The Biodiversity of Moss: North Shore vs. South Shore

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Abstract:

The collection of mosses in this project will show the biodiversity of mosses between the South shore and the North shore of Long Island. The samples will be collected from Babylon, Glen Cove, Greenport, Lindenhurst, and Southampton, with three places being on the South shore and two being on the North shore. Three samples will be collected from each location so we end up with fifteen samples in total. Each sample will measure 5.08 x 5.08 cm and the surrounding environmental factors will be observed and recorded. After collecting the samples we will go to an open lab at Cold Spring Harbor Laboratory where we will extract and sequence the DNA following the Cold Spring Harbor Laboratory protocol being careful to avoid cross contamination and mislabeling. We aim to show how different environments can influence the types of mosses in different areas.

Introduction:

Mosses are a group of nonvascular, spore producing plant species that thrive in moist environments (4). Like other plants, mosses make their own food by photosynthesis. Mosses can photosynthesize in all of their cells, so they don't need a vascular system (2). To grow larger, mosses make new cells through mitosis. When they want to reproduce, mosses use meiosis to produce spores, which blow away in the wind and new mosses form (3). Water is an important factor in the reproduction of moss, which provides an explanation for why we tend to find moss near water, such as lakes, rivers, canals, etc… Over 10,000 different species of moss grow around the world, from the tropics to the arctic, in water and on land.

Mosses play an important role in the environment. They are large contributors in nutrient cycling and in the long-term storage of carbon dioxide and other forms of carbon (carbon sequestration). Carbon sequestration has been proposed as a way to slow the atmospheric and marine accumulation of greenhouse gases released by burning fossil fuels (5), which means moss could be a contributing factor in help to defer global warming. Mosses are able to grow on most surfaces making them more durable and widespread in comparison to grasses. This allows for a heightened capacity for carbon sequestration therefore increasing the amount of carbon that could be stored. Ground layers of mosses often have functional impacts disproportionate to their biomass, and are responsible for sequestering one-third of the world's terrestrial carbon as they regulate water tables, cool soils and inhibit microbial decomposition (5). This is important because without reliable assessment tools the potential effects of climate and land use changes on these functions remain unclear (1). When identifying mosses, DNA barcoding is more efficient and practical than using a field guide. It is easier to mix up the different species of mosses when using a field guide but DNA barcoding prevents any possible errors that can be made by us humans. DNA barcoding also allows for any new unidentified moss species to be identified and documented.

Materials and Methods:

The samples will be collected from Lake Agawam in Southampton, Argyle Lake in Babylon, Pratt Park in Glen Cove, 1.2 miles SE of Mitchell Park and Marina in Greenport, Ocean Beach Park in Long Beach and Mill Dam Park in Huntington.

To collect the moss samples, we will bring sterile tupperware containers to put each sample in with enough room to hold the moss and 25 ml of water from Poland Spring water bottles in order to keep the moss moist. Gloves will be used to avoid the possibility of any cross contamination. We will be using one of our cell phone cameras, to take pictures up close of the samples. This is done so we can get a close look at the samples. After this is done, we will be using Google Maps to record the exact location that the samples are collected at and will be writing them down in our notebook. We will then use a ruler to measure exact dimensions of 5.08 cm. X 5.08 cm., to then use sterilized scissors to cut the sample out of the ground. Then, we will record some environmental factors that are around the site of collection (such as if rocks are present, shade/sunshine). In order to try and avoid the possibility of getting the same type of moss during the collection, we will go to three different areas from each location, that are far enough apart from each other, to hopefully collect different types of moss. After all of the data is collected, the findings will be uploaded from the notebook to the data table, seen in figure 1. In order to keep the samples moist, the samples will be kept in one person's refrigerator until the next available school day where the samples will be transferred to a refrigerator that is located in the classroom.

Then, a very small piece of DNA will be extracted at Cold Spring Harbor Laboratory from each sample, and putting it in small tubes that will be carefully labeled. When extracting the DNA, we will use precautions to avoid the possibility of cross contamination such as, switching gloves when collecting every sample and sterilizing the scissors used to help cut the sample out of the ground. A lysis solution will be added to the tubes containing the samples to break up the DNA, and then the samples will be grinded up to separate the DNA. We will then go to Cold Spring Harbor Laboratory for an open lab where we will do the DNA sequencing with researchers present.

Results:

The first figure represents the data table of the collection of moss samples from all five locations, across Long Island, and the observations and conclusion that were made. We decided to include factors such as latitude and longitude, weather, area sample was founded etc… The second figure is the gel electrophoresis that was run at Cold Spring Harbor Laboratory. Each sample that was tested showed in the gel electrophoresis meaning the process was effective and that all for the samples are able to be amplified. The third figure is the PHILIP ML genetic tree. From this tree we were able to conclude many of the samples were closely related to each other as well as to the chosen species. The fourth figure is the PHILIP NJ genetic tree revealed that while many of samples had genetic sequences that were similar between the sample and the chosen species, some of the sequences differed into a separate branch.

Figure 1.- Image of sample PCT- 009 from Southampton.

Figure 2.- Image of sample PCT-007 from Southampton.

Figure 3.- Image of sample PCT-00 from in a tupperware container.

Figure 5.- Image of the collection of sample PCT-00 from 7

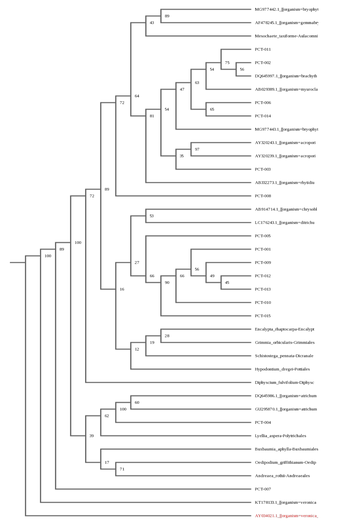

Figure 5.- PHYLIP NJ: Shows that most of the moss species collected are closely related. Samples PCT-006 and PCT-14 are very closely related to each other but are not as related to the rest of the mosses. PCT-007, PCT-004, and PCT-008 all come off of totally different branches and are very far off from the main cluster showing that they are not as genetically similar as the other samples.

Figure 6.- PHYLIP ML: Shows that most of the moss species collected are closely related. Samples PCT-006 and PCT-014 are very closely related to each other but are not as related to the rest of the mosses. PCT-003, PCT-004, and PCT-008 all come off of totally different branches and are very far off from the main cluster showing that they are not as genetically similar as the other samples.

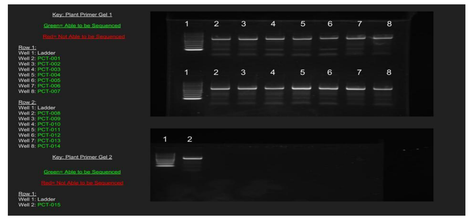

Figure 77.- Image shows which samples are able to be sequenced. Green= Able to be sequenced. Red= Unable to be sequenced.

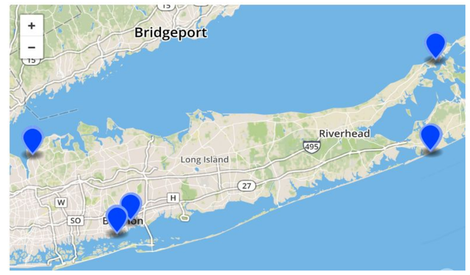

Figure 8- Map of the places the samples were collected from. Those places being Babylon, Copiague, Glen Cove, Greenport, and Southampton

Samples	Latitude	Longitude	Environmental Factors (such as if rocks are present, sample found in a shaded area vs. non-shaded area):	Location: North Shore or South Shore
PCT-001	40.8632744977	-73.6359920919	By a lake. Grassy area with some dirt patches.	North- Glen Cove
PCT-002	40.8034148344	-73.6896371841	Grassy area. More pebbly soil.	North- Glen Cove
PCT-003	40.8637037231	-73.6347359061	Grassy area. Closer to sidewalk.	North- Glen Cove
PCT-004	41.0951178164	-72.3777763456	Collected from a large grassy backyard.	North- Greenport
PCT-005	41.0950389427	-72.377717337	Large, grassy, backyard area.	North- Greenport
PCT-006	41.0950898509	-72.3780807763	Large, grassy, front yard area closer to road.	North- Greenport
PCT-007	40.8698134742	-72.3914014568	Sample site was next to a lake. Across the street from St. Andrews Church	South- Southampton
PCT-008	40.869435807	-72.3919378996	Collected from next to Agawam Lake. Across the street from St. Andrews Church.	South- Southampton
PCT-009	40.8691287226	-72.3936008692	Collected from next to Agawam Lake. Across the street from St. Andrews Church.	South- Southampton
PCT-010	40.6988475241	-73.3279323398	Next to the pathway that goes around Argyle Lake which is a man-made Lake.	South- Babylon
PCT-011	40.6967492138	-73.3279644728	Next to the path that goes around Argyle Lake which is a man-made lake.	South-Babylon
PCT-012	40.6979742886	-73.3310168802	Next to path that goes around Argyle Lake which is a man-made lake. Large patch of moss found in between a cluster of 4 trees.	South- Babylon
PCT-013	40.6668537712	-73.3718597889	Collected from Copiague Neck County Park which is located at the mouth of the Great South Bay. Sample was found off the shore line close to where the trees start.	South- Copiague
PCT-014	40.6672037019	-73.373303555	Collected from Copiague Neck County Park which is located at the mouth of the Great South Bay. Sample was collected closer to the trees of the Park.	South- Copiague
PCT-015	40.6673420461	-73.3738017082	Collected from Copiague Neck County Park which is located at the mouth of the Great South Bay. Collected closer to the tees of the Park. Soil more sandy.	South- Copiague

Figure 5.- This is the data table that represents the collection of moss samples from all six locations, across Long Island, and the observations and conclusion that were made. We decided to include factors such as latitude and longitude, weather, area sample was founded etc…

Discussion:

From the results, the gel electrophoresis worked effectively and each of the fifteen samples of DNA were able to be amplified successfully. The PHILIP ML genetic tree revealed common relationships between the mosses and the species to compare them with, as well as other mosses that weren't paired, possibly a new sequence. An example of a commonality can been seen between samples 6 and 14 which is interesting because sample 6 was from Greenport and 14 was from Copiague. The PHILIP NJ genetic tree revealed common relationships between the mosses and the species to compare them with. An example of a commonality can be seen between samples 2 and 11 which is interesting because sample 2 was found in Glen Cove whereas sample 11 was found in Babylon. Some things in the future, we would want to examine is a larger area, including the 5 boroughs of New York City and then compare the results to what we found in both NYC and Long Island.

References:

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