

# Biodiversity of Sandy Beach Invertebrates Along Long Island Shores



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## Abstract

Biodiversity is the foundation for human health. The purpose of this research was to determine biodiversity of sand dwellers on Long Island's sandy beaches in order to investigate the health of beach environments. Twenty sand dwellers were collected and documented from Robert Moses and Hither Hills beaches. Using Barcode Long Island's protocol, DNA extraction, PCR, and gel electrophoresis were performed to look for the approximately 648bp CO1 gene. Then the samples were sent to a lab for Sanger sequencing. DNA Subway was used for analysis. 8 samples were successfully sequenced and BLASTED to look for similarity among sequences in GenBank. The percent similarity ranged from 64.04-100%. Phylogenetic trees compared the samples to each other. 5 samples did not match with any organisms in BOLD or GenBank databases when BLASTED. This means the samples have not been documented yet. These results show some biodiversity among sandy beach invertebrates along Long Island's south shore.

## Introduction and Hypothesis

- Without a global environment that is healthy and capable of supporting a diversity of life, no human population can exist ("Cohab Initiative", 2010).
- Biodiversity aids in the development of human medicine to fight diseases and biodiversity loss can increase the risk of infectious diseases among all organisms ("Cohab Initiative", 2010).
- The purpose of the experiment was to determine the biodiversity of sand dwellers (Ex. beach hoppers, beetles, bloodworms, copepods) on sandy beaches because the greater the biodiversity among the organisms, the healthier and more stable the environment is.
- The biodiversity of invertebrate sand dwelling marine organisms located along Long Island Shores will be high because the surrounding bodies of water have a high biodiversity rate which means the shores will as well.

## Materials and Methods

### Sample Collection

Samples were collected along Long Island Shores.  
 \*NO ISOPODS OR SAND CRABS WERE COLLECTED\*



Figure 1: Map of the locations where collection of samples occurred ("Barcode Long Island Sample Database", 2017).

### Sample Documentation

All metadata was recorded at the collection locations on a data table. Samples were scientifically photographed with a Ken-a-vision microscope.



Figure 2: Scientific photo of sample PCC-008. Photo taken by researchers.

### DNA Barcoding

DNA Extraction - Barcode Long Island DNA Protocol, PCR - Isolated the CO1 gene, Gel Electrophoresis - Looking for the 648bp CO1 Gene

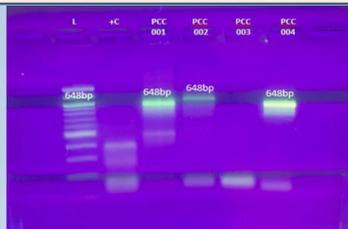


Figure 3: Gel electrophoresis of samples PCC-001, PCC-002, PCC-004. \*Sample PCC-003 was not used\*. Photo courtesy of research teacher.

### Sequencing and Analysis

Results were sent out to a lab for Sanger sequencing and DNA Subway analysis was performed.

## Results

Table: MetaData and data from comparisons of samples to GenBank and BOLD databases

Sample MetaData		GenBank Data			BOLD Data		
Sample ID	Beach	Alignment Length	Bit Score	e Value	# Mismatches	Matches	Sci Name
PCC-001	Robert Moses	503	984	0	0	100%	<i>Americorchestia megalophthalma</i>
PCC-002	Robert Moses	546	544	1 (151)	98	No Matches	No Matches
PCC-004	Robert Moses	650	645	0	117	No Matches	No Matches
PCC-005	Hither Hills	661	645	0	119	No Matches	No Matches
PCC-006	Robert Moses	476	838	0	3	99.36%	<i>Americorchestia megalophthalma</i>
PCC-007	Robert Moses	658	1166	0	3	99.39%	<i>Ocypode quadrata</i>
PCC-008	Robert Moses	644	643	0	115	No Matches	No Matches
PCC-011	Hither Hills	658	646	0	118	No Matches	No Matches

#	Accession #	Details	Aln. Length	Bit Score	e	Mis-matches
1(1)	KT958150.1	Uniothidae sp. - ST132_10311_NAMBI cytochrome oxidase subunit 1 (CO1) gene, partial cds; mitochondrial	585	578	2e-162	106
2(2)	KX812479.1	Bellorchestia pravidactyla - cytochrome c oxidase subunit 1 (COI) gene, partial cds; mitochondrial	584	576	2e-161	106
3(3)	KX812478.1	Bellorchestia pravidactyla - cytochrome c oxidase subunit 1 (COI) gene, partial cds; mitochondrial	584	576	2e-161	106
4(4)	KX812477.1	Bellorchestia pravidactyla - cytochrome c oxidase subunit 1 (COI) gene, partial cds; mitochondrial	584	576	2e-161	106
5(5)	KT958048.1	Chiltoniidae sp. - ST187_8WA cytochrome oxidase subunit 1 (CO1) gene, partial cds; mitochondrial	589	572	2e-160	110
6(6)	KX812484.1	Bellorchestia pravidactyla - cytochrome c oxidase subunit 1 (COI) gene, partial cds; mitochondrial	584	571	8e-160	107
7(7)	KX812483.1	Bellorchestia pravidactyla - cytochrome c oxidase subunit 1 (COI) gene, partial cds; mitochondrial	584	571	8e-160	107
8(8)	KX812482.1	Bellorchestia pravidactyla - cytochrome c oxidase subunit 1 (COI) gene, partial cds; mitochondrial	584	571	8e-160	107
9(9)	KX812481.1	Bellorchestia pravidactyla - cytochrome c oxidase subunit 1 (COI) gene, partial cds; mitochondrial	584	571	8e-160	107
10(10)	KX812480.1	Bellorchestia pravidactyla - cytochrome c oxidase subunit 1 (COI) gene, partial cds; mitochondrial	584	571	8e-160	107
11(11)	KX812476.1	Bellorchestia pravidactyla - cytochrome c oxidase subunit 1 (COI) gene, partial cds; mitochondrial	584	571	8e-160	107
12(12)	KX812474.1	Bellorchestia pravidactyla - cytochrome c oxidase subunit 1 (COI) gene, partial cds; mitochondrial	584	571	8e-160	107

Figure 6: BLAST results for sample PCC-002 show how it does not have a favorable/precise match to anything else in the GenBank database.

	C	1	2	3	4	5	6	7	8	9	10	11
<i>Ocypode quadrata</i>	-	76.78	73.58	76.26	96.65	96.94	96.66	96.93	96.90	77.80	78.33	77.73
<i>Stonefly-Plecoptera</i>	1	76.78	-	76.10	76.26	73.74	73.63	73.74	73.63	73.73	71.38	72.17
<i>Lacewing-Neuroptera</i>	2	73.58	76.10	-	76.89	70.44	70.75	70.75	70.75	71.38	72.37	72.21
PCC-008	3	76.26	76.26	76.89	-	73.27	73.11	73.11	73.11	67.52	68.39	67.16
PCC-011	4	96.65	73.74	70.44	73.27	-	99.44	99.16	99.44	99.58	73.94	74.16
PCC-002	5	96.94	73.63	70.75	73.11	99.44	-	99.86	100.00	100.00	73.76	73.96
PCC-005	6	96.66	73.74	70.75	73.11	99.16	99.86	-	99.86	99.86	73.76	73.96
PCC-004	7	96.93	73.63	70.75	73.11	99.44	100.00	99.86	-	100.00	73.76	73.96
<i>Americorchestia megalophthalma</i>	8	96.90	73.73	70.75	73.11	99.58	100.00	99.86	100.00	-	73.76	73.96
<i>Americorchestia megalophthalma</i>	9	77.80	71.38	71.38	67.52	73.94	73.76	73.76	73.76	-	100.00	99.37
<i>Americorchestia megalophthalma</i>	10	78.33	72.17	72.37	68.39	74.16	73.96	73.96	73.96	100.00	-	99.37
<i>Americorchestia megalophthalma</i>	11	77.73	72.00	72.21	67.16	73.47	73.26	73.26	73.26	99.37	99.37	-

Figure 7: A percent similarity table among all of the sample sequences, as well as the top related matches.

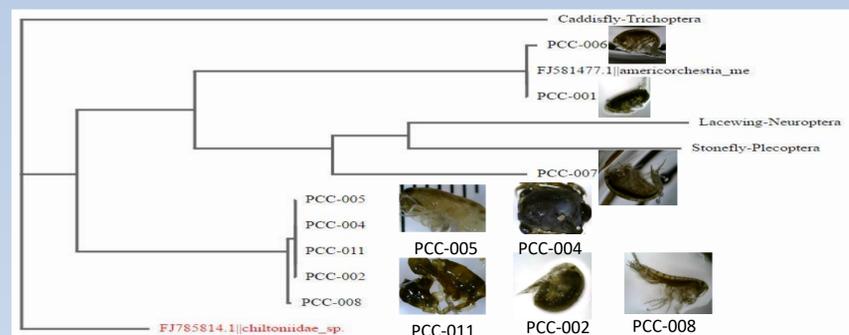


Figure 8: Phylogenetic tree shows the diversity of the samples that were sequenced, along with the top related organisms. All photos taken by researchers.

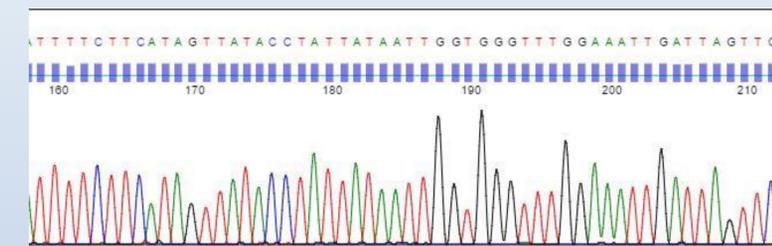


Figure 4: The electropherogram for sample PCC-007. The higher the colorful peak, the higher the intensity of the nucleotide at a specific location in the gene. The blue bars show the quantity of the sequence result.



Figure 5: The alignment viewer displays the similarity of the bases between collected organisms and related matches.

## Data and Results

- 8 out of the 20 samples were BLASTED on DNA Subway to look for similarity among DNA alignments.
- The samples were composed into a table showing percent similarity ranging from 64.04-100% among all of the samples.
- A phylogenetic tree shows much similarity between five of the samples that were not able to be identified in either GenBank or BOLD.

## Conclusions/Future Research

- Our hypothesis was supported because some of the organisms identified were indeed diverse supporting the biodiversity among sand dwelling invertebrates.
- This tells us that the ecosystem of Long Island shores are healthy and stable due to the high biodiversity rates.
- During our research it was found that five of our samples did not get direct matches in the BOLD database and GenBank. This means that we may have found novel sequences.
- For future research we will be comparing these results to past results done in the same environment to see how the health has change over time. Also, comparing the health and stability of the beach environment to an inland body of water like a river or lake environment.

## References

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