

Determining the Evolutionary Diversities Between the Forms of a Diverged Common Ancestor Throughout Time

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Abstract

Barcoding of organisms can help determine the evolutionary differences between aquatic and terrestrial invertebrates based on a common ancestor. If the DNA between terrestrial and aquatic invertebrates are similar then there must have been a common ancestor. After the invertebrates were collected, the team amplified the DNA of each invertebrate using micropipettes, and a variety of chemicals that were supplied by CHSL. PCR was then used to amplify the CO1 gene. Samples PGD-002, 003, 004, and 005 showed DNA bands after electrophoresis and were sent for sequencing. After being analyzed in GenBank, samples PGD-003 and PGD-005 showed 79 mismatches. We then used BOLD to compare these samples to other invertebrates, and they showed a similarity percentage of 89%. The similar DNA between the types of organisms helps to show a lacking biodiversity in the Long Island area, which is bad for the ecosystem.



Figure 1: Picture of Gardiners Park taken from Google Earth

Methods And Materials

Sample and Metadata Collection

20 organisms were collected from Gardiners Park. Terrestrial insects were collected at area 1 listed on the map (figure 1). Aquatic insects were also collected at area 2 on the map. All metadata was collected with weather probes.

Sample Documentation

At the lab all the organisms were frozen. Two pictures were taken of each organism.

DNA Barcoding

For DNA extraction day one, the organisms were crushed with lysis buffer and a silica pellet that binded to the DNA was formed. For DNA extraction day two, wash buffer was added to the pellet and the DNA was separated from the silica pellet with distilled water. For PCR, the CO1 gene was amplified by putting the DNA and primers into the thermo cycler for 35 cycles. The DNA after PCR was electrophoresed to determine which samples could be sequenced. Samples were sent for sequencing and then analyzed using DNA Subway.

Discussion

- Uncontrolled events that could have affected the results were the amount of organisms that were present, the season that the organisms that were collected, and the weather.
- Some improvements for future research include utilizing the map to find better locations for aquatic organisms, having more time to collect the organisms, and locating more areas to collect the organisms from.
- Once our results were finished sequencing, we analyzed them using DNA subway, and discovered that two out of the four organisms have a chance to be novel because they had a large number of mismatches compared to the other organisms in the database. They showed mismatches in the range of 70-80. We then compared them to sequences in BOLD systems and found less than 90% similarity which suggests they are novel.
- For future research we would like to revisit the area in which we collected the samples, at a better time to collect more samples especially aquatic insects, as well as get more involved in studying organisms with a common ancestor.



Figure 3: Phylogenetic tree showing relationships between samples sequenced

Introduction

- Our team compared the similarities and differences between types of terrestrial insects in order to determine the evolutionary diversities between the forms based on a single common ancestor.
- All organisms serve a place in the food web that ensures stability in Long Island ecosystems; the depletion of organisms could lead to a collapse in the ecosystem that would cause an increase in wastes and a decrease in life on Long Island.
- This could affect human health by leading to lower amounts of locally grown, fresh, and healthy foods, which in turn will lead to a supply of food that does not satisfy the nutritional values that are needed to maintain a healthy lifestyle based on solely local fresh food.

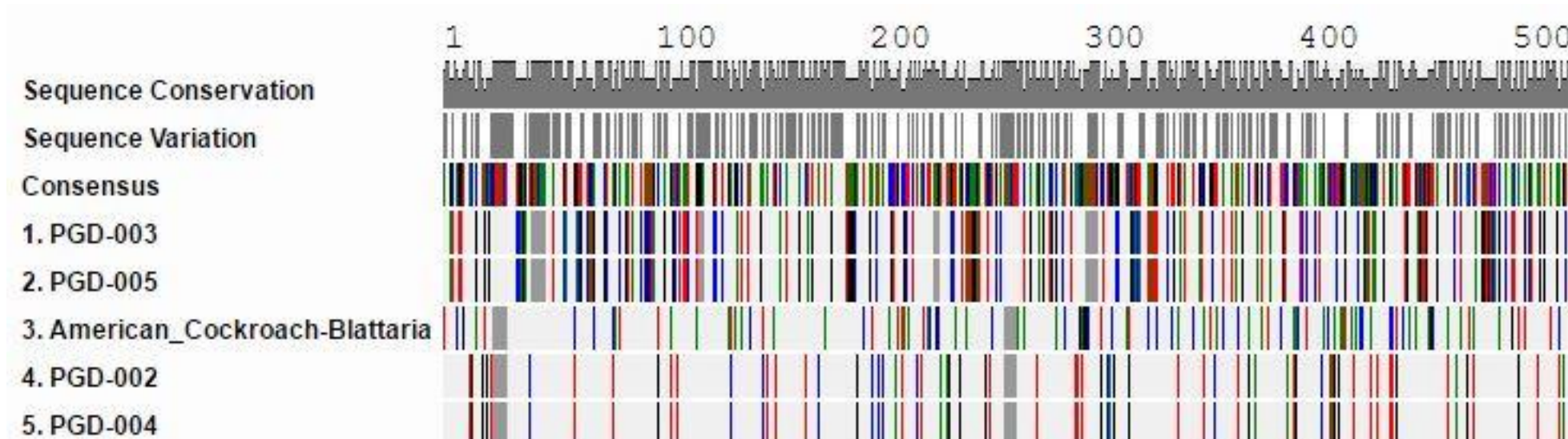


Figure 2: Alignment showing similarities and differences between samples sequenced

Results

The data shows that this experiment can be repeated and the organisms that were collected were diverse. Similar organisms based on DNA were found in proximity to each other. Two out of the twenty organisms found are likely to be novel, PGD-003, and PGD-005.

Table: Data of Sequenced Results

Sample ID	Latitude	Longitude	Posts Description	Bit Score	E Value	Mismatches	Scientific Name	Similarity percentage via BOLD systems
PGD-002	40° 41' 42.8 N	73° 16' 18.8 W	wood	1180	0.0	0	Isopoda sp.	100%
PGD-003	40° 41' 52.8 N	73° 16' 26.9 W	wood	787	0.0	79	Unknown	82.43%
PGD-004	40° 41' 42.8 N	73° 16' 18.8 W	metal	1189	0.0	5	Isopoda sp.	100%
PGD-005	40° 41' 42.8 N	73° 16' 18.8 W	wood	787	0.0	79	Unknown	89.12%

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