Analyzing the Diversity of Ants in the Commack Community

Authors: Mia Goren & Emma Karadenes
Teacher: Jeanette Collette
Commack High School

Abstract

There are over 12,000 species of ants, each with their own unique characteristics which allow them to survive in their own environments. Recently, ants have been used as a model to study disease transmission. Some ants' species, such as the Pharaoh ant, can carry pathogens that are harmful to humans. The purpose of our study is to investigate the biodiversity of ants in Commack, NY. We performed DNA Barcoding utilizing Polymerase Chain Reaction (PCR) to isolate the Cytochrome Oxidase I gene within the mitochondrial DNA region. Gel electrophoresis was performed to verify DNA was obtained. Afterwards DNA was sent to be sequenced and analyzed through the DNA Learning Center's DNA subway we will look at the ants phylogeny to classify them.

Introduction

Ants play a key role in their environment, most importantly through their nest building and diet. When building nests, ants spread out the soil and making it more nutrient rich by decomposing organic matter, providing better soil for plant growth (3). Another key role ants play is in seed planting, because seeds are waste from their food. (3).This study assessed the different species of ants found in the Commack and any pathogens or bacterial transmissions that may be carried. Different ant species have completely different types of behavior. They eat different substances and can hunt in large numbers or small packs depending on the species. The ants were located around more suburban areas for the project, spanning the most in driveways, parks, and near houses. The ants were collected in a number of different ways, all such involving trapping and storing them.

DNA Barcoding is a technique that has revolutionized in the field of taxonomy, or the classification of species. It uses each species' own DNA to classify it instead of analysis based on physical traits alone. It is revolutionary due to the fact that it shows that each species has a precise code, and see the relationship between each organism, or to see any mutations between them. DNA barcoding can be used here to see the different ant species in the community. This also can help identify if there are any invasive species by comparing them to a list of native species, since ants are an organism found all over the world. It would also help us see if there might be a novel sequence in the local area. In DNA barcoding, the CO1 gene is compared, because it is present in all animals, and sets a baseline for the comparison of the diversity between the ant species.

Results

Figure 1: **A:** The sample picture of NZF-005 in the area near Bread and Cheese Hollow Road.
B: Sample of ant collected from the area.

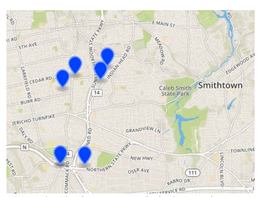

Figure 2: The locations in which the samples were located and collected. Locations varied from inside homes to anthills by telephone poles outside.

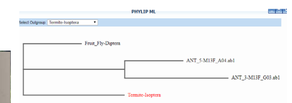

Figure 3: The ML phylogenetic tree with the sequenced compared to Fruit flies and termites for NZF-004 and NZF-005, the remining ants had bad sequencing data.

Note: All Sanger Sequencing Results are accessible for 2 years after which time the data will no longer be available

	Reaction	Tube	#	Sample	Q1	ORL	Failure Cause	Seq File (+Fasta Trim)	Trace File	Phd.1 File
ⓘ	JC01	JC1	1	ANT_1-M13F	12	6	No Primmg			
ⓘ	JC02	JC2	2	ANT_2-M13F	21	242	No Primmg			
ⓘ	JC03	JC3	3	ANT_3-M13F	24	412	Poor Quality			
ⓘ	JC04	JC4	4	ANT_4-M13F	12	1	No Primmg			
ⓘ	JC05	JC5	5	ANT_5-M13F	44	627				

Figure 4: Sample of the Genewiz results showing Sample # 5 being adequate and Sample # 3 being poor quality.

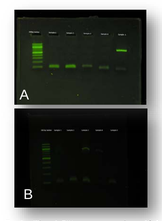

Figure 5: **A:** The 1.5% agarose gel verifying the CO1 gene was isolated for NFZ-005. **B:** The 1.5% agarose gel verifying the CO1 gene was isolated for NFZ-003.

Materials & Methods

The group collected ants from around the Commack Community. Sampling was performed on 7 total ants from 6 different locations in the Commack Community to find the variety of species. Ant traps were set using either a honey and water solution, or pumpkin pieces. Ants were also found by turning over large rocks and bricks. These ants were collected using a spoon or other object to help place them in a bag. Using an I-phone app, the GPS coordinates were determined in reference to a fixed-point in the ant's vicinity. The ants were digitally documented and geo-mapped. The DNA Barcoding Procedure was based on DNA Learning Center protocols, and performed mostly with their supplies. DNA was isolated using a Qiagen kit initially, then changing to the Rapid DNA isolation method. The DNA was amplified by Polymerase Chain Reaction (PCR) using primers for the COI gene. Gel electrophoresis was performed to verify the DNA was properly isolated for the COI gene. The amplified DNA was then sent to Genwiz for sequencing. The resulting FASTA files were uploaded into DNA Subway where a phylogenetic analysis was performed.

Discussion

The results were inconclusive as we had difficulty isolating DNA from the ants. We tried 2 separate techniques and even attended one of the DNALC workshops but still could not obtain good results. We believe we are not sufficiently grinding the ants, which shows how sensitive some of the procedures can be. We do not believe it was the reagents as we had 3 different sets of reagents and still could not obtain good results. We still have left over ants and plan to increasing the grinding time and hope to obtain sufficient results to determine the biodiversity of ants in the Commack Community.

References

- Doyle, P. S., Bibette, J., Bancaud, A., & Viovy, J. L. (2002). Self-assembled magnetic matrices for DNA separation chips. *Science*, *295*(5563), 2237-2237.
- Folgarait, P. J. (1998). Ant biodiversity and its relationship to ecosystem functioning: a review. *Biodiversity & Conservation*, *7*(9), 1221-1244.
- Frézal, L., & Leblois, R. (2008). Four years of DNA barcoding: current advances and prospects. *Infection, Genetics and Evolution*, *8*(5), 727-736.
- Hajibabaei, M., Singer, G. A., Hebert, P. D., & Hickey, D. A. (2007). DNA barcoding: how it complements taxonomy, molecular phylogenetics and population genetics. *TRENDS in Genetics*, *23*(4), 167-172.
- Hebert, P. D., & Gregory, T. R. (2005). The promise of DNA barcoding for taxonomy. *Systematic biology*, *54*(5), 852-859.
- Heller, C. (2001). Principles of DNA separation with capillary electrophoresis. *Electrophoresis*, *22*(4), 629-643.
- Ratnasingham, S., & Hebert, P. D. (2007). BOLD: The Barcode of Life Data System (http://www. barcodinglife. org). *Molecular Ecology Resources*, *7*(3), 355-364.
- Smith, M. A., & Fisher, B. L. (2009). Invasions, DNA barcodes, and rapid biodiversity assessment using ants of Mauritius. *Frontiers in Zoology*, *6*(1), 31.