Night vs Day Ant Biodiversity

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ABSTRACT

In order to do this experiment, we relied on DNA Barcoding. DNA Barcoding allows us to correctly identify the ants we collect and allow us to view the biodiversity of ants in the day and night. The question we wanted answered was "What types of ant species are present in Wheatley Heights during the day and during the night?" Our objective is to correctly identify the ant species that we collect during the day and night. We used a couple of sample collection methods to collect our ant species. We performed DNA Isolation and DNA Amplification so that we could sequence their DNA. Before collecting our specimens, we expected to find a greater biodiversity of ants. Since we have found very few species, we did further research to see why that is and concluded that it may have something to do with our collection methods and other environmental factors.

INTRODUCTION

The goal of this project is to identify the different ant species that are found during the day and night and view the biodiversity of the area we chose in Wheatley Heights.

In collecting and identifying the specimens, we hoped to view the biodiversity of the area. Biodiversity is an important factor to the ecosystem and environment. Determining the biodiversity of our location can determine the state and stability of the ecosystem. Greater biodiversity leads to a stable ecosystem, while a low biodiversity means a weaker ecosystem. Depending on the results, our group will experiment with other environmental factors in the future.

COLLECTION METHODS

We used sifting and baiting techniques. We used honey to bait the ants because ants are naturally attracted to sugar since it is the equivalent of energy. This causes them to wander farther to seek out honey. We coated a piece of cardboard with a layer of honey and placed it on the ground for a few hours.

We sifted the dirt with a sifting pan and a white poster board.

DNA ISOLATION PROCEDURE AND MATERIALS

We isolated the DNA with the Chelex solution method. We took the whole specimen and grinded each of them in a 10% chelex solution. We then incubated the samples in a water bath for 10 minutes at 95 degrees followed by centrifuging it for 30 seconds. We separated the supernatant from the chelex pellet and transferred 30µl into a new microfuge tube and then added 6µl to the reagent. We then did PCR to amplify the CO1 gene.

After we did PCR we did gel electrophoresis to determine if the DNA was amplified. We added both 5µl from the PCR tube into a new tube and transfer 5µl into each well. The gel then ran for 30 minutes at 130 volts.

RESULTS

When collecting our insects, we attempted both sifting and baiting techniques. The sifting technique was a success while the baiting technique was not effective.

When we did PCR on the 14 specimens we have collected, one of them was unsuccessfully amplified and couldn't be sequenced. When we sequenced all of the specimens, we found in total 4 different species. The species we identified were the Monomorium emarginatum, Lasius claviger, Tetramorium caespitum, Lasius neoniger.

DISCUSSION

Our results were not what we expected. We thought we would find a great biodiversity, yet we only were able to identify four species. After some time and further research, we were able to identify the factors that may have led to our results.

We think the reason why we didn't find many ant species is because the area that we collected them from was nearby a street. Although there was rarely any disturbances, there may have been enough disturbance that could result in the lack of biodiversity in the area. We also think we should have tried various other collection methods (searching in trees and trying other baits) to broaden our chances of collecting a variety of ants. We also found that our baiting technique wasn't as effective because we used processed honey, which doesn't contain all of the nutritional compounds ants desire.

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