Barcoding Native and Invasive Species in the Hempstead Plains, New York

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Abstract

The Hempstead Plains is a historic landmark of Long Island, first discovered in the 1800s by the Europeans. These plains were at one time used as a vast landing strip for planes before being cut down. Now, all that remains is a small preserve located in Nassau Community College, infested by invasive species. The invasive species kill the thriving grasses and plants that are currently in the Hempstead Plains, and if they do not get removed, they can take over the entire plains. We plan to barcode unknown species in these plains as a part of the Long Island Barcoding Grant. Our aim is also to assist in the restoration of this process at the Wheatley School in the Wheatley Woods. We will collect samples of unknown grass from the plains preserve to barcode them, discovering which are invasive, which are native, and which have evolved. We conducted our barcoding in the Cold Spring Harbor Laboratory, through a DNA extraction and PCR test to separate the DNA. We used the program BLASTN to analyze the samples and match them with other species which have identical or highly similar gene sequences. After barcoding these species, we were able to identify which species are invasive or native, which will aid in the restoration process of the Hempstead Plains, finding two unknown species, *Linaria vulgaris*, toad flax, native to most of Europe, northern Asia, the United Kingdom, and *Solidago canadensis* a perennial plant, found in North Central North America.

Introduction

The Hempstead Plains once covered forty acres of land before they were destroyed by urban developments. The plains support populations of endangered plants and 250 different kinds of vegetation. The hempstead plains have great management and protection, which prevents weeding and littering. These plains are located in Nassau Community College. This section of Long Island is the only portion left of the original landscape and native species of Long Island, which was originally made up of the Hempstead Plains("About the Plains," 2008). Instead, when this area was first settled, the Europeans brought along invasive species such as European weeds. Now, this area is being trashed with litter and taken over by unknown weeds and brush. Today, it is one of the most rapidly vanishing habitats in the world and many animals and insects are disappearing with it . These plains have beens homes to many animals, insects, and plants, and were once an area for early airplane journeys("About the Plains," 2008).

The prairie grass of these original plains are near extinction and hard to find nowadays and are not the same as the original prairie grass found when colonists first came to Long Island. The main grasses found in the small preservation of Hempstead Plains include Big Bluestem, broomsedge, Indian Grass, Little Bluestem, Pennsylvania Sedge, and Switchgrass. These grasses are important in maintaining the biodiversity of the Hempstead Plains and providing food and energy for the other animals, but they also add beautiful decor to these plains which make them attractive, for example the Bluestem, as their name implies, has a rich violet color. Also, it is drought resistant and therefore an important plant as it can survive unsuitable conditions which other plants could not cope well in (Harper 1911).

Materials & Methods

We obtained small pieces of unknown and known plants from the Hempstead Plains, which Ms. Betsy Gulotta, the director and caretaker of the Hempstead Plains instructed us on. Ms. Gulotta informed us about key species that were unknown on the prairie and key invasive plants that she wanted to investigate. We obtained about twenty five samples, some of these samples were known and treated as a control group for the purposes of our experiment.

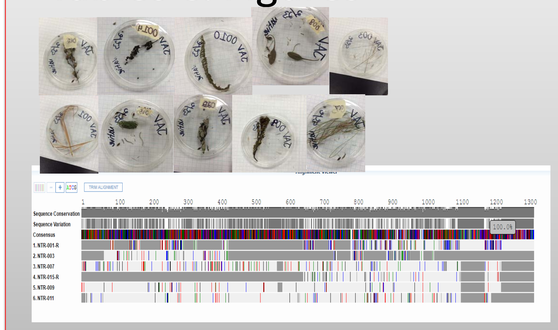
After we obtained these samples, we kept them in a fridge until it was time to isolate the DNA. For the first attempt at isolating the DNA, we went to the Cold Spring Harbor Laboratory and followed the Barcode LI protocol for isolating and amplifying the DNA from the samples.

Results

We first went to The Hempstead plains and retrieved numerous samples. We chose 10 of the samples to work with and used the native species as our control and the unknown species as our experimental group in which we tried to identify. We did a PCR and a gel electrophoresis in order for us to help identify the species. About six out of the ten samples showed up when we completed the gel electrophoresis. These samples included 2, 3, 4, 6, 7, and 11.

Next we sent our samples to be sequenced. Our next step was to try to determine the species. Sample 7 we found as *Festuca rubra*, which is a species of grass, red fescue, and is greatly widespread across the Northern Hemisphere. Sample 9 we found as *Solidago canadensis,* which is a perennial plant, found in North Central North America. Sample 11 we found as *Linaria vulgaris* which is toadflax, a native to most of Europe, northern Asia, the United Kingdom, and has been introduced and is now very common in North America. However, our Sample 3 had 25 mismatches, making it difficult to identify to a species.

Tables & Figures



Sample	Believed Species	Mismatches
003	*Schizachyrium sanguineum:* (Crimson Bluestem): species of grass, found in the south of North America	25
007	*Festuca rubra:* species of grass, red fescue, widespread across Northern Hemisphere	1
009	*Solidago canadensis:* perennial plant, found in North Central North America.	3
011	*Linaria vulgaris*: toad flax, native to most of Europe, northern Asia, the United Kingdom, has been introduced and is now common in North America.	5

Discussion

25 samples from the Hempstead Plains reserve in Nassau Community College were collected. After these samples were collected, DNA had been extracted out of 10 samples. Out of these 10 samples, samples 1-7 are considered as the control samples. Out of the 10 samples that we have extracted DNA out of, 6 samples were extracted successfully. Out of those 6 successful samples, 4 of them were sequenced successfully. Out of these four that were successfully sequenced, 1 sample was the control sample, and 3 were the experimental samples.

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