

Comparative Analysis of Field Trap vs Forest Trap for Diptera at Farmingdale State College

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Figure 1 - Image of Sample CRZ-013



Figure 2 - Image of Sample CRZ-018

Abstract

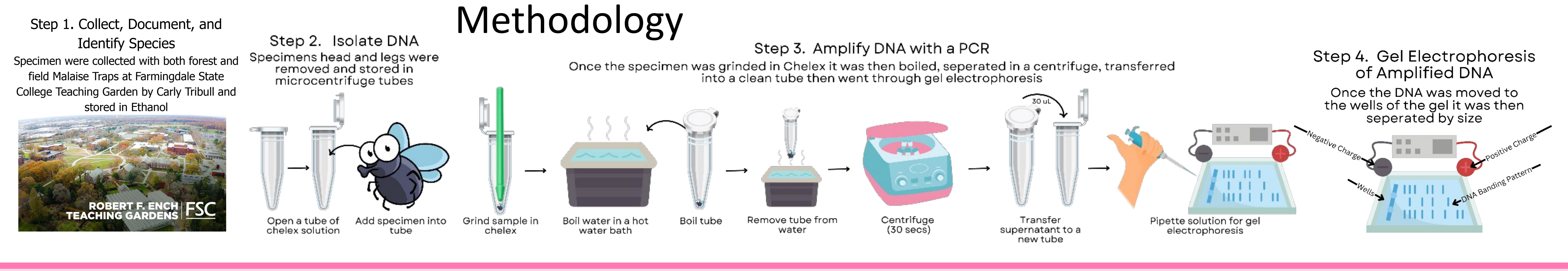
Diptera are well represented as ecosystem engineers and are classified as a keystone species that can alter environments and even indicate the quality of water. As insects provide many essential services and are vital for our ecosystems (Costanza et al., 1997; Dainese et al., 2019; Reid, 2005), it is critical to continuously monitor insect communities in order to determine when and where populations are declining, identify drivers of declines, and develop targeted mitigation measures. 20 specimens were caught from Farmingdale State College teaching gardens by Dr. Carly Tribull using a malaise trap set in a field (40.754930-73.432509) and a forest (40.756139-73.433833). A malaise trap is a tent-like structure that is an efficient method for collecting flying insects. Our research aimed to compare the specimens caught in a field trap versus a forest trap. DNA from each sample was extracted using the chelex protocol isolating the Cytochrome c oxidase I (COX1) gene. Sample DNA was then isolated and amplified utilizing a Polymerase Chain Reaction (PCR). Species samples were run using a gel electrophoresis chamber. The samples were then accessed on the DNA Subway platform, and the Barcode of Life Data System (BOLD) and Basic Local Alignment Search Tool (BLAST) programs were accessed to identify species using nucleotide sequences. Data was organized using the Multiple Sequence Alignment created by MUSCLE through DNA Subway. A phylogenetic tree was built and analyzed for common ancestry. A pie chart was built to demonstrate which families were found in only forest traps, only in field traps, or found in both forest and field traps. Results indicated that some species of Diptera were found only in forests, further stressing the urgency to preserve biodiversity moving forward.

Introduction

- A malaise trap, usually set in forests is a large, tent like structure used to catch or preserve insects (Michael J Skvarla, Jonathan L Larson, J Ray Fisher, Ashley P G Dowling, 2021)
- A type of field trap (sticky trap) which is often applied to Diptera and Hemiptera, efficiently sampled many families of Hymenoptera and Coleoptera, as well as Diptera after a study of field traps with identification. (Mito Ikemoto & Kazumu Kuramitsu, 2021)
- Insects play an extremely important role in ecosystems such as pollinators, decomposers, predators, and prey - they make up about 80% of all life on Earth (Min Li, Ting Lei, Guobin Wang, Danli Zhang, Huaxi Lu, Zhiwei Zhang, 2023)
- 2.5 billion people worldwide depend on insects as their supplementary food source (Owusu Fordjour Aidoo, Jonathan Osei -Owusu, Kwasi Asante, Aboagye Kwarteng Dofuor, Belinda Obenewa Boateng, Shadrack Kwaku Debrah, Kodwo Dadzie Ninsin, Shahida Anusha Siddiqui, Shaphan Yong Chia, 2023)
- Larval flies are well represented as ecosystem engineers and keystone species that alter the abiotic and biotic environments through activities such as burrowing, grazing, suspension feeding, and predation. (Muhammad Ashfaq, 2022)
- Genetic species identification works by matching unknown samples to reference samples in the data bases (Nick Dawnay a, Rob Ogden b, Ross McEwing b, Gary R. Carvalho a, Roger S. Thorpe, 2007)
- Identification is performed by using the CO1 gene. It is easy to amplify and only one variant of the gene exists (Nick Dawnay a, Rob Ogden b, Ross McEwing b, Gary R. Carvalho a, Roger S. Thorpe, 2007)
- The CO1 gene is encoded in the mitochondrial genome for all living insects (Nick Dawnay a, Rob Ogden b, Ross McEwing b, Gary R. Carvalho a, Roger S. Thorpe, 2007)

Research Question and Hypothesis

Would a field trap or forest trap capture more Diptera?
 H₀ - The results from the CHELEX DNA extraction protocol will not indicate high levels of biodiversity in a forest when compared to a field.
 H_a - The results acquired from the CHELEX protocol will indicate high levels of insect biodiversity in a forest when compared to that of a field.



Results and Data

Family Samples Collected from Malaise Field Traps

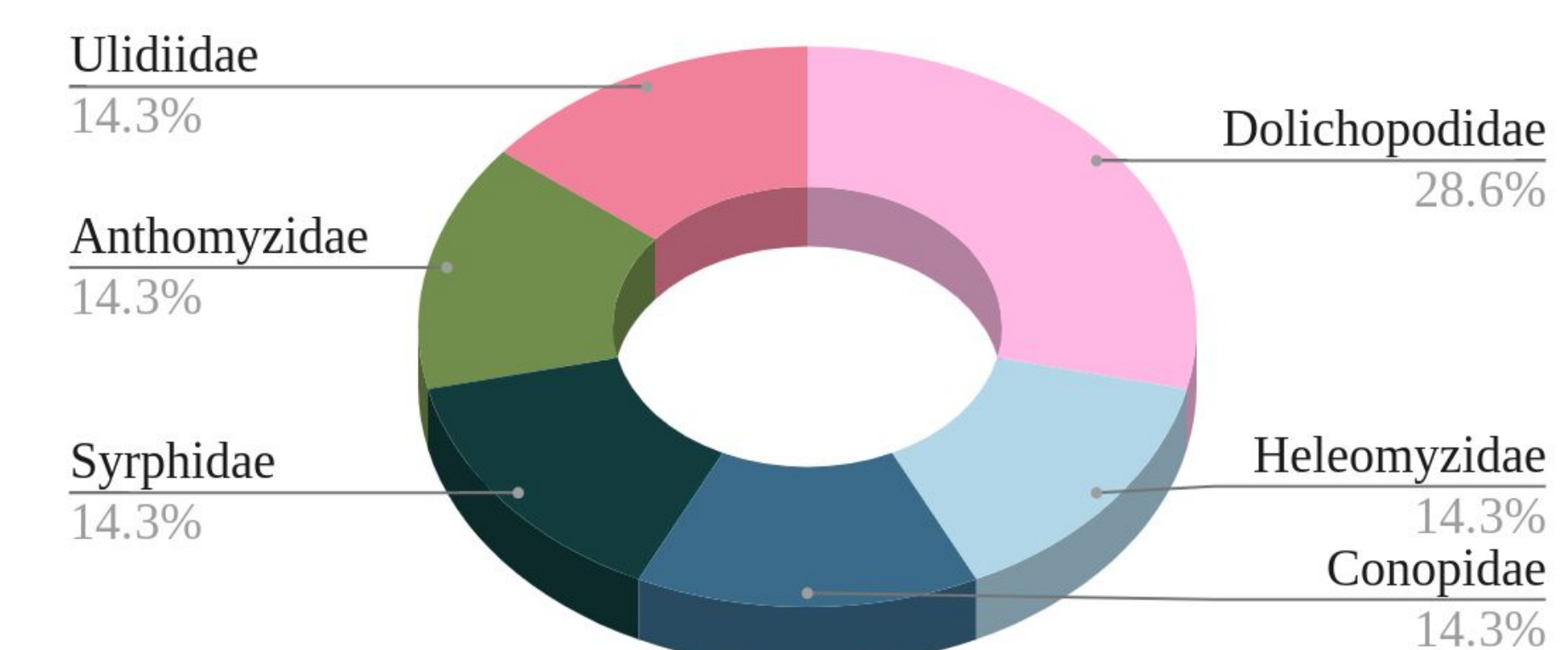


Figure 3 - Pie graph showing the families of samples collected from Malaise field traps.

Family Samples Collected from Malaise Forest Traps

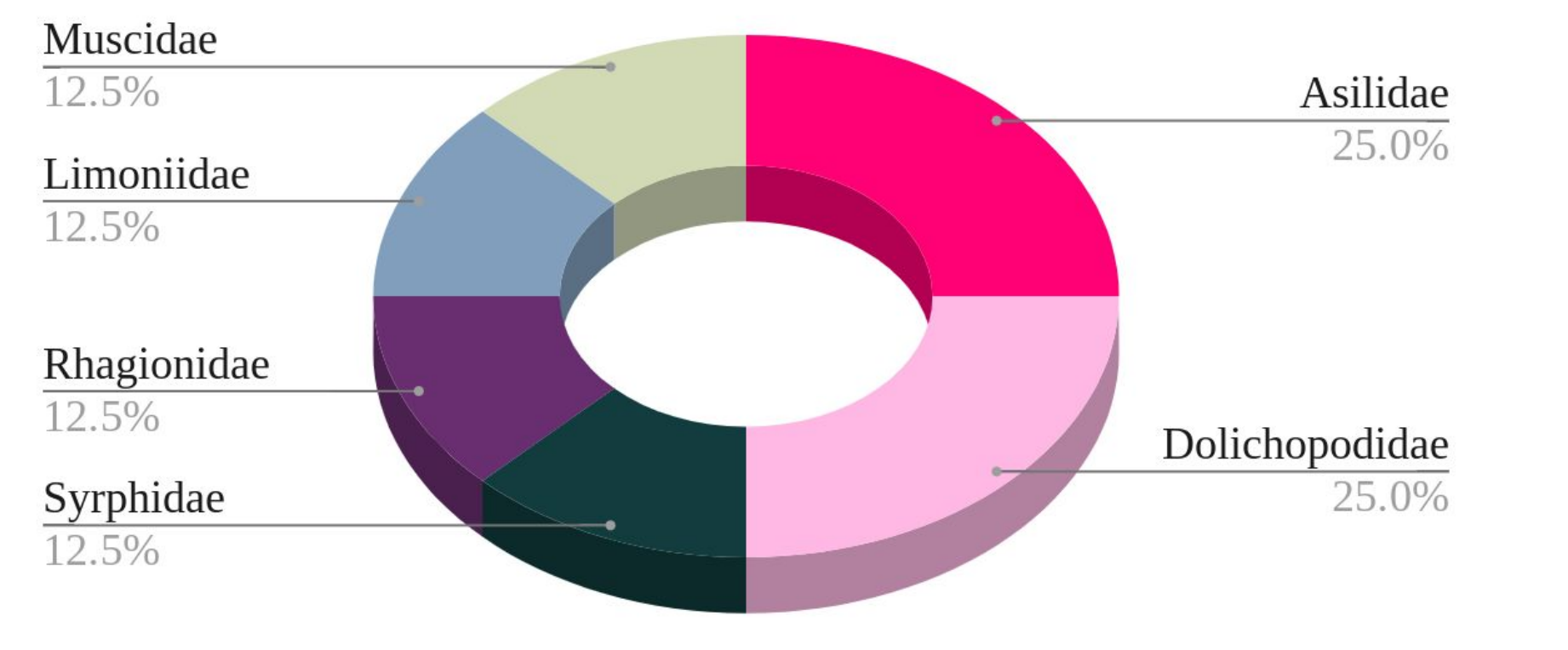


Figure 4 - Pie graph showing the families of samples collected from Malaise forest traps.

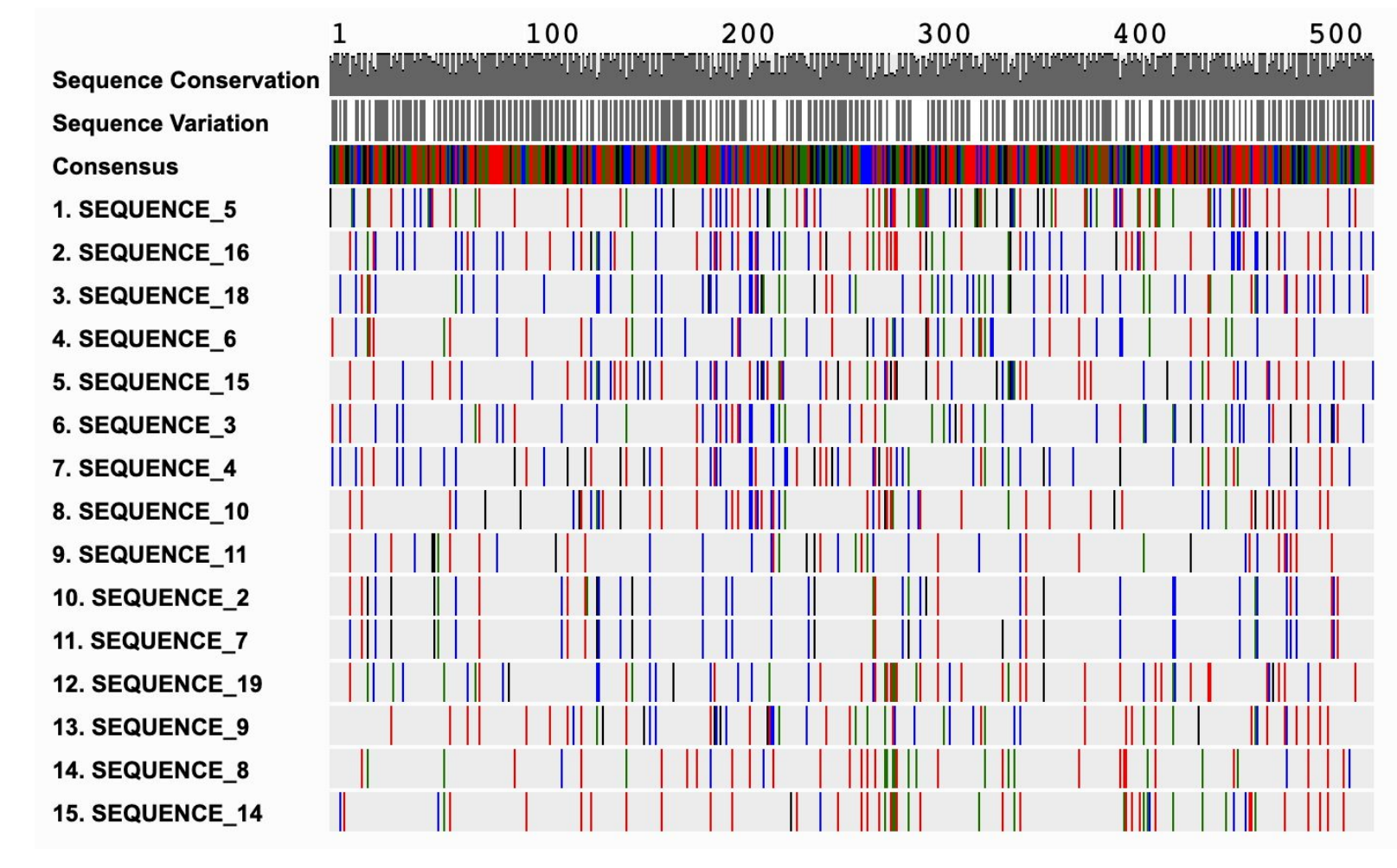


Figure 5 - Multiple Sequence Alignment created by MUSCLE using DNA Subway

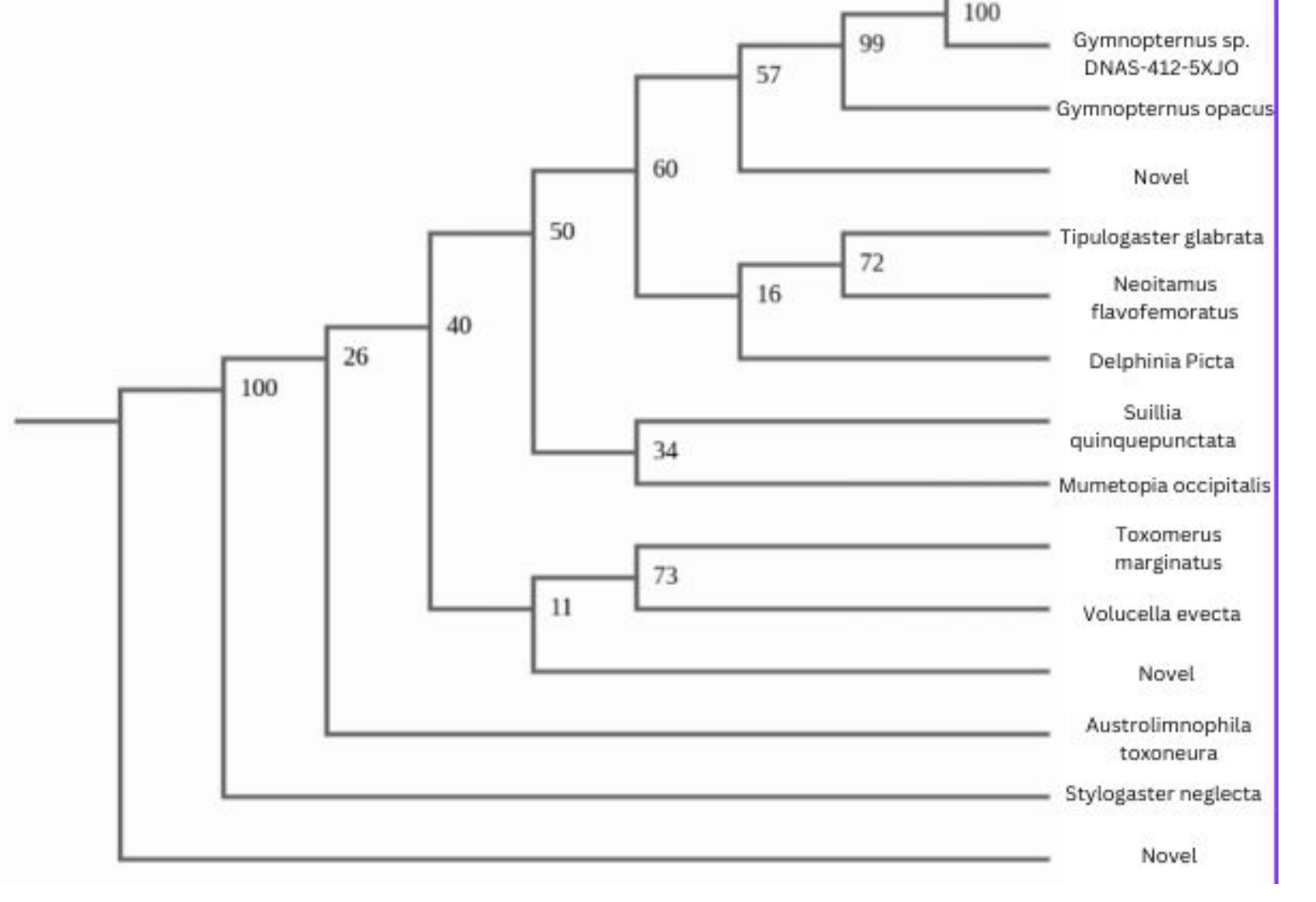


Figure 6 - Phylogenetic tree created with DNA Subway

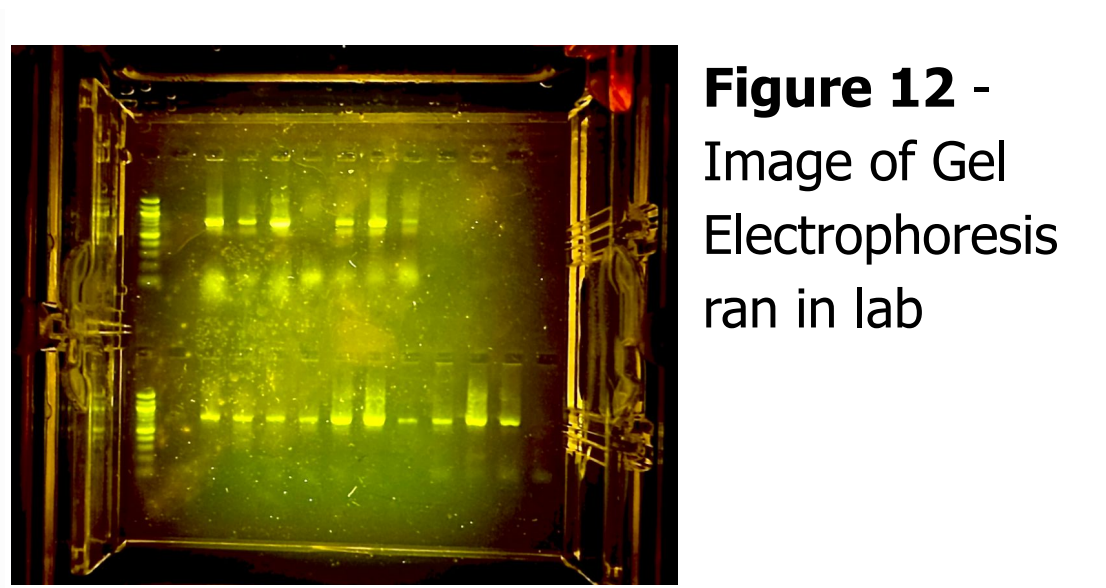


Figure 12 - Image of Gel Electrophoresis run in lab



Figure 8 - Image of Sample CRZ-003, novel species

Sample ID	GPS Cordiantes	Trap	N - Novel
CRZ-002	40.754930-73.432509	Field	
CRZ-003	40.754930-73.432509	Field	N
CRZ-004	40.754930-73.432509	Field	
CRZ-005	40.754930-73.432509	Field	
CRZ-006	40.756139-73.433833	Forest	
CRZ-007	40.756139-73.433833	Forest	
CRZ-008	40.756139-73.433833	Forest	
CRZ-009	40.756361-73.433583	Forest	N
CRZ-010	40.756361-73.433583	Forest	
CRZ-011	40.756361-73.433583	Forest	
CRZ-014	40.756361-73.433583	Field	
CRZ-015	40.756361-73.433583	Field	
CRZ-016	40.756361-73.433583	Field	
CRZ-018	40.755583-73.433778	Forest	
CRZ-019	40.755583-73.433778	Forest	N

Figure 7 - Shows GPS coordinates, field or forest trap, and novel species



Figure 9 - Image of Sample CRZ-003, novel species



Figure 10 - Image of Sample CRZ-009, novel species

Discussion

- Pie chart displays the percentages of insect caught in both field and forest traps broken down into identified families.
- 25% Asilidae and 25% Dolichopodidae species were captured in the malaise forest trap.
- 28.6% Dolichopodidae species were captured in the malaise field trap.
- The Heleomyzidae, Conopidae, Anthomyzidae, and Ullidae species were only found to be caught in field traps
- The Asilidae, Muscidae, Limoniidae, and Rhagionidae species were only caught in forest traps
- The species of Gymnopternus and Gymnopternus sp.DNAS-412-5XJO scored 100 on Phylogenetic tree indicating they are most closely related
- Multiple Sequence Comparison by Log-Expectation results indicated that Sequence 002 and 007 had DNA fragments similar to one another suggesting that these two specimens are closely related.
- 1 novel specie was captured in malaise field trap
- 2 novel specie was captured malaise forest trap
- The program DNA Subway was used to create Phylogenetic Tree, Multiple Sequence Comparison by Log-Expectation as well as BLASTIN the species for identification
- 7 specimens were collected in a field and 8 were collected in a forest. Increased levels of biodiversity are located within forests.



Figure 11 - Image of Sample CRZ-019, novel species



Figure 12 - Image of Sample CRZ-006, novel species



References and Acknowledgements