Identification of Curated Butterfly Species Using DNA Barcoding

John Berkowitz, Jake Coggin, Jameson Mortenson

Eastport South Manor Junior-Senior High School

Abstract

This study uses DNA barcoding to identify butterfly species by analyzing a short region of mitochondrial DNA known as the CO1 gene. Butterflies play an important role in ecosystems as pollinators, making accurate identification important for understanding biodiversity. Specimens were obtained from the Long Island Aquarium and prepared for genetic analysis through DNA extraction and PCR amplification.Gel electrophoresis results showed successful amplification of the CO1 gene in most samples, indicating that the DNA was properly extracted and suitable for further analysis. The amplified samples are being sequenced to compare their DNA barcodes to reference databases for species identification. These results demonstrate that DNA barcoding is an effective method for identifying butterfly species and supports its use in studying biodiversity.

Introduction

DNA barcoding identifies specimens using short, standardized segments of DNA from the mitochondrial COI gene. Each species has a unique DNA barcode, comparable to a fingerprint, which can be matched against a reference library for identification.

Studying butterfly biodiversity is crucial because they are vital pollinators. Stable butterfly populations are necessary for healthy ecosystems. Conserving butterflies improves the environment for wildlife, enriches human life, and provides intrinsic, aesthetic, and educational value.

Biodiversity ensures ecosystem stability, preventing species loss and allowing plants and animals to thrive

Materials and Methods

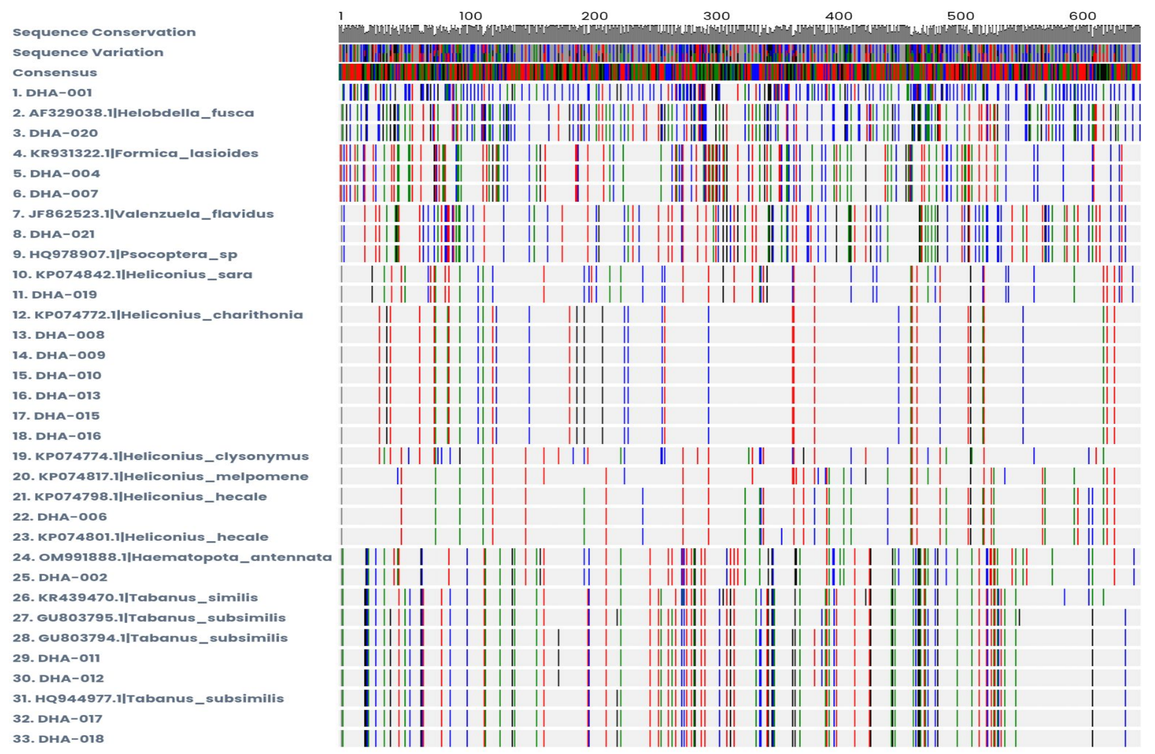
20 different butterfy chrysalises were received from the Long Island Aquarium in marked resealable plastic bags, photographed, and stored in freezer until DNA extraction

Samples were labeled and organized in plastic bags, then crushed them into smaller pieces that can be used for PCR

Samples were amplified with PCR and then gel electrophoresis was used to identify any CO1 genes that were copies successfully These copies were sent for nanopore sequencing at DNALC

References

Results



SAMPLE ID NUMBER	AQUARIUM IDENTIFICATION	DNA BARCODE ID	COMMON NAME
DHA-001	*Dryas iulias*	*Homo Sapiens*	Human
DHA-002	*Dryas iulias*	*Haematopota antennata*	Horsefly
DHA-003	*Dryas iulias*	*Homo Sapiens*	Human
DHA-004	*Dryas iulias*	*Formica lasioides*	Fuzzy Mound Ant
DHA-006	*Heliconius hecale*	*Heliconius hecale*	Tiger longwing
DHA-007	*Heliconius hecale*	*Formica lasioides*	Fuzzy Mound Ant
DHA-008	*Heliconius charithonius*	*Heliconius charithonia*	Zebra longwing
DHA-009	*Heliconius charithonius*	*Heliconius charithonia*	Zebra longwing
DHA-010	*Heliconius charithonius*	*Heliconius charithonia*	Zebra longwing
DHA-011	*Heliconius charithonius*	*Tabanus subsimilis*	Striped horse fly
DHA-012	*Heliconius charithonius*	*Tabanus subsimilis*	Striped horse fly
DHA-013	*Heliconius charithonius*	*Heliconius charithonia*	Zebra Longwing Butterfly
DHA-014	*Heliconius charithonius*	*Tabanus subsimilis*	Striped horse fly
DHA-015	*Heliconius charithonius*	*Heliconius charithonia*	Zebra Longwing Butterfly
DHA-016	*Heliconius charithonius*	*Heliconius charithonia*	Zebra Longwing Butterfly
DHA-017	*Heliconius charithonius*	*Tabanus subsimilis*	striped horse fly
DHA-018	*Heliconius charithonius*	*Tabanus subsimilis*	striped horse fly
DHA-019	*Heliconius sara*	*Heliconius sara*	Sara Longwing
DHA-020	*Heliconius sara*	*Helobdella fusca*	Dark Leech
DHA-021	*Heliconius ismenius*	*Valenzuela flavidus*	Yellow barklouse

Discussion

Most butterfly samples showed successful amplification of the CO1 gene because clear DNA bands and readable sequences were obtained. This indicates that the PCR process and DNA extraction methods were effective for most specimens. Differences seen in the sequence alignment suggest genetic variation between butterfly species. A few samples produced weak or unclear results which may have been caused by low DNA quality or errors during amplification. Overall the results support the use of DNA barcoding as an effective method for identifying butterfly species and studying biodiversity.

Future Directions

Sequence CO1 gene samples to identify species using reference databases. Increase sample size to improve accuracy and reliability. Compare DNA results with physical identification methods. Improve lab techniques to reduce inconclusive results. Apply findings to support biodiversity research and conservation.

Acknowledgements

Thank you to the DNA Learning Center Staff for support with proposals, providing laboratory equipment, and supporting sequence analysis. Special thanks to Jeff Petracca for assistance with nanopore sequencing.