

Macroinvertebrate Indicators of the Health of the Connetquot River



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Abstract

The process of “barcoding” organisms has been increasingly adopted by scientists as a simple, accurate and cost effective means of species identification. DNA barcoding relies on sequencing the DNA of a particular gene and comparing it to an international database of samples. Barcoding can be used to identify key benthic organisms that can help predict the health of a river. Genetic testing of organisms, rather than taxonomic key, is highly accurate, and requires less formal training. A key flaw in taxonomic keys are the presence of cryptic species, which are two species that look the same but are composed genetically different. Using basic genetic extraction procedures, we have barcoded in total, eight samples in which has been sequenced and analyzed. Based on our results, we are very confident that sample PDJ-010 may have yield a novel sequences.

Introduction

A healthy Connetquot river system is important as it is a valuable part of the Long Island ecosystem and provides area residents with outdoor recreation. Surrounded by increasing human development there is concern that pollution and other human activities could threaten this delicate ecosystem. What would indicate that the stream is healthy and able to provide the proper ecosystems is the balance of the biological community¹. Benthic macroinvertebrates (bottom-dwellers) are especially useful to determine the quality because they have large populations and varied life spans and are greatly dependent on the land around the stream¹. Our group needs a way to accurately identify the sample species. Therefore, the DNA Barcoding is very useful for us and other scientists conducting similar projects.

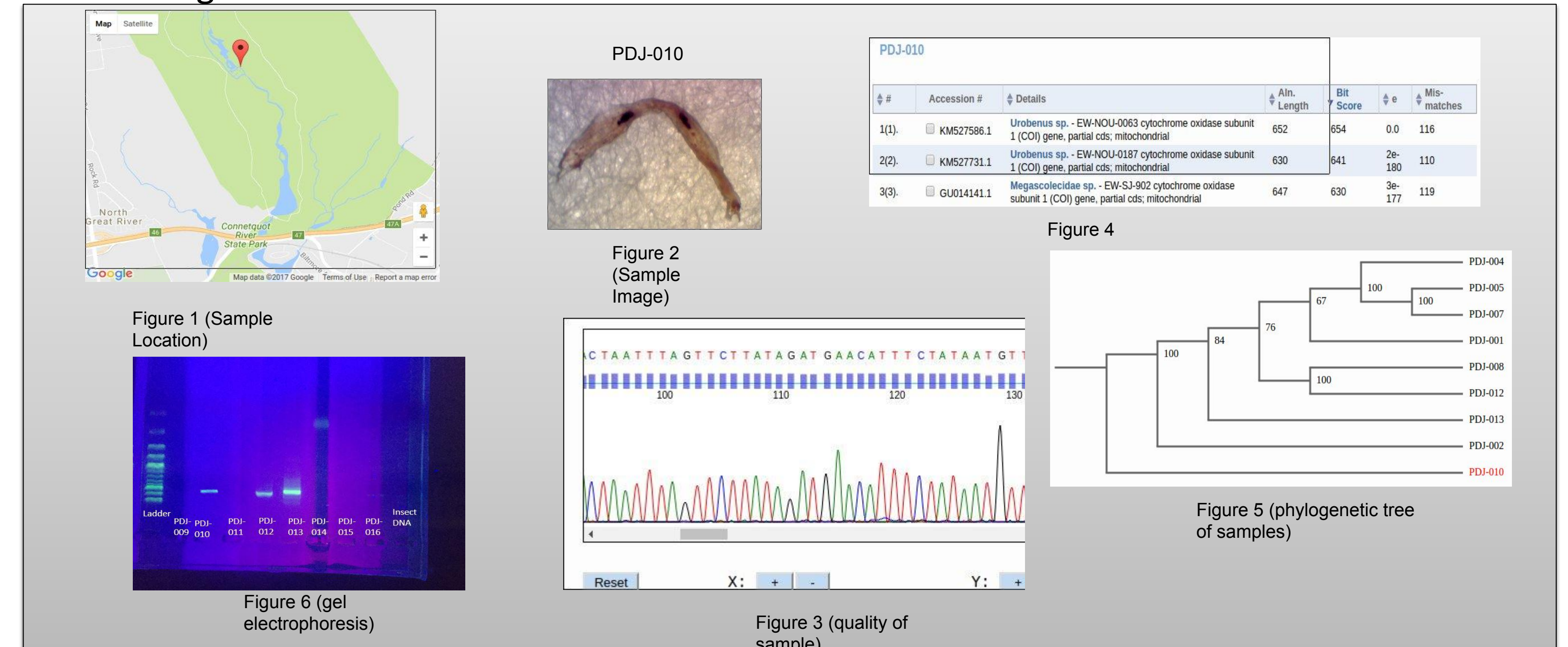
Materials & Methods

Before acquiring the samples, we submitted plans with the NY State Parks Department to obtain the proper permits for sampling on state owned lands. Once we did, we gathered materials which consisted of nets (poles), glass jars, buckets, and gloves. Once we arrived at the river, we found our way to the posts which we have coordinates for³. For each post, we had a large bucket in which we dumped the sediment and organisms into after scooping it up from the floor of the river. We used gloves to go through the bucket looking for any insects and whenever we found any we moved it into its own glass jar which we then labeled. then we cleaned out what was left in the bucket and put it back in the water and continued. After we received reagents and primers from Cold Spring Harbor Laboratories, we proceeded to carry out a genetic extraction protocol for macroinvertebrates, using silica. This was followed by PCR using primers for the COI gene. The success of PCR was verified by gel electrophoresis. Those samples with bands that matched the DNA Ladder in the 700 - 800 bp range, were sent to Genewiz for sequencing. Results were finally upload and analyzed using the Blue line of the DNA Subway program.

Results

Most of our samples were found to be closely related to an already recorded species. However, our sample PDJ-010 seemed to have the most mismatches when we got our BLAST results back. This is the sample that is seen along with its figures in the box above. So far, we have not yet confirmed a species match for it. For the rest of our samples, we have found both their genus' and species'. We plan on arriving to a conclusion about the biodiversity/health of the stream soon. Putting our collected specimens through the process of DNA Barcoding has been successful so far and even if in the end we don't come to our hoped conclusion, it would still be very useful for any future projects.

Tables & Figures



Discussion

We would use DNA Barcoding to find the species of our samples; so all together they would be good indicators to evaluate the health of the Connetquot River. This is because different organisms are known to have different levels of tolerance the pollution which would help especially if we have a larger range of the tolerance levels within our samples. So, if we have more samples that have high tolerances and less that have low tolerances, we can make a fair presumption that the Connetquot River and its inhabitant species are at risk. But we hope to see the opposite for our conclusion, and if not we know that something must change to help reverse the problem.

References

- 1) “Macroinvertebrates as Indicators of Water Quality.” Water Quality (Penn State Extension). N.p., n.d. Web. 01 Nov. 2016
- 2) “Using DNA Barcode to Identify and Classify Living Things” “Home | DNA Barcoding 101.” Home | DNA Barcoding 101. N.p., n.d. Web. 14 Oct. 2016
- 3) Lat/Long for the Three Sample locations:
40.764811, -73.154290
40.764771, -73.154075
40.764437, -73.153601

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