DNA Barcodes at Two Different Preserves on Long Island

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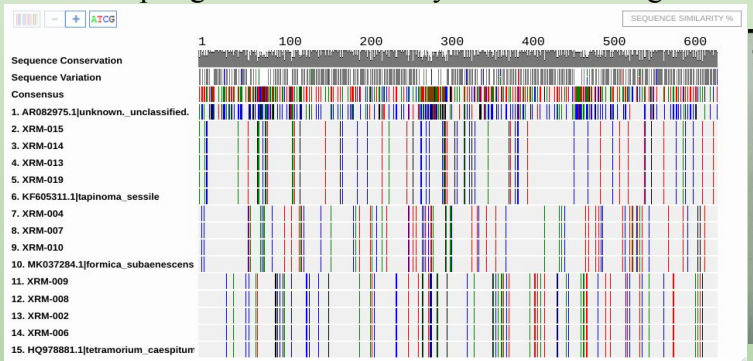
Abstract:

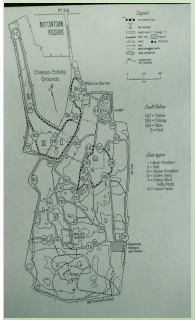
In this research project we wanted to see if there was a difference between ants that live near a high concentration of humans and ants that lived near a low concentration of humans. To do this we took ants from two locations. The Muttontown preserve is the area with low human activity, and the Massapequa preserve is the area with high human activity. After collecting samples we isolated the ant DNA, amplified the DNA and used gel electrophoresis to compare the size of the different ant DNA. All the samples had the same size bands.

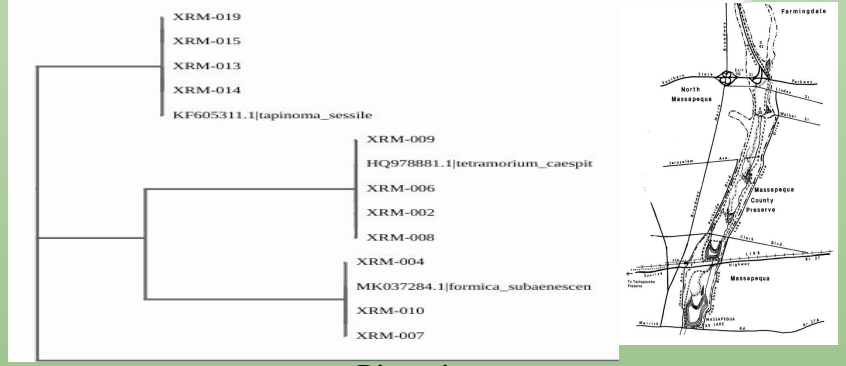
Introduction:

The purpose of our project was to find out whether the biodiversity of ants is different in areas with high human activity compared to areas with low human activity. These two areas vary in soil quality and therefore, food quality. Our goal was to find out if human interference on Long Island affects how ants live and where they chose to live and move throughout (Moffett). Finding this information out is important because depending on what our results come out to be, it can show the effects of how humans are interfering with how some ants are able to live (Dunn). The research that was conducted involves capturing sixteen ant samples, eight from the Muttontown preserve, and eight from the Massapequa preserve. The Muttontown preserve with a population of 3,669 as of 2020 is the area with low human activity, and the Massapequa preserve with a population of 17,105 as of 2020 is the area with high human activity.

Our hypothesis is that if we test the biodiversity of ants on the Muttontown preserve and the Massapequa preserve, there will be a larger variety of ants in the Muttontown preserve (King, Tschinkel). We predict this because we think that certain types of ants will not be equipped with the requirements needed to be able to live in polluted areas that tend to have high human activity (Cammaerts, Cammaerts). The habitat will not be suitable for them to survive (Delable, Paim, et al).







Discussion:

These results mean the DNA from our ant samples were successfully extracted and amplified. These results are important because this means we can observe the biodiversity of ants from each preserve. During our study, we did encounter some problems. We originally were supposed to use 20 ant samples, but instead we settled for 16 ants because 4 of the ants became unusable for our procedure. We also did not properly label some of our materials, which led to a little confusion. For any future studies, we will make sure to label everything thoroughly beforehand so there is no confusion. We will also handle samples with more care so no samples become unusable.

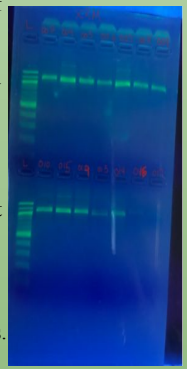
Materials and Methods:

We collected our samples for a span of several hours. We used an aspirator to collect our ant samples while going to various locations. We picked 8 ants from all around each preserve using bait to attract them. After that, we put the ants from each preserve into their own plastic ziplock bags, and we stored them in a freezer to preserve the DNA. Our samples were processed for barcoding through the chelex solution method. After completing the chelex solution method, we amplified the using CO1 primer and all verified samples sent to GENEWIZ for sequencing. Then used DNA subway to the analysis.

While doing the procedure, first we had to obtain our tissue. Some ants are extremely small, so for ants that are smaller than a grain of rice, we had to use the entire ant as our tissue sample. For larger ants, only one or two legs would be needed for the highest quality sequence possible. Next, after our tubes were labeled, we gently placed the tissue sample in the tube containing 100 microliters of the 10% chelex solution. After every sample was crushed in its own chelex solution, all the samples incubated in the water bath at 95 degrees celsius for approximately 10 minutes. After the samples were taken out, they rested for another 10 minutes. The samples spun at max speed for 30 seconds in the centrifuge afterwards. Following this step, we transferred 30 microliters of supernatant from the chelex tube, avoiding the chelex, into a clean, 1.5 mL tube, to be stored in a freezer. Finally, we then used gel electrophoresis. From this, we will get the results of the ant samples that we tested from DNA Subway.

Results:

The results of our samples after the gel electrophoresis process showed that each one of our samples were clearly shown by the thick, bright bands on the sequenced DNA. Our hypothesis was partially correct since there was a diversity of two different species of ants at both Massapequa and Muttontown. The Massapequa preserve was mostly the Tapinoma sessile species.



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