THE IDENTIFICATION OF DIFFERENT THERAPHOSIDAE SPECIES AND GENERA THROUGH THE USE OF DNA BARCODING

Your Logo Here

Authors

Authors: Mauricsha Murray, Gleydy Diaz-Rodriguez, Grace Garcia, Deborah Adjei, Sean Merritt

Affiliations

Wyandanch Memorial High School, Cold Spring Harbour Laboratories

Abstract

The term "Tarantula" is generally used to describe members of the family Theraphosidae. Theraphosidae samples were collected from multiple habitats with collaboration with Kansas State University and Disney's Animal Kingdom. The goal of our research was to provide identification of specific species of tarantula in conservation efforts such as preventing habitat loss along with support for potentially endangered species. Some essential methods and materials that we used to prove our hypothesis were a microcentrifuge, to effectively separate the DNA, and the process of PCR, which was used to amplify the amount of DNA in a sample. We discovered the specific Theraphosidae species out of these sample molt skins. This non-invasive barcoding project supports species verification for endangered or captive-bred tarantulas. Identifying species can help in conservation. As students, we contributed to this project by processing molt skins using specialized DNA barcoding protocols.

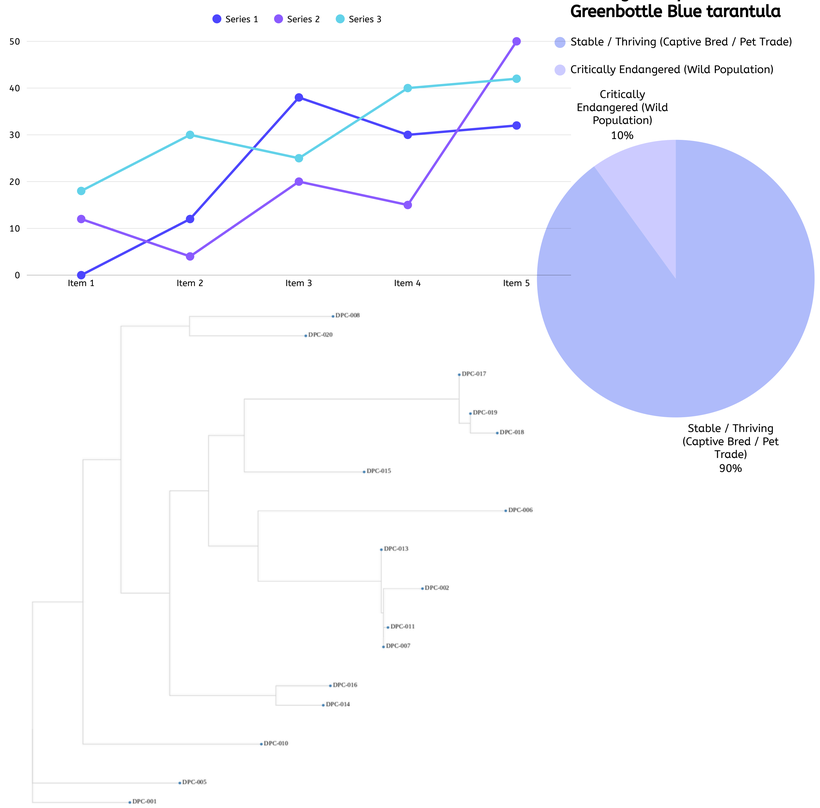
Objective

How can we understand the differences as it relates to species identification in terms of understanding the ecology and population? This DNA Barcoding project addresses meticulous species within the Theraphosidae family, which consists of over 1,100 species with distinct behaviours and lifespans. While having similar anatomy makes differentiation difficult, DNA barcoding provides an efficient tool to catalog genetic variations. Accurate identification provides the data needed to record unique and evolutionary traits,as well as demographics such as lifespan and molting. This project contributes to identification, population tracking, ultimately providing the aid needed to design effective conservation strategies for threatened tarantula populations.

Methodology

1. We were provided frozen tarantula molt samples of various species from an outside source. Most of our chemicals and equipment were also provided from an outside source. Each member was responsible for
2. extracting the DNA from a few samples. We used a silica resin DNA extraction protocol. It involves binding the extracted DNA to silica resin and
3. washing it to remove impurities. After selecting viable samples, they were sent to Cold Spring Harbor Laboratory for sequencing. After obtaining the sequencing results, they will be compared to
4. available information on the DNA Subway and Bold Systems websites. (dnasubway.org) (id.boldsystems.org) After comparison, the species of
5. the tarantula can be identified.

Query ID	Tree	Tax Rank	Phylum	Class	Order	Family	Subfamily	Tribe	Genus	Species	Confidence
DPC-015	Tree	FAMILY	Arthropoda	Arachnida	Araneae	Theraphosidae					100.0
DPC-001	Tree	GENUS	Arthropoda	Arachnida	Araneae	Theraphosidae			Acanthoscurria		100.0
DPC-005	Tree	SPECIES	Arthropoda	Arachnida	Araneae	Theraphosidae			Tliltocatl	Tliltocatl albopilosus	100.0
DPC-007	Tree	SPECIES	Arthropoda	Arachnida	Araneae	Theraphosidae			Chromatopelma	Chromatopelma cyaneopubescens	100.0
DPC-011	Tree	SPECIES	Arthropoda	Arachnida	Araneae	Theraphosidae			Chromatopelma	Chromatopelma cyaneopubescens	100.0
DPC-013	Tree	SPECIES	Arthropoda	Arachnida	Araneae	Theraphosidae			Chromatopelma	Chromatopelma cyaneopubescens	100.0
DPC-006	Tree	GENUS	Arthropoda	Arachnida	Araneae	Theraphosidae			Caribena		100.0
DPC-008	Tree	GENUS	Arthropoda	Arachnida	Araneae	Theraphosidae			Nhandu		100.0
DPC-020	Tree	GENUS	Arthropoda	Arachnida	Araneae	Theraphosidae			Lasiodora		99.85
DPC-002	Tree										



Discuss & Results

We used BOLD SYSTEMS and placed our DNA sequences in their identification engine and it successfully identified the tarantula species of the samples. While doing the DNA extraction and gel electrophoresis within a class period, which is 45 minutes, it was not optimal and we had to restart over. When we did the gel electrophoresis, some of the samples were very faint and fuzzy, in contrast to the clarity we should have had as the result. But at the end we managed to successfully get the DNA sequences of our samples, the results are detailed below. Using DNA barcoding, it made it easier to identify species with their sequences.

This connects to the goal of our research which was to provide identification of specific species of tarantula in conservation efforts such as preventing habitat loss along with support for potentially endangered species by using an efficient way to identify these species.

For example: The chromatopelma cyaneopubescens (See in FIgure 2)

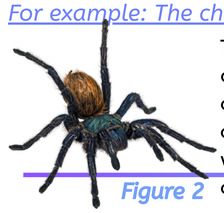
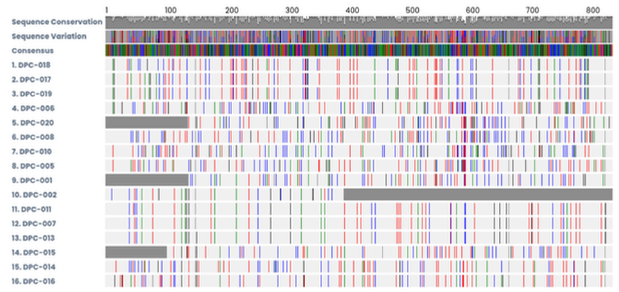


Figure 2

The Chromatopelma cyaneopubescens (Greenbottle Blue tarantula) is classified as Endangered in Venezuela. In 2013, Venezuelan scientists announced that Greenbottle blue tarantulas were threatened by overgrazing that is destroying their habitat. Identifying these species with much efficency and accurately can assist on bringing awareness and catch statuses of these species before its too late.

Conclusion

The conclusion summarizes the main findings of the study and restates the research objective. It highlights the significance of the findings and discusses their implications for future research and practice. The conclusion should provide a concise and clear summary of the study, reinforcing the key points and emphasizing the contributions of the research.



Key Sources & Acknowledgements

We would like to thank Dr. Christina Fernandez-Marco of CSHL and Jeffry Petracca for assisting our research.