



Abstract

This study created the first ever phenology trail in Central Park to study physical changes in plants over time and used DNA barcoding to confirm the visual identification of the plant species on the trail. The DNA barcodes were isolated from thirteen leaf samples by running the DNA extraction process, PCR, and gel electrophoresis, before sending the samples to Genewiz for sequencing. The map of the phenology trail was created online using the program iNaturalist, enabling it to be used by future researchers and citizen scientists. We hypothesize that the phenophases of our plants will differ from their typical stages due to the urban heat island effect. Our results showed that, although the phenophases of six of our plants matched up with typical trends, there were distinct changes in the phenophases of the other seven (Christmas fern, Tulip Tree, Northern maidenhair fern, Pokeweed, *Phragmites*, Spotted Lady's Thumb, and Japanese Maple), possibly resulting from the urban heat island effect.

Introduction

Phenology is the process by which seasonal variations and other environmental changes affect organisms, both plants and animals. These conditions can have an effect on both the organism's appearance and how it interacts with its environment. Biologists utilize phenology to observe the effects of environmental changes, both organic and inorganic, on the natural world (1). Phenology is also useful for citizen science projects, allowing non-scientists to observe and document the same organism over long periods of time. Phenology trails contain various organisms within their borders, which can be observed repeatedly in the same locations in an attempt to discern changes in the species (1).

Central Park, a large tract of parkland inside the metropolis of New York City, was designed by Frederick Law Olmsted. The park was designed to enable visitors to enjoy the beauty of nature while surrounded by the towering buildings of an urban metropolis. It is home to a wide variety of flora and fauna, both cultivated and natural. Central Park is an example of broad biodiversity in a densely populated urban area (3).

Central Park resides within a metropolitan area which is known to be 2 to 3 degrees hotter than surrounding rural areas due to the urban heat island effect, creating a microclimate (5). The urban heat island effect results from an increase in heat energy in metropolitan areas compared to rural areas due to the high concentration of people, cars, and buildings in cities (4). Therefore, we predict that the plants within it will have a different phenophase calendar due to the warmer temperatures.

This project established the first phenology trail around The Pond in Central Park to collect data on the phenology of thirteen plant species in the area. It aims to ensure the continued use of this data by researchers and citizen scientists alike.



Figure 1: Map of the phenology trail

Central Park Pond Phenology Trail

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Materials & Methods

Thirteen species were selected along the trail surrounding the Central Park Pond. The species were chosen based on their location and in order to have representatives of many different plant families. Each plant was monitored as often as possible over a period of eight months. Each observation consisted of measuring the height, width/diameter, leaf number, phenophase, and any additional observations. Species were photographed and the data was recorded within the iNaturalist project "Central Park Pond Phenology Trail." Physical samples of the plants were collected with permission from the Parks Department. A small piece of a leaf from each species was collected which were placed in a plastic bag for. The samples were stored in a fridge in the science lab at the Browning School.

The DNA was extracted and amplified using the DNA Learning Center Barcoding Procedure. Ready To Go PCR beads and rbc1 primers were used during the amplification process. We followed the PCR protocol outlined in the DNA Learning Center procedure. These samples were then loaded into a gel machine and the resulting gel signatures were analyzed in order to insure that the rbc1 gene necessary for the DNA barcoding of these samples was present. Once the analysis was complete, the barcodes were sent off to GeneWiz for sequencing and DNA Subway was used to identify the species. The DNA barcodes will be published to GenBank.



Figure 2: Phenophase calendar for monitored and typical phenophases



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Visit Central Park Pond
Phenology Trail

Results

Phenology Observations:						
Date		Start Time		End Time	Weather	
Species	Height (cm)	Diameter (cm)	Stage	Number of leaves	Other Observations	
American Yew						
Ostrich Fern						
Common Jewelweed						
Christmas Fern						
Tulip Tree						
Northern Maidenhair Fern						
Pokeweed						
Phragmites						
Sumac						
Sassafras						
American Holly						
Spotted Lady's Thumb						
Japanese Maple						

Figure 3: Monitoring sheet used to fill in observations during monitoring sessions



Figure 4: Monitored ostrich fern being measured

BLASTN		
Name	Sequence	Action
OF-M13_A0.ab1	CNGCTATGACACATCCGCGGATATCTTTTGATTCNAGCTGTGTCAAGATATM	View Results
PB-M13_D0.ab1	TGTTGGATTAAAGCTGGTGTAAAGATTACAAATGATATATATCTCTCGATATATM	View Results
SC-M13_F0.ab1	TCAAGCCGGCTTAAAGACTATAATGACTTATTATATCTCTCGATATATATM	View Results
TT-M13_C0.ab1	GGATTCAAGCTGGTGTAAAGATTACAAATGATATATATATCTCTCGATATATM	View Results

Figure 5: Example Nucleotide BLAST for Four Study Plants (DNA Subway)

Discussion

The results of this study support our hypothesis that the phenophases of our study plants would differ from typical trends, although we can not say for certain if this is due to the urban heat island effect. Although some of our study plants, such as the American yew and the ostrich fern, showed similar phenophases to those seen in typical members of their species, other species, such as the pokeweed and the *Phragmites*, showed some phenophase differences in regard to timing of dormancy and late presence of flowers, respectively.

During our first sequencing session, a contamination event occurred between some of our samples and those of a concurrent student project studying fish DNA. Due to this, the original DNA sample of staghorn sumac returned as *Scomber scombrus*, the Atlantic mackerel, instead of the expected *Rhus typhina*. Due to an additional error, the samples of the American yew, northern maidenhair fern, staghorn sumac, and Japanese maple were attached to the wrong sequences, although all four sequences did return with the correct species at the genus level. This prevented us from attaching these sequences to our samples, although we could confirm the presence of the species in our study site. Finally, three sample extractions, the Christmas fern, American holly, and sassafras, were unable to be completed before the publication of this study, due to late sample collection, late changes in which species we were sampling, and repeated failure of original specimen extractions respectively.

The results of this study are significant since they are part of the first phenology trail in the Central Park area. This data can be used in the future to provide information about the status of these plants in the park at specific times and under specific conditions, which could be helpful for future environmental decision making. This data and all future data gained from this trail will continue to be used by researchers, citizen scientists, and Browning School students to observe the phenological changes on this trail long after the end of this study.

Future studies that can originate from this project could include a continued study of this phenology trail. After the end of this initial study, the phenology trail will remain intact and online for future use. Another potential future study option could be the creation of further phenology trails in Central Park or in other areas of New York, such as Black Rock Forest, an area that is not influenced by the urban heat island effect, which could show if the changes seen in this study are a result of the impact of this effect.

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