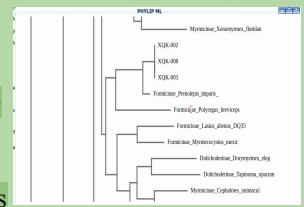


Examining the biodiversity of ants in comparison to climate change

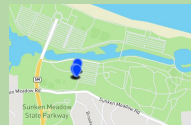


The Phylogenetic Tree draws a relationship between samples 3,4 and 8 with formicine prenolepis imparis

Abstract : The purpose of this study is to examine the Biodiversity of ants over many months to observe the effects that climate change has on the ant species. This project will not only be performed over the span of a few months, but it is also expected to proceed in the upcoming years. The reason this will be helpful for science to continue this project yearly is to see the impact of climate change, a major issue in our world today, affecting the biodiversity of a species in an area we live in. We expect to see an increase of biodiversity over several years of this study, because as climate change shows, temperatures of this earth are rising and will continue to.

Introduction: The purpose of this project is to identify the biodiversity of ants collected at one specific location on Long Island, Sunken Meadow State Park, at both the rocky area, along with the grassy area. We predict that as temperatures increase, so will biodiversity. We will begin collections in March, and we expect the biodiversity to increase as the collection times get warmer over the span of our collecting months. "Ants are ideal organisms for biodiversity studies due to their stability in a habitat over time." (Wilson, pg. 25). We are studying ant biodiversity for similar benefits such as analyzing the impact climate change has on each individual species on the earth. We are focusing on ants, so a connection can be made for a more in depth understanding of climate changes and harmful impacts to their habitat. Studying this is important because if our prediction and hypothesis are correct, this means climate change has continued to worsen, and change has to happen in human behavior towards the earth, before ant species become at risk in their own habitats.

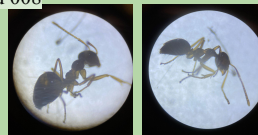
Map of collection cite: Sunken Meadow Beach



References:
<https://link.springer.com/article/10.1023/A:100889190195>
<https://link.springer.com/article/10.1007/s10531-017-1474-x>
<https://dnabarcoding101.org/lab/protocol-2.html#alternatee>
<https://animals.mom.com/ants-hibermate-cold-10899.html>

Methods and Materials: Our data was collected at Sunken Meadow State Park. We collected 20 ants total from rocky and dirt areas and put them inside of a micro centrifuge tube tube with 95% ethanol in it to preserve it. Next, we started DNA extraction using a method called Chelex DNA extraction. This method allowed us to extract the ants DNA in the lab. To begin Chelex isolation we cut off 1 leg per sample and placed them into a chelex microcentrifuge tube. Then each leg was grinded and broken down using plastic pestles, then placed the chelex tubes in a hot water bath for 10 minutes allowing the DNA to heat up and then centrifuged for 30 seconds to create a supernatant. To amplify DNA we added primer PCR beads with DNA into PCR tubes and placed them in the thermocycler. We sent the PCR tubes to GeneWiz to receive our sequences back. Samples 3,4,8 and 12 amplified. We used DNA Subway to track, compare and analyze the DNA from our samples after isolating the DNA to determine the effects of climate change on the biodiversity of ants at Sunken Meadow State Park.

Gel Electrophoresis of samples 3,4,8 & 12 XQK-003 and 008



Alignment Viewer
XQK-002,3,8

Discussion: Unfortunately due to limited time, a direct conclusion to this experiment can not be made, however as we plan to continue this for more accurate results next year, we predict to see an increase in biodiversity as temperatures rise due to Global warming.

Reasons we did not get our expected results :

- Our samples had to sit in the fridge for an extended period of time because of quarantine protocols from COVID-19 and it most likely deteriorated.
- Possible isolation issue due to ant leg samples not being completely crushed using the pestle.

Based on the 3 samples however we can conclude that we successfully amplified the DNA correctly because all 3 samples that came from the same day and same location had exact DNA nucleotide sequences..

We predict these ants to be the same species and can hopefully use their DNA sequences to compare ants in the years to come. The pedigree attached above also indicates that a closely related species to these ants was the **formicine prenolepis imparis**. Although these results could not help us come to a conclusion of how ant biodiversity has been affected, we can use the results to better our experiment next year by preventing our ant DNA from deteriorating, and prevent isolation issues that occurred in this experiment. Another way we would like to improve this experiment is to collect more frequently. The more DNA and different samples we have, the more accurate of a conclusion we will be able to draw.

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