

Biodiversity Analysis Using CO1 Barcode for Coleoptera at Farmingdale State College

CSH Cold Spring Harbor Laboratory
DNA LEARNING CENTER

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Abstract

Healthy communities rely on well-functioning ecosystems. Without the presence of genetic, species and habitat diversity, the biosphere will deteriorate. The order Coleoptera play a vital role in the decomposition of organic material, stability of food webs and contributes to a large portion of the world's insect species. Due to a steady rise in local carbon dioxide emissions, biodiversity has declined on a massive scale, putting Coleoptera and many other species at the forefront of the climate crisis within Long Island.

Malaise traps are apparatuses designed to capture various species of insects at various elevations. Malaise traps utilize killing agents to increase specimen collection. 20 Coleoptera samples were collected by Dr. Carly Tribull, an entomologist and professor at Farmingdale State University, within the nearby field and forest habitats. To determine the species of these specimens, a chelex protocol was performed. This specific sequencing targets the COI gene, which amplifies insect DNA in order to accurately identify species. To begin, specimen legs and heads were removed and ground up for DNA extraction. The Polymerase Chain Reaction was then utilized to process amplified DNA fragments. Samples were then aliquoted into gel electrophoresis wells to test for DNA efficacy. Genetic diversity was determined using MUSCLE Sequencing. Species diversity was expressed with the creation of a pie chart and phylogenetic tree. To determine species, sequences were put through BOLD Systems' Taxonomy Browser. After the search, two novel species were identified, these specimens being (DAG_005) and (DAG_012).



Introduction

- CO1 (cytochrome c oxidase subunit I) is a vital genetic region located within mitochondria, and is utilized in the process of DNA Barcoding because of its large patterns of variation and relative ease of obtainment (Pentinsaari et. al, 2016).
- Malaise traps are highly-productive, adaptive apparatuses that are utilized to capture insects at varying elevations. These traps are often lined with killing agents to ensure maximum collection of specimens (Skvarla et. al, 2020).
- Beetles play an important role in ecosystems as decomposers of dying plants and animals (Nadeau et. al, 2015).
- Beetles are the most species-rich order of insects, and account for roughly 25% of all described species. This large variance within the beetle family indicates that beetles are necessary indicators of biodiversity (Stork et. al, 2015).
- Propylea quatuordecimpunctata* are vital for ecosystems as they keep the growth of aphid populations in check. If these species were to vanish, induced growth of aphid populations would cause excessive consumption of trees and shrubbery in the Teaching Gardens (Pervez & Omkar, 2011).
- Small shifts in Celsius temperatures are detrimental to the behavioral and physiological parameters of *Propylea quatuordecimpunctata* and *Hippodamia variegata* populations (Yang et al., 2022).
- Temperatures in New York have been increasing (Lamie, C, et. al, 2024).
- Coccinellidae are bioindicators of a healthy ecosystem (G. Ipert, 1999).

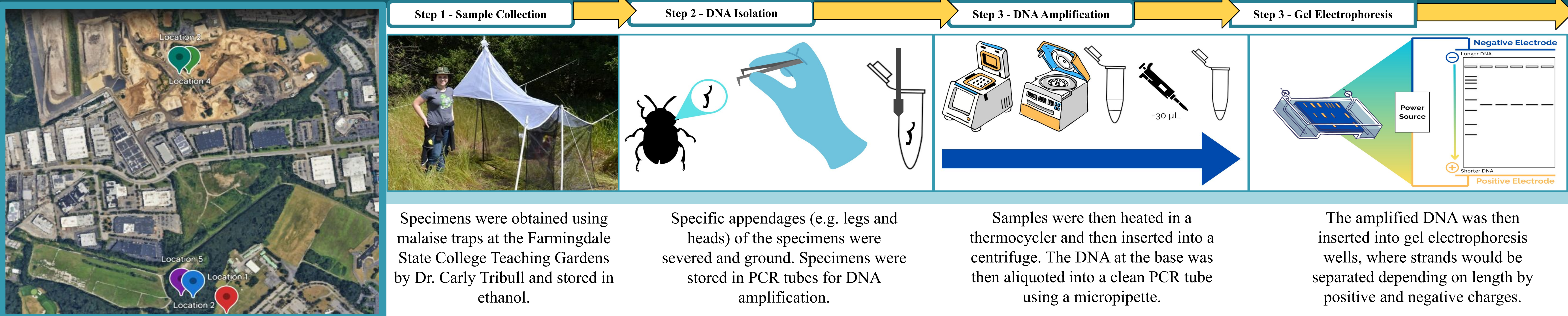
Research Question

How is the Biodiversity of Coleoptera influenced by external human influences?

References



Methodology



Data + Results

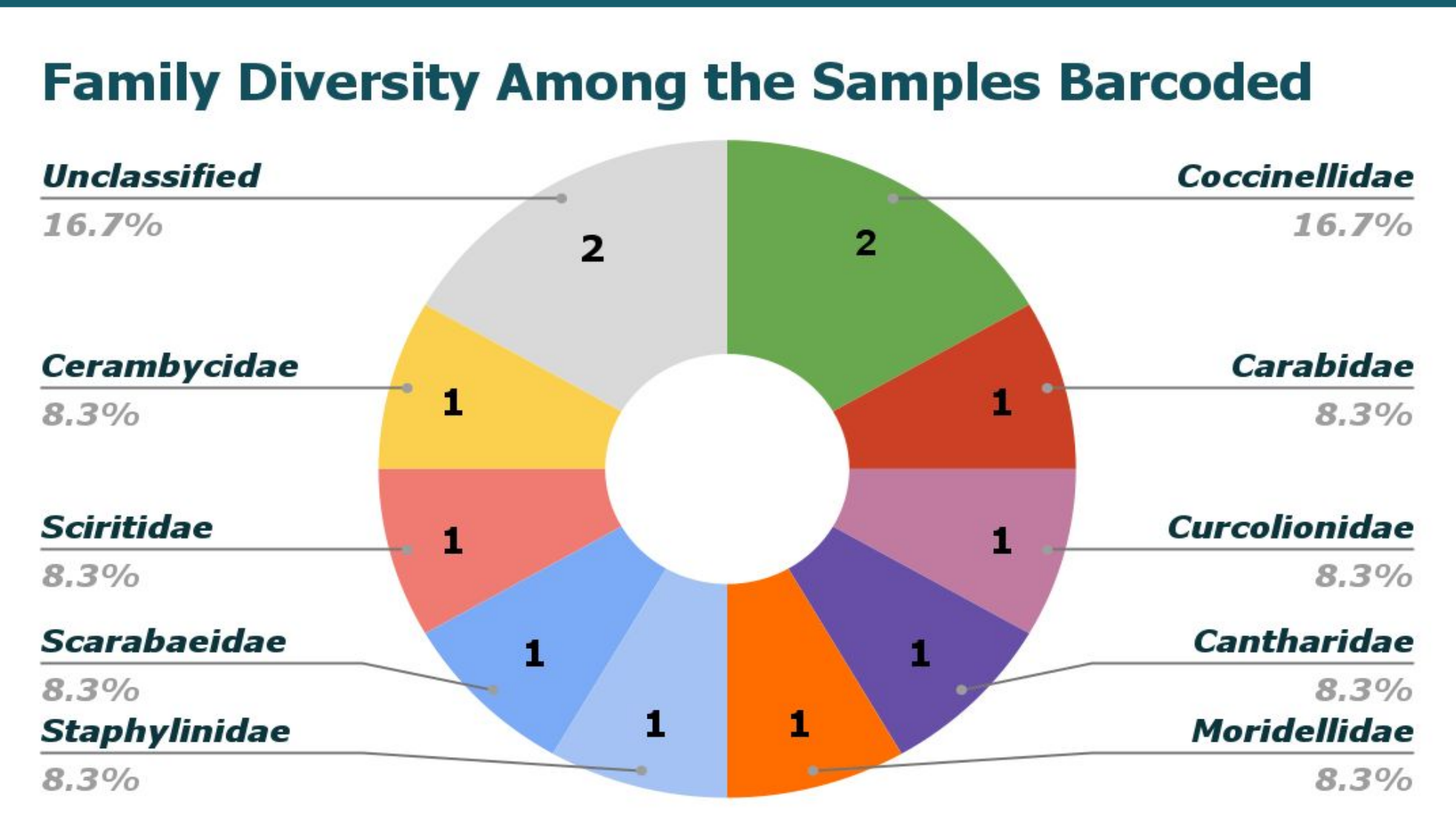


Figure x: A pie chart analyzing the diversity of families for the samples collected. (N=12)

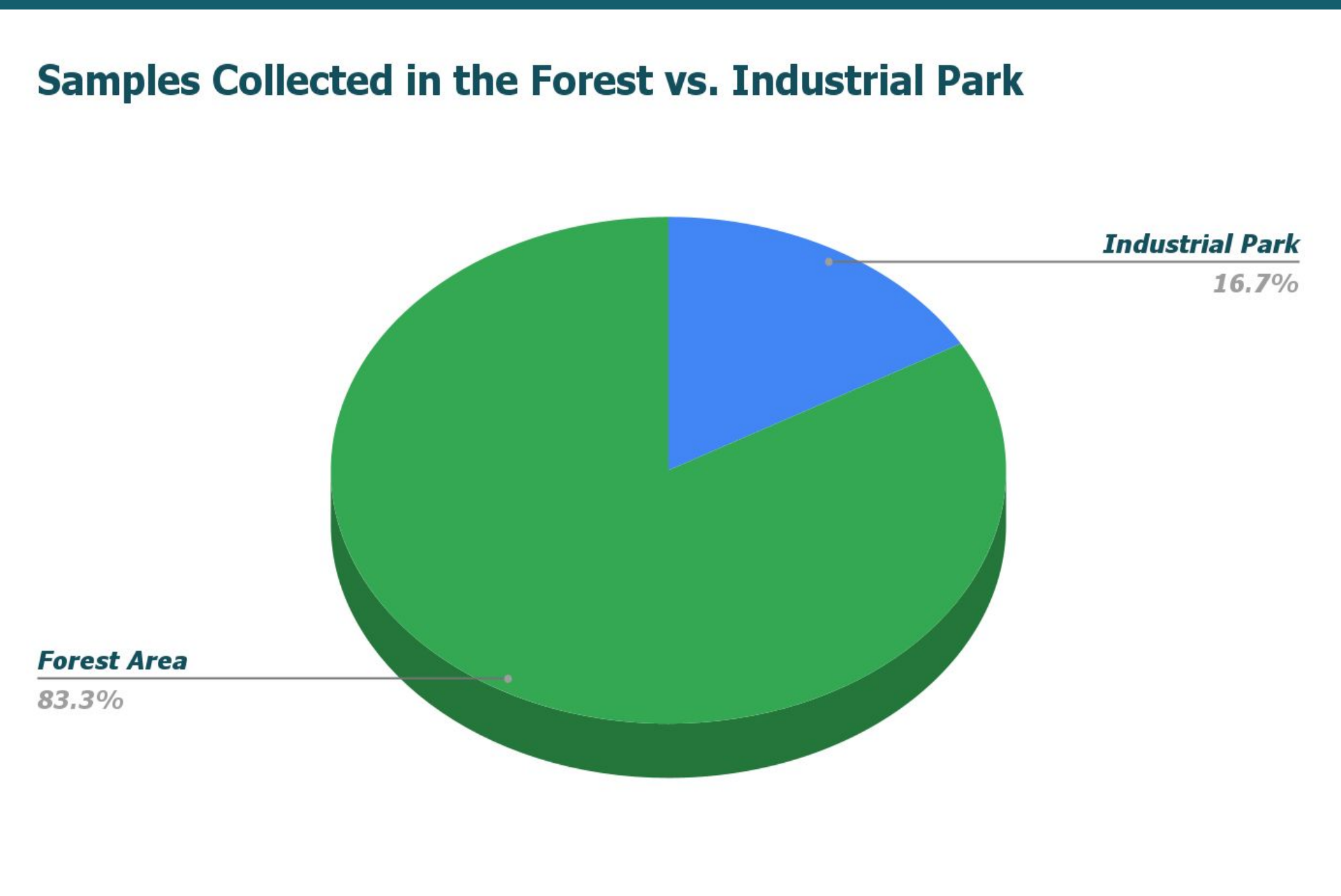


Figure x: A pie chart analyzing the environments where samples were collected.

Phylogenetic Tree of Collected Samples

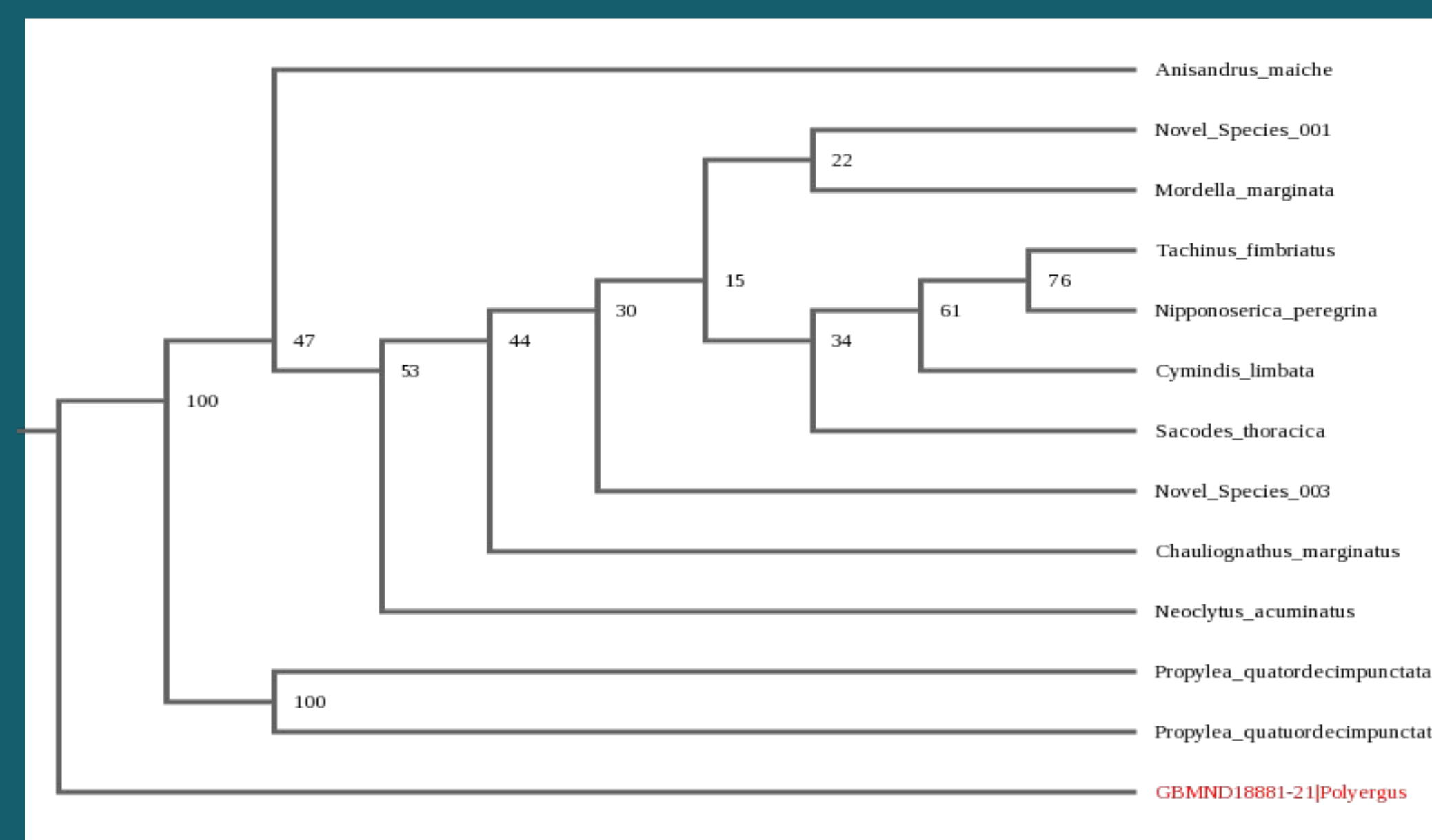


Figure x: Phylogenetic tree composed of all sample specimen (N=20) Branches connect species with similar genetic makeup identifying closely related species. GBMND18881-21 | Polyergus was used as a control in sample collection.

MUSCLE Multiple Sequence Alignment by Log-Expectation

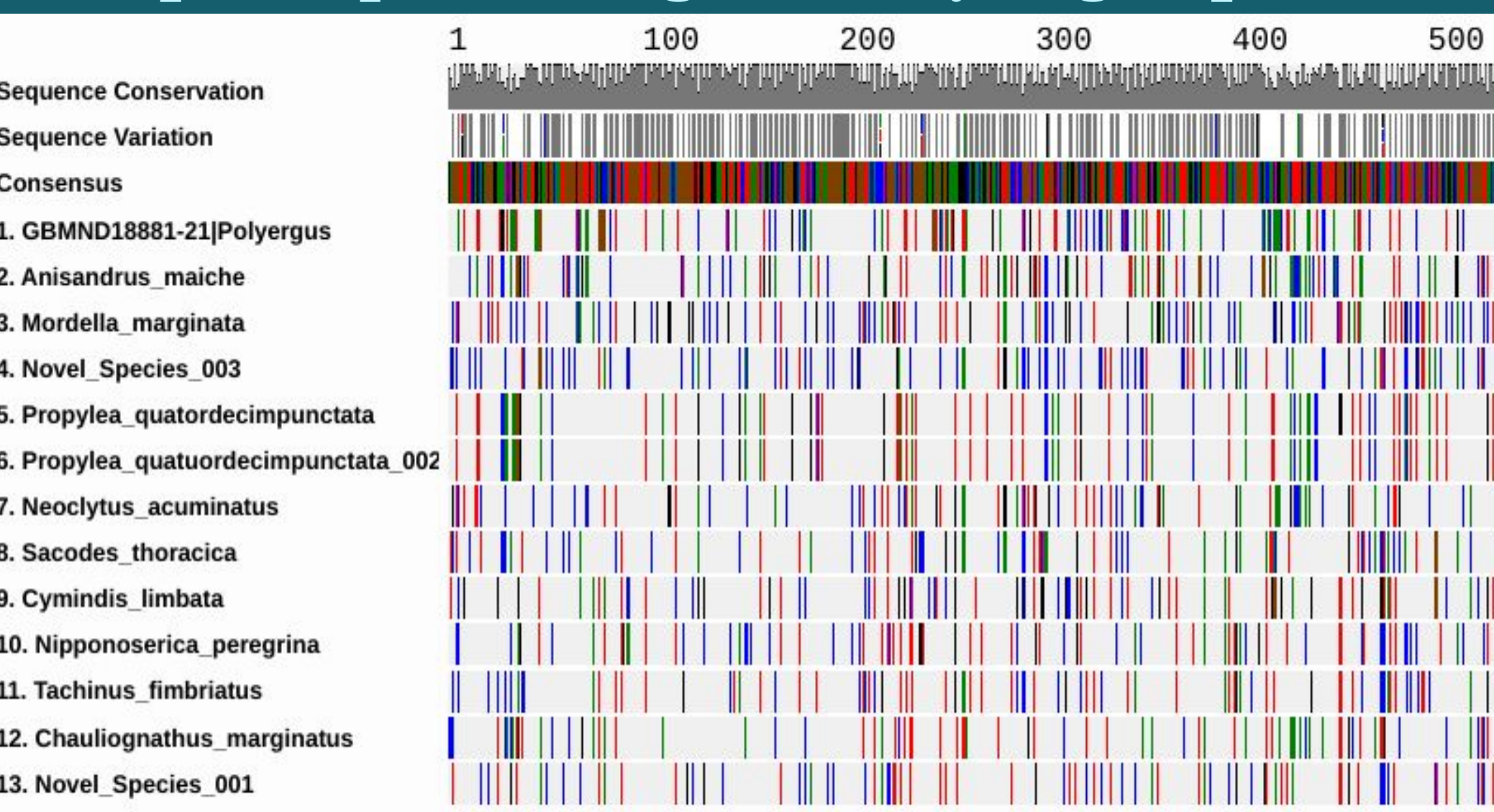


Figure x: Figure x: A visualization of the CO1 gene sequence for all the samples collected in Farmingdale.

Discussion

- Samples DAG_005 and DAG_012 were unable to be identified through the BOLD or BLAST system and therefore have been determined as novel.
- The pie chart suggests a greater population of Ladybugs (*Coccinellidae*) than other species.
- The MUSCLE shows some similarities at the 70 base pair mark between two novel species and *Chauliognathus Marginatus*, *Tachinus Fimbriatus*, and *Cymindis Limbata*
- Phylogenetic tree shows one a 76% match between *Tachinus Fimbriatus* and *Nipponoserica Peregrina* and a 100% match with both *Propylea Quatuordecimpunctata*
- We used the BOLD System during the BLAST species identification process, and this helped as it gave us multiple sources of BLAST data to cross reference, and the BOLD system gives us a more nuanced representation of data, as it gives us a percent match and graph as opposed to number of mismatches
- Our data shows ~29% of samples collected were *Propylea Quatuordecimpunctata*, and we expect these species to decline as temperatures continue to rise, but these species are also known bioindicators of ecosystem health, so we believe that temperature has an inverse relationship with ecosystem health.
- Forest Vs Industry - There was more biodiversity in the forest, suggesting that industrial emissions contribute to a decrease in biodiversity

Species Identification

Samples	Species ID	GPS Location
- DAG_001	<i>Propylea quatuordecimpunctata</i>	• 40.755493, -73.432509
- DAG_005	NOVEL SPECIES	40.755493, -73.432509
- DAG_006	<i>Cymindis limbata</i>	40.7656139, -73.433833
- DAG_007	<i>Anisandrus maiche</i>	40.756139, -73.433833
- DAG_009	<i>Chauliognathus marginatus</i>	40.7656139, -73.433583
- DAG_011	<i>Mordella marginata</i>	40.7656139, -73.433583
- DAG_012	NOVEL SPECIES	40.756139, -73.433778
- DAG_014	<i>Tachinus fimbriatus</i>	40.755493, -73.432509
- DAG_015	<i>Nipponoserica peregrina</i>	40.755493, -73.432509
- DAG_016	<i>Propylea quatuordecimpunctata</i>	40.755493, -73.432509
- DAG_017	<i>Neoclytus acuminatus</i>	40.755493, -73.432509
- DAG_020	<i>Sacodes thoracica</i>	40.755493, -73.432509