

Aayusna Poudel, Aastha Budhathoki, Babita Jamkatel, Sonam Sherpa Mentor: Dr. Maria Entezari ¹Department of Natural and Applied Sciences, LaGuardia Community College, Long Island City, NY 11101

Introduction

The ecological indicators impacts the standard of water quality. The fluctuation in biological and physiochemical indicators results in alteration of bacterial community. Human activities such as improper sewage disposals, urbanization, pumping station bypasses, storm water run off etc results to form suitable habitat for microbial community to exist [10] Our study focuses on the bacterial community abundant in the depths and surfaces of East river and Long Island river. Metagenomics analysis is the effective approach to study the whole microbial community with broad access to the functional gene composition and description [6]. We did DNA extraction using MoBio Water Power Kit and amplified our DNA samples using PCR technique which resulted in the findings of the microbial community. Bacteria such as Enterococcus can be detected simply by culturing but there are bacterial communities that need 16s rRNA gene sequencing [1] which is what we did with our samples. The most abundant bacterial community found were Alpha, Beta and Gammaproteobacterial, Flavobacteria, Actinobacteria and Planctomycetes. The aim of this investigation is generally reporting of cumulative finding of bacterial community present in the east river to give an overview of how safe it is for human consumption or aquatic life. The findings of our project serves the purpose of creating a scope for future researchers in terms of what more can be done to improve the current status of East River.

QUESTION/PROBLEM

- What kinds of bacterial community exist in East River?
- What is the cause of abundance of certain bacteria?
- Are those harmful to human and aquatic lives?

HYPOTHESIS

The abundance of the particular bacterial community in Long Island and East river is reflected by the type and amounts of pollutants in each area.

METHODS

Metagenomic Analysis

- DNA extraction
- Polymerase Chain Reaction



Courtesy of Google

BACTERIAL COMMUNITY AND POLLUTANT







Water sample Area	A-proteobacteria	Flavobacteria	G-prote bacteri
Long Island Deep	*	29%	32%
Long Island Surface	36%	16%	18%
East River Deep	30%	17%	19%
East River Surface	28%	18%	26%
types	aerobic pathogens	Aerobic pathogen	Faculta anaerot ferment pathoge
	Deep oceanic sediments, glacial ice, deep undersurface soil.	Fresh meat poultry products	

East MapsRiver Running Map.



DISCUSSION

- receptacle of Hospital sewage.
- 2017)
- Microbiology, 2016)
- pollution.[9]



The amount of pollutants reflects the kind of bacterial community that is inhabiting the water source matches

-Our hypothesis was to find what type of bacterial community resides in the water samples and why they are varying in the quantity is approved by our findings. Many initiatives have been started in NYC. The Department Of Environment Protection conducts Statewide Monitoring Programs such as Stream Biomonitoring, Lake Classifications and Inventory, Water Assessments by Volunteer Evaluators, Toxicity Testing Program etc... Projects such as Greening the Gap works on developing green infrastructure and waterfront access, controlling the pollutants and improving the water sanitation. Significant changes such as nitrogen reduction, hypoxia management are the results of these initiations but as the pollutants that goes into these water sources are results of human behaviors, water quality is still at high risk. The abundance of certain bacterial communities among others are because of pollutants in the water resources that leads to high oxygen level, CO2 level and salinity in east River and Long Island. Abundant rate of flavobacteria, Actinobacteria, Planctomycetes and proteobacteria found in certain parts of river were identified and studied for its effects to the aquatic life and humans as well. The main thing to focus here is how these pollutants are released to the water and the answer is human behavior. We have come to determine through this research that it a high time human control their actions against degrading environment. We would need to go in depth with the bacterial profile and need more statistics of Water Quality in different parts of the city to further research on this topic.

1. Retrived from https://www.illumina.com/areas-of-interest/microbiology/microbial-sequencingmethods/16s-rrna-sequencing.htm

- doi:10.2174/1874401x01104010040
- 3. Greening The Gap. (2013, May). Retrieved from https://eastharlemstudio.wordpress.com/ 4. Long Island Sound Study. 2017. Area of Hypoxia. Available from:
- http://longislandsoundstudy.net/indicator/area-of-hypoxia/. 5. Long Island Sound | EcoHealth Report Cards. (2015, June). Retrieved from
- https://ecoreportcard.org/report-cards/long-island-sound/
- doi:10.1155/2017/9351507
- Horan, Authors). London: Academic Press
- 9. Long Island Nitrogen Action Plan, 2017. Retrieved from https://www.dec.ny.gov/chemical/111155.html
- on-long-island.html





• High abundance of proteobacteria in Long Island Sound than in East river because of pollutant loads entering Long Island sound (Save the Sound Org.) Flavobacteria has highest abundance in Long island river due to the area being the

• Excess nitrogen causing toxic algal blooms, maintaining suitable condition for microbes to exist. Algal blooms leading to eutrophication-low water quality (DOEC,

• Long Island joins to the Atlantic ocean which itself has high salinity in addition to the salinity level increased by the pollutants (Long Island Sound study)

• Abundance of Actinobacteria on the deep than on the surface as they are surface dwelling and can sustain under nutrient limited conditions (American Society for

• More than 100,000 miles of rivers and streams, close to 2.5 million acres of lakes, reservoirs and ponds, and more than 800 square miles of bays and estuaries in the United States have poor water quality because of nitrogen and phosphorus

CONCLUSIONS AND **FUTURE STUDY**

REFRENCES

2. Barnes, M. E. (2011). A Review of Flavobacterium Psychrophilum Biology, Clinical Signs, and Bacterial Cold Water Disease Prevention and Treat. The Open Fish Science Journal, 4(1), 40-48.

6. Thomas, T., Gilbert, J., & Meyer, F. (2012). Metagenomics - a guide from sampling to data

analysis. *Microbial informatics and experimentation*, 2(1), 3. doi:10.1186/2042-5783-2-3

7. Rizzatti, G., Lopetuso, L. R., Gibiino, G., Binda, C., & Gasbarrini, A. (2017). Proteobacteria: A Common Factor in Human Diseases. BioMed Research International, 2017, 1-7.

8. Undefined, U. U. (2003). Handbook of water and wastewater microbiology (D. D. Mara & N. J.

10. W.F, Lisa, 2017 'Dead Rivers, Closed Beaches': A Water Crisis on Long Island,

https://www.nytimes.com/2017/05/08/nyregion/dead-rivers-closed-beaches-an-acute-water-crisis-