

Biodiversity and Evolution: Bees, Ants and Wasps of the Hymenoptera Order

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Abstract

This study investigated the biodiversity and evolutionary relationships between bees, ants, and wasps collected from Nassau County, New York.

We hypothesized that DNA sequence identification using DNA Subway and BLAST will yield taxonomic identifications consistent with those obtained through image-based identification using iNaturalist, and that sequences of the COI barcode region will provide sufficient genetic information to construct a phylogenetic tree.

DNA was extracted, amplified by PCR, put through gel electrophoresis, and the sequenced data was analyzed using DNA Subway and BLAST to identify specimens and construct a phylogenetic tree.

The results yielded a sufficient phylogenetic tree of our specimens and also suggested that using both DNA and morphological identifications does not necessarily increase accuracy, since species level identifications did not coincide often.

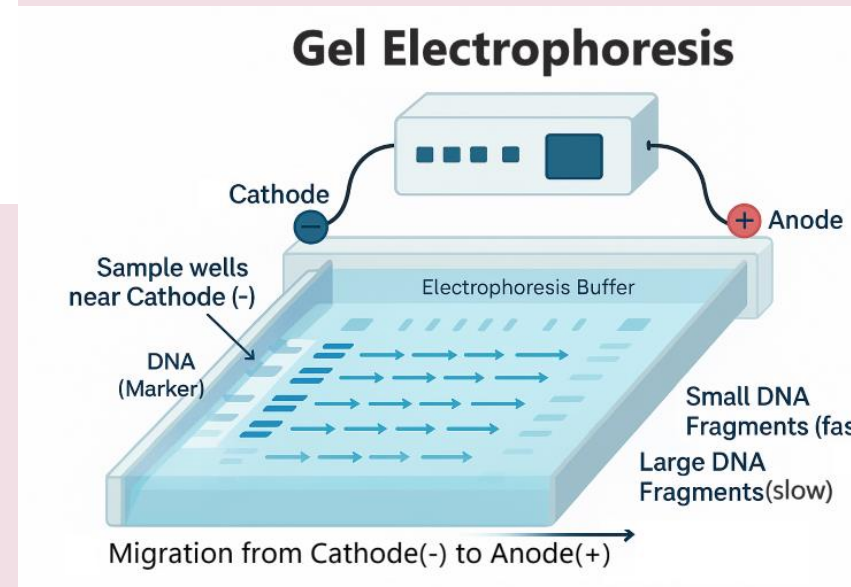
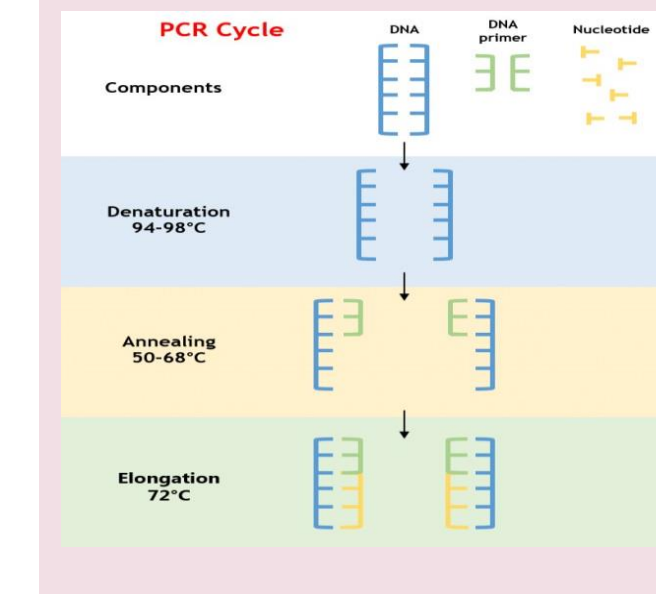
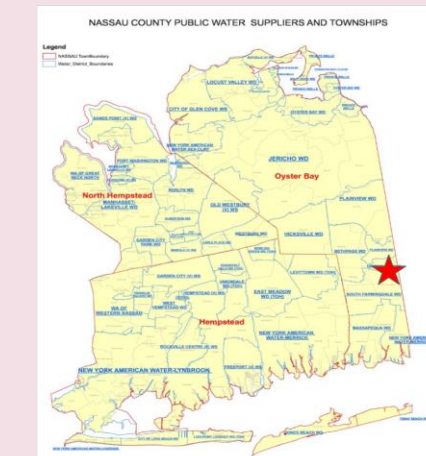
Introduction

The Hymenoptera Order, which includes bees, ants, and wasps, is one of the most diverse and important orders of insects.

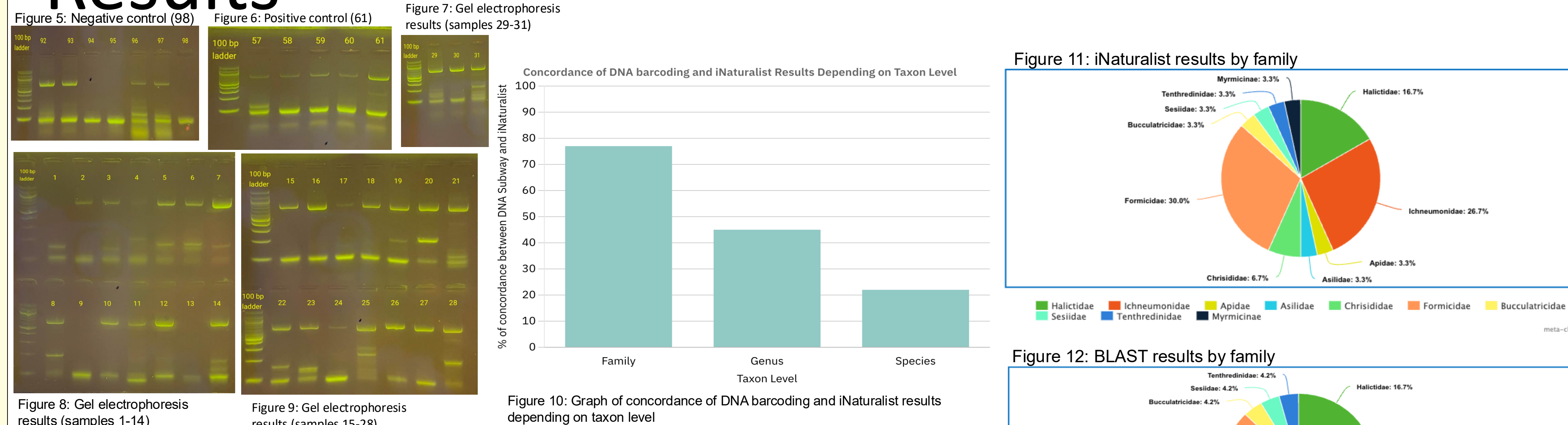
Insects in this order are ecologically significant, playing various key ecological roles like pollination, population regulation of pests, soil aeration, and nutrient recycling. Phylogenetics: the study of evolutionary relationships between organisms. Phylogenetic trees: visual diagrams which demonstrate the origin of species and their shared ancestry.

Materials & Methods

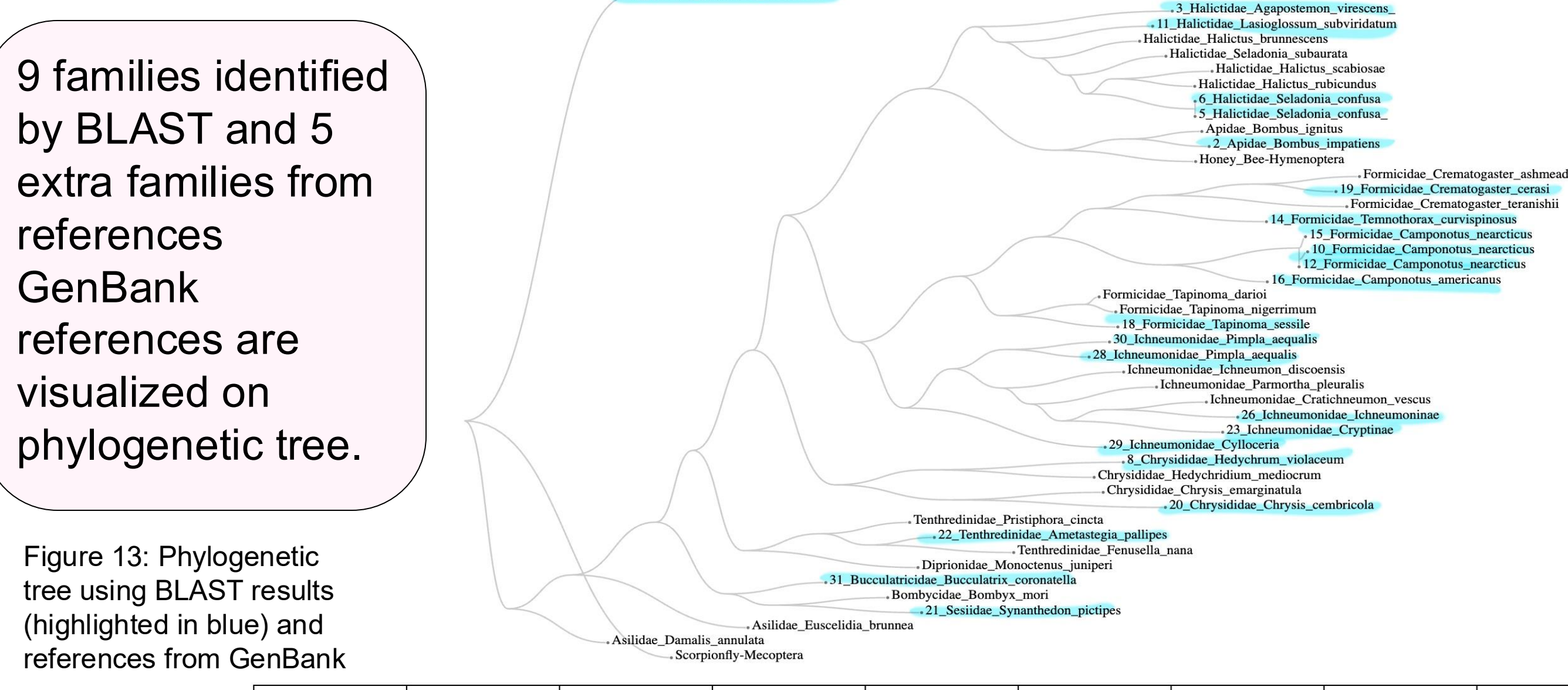
- Collection**
 - The specimens were collected on 06/20/2022 and 07/26/2022 at two locations in Farmingdale, NY.
- Specimen Photography**
 - A handheld microscope and an iPhone were used to take photos.
 - These pictures were uploaded to citizen science platform iNaturalist for identification.
- Extraction**
 - DNA was extracted using the Chelex resin method.
 - Supernatant was collected from the Chelex tube, and it was frozen for storage.
- PCR**
 - PCR was conducted to amplify the extracted DNA.
- Gel Electrophoresis**
 - Gel electrophoresis was utilized to visualize results of PCR.
 - The gel was viewed using an LED transilluminator and photographed using an iPhone.
- Analyzing**
 - The DNA sequences were trimmed using DNA Subway 2.0 and ran through BLAST to compare sequences with other sequences in the database.
 - PHYLIP ML on DNA Subway 2.0 was used to create a phylogenetic tree of our specimens.



Results



Results of gel electrophoresis: 27 specimens showed band of amplified DNA (658bp) consistent with COI amplicon. The DNA of these 27 specimens was sent for sequencing. In gel electrophoresis, both negative and positive controls showed successful results.



iNaturalist classified species into 10 families, while BLAST classified species into 9 families.

- The results showed that out of the 31 specimens, there were 8 bees, 10 ants, 9 wasps, 2 flies and 2 moths.
- Between the iNaturalist and BLAST results, 6 samples had matching identifications down to the species.

Discussion

- DNA barcoding using the COI gene successfully identified insect families and produced a phylogenetic tree showing expected relationships (Fig. 12).
- Most samples yielded usable DNA sequences, confirming the effectiveness of the methods used (Figs. 5–9).
- BLAST and iNaturalist identifications showed partial agreement (Fig. 10), likely due to limitations in image-based identification and DNA databases.
- Overall, the results demonstrate that DNA barcoding is a useful tool for biodiversity studies.

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