



Biodiversity of Central Park

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Abstract

We collected plants from different locations. We took a sample (piece) of each plant and used methods of DNA extraction such as PCR for each plant. We then analyzed our findings to determine the range of biodiversity in Central Park.

Introduction

According to National Geographic, “Biodiversity refers to the variety of all living things in a selected area, or furthermore, the entire planet” (Lanting, 2019). Biodiversity is important because it is essential to the survival of life on Earth; it ensures the continuous survival of the planet’s life. It is essential to the functionality of life within an ecosystem because all organisms work together to move on their own accord. Every ecosystem has a balanced cycle that makes it what it is, and maintains the dynamic (Morel & Nogué, 2019). However, in this experiment, the biodiversity of trees, plants, and insects in Central Park and Riverside park are being studied. Parks are not only beneficial to the functioning of human society, but also provides for an increase in the biodiversity of non-human animal and plant species. Central Park and Riverside Park are both considered urban parks in the borough of Manhattan of New York City. According to research conducted on the effect(s) of urban parks on the environment, they are beneficial to the preservation and diversification of the environment (Urban Parks Access: Trends, Issues, Challenges, n.d.).

Materials & Methods

The methods that we used throughout the experiment was a PCR test, and gel electrophoresis. The materials were buffer, micropipettes, microvials, centrifuge, lysis solution, incubator, specimens, Silica resin, thermal cycle, and argos gel.

The Methods/ Steps that we took for DNA Barcoding are:

I. Collect, Document, and Identify Specimens

1. Collect specimen
2. Document Specimen
3. Identify Specimen
4. Store Specimen

II. Isolate DNA from Plant, Fungal, or Animal Species

1. Add specimen tissue sample
2. Add lysis solution (300 microliters)
3. Grind sample in solution
4. Incubate 10 minutes (at 65 degrees celsius)
5. Centrifuge 1 minute (centrifuging allows us to separate the components and after the DNA will be a supernatant)
6. Transfer supernatant to fresh tube (150 microliters)
7. Add silica resin (we add silica resin to bind the DNA)
8. Mix
9. Incubate (5 minutes at 57 degrees celsius)
10. Centrifuge for 30 seconds (after this the DNA will be a pellet)
11. Remove supernatant
12. Add wash buffer (500 microliters)
13. Mix
14. Centrifuge 30 seconds
15. Remove supernatant (500 microliters)
16. Add wash buffer (500 microliters)
17. Mix
18. Centrifuge for 30 seconds
19. Remove remaining supernatant (500 microliters)
20. Centrifuge 15 seconds
21. Remove remaining supernatant (50 microliters)
22. Add dH2O (100 microliters, the distilled water was added to clean the DNA)
23. Mix by pipetting in and out
24. Incubate 5 minutes (57 degrees celsius)
25. Centrifuge 30 seconds
26. Transfer supernatant to fresh tube (50 microliters)
27. Chill on ice or store at 4 degrees celsius overnight

III. Amplify DNA by PCR

1. Add PCR reagents (23 microliters primer mix to PCR beads)
2. Transfer DNA to PCR tube (2 microliters, directly into the PCR mix)
3. Amplify in thermal cycler
4. Chill on ice (or store at 4 degrees celsius)

IV. Analyze PCR Products by Gel Electrophoresis

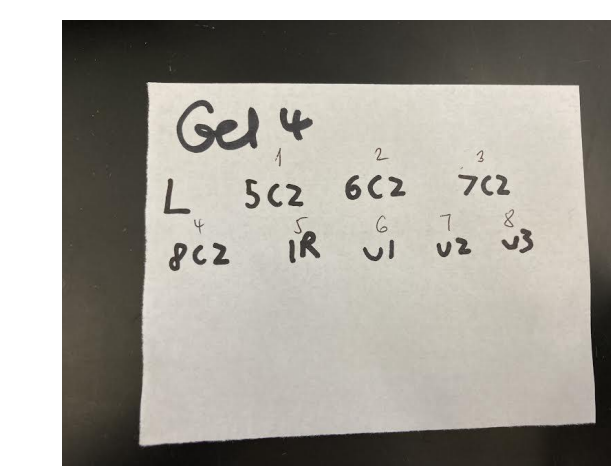
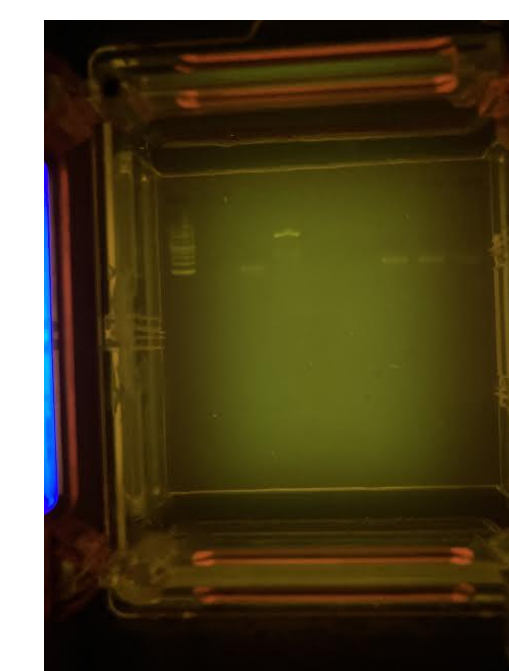
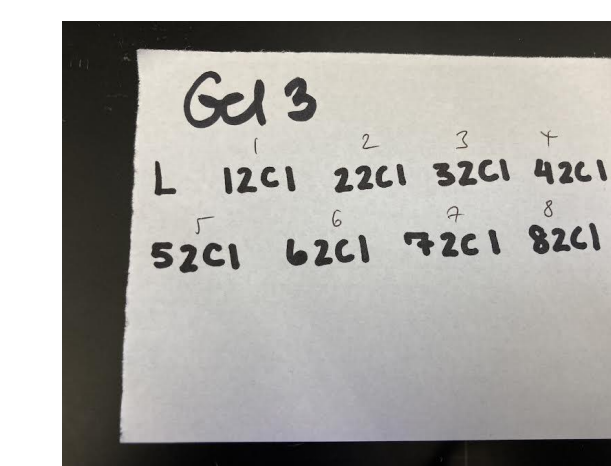
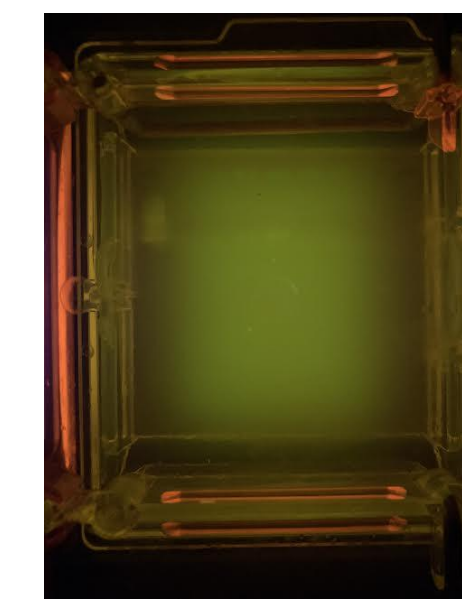
1. Melt agarose at 30 second intervals (loosen cap, be careful this will be hot, the agarose should be clear and boiling)
2. Cool for five minutes
3. Pour gel
4. Set for 20 minutes
5. Add SYBR green to fresh tube (2 microliters)
6. Transfer DNA from PCR tube to SYBR green tube (5 microliters)
7. Load gel (Caution! Do NOT load all 23 microliters of sample into the gel or there will be no sample left to sequence) 5 microliters per sample
8. Store PCR tube with remaining 20 microliter sample
9. Electrophorese (130 volts, 400 mA, 30 minutes)
10. Photograph and upload

V. Sequence PCR Product and Analyze Results

1. Send sample for sequencing
2. Analyze results using bioinformatics

Results

The results of our investigation is that we only got 2 out of the 36 DNA samples to “light up,” meaning that there was not sufficient DNA. It is possible that we took too much of a sample, meaning that we took too much DNA. Another possible source of error is the fact that the might not work well in the downstream application and/or the quality of the genomic DNA is poor meaning that the stating sample was not stored properly



Discussion

Our hypothesis indicates that we think that Central Park would have a wider range of biodiversity. Because we were only able to synthesize 2 samples out of the 36 that we collected. This means that there could have been a multitude of both human and testing errors during the experimental process. An error that occurred in the process was a mix-up of the collected samples among our group and the other group that tested. One possible error that could have occurred was poor grinding of the sample, which could have caused an error in DNA analysis. Another thing that could have occurred was the insertion of the sample into the gel chambers.

References

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