

Characterizing the new life forms present in affected New York City lakes after Hurricane Sandy flooding

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Abstract

Hurricane Sandy, a devastating hurricane, hit NYC on October 29, 2012, flooding many regions of the city. We predicted that Hurricane Sandy introduced new organisms to NYC's aquatic biodiversity, including invasive species. It was our objective to characterize some of these species by comparing organisms in samples collected from flooded and non-flooded regions. While collecting samples, we took into account other environmental factors such as temperature and pH in order to arrive at the most valid results. Using DNA Extraction, PCR, and Gel Electrophoresis, we were able to attain DNA that was sent to a lab for sequencing. As of now, we are still waiting for the results to come back.

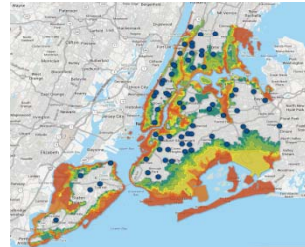
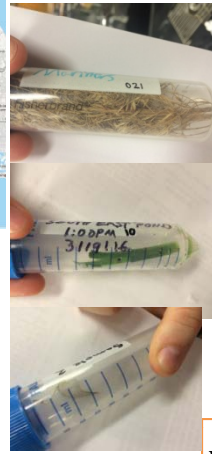


Figure 1. Red indicates regions heavily flooded by Sandy (Edwards 2013)



Pictures of several samples collected

Introduction

-Hurricane Sandy began as a tropical wave on the west coast of Africa, but built up into a tropical storm in the Caribbean, then passing by Jamaica, Cuba, Bahamas, and the entire US East Coast (Drye 2012). It hit NYC on October 29, 2012, with Lower Manhattan, Long Island, and Rockaways receiving the hardest blows and most flooding (NYC 2013) (see Fig. 1).

-As the hurricane passed through lands and bodies of water, it picked up different debris and organisms and left behind others. We suspect that some of these left behind organisms will not be native to NYC

-We sought to examine the effects of Hurricane Sandy by identifying organisms, especially plants, algae, and microorganisms, in rivers and ponds from all over NYC, testing both flooded and non-flooded regions

-While comparing the aquatic biodiversity among bodies of water, we will identify potential invasive species, which are organisms that are introduced to a new environment and may be harmful because they bring in more competition, threatening natural resources (NOAA).

Materials and Methods

-We collected 27 samples in total from five boroughs and Long Island. At the site of collection, we recorded temperature, pH, nitrite, and phosphate, as well as took note of the environment (see Fig. 2)

-We performed DNA Extraction on nearly all of the samples. Extraction involved lysing the cells to get the DNA, using silica resin to bind to the DNA, and washing to remove unnecessary substances

-Next was PCR, which is used to amplify the DNA. PCR tubes contained Taq master mix (with Tag DNA polymerase, buffer, and dNTPs) and forward/reverse PCR primers. At one point we ran out of Taq Master Mix, so we used Taq beads. The primers we used were rcbl plant, rcbl algae, COI fish, and COI invertebrate. We used both the mini PCR and the mastercycler

-To make sure Extraction and PCR were successful, we ran the amplicons through an agarose gel (gel electrophoresis). DNA was stained with SYBR green dye and pipetted into a gel, through which a low voltage current passed. The gel was placed under UV transillumination in order to see the bands and determine if the entire procedure was successful

Results

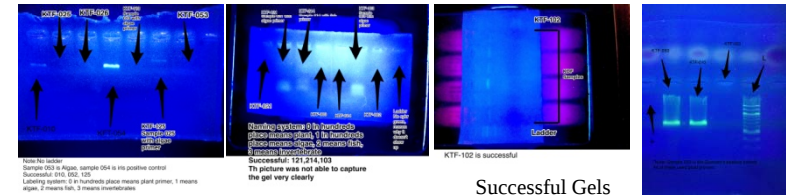
-PCR products have been sent for sequencing but have not yet returned

-Samples approved for sequencing: 002 (sample 002 with algae primer), 003 (sample 003 with algae primer), 009 (sample 010 with algae primer), 010 (sample 014 with fish primer), 014 (sample 021 with algae primer), and the iris positive control

-We received some sequencing results and are currently working on analyzing them via DNA subway

-We received results of samples 002, 009, 014, and 017 (iris + control)

-We are waiting for results of samples 003 and 010. There were problems sequencing these most likely due to very small amounts of DNA



Successful Gels

Discussion

-We are awaiting sequencing results; once these arrive, we will analyze the data and make conclusions.

-We noticed that Mini PCR produced better gels. It may be due to how the standard protocol affected the PCR machine.

-Additionally, we had a lot of trouble getting successful results. This may have been due to the PCR machine, but other predictions we had were: Taq polymerase or primers were left out for too long, not enough dye, or if the DNA was hard the extract from samples (particularly dry plant samples and the feather).

Acknowledgments

We would like to give tremendous thanks to Mrs. Jessica Quenzer, our tireless and supremely dedicated advisor, for spending hours helping us in the school laboratory after school for the past month. Additionally, we would like to thank the members of the other groups representing Stuyvesant at this year's UBP symposium, especially Lawrence Kwong, for assisting us with the many procedures we had trouble with. Finally, we would like to thank the teachers running the Urban Barcode Project and the Cold Spring Harbor DNA Learning Center for giving all of us this wonderful and inspiring opportunity to learn about the city around us in terms of molecular genetics.

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Sample Information									
Sample number	Date collected	Collected by who?	Which pond?	Physical characteristics	Species Identification	Additional Observations			
Sample 001	3/16/16	Marta	Prospect Park (water sample) 40°39'22.3" N 73°58'16.8" W	black specs, slightly green, several air bubbles, several brown pieces of sticks, 35mL.					
Sample 003	3/16/16	Marta	Prospect Park	Piece of dried up plant that was					
Environmental Monitoring									
Body of Water	Borough	In affected or non-affected area	Observations of surrounding environment	Observations of water (include if it's freshwater or saltwater- prediction)	pH	Temperature (°C)	Nitrite	Phosphate	
Prospect Park	Brooklyn	Non-affected	Dried up plants, bare trees	Several feathers, green murky, logs, a little garbage nearby, several branches; freshwater	on site: 6 In lab: 7.53 (tested 3/22/16) (we put the sample tested for pH back into the test tube	5.6	0	.25	
Coney Island	Brooklyn	Affected	rocks and wooden	no debris, barely any	on site: 5.5 In lab: 7.45	11.8	.05	.15	

Figure 2: Charts with data recorded about samples