Peconic River Barcoding of Macroinvertebrates

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Abstract

This project focuses on the biodiversity of an estuary ecosystem. Our group has collected various specimens to analyze their genetic makeup. We utilized the genome of Mitochondrial cytochrome oxidase (C01) to conduct DNA barcoding. We used the C01 gene for DNA barcoding which has been proven a reliable source of identifying species and relationships. The goal is to help us identify different species to assess the biodiversity in the Peconic river. A non-native species of leech, *Helobdella fusca,* was preliminarily identified.

Introduction

DNA Barcoding is the identification and analyzation of a specimens genetics using the CO1 gene. It can be used to identify a specific specimen in a group of organisms. DNA Barcoding is useful for this with an accuracy around 99%. The goal of this study is to barcode a group of specimens from the estuary. This can be helpful to help and prevent death of major ecological species, while attempting to find a rare species or a unique genetic code. Our goal from this is to identify the organisms in this estuary to measure biodiversity and determine if any are invasive, novel, and are indicators of water quality.

Materials and Methods

20 different specimens were collected from the Peconic River. They were preserved in ethanol, before four photos were taken from four different side of each specimen..

Samples were taken from each specimen. DNA was extracted using the Chelex protocol from the DNACL and amplified using PCR. Amplicons were sequenced.

DNA sequences were submitted into DNA Subway, refined, and compared to other sequences to identify the taxonomy of each species. Barcodes were generates with DNA Subway.

Results

Figure 1 : DNA Barcode of DNA sequences from samples amplified with PCR

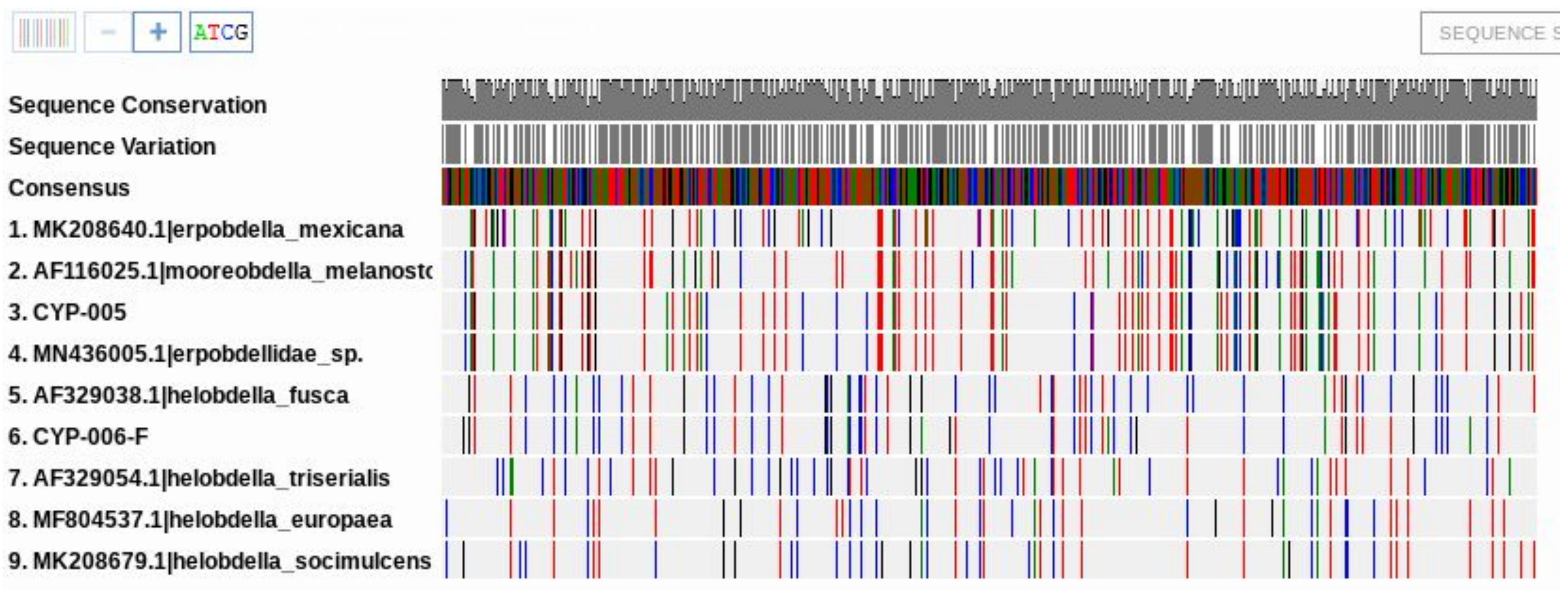


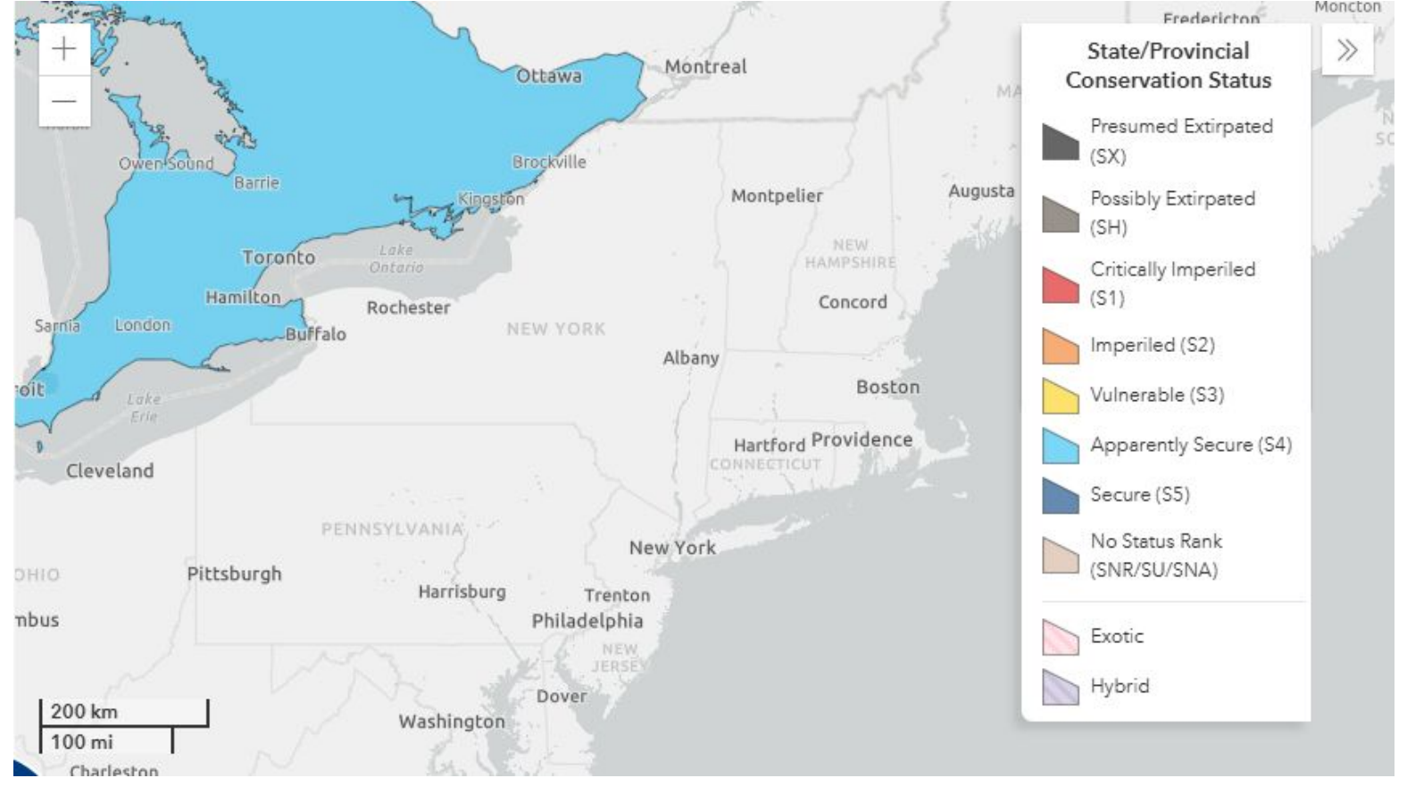
Figure 2: Sequence similarity grid illustrating the samples collected that match the BLAST results.

	C	1	2	3	4	5	6	7	8	9
C	-	81.62	84.01	84.98	84.44	89.17	88.70	89.80	92.45	91.49
1	81.62	-	86.18	87.60	87.46	72.99	72.33	74.53	75.73	75.00
2	84.01	86.18	-	92.39	92.22	74.70	73.50	74.70	77.44	75.86
3	84.98	87.60	92.39	-	100.00	74.87	73.67	74.53	76.41	75.86
4	84.44	87.46	92.22	100.00	-	74.96	73.75	74.61	76.50	75.95
5	89.17	72.99	74.70	74.87	74.96	-	97.33	85.95	85.17	85.14
6	88.70	72.33	73.50	73.67	73.75	97.33	-	86.12	85.71	86.09
7	89.80	74.53	74.70	74.53	74.61	85.95	86.12	-	89.80	89.45
8	92.45	75.73	77.44	76.41	76.50	85.17	85.71	89.80	-	96.55
9	91.49	75.00	75.86	75.86	75.95	85.14	86.09	89.45	96.55	-

Figure 3 : Table of samples, species identification, BIT scores, and number of mismatches * indicates a novel specimen to the estuary that has not been recorded

Sample Number	Species Identification	BIT Score	Mismatches
CYP-005	*Erpobdellidae*	1137	0
CYP-006F	*Helobdella fusca**	1011	16

Figure 4: Map of known *Helobdella fusca* species around Canada and North America



Discussion

The two samples, CYP-005 and CYP-006F have been identified using their DNA barcodes. Sample CYP-005 identified as Erpobdella , a part of the leech family. The other species being CYP-006F was identified as *Helobdella fusca. Helobdella fusca* is a part of the leech family. They are polymorphic, meaning that the species comes in different colors and patterns. This species is unique to the Peconic River because it is not native to New York. This species of leech is native to Canada and may have been imported into the Peconic. Since this species in non-native to the area, it has potential to become a invasive species.

Future Directions

Our future goal is to monitor the Peconic River Estuary and discover more about the species that live and thrive in there, as well as discovering new information about them.

References

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