Can Emission Standards Improve Plant Biodiversity in a Metropolis

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Abstract

Recognizing pollution as one of the largest threats to human health and our planet's biodiversity, the United States Environmental Protection Agency (EPA) established National Ambient Air Quality Standards (NAAQS) under the Clean Air Act, and these limits have led to a 36% decline in Nitrogen Dioxide (NO_2) pollution in New York City since 2009. Our goal for this research project is to study how lower NO_2 pollution correlates with biodiversity. We hypothesize that a visible payback of higher biodiversity in regions with lower pollution over the past 15 years in New York City, a very short period when climate cycles historically have been viewed as lasting hundreds if not thousands of years, can be a strong motivator for continuing strong emission regulations. Using plant samples collected from the lower regions of Central Park in Manhattan, we tried to determine if mutations are connected to the presence of NO_2 in a given area.

Introduction

- New York City may be home to 28,000 acres of municipal parkland, but over time, its rich biodiversity has slowly deteriorated due to urbanization. Large shifts in the environment are an inevitable consequence of the human population of New York City increasing from 33,131 in 1790 to over 8 million by 2000.[1] Millions of people cannot survive in a confided area without efficient transportation. Over 120 million vehicles crossed into Manhattan through bridges and tunnels in 2022.[2] Unfortunately, cars, trucks, and buses are the country's largest sources of NO_2 emissions.[3]
- DNA barcoding similar plant samples allows us to determine the mutations in the species that are the same.

Materials and Methods

- Plant specimens were collected from lower Central Park between Central Park South (59th Street) and 63rd Street to see if mutations are connected to the presence of NO_2 in a given area. This area was separated into five quintets, with successful barcoding done for samples from Quintet
- DNA was extracted from plant tissue and a polymerase chain reaction (PCR) was performed to amplify the rBCL genes of the samples.
- Positive PCR results were sequenced, and BLAST was used to determine the identity of the plant species.
- Once the rBCL genome was fully sequenced, we were able to use Subway to identify gene mutations, and proceed with our alysis of the data

Results

Sample ID	Number of population	BLASTN Species Results
KJW001	1000+	Negative
KJW002	1000+	Fortune's Spindle
KJW003	1000+	Negative
KJW004	1000+	Negative
KJW005	1000+	Negative
KJW006	1000+	Negative
KJW007	1000+	Burk Oak
KJW008	1000+	Burk Oak
KJW009	1000+	Fortune's Spindle
KJW010	1000+	Negative
KJW011	1000+	Negative
KJW012	1000+	Negative
N/A		
KJW013	1000+	Negative
KJW014	multiple thousands	Negative
KJW015	1000+	Negative

Table 1: Species identification. This table contains results from the DNA sequencing. The sample ID is on the left. The center contains the population count we logged during our collection process. The BLATN species result is on the right most column.

New Grass


Negative/KJW013


Negative/KJW014


Negative/KJW011


Negative/KJW006


Negative/KJW004


Negative/KJW001


Fortune's Spindle/KJW002


Negative/KJW015


Negative/KJW012


Bur Oak/KJW007


Negative/KJW005


Negative/KJW003

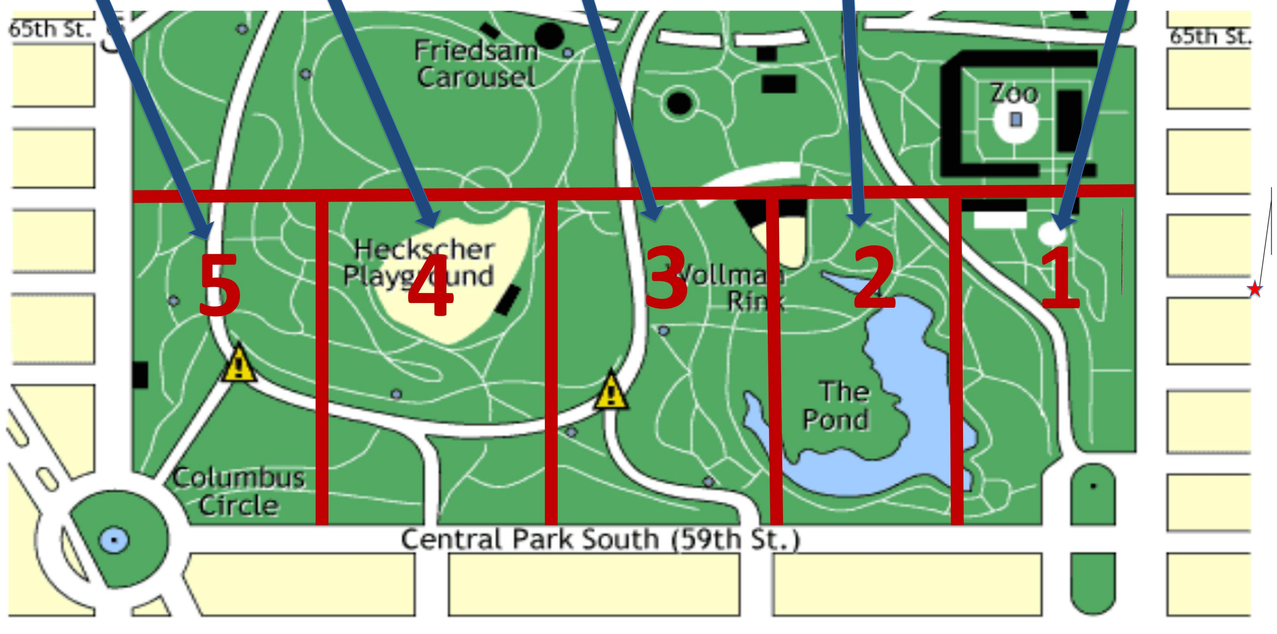

Figure 1:Map of Central Park and the plants identified. This map shows the plants identified around five quintets

Discussion

- We were unable to verify if the mutations in the plant samples collected were caused solely by NO_2 pollution. There are many causes for mutations in plants, and other environmental conditions may have caused the mutations. We would need to do further testing, through the utilization of an NO_2 meter, to truly determine the correlation between NO_2 and plant mutations.
- This year, our group suffered from a variety of setbacks, particularly when a large number of our samples did not work through the sequencing phase. As a result, this largely reduced the size of the sample pool that we had available to us. Furthermore, we were not able to have access to an NO_2 meter, which once again reduced our ability to gauge the number of N02 in a given area. This meant that the difficulty of correlating the NO_2 count to mutations in the plants was virtually impossible.
- Despite these setbacks, we believe that our experiment is a strong start in the right direction. In future years, we plan to work on obtaining a reliable NO2 meter that we can use to measure the count in the atmosphere. Once we have accomplished this goal, we can then view the correlation between NO_2 and mutations in plants.

Selected References

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