Beetle biodiversity at Bailey's Arboretum Authors: Gen Decker^{1,2} and Juliana Pecoraro^{1,2} Mentor: Ms. Shanley^{1,2} ¹Cold Spring Harbor Laboratory DNA Learning Center; ²St. Dominic High School

<u>Abstract</u>

DNA barcoding is a process that allows us to match our collected DNA and compare it to other DNA remaining blood and tissue samples to be run through gel electrophoresis. This allowed us sequences in known databases. By observing the DNA sequences and identifying the specific species, to see the amount of base pairs in our solution, by comparing it to a ladder in the first we're able to examine the biodiversity of the selected site. The purpose of our study was to observe and well. We then ran our samples through DNA Subway and were able to determine our identify the biodiversity of beetle species at Bailey Arboretum, an estate filled with various organisms beetle invertebrate species. and life. The most essential materials and procedures that were necessary to perform the DNA barcoding process were the net and shovel to collect the beetles and store the species. The components to perform the Chelex method and gel electrophoresis were also crucial to perform the experiment. We expected the results of our experiment to show that we found various beetles species and some beetles in the same family. Unfortunately, most of our samples failed after using the chelex method, so we processed the remaining samples and chelex solutions. Majority of the remaining blood and tissue samples were able to be processed and identified. By examining the results of the DNA barcode sequences, our group was able to identify the biodiversity of beetle species at Bailey's Arboretum.

Introduction

To determine the biodiversity of the site, our group planned on collecting DNA data samples of multiple different beetle species located within the arboretum, in different locations. A common method used by scientists is DNA barcoding, which allows us to target the COI gene and compare the sequence to other COI known sequences that are already associated with beetles. Once each invertebrate sample was collected, we isolated and amplified the samples' DNA that were used for DNA barcoding. The DNA barcode process enables us to identify the most closely related invertebrate beetle species to our sample.

<u>References</u>
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https://www.pnas.org/doi/10.1073/pnas.1909655116





Methods and Materials

We started by collecting our beetle invertebrate from Baileys Arboretum. We originally planned on using a net with small holes and sweeping it across the bushes and trees to collect the beetles, but the method was unsuccessful in capturing any invertebrate species. Our aim was to collect a large variety of invertebrates so we also used a shovel to scoop up dirt and debris onto a large white piece of paper. We then shifted the dirt and debris collection and removed the living invertebrates and placed them into a container. The samples we found were put directly into a freezer to preserve the tissue.Next we started the process of DNA isolation. We attempted to use the Chelex method to isolate our specimen's DNA but our samples were unable to be successfully amplified. We ran our

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Results

After multiple trials, we ended up with matches for nine out of twelve of our samples. We had two groups of matching results. At the end of our research we ended up with seven different species. It is likely our three samples; CSZ-002, CSZ-010, and CSZ-012, didn't work because beetles have a very strong exoskeleton making it difficult to crush and extract DNA from. Another possibility is that too much of our sample was added in the beginning of the process.

Discussion

While collecting invertebrate species we faced a few challenges. We collected our samples between the months of March-April and had trouble finding multiple beetle invertebrates out in the open. We were able to collect 12 beetles to be sampled for the process. This affected the experiment because there was less of a variety to compare each species to. Once we brought our samples to Cold Spring Harbor Laboratory to be amplified we were unable to successfully process the samples due to too much DNA being extracted from samples. Our group had to re-run our leftover blood and tissue samples of the remaining beetle samples to amplify their DNA.



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Number	Species	Accession Number
CSZ-001	Pterostichus corvinus voucher	OR001776
CSZ-00 3	Sphaeroderus stenostomus voucher	OR001777
CSZ-00 4	Sphaeroderus stenostomus voucher	OR001778
CSZ-00 5	Philoscia muscorum voucher	OR001779
CSZ-00 6	Acrosternum hilare voucher	OR001780
CSZ-00 7	Lilioceris lilii voucher	OR001781
CSZ-00 8	Lilioceris lilii voucher	OR001782
CSZ-00 9	Scarites subterraneus voucher	OR001783
CSZ-011	Harmonia axyridis voucher	OR001784



