Reaction (PCR), and raw data was analyzed using QIIME (Caporaso, J. G. et al. (2010). Gene sequences were analyzed using Basic Local Alignment Search Tool (BLAST).

Water analysis:

Water samples were tested for dissolved O_2, dissolved CO_2, and salinity. pH and temperature were measured at time of collection with handheld readers and thermometers. Salinity was measured using the evaporation method as well as via a standard curve determined by dialysis bags with known NaCl concentrations. Dissolved Oxygen was measured with a LaMotte titration kit for dissolved oxygen in water (Winkler titration all –liquid system). Oxygen was fixed with manganous sulfate and Alkaline potassium at time of collection; sulfuric acid was added to complete the fixation process. Dissolved Carbon Dioxide was

Results

Site Locations

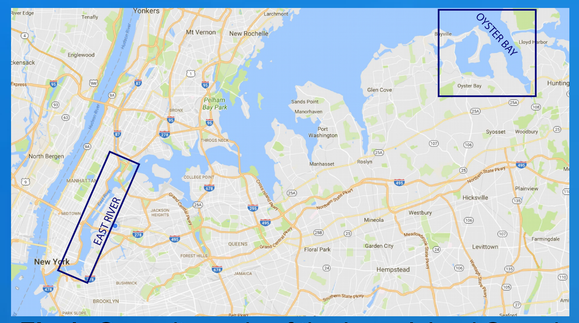

Fig 1: Opposite ends of the Long Island Sound.

Alpha Diversity by Location

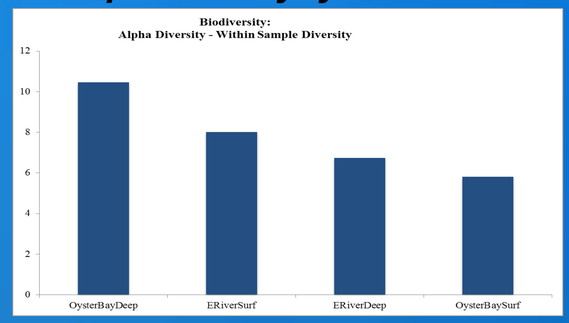

Fig 2: Oyster Bay shows greater bacteria diversity.

Class-Level Bacterial Diversity in the East River and Oyster Bay

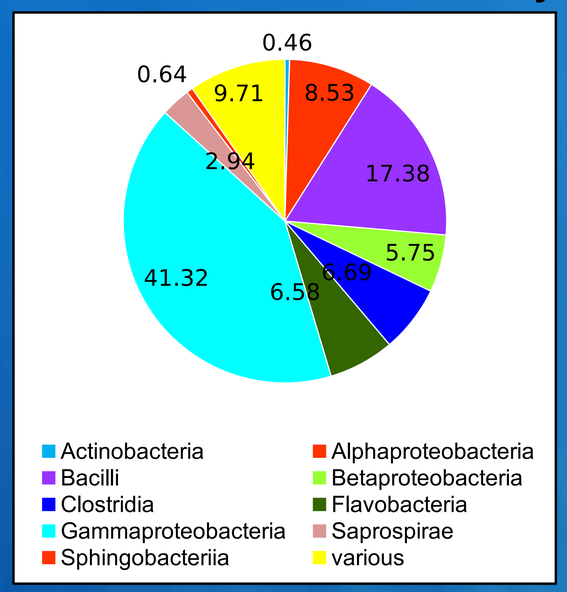

Fig 3a: East River

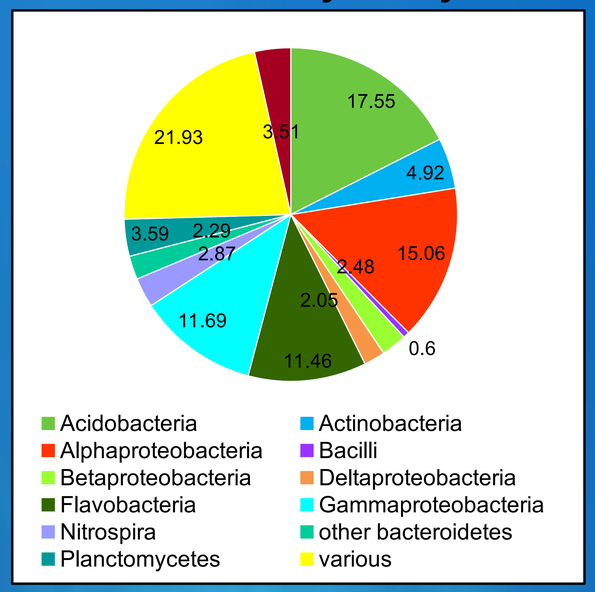

Fig 3b: Oyster Bay

East River has greater abundance of Gammaproteobacteria and Bacilli than Oyster Bay. Acidobacteria, which is mostly represented by aerobic or photosynthetic bacteria, is the most abundant group in Oyster Bay, yet is not found in East River. However, anaerobic Clostridia is found in East River, and not in Oyster Bay.

Physico-Chemical Analysis

Parameters	East River	Oyster Bay	EPA Standards
Dates of Collection	3/13, 3/27, 4/17, & 5/1/2017	3/13, 3/27, 4/14, & 5/1/2017	
Temperature	6 ˚C – 3/13/17 & 3/27/17 8 ˚C – 4/17/17 13 ˚C – 5/1/17	6 ˚C – 3/13/17 & 3/27/17 8˚C – 4/14/17 12˚C – 5/1/17	
pH	8.5 pH – 3/13/17 & 4/17/17 8.25 pH – 3/27/17 9 pH – 5/1/17 *	8.5 pH – 3/13/17 3/27/17 8 pH – 4/14/17 & 5/1/17	6.5 - 8.5 = preferred pH < 5 and > 9 = difficult pH Environments for marine organism survival.
Salinity	30,000 mg/L	33,333 mg/L	35,000 mg/L = average for seawater. 1,000 mg/L = limit for drinking water.
Dissolved Oxygen	8.2 ppm	7.6 ppm	5ppm and above = appropritate 3-4 ppm = stressful 0-3 ppm = fatal For most aquatic life.
Dissolved Carbondioxide	28 mg/L	16.25 mg/L **	< 20 mg/L = fatal for more sensitive aquatic life.

Fig 4: * A pH of 9 is approaching a difficult environment for marine organisms.
** Less than 20 mg/L is typically fatal for more sensitive aquatic life.

Discussion

- ✓ Greater abundance of Oceanospirillales in East River is consistent with oil contamination.
- ✓ Greater abundance of Enterobacteriaceae in East River is consistent with high fecal matter contamination.
- ✓ Greater abundance of Bacilli, specifically Paenibacillus, in East River is consistent with fluctuations in pH in East River over a short period of time.
- ✓ Increasing alkalinity in East River is consistent with higher levels of calcium carbonate and waste release from a nearby Con Edison dumping.
- ✓ Greater abundance of Bacilli in East River is consistent with the lower alpha diversity in this area.
- ✓ Presence of Paenibacillus in East River and Rhiziobiales in both Oyster Bay and East River is consistent with higher levels of nitrogen in these water bodies.
- ✓ Greater relative abundance of Chloracidobacteria in oyster Bay is consistent with the higher levels of dissolved O_2.
- ✓ Presence of Clostridia in East River is consistent with lower levels of dissolved O_2 and presence of sewage sludge.

Conclusion

- ✓ Our results support our hypothesis
- ✓ Overall, Oyster Bay had greater alpha diversity (diversity within site) than East River.
- ✓ Pollution, pH, and temperature are among the factors that can change the biodiversity of bacteria in water bodies.
- ✓ Human activities around water bodies are important factors affecting water ecology and may cause loss of diversity.
- ✓ Bacterial diversity assessment is a reliable technique to identify the effect of physico-chemical properties of water bodies on biodiversity.

References

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