Analyzing the Biodiversity of Beetles on the South Shore of Long Island

Authors: Gizela Maksym[1], Christina Schaake[1]
Mentors: Mary Kroll[1], Cristina Fernández-Marco[2], Sharon Pepenella[2]
[1]West Islip High School; [2]Cold Spring Harbor Laboratory's DNA Learning Center

Abstract

Beetles are responsible for decomposition of plants in gardens and farms on Long Island, creating financial problems for growers that depend on the plants for produce. To prevent crop decomposition in New York, the biodiversity of beetles must be studied to identify species that decompose plants, therefore minimizing farming issues. Beetle samples were collected at Gardiner Park and their DNA was copied using an extraction protocol, PCR of the CO1 gene, and gel electrophoresis. The genes were sequenced and analyzed using DNA Subway. By identifying decomposing beetles, farmers can take action to keep the pests out of their crops, preventing a decrease in product produced due to infestation.

Introduction and Hypothesis

- Beetles that decompose fruit-bearing trees on farms create financial problems for growers who depend on the trees for their fruits. A past problem in New York has been the infestation of Prionus Root-Boring Beetles of apple orchards, which affected the business local farmers (Agnello, 2011).
- It is hypothesized that the beetles collected around trees and decayed material are those that assist in the decomposition process of surrounding plants.
- This research project is unique to New York beetles on Long Island farms, gardens and forests.

Methods

Figure 1. Identifies the sites of collection for all beetle samples, in both Gardiner Park and Manorville on the South Shore of Long Island.

Figure 3. This close-up image depicts NZG-009 which was sent to the Barcode Long Island Database and was not discovered in GenBank or BOLD. *Photo taken by researchers.*

Sample Collection: 20 samples from Gardiner Park, Manorville, and West Islip using scoopulas, tweezers, gloves and test tubes.

DNA Collection: For each sample, a DNA extraction protocol was followed to obtain a purified DNA sequence.

Sample Documentation: NZG Samples are documented in pictures using digital microscope, camera, rulers and tweezers are sent to Barcode Long Island.

DNA Barcoding: Positive results are sent out to Cold Spring Harbor Laboratory for Sanger Sequencing, after PCR and gel electrophoresis, to isolate the CO1 gene.

DNA Subway Analysis: Accepted samples on DNA Subway are analyzed. The DNA of the organisms are compared to similar sequences using the program, representing the experimental results.

Figure 2. This photograph depicts the process of DNA extraction with micropipettes. *Photo taken by research teacher.*

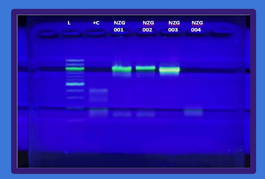

Figure 4. Gel electrophoresis results for samples NZG-001 to NZG-004 with a positive control and a ladder. The brightness of the bands indicate positive results, while the missing NZG-004 band means not enough DNA was collected to obtain results. *Photo taken by researchers.*

Results

Table 1. The metadata and information from GenBank and BOLD for each analyzed species

Sample ID	Quadrat Location	Habitat Description	Aln. Length	Bit Score	e Value	# Mis-matches	GenBank Scientific Name	% Similar in BOLD	BOLD Scientific Name
NZG-001	Gardiner Park	Rotting Log	639	1119	0	0	*Carabidae sp.*		
NZG-002	Gardiner Park	Tree stump	644	1142	0	1	*Forficula cf.*		
NZG-003	Gardiner Park	Forest Floor	652	1177	0	0	*Forficula aff*		
NZG-007	Gardiner Park	Forest Floor	637	921	0	49	*Not Available*	100%	*Pterostichus tristis*
NZG-009	Gardiner Park	Forest Floor	626	655	0	105	*Not Available*	No Matches	
NZG-015	Gardiner Park	Leaf Litter	656	1155	0	2	*Pterostichus tristis*		
NZG-016	Manorville	Pine Barrens Floor	560	888	0	30	*Parcoblatta sp.*	98.91%	*Parcoblatta uhleriana*
NZG-017	Manorville	Pine Barrens Floor	602	760	0	67	*Not Available*	99.06%	*Parcoblatta uhleriana*
NZG-019	Manorville	Pine Barrens Floor	657	1097	0	17	*Not Available*	100%	*Philoscia muscorum*

Table 2. This table is the similarity chart generated by DNA Subway, showcasing percentages of similarity between organisms; numbers on the y-axis of the table, along with the scientific name identified by GenBank and BOLD databases, correspond with numbers along the top of the table.

Sequence Variation	1	2	3	4	5	6	7	8	9	10	11	12	13
1. Consensus	-	60.43	82.14	82.67	82.67	78.48	78.53	82.32	85.9	85.88	85.87	89.51	89.36
2. Oniscus Asellus	60.43	-	55.99	56.37	56.37	54.04	53.58	53.35	54.68	54.67	56.12	55.26	55.7
3. Forficula cf.	82.14	55.99	-	99.84	99.84	69.83	68.91	67.32	70.48	70.34	73.53	73.68	73.72
4. Forficula aff.	82.67	56.37	99.84	-	100	70.35	69.07	67.32	70.68	70.54	73.86	74	74.42
5. Forficula aff. (BLAST)	82.67	56.37	99.84	100	-	70.35	69.07	67.32	70.68	70.54	73.86	74	74.42
6. Philoscia uhleriana	78.48	54.02	69.83	70.35	70.35	-	71.63	70	73.11	72.88	74.84	75.44	75.04
7. Stag Beetle Coleoptera (BLAST)	78.53	53.58	68.91	69.07	69.07	71.63	-	71.79	73.82	73.4	77.26	78.1	78.69
8. Parcoblatta Sp.	82.32	53.35	67.32	67.32	67.32	70	71.79	-	94.61	94.51	75	75.89	76.43
9. Parcoblatta uhleriana	85.9	54.68	70.48	70.68	70.68	73.11	73.82	94.61	-	100	78.12	79.02	79.67
10. Parcoblatta uhleriana	85.88	54.67	70.34	70.54	70.54	72.88	73.4	94.51	100	-	78.32	78.76	79.5
11. Pterostichus tristis	85.87	56.12	73.53	73.86	73.86	74.84	77.26	75	78.12	78.32	-	87.44	88.05
12. Carbadae sp.	89.51	55.26	73.68	74	74	75.44	78.1	75.89	79.02	78.76	87.44	-	99.21
13. Pterostichus tristis	89.36	55.7	73.72	74.42	74.42	75.04	78.69	76.43	79.67	79.5	88.5	99.21	-

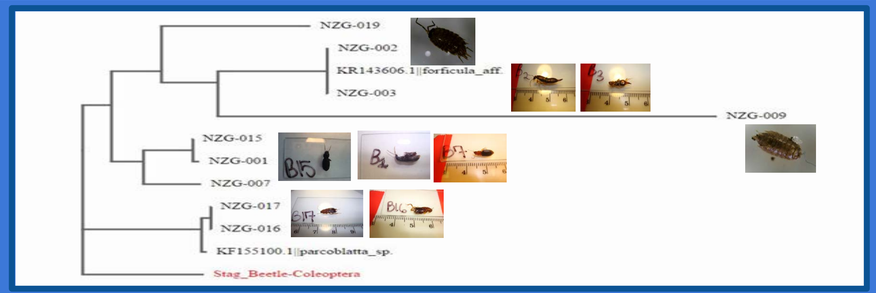

Figure 5. PHYLIP ML tree of the NZG collected samples and related selected organisms (*Parcoblatta sp*, *Forficula aff*) with outgroup as the Stag Beetle Coleoptera. *All photos taken by researchers.*

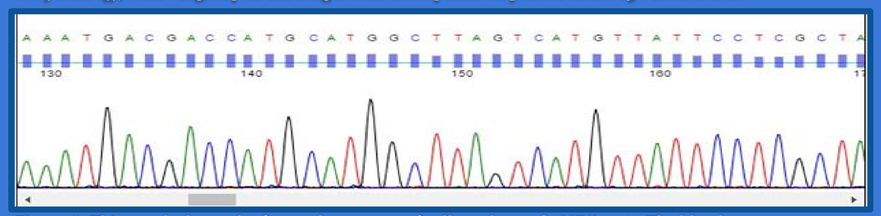

Figure 6. This graph shows the forward sequence of collected sample NZG-009. The blue bars up top represents the quality of the sequence. The height of the peak tells you how reliable each nucleotide identification is (the higher the peak, the more reliable the sequence is).

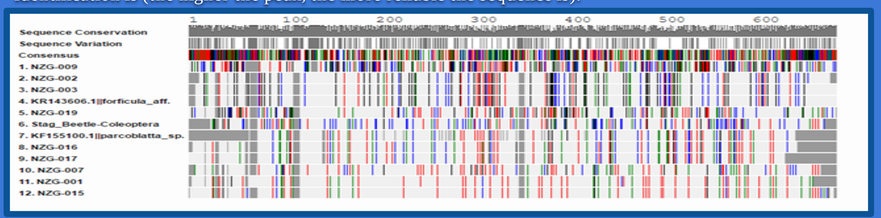

Figure 7. Sequence relation of collected organisms, BLAST hits (*Parcoblatta sp.* and *Forficula aff.*), and reference data of the stag beetle *Coleopteran* species

Conclusions

With the data and information collected, our hypothesis can be considered accurate. This is because all of the beetles identified are decomposers that may aid in the process of plant decomposition.

- NZG-001: Commonly known as the "Ground Beetle" for inhabiting soil in crops and forests; Native to North America (Regents of the University of Minnesota. n.d).
- NZG-002 and NZG-003: Commonly known as "European Earwig" and can create economic damage to vegetable and flower gardens. Native to Europe and Western Asia. In the early twentieth century it was accidentally introduced into North America (Maczey, 2015).
- NZG-007 and NZG-015: Native in the U.S and inhabits soil and compost; Native to North America.
- **NZG-009: An exception to the hypothesis; Identified as "Oniscus asellus" with 105 mismatches in GenBank; no matches in BOLD database. This indicates that NZG-009 has a potentially novel barcode.**
- NZG-016 and NZG-017: Commonly known as "Uhler's Wood Cockroach" and inhabits forests and scrubland; Native to Canada and Eastern United States, including New York (Encylopedia of Life n.d).
- NZG019: Commonly known as "Woodlice" and thrive in grassland, living in decomposed wood; Native to England and Scotland (NBN Species Dictionary, 2003) and (BMIG, n.d).

Future Research: For future research, we would like to look into sample NZG-009 because the sample had no found results in GenBank and BOLD databases with less than 150 mismatches. Although this organism appeared to be a common isopod insect, both databases showed no clear relation to the insect.

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