



# Utilizing the CO1 Gene to Navigate Lepidoptera **Biodiversity in Farmingdale State University Forest**

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### Abstract

#### Biodiversity is crucial for ecosystem stability and can be effectively studied using DNA barcoding. DNA barcoding identifies species using shortened DNA sequences. These DNA sequences are compared to other genus and species of Lepidoptera. When all compared sequences have over 15 mismatches, it can be named as a novel species. The purpose of this study is to investigate Lepidoptera biodiversity on Long Island by using DNA barcoding techniques. DNA Isolation was practiced to lyse the cells. To conduct this research, insects were photographed and documented after collection from a Malaise trap located in Farmingdale State University Teaching Gardens. DNA was extracted using the Chelex method. The cytochrome oxidase I (CO1) gene was amplified through polymerase chain reaction (PCR). Confirmation of successful amplification was achieved using gel electrophoresis. The resulting sequences were then analyzed in DNA

### Methodology



Subway to identify and compare species. DNA Subway was also used to trim the DNA sequence of mis-reads. A Simpson's index was used to calculate biodiversity. The results indicated a high level of biodiversity, reading at a number of 0.99. Future research could explore comparing forest Lepidoptera and field Lepidoptera to obtain differences when in opposite habitats.

llination

Food Source for

**Other Predators** 

he bioinformatics of the data collected

### **Data & Results**

electrophoresis conducted



DNA amplification procedure





Figure 18 - image of sample DGQ-009



Figure 17 - image of sample DGQ-00





igure 8 - phylogenetic tree of Lepic





Ha - The CO1 gene can be used to effectively measure and compare Lepidoptera biodiversity within forest habitats.

## **Key References**

**ARTICLE #1:** Malaise trap and insect sampling: Mini Review Sheikh, A. H., Thomas, M., Bhandari, R., & Meshram, H. (2016). Malaise trap and insect sampling: Mini Review. Bio Bulletin, 2(2), 35-40.

**Goals** - The goal of this study was to relate contrasting and comparing aspects of different malaise traps into a single window system

**Findings** - Malaise traps are able to collect diverse insect groups efficiently, but certain factors such as collectors, tap location, killing agents, and trap dimensions have impacted certain aspects of collection

**ARTICLE #2:** DNA Barcoding for Identification of Agriculturally Important Insects

Jalali, S. K., Ojha, R., & Venkatesan, T. (2015). DNA barcoding for identification of agriculturally important insects. New horizons in insect science: Towards sustainable pest management, 13-23.

Goals - The goal of this study was to examine the ability of DNA barcoding in identifying and assigning unknown specimens to species besides facilitating the discovery of new species.

Findings - DNA barcoding is favorable as it is a decisive tool in quick and reliable identification of insects.

# Figure 11 - image of sample DGQ-00. igure 10 - image of sample DGO-00

Sample ID	Genus	Specie	ORDER	Trap Location
DGQ-001	Apogeshna	stenialis	Lepidoptera	Forest
DGQ-003	Polypogon	obscuripennis	Lepidoptera	Forest
DGQ-004	Tineidae	sp.	Lepidoptera	Forest
DGQ-006	Notocelia	rosaecolana	Lepidoptera	Forest
DGQ-008	Apogeshna	stenialis	Lepidoptera	Forest
DGQ-009	Acrolophus	sp.	Lepidoptera	Forest
DGQ-010	Pandemis	limitata	Lepidoptera	Forest
DGQ-011	Glauce	pectenalaeella	Lepidoptera	Forest
DGQ-012	Anageshna	primordialis	Lepidoptera	Forest
DGQ-013	Aphomia	sociella	Lepidoptera	Forest
DGQ-014	Holcocera	chalcofrontella	Lepidoptera	Forest
DGQ-015	Acleris	semipurpurana	Lepidoptera	Forest
DGQ-016	Zale	horrida	Lepidoptera	Forest
DGQ-017	Protoboarmia	porcelaria	Lepidoptera	Forest
DGQ-019	Orthodes	detracta	Lepidoptera	Forest
DGQ-020	Noctua	pronuba	Lepidoptera	Forest
DGQ-021	Tineidae	sp.	Lepidoptera	Forest



Figure 9 - image of gel electrophoresis

Figure 16 - image of sample DGQ-00

Species	# of insects (n)	(n-1)	n(n-1)
Polypogon	1	0	С
īneidae	2	1	2
lotocelia	1	0	С
pogeshna	1	0	С
Acrolophus	1	0	C
Pandemis	1	0	С
Hauce	1	0	С
nageshna	1	0	С
phomia	1	0	С
lolcocera	1	0	C
Acleris	1	0	С
Zale	1	0	С
Protoboarmia	1	0	С
Drthodes	1	0	С
loctua	1	0	С
	N = 16		SUM = 2

Figure 14 - graph depicting the number, genus ecie, order, and location of each specimen

Figure 15 - graph depicting the Simpsons Inde breakdow

### Simpson's Index

#### 100% of insect specimens are from the forest.

Simpson's diversity index was calculated to determine the biodiversity score of 0.99. This indicates a significantly high level of biodiversity in the area as 0.99 is very close to 1.

Discussion

The phylogenetic tree indicates a 100 score between specimens DGQ-004 & DGQ-021 as shown in Figure 8.

• Samples DGQ-004, DGQ-009, and DGQ-021 were unable to be identified through the BOLD or BLAST system and

therefore have been determined as novel species.

• According to the MUSCLE, specimens DGQ-004 and DGQ-021 are most likely related genetically, as they have significantly similar barcodes.

• The largest percentage of Lepidoptera was from the family Tineidae and represented 12.5% of the samples.

