Comparing the Biodiversity of Crustaceans along the South Shore of Long Island

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Abstract

The genetic diversity and spread of the crustacean population is very important to Long Island. The objective was to see the see if there was a large variety in the gene's of similar crustaceans located on the island. We commenced the project after collecting the crabs by taking the DNA samples from the crustacean. After we took the DNA samples, we put the DNA under gel electrophoresis to make sure the samples were viable and then sent them to Cold Spring Harbor to have them sequenced. When we received the DNA we found that the crabs were from the same genetic path and had a number of similarities between them. We also found that there we some variation in the species, with one of our crabs branching to a second one in a short amount of time, denoting a presence or lack of genes found in other crabs of the same species. The results provided us with an excellent way to view the crabs genetic code, and allowed us to successfully identify the genetic similarities found between the crabs.

Introduction

Throughout Long Island there are at least seven different genuses (2) of crabs that reside in the Long Island Sound, and those species, and perhaps even more, exist in the Great South Bay (3). This project will observe the genetic makeup of the crustaceans that live in the South Shore bay areas of Long Island and observe the similarities and differences in the CO1 gene.

The testing of these animals will allow for a broader understanding of the local crustaceans for both research and public knowledge. DNA Barcoding is the way that we will test the species, allowing us to catalogue the species and create a phylogenetic tree which will help illustrate how closely related each species is.

DNA barcoding is a system developed by Paul Herbert of the University of Guelph in Ontario, Canada. This system allows for quick and easy access to a database of different species, genetic sequences, making species identification easier. By using the database to identify different species of crabs in the South Shore bay area we will be able to spot and identify the different species of crab that contribute to the overall local ecosystem biodiversity.

Figure 1: Google Map indicating the area the crustaceans were collected

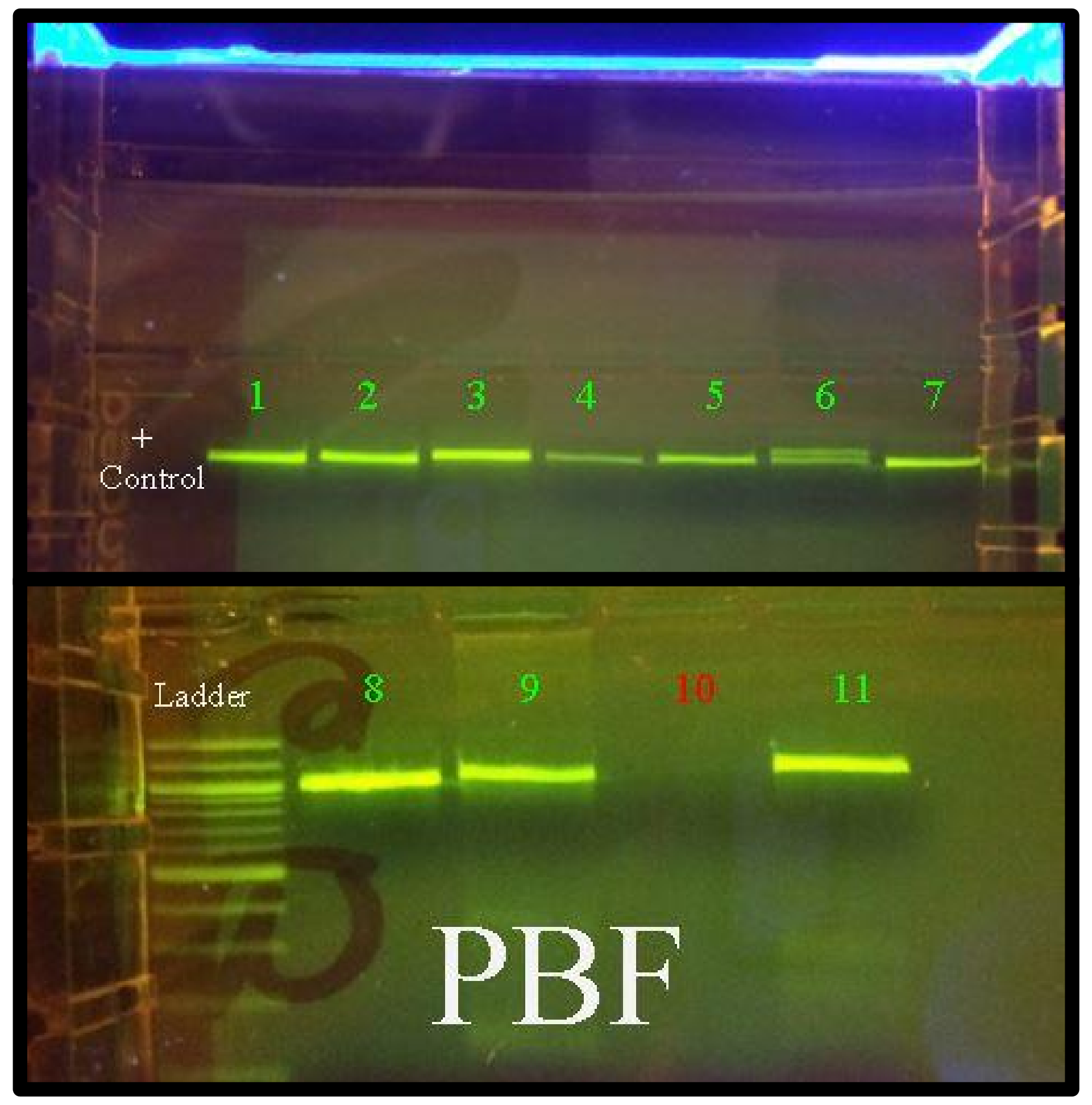

Figure 2: Image of gel showing that all samples were able to be sequenced due to band strength

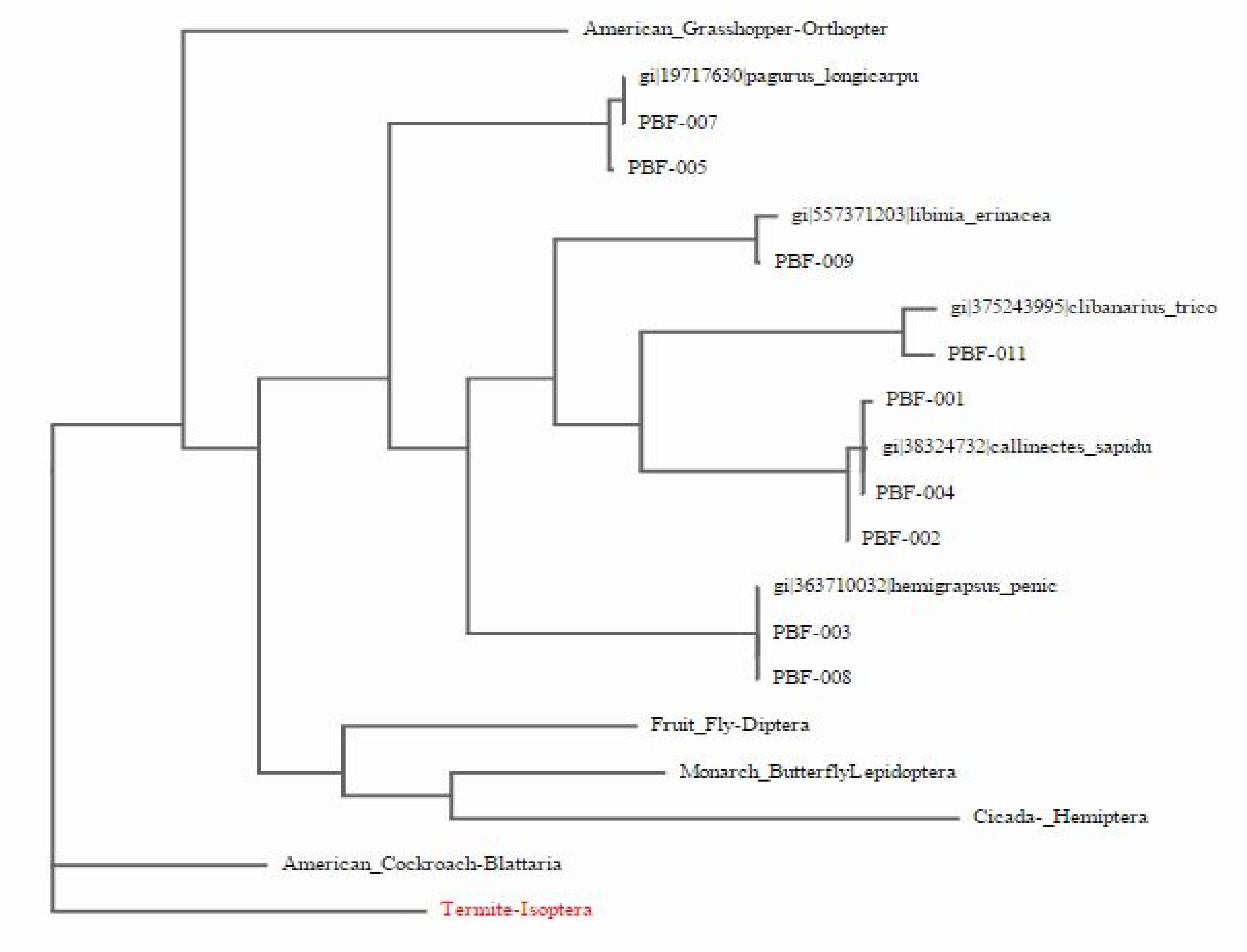

Figure 3: ML tree indicating relationships between collected specimen and BLAST results/reference data, using Termites as the outgroup

Methods:

The live samples will be terminated, by being placed in a freezer located within Babylon Jr/Sr High School. The samples that were not caught in Babylon will be preserved in a freezer bag then transported via cooler to a freezer in Babylon Jr. Sr. High School.

To process the crab DNA, we will use the standard DNA extraction techniques and laboratory equipment provided by Cold Spring Harbor Laboratory, SUNY Stony Brook Laboratory or Brookhaven National Laboratory. We plan on using the laboratory time and equipment to assist us in carrying out our experiment. We plan on conducting the most essential part of our experiment, DNA extraction and PCR analysis, at one of the three laboratories listed above. Following DNA extraction and PCR analysis, samples will be sequenced according to Cold Spring Harbor Laboratory protocols. After the samples are analyzed, we plan on comparing the genes from each specimen to each other and hope to create a phylogenic tree utilizing bioinformatics.

Discussion:

The project shows the single similarities in the genetics of the crabs, as well as a broad view of the way that the crabs developed and evolved from previous crustacean. These results prove that the crabs came from a unique species of crustacean. This means that even though the crabs had different sizes and structures, they all developed along the same genealogical path, and were able to develop different ecological niches in the bay. These results are important because they help to solidify and make clear the development and growth of the local crustacean community here on Long Island. If this project were to be followed up, there are several things that could be done differently. One of the main things would be to get a larger variety of crustacean species in an attempt to better understand the development of the community.

References

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3) Conservation Library "Great South Bay" http://nctc.fws.gov/resources/knowledge-resources/pubs5/web_link/text/gsb_form.htm Accessed on October 28, 2015