# **Invasive Plants vs Native Plants: The Battle for** Survivelderman, Eliana Ellerton, Leah Goykadosh Mentors: Shulamith Biderman, Ruth Fried Yeshiva University High School For Girls

# Abstract

Invasive plants threaten the environments they encroach upon as they are highly aggressive, possessing the ability to out-compete native plants for resources. We compared the chloroplast rbcL DNA of native and invasive plants found in the same order or family but different species in order to search for a genetic reason invasive plants have the ability to outcompete native plants, even those of the same genus.For example what allows invasive Common Reed (of order Poales and family Poaceae) to outcompete Native Cat-Tail Reed (of order Poales and family Typhaceae) along with other native plants in the environment Common Reed invades? We aimed to test whether a plant's survival was due to chloroplast genetic differentiation, or if it was due to other factors, such as the environment or nuclear DNA. We hypothesized that there would not be much difference between the chloroplast DNA of all compared plants, and that survivability would be linked to other factors. We sequenced and compared the chloroplast DNA of five different plants, two native and one invasive. We found no correlation between chloroplast DNA of invasive or native plants, proving our hypothesis correct.

### Introduction

Through comparing chloroplast rbcL DNA, we wanted to determine if there was a genetic explanation to the question of why foreign families of plants seem to outcompete plants that are native to the region. Our research is important because if left without intervention, invasive plants can cause widespread damage to an ecosystem due to their potential to out-compete native species for space and resources.

Native species, which have been in the New York environment for millennia, are fundamental pillars of the ecosystem and irreversible damage would be caused by their disappearance. Invasive plants, on the other hand, can cause all kinds of problems to the environment including habitat degradation or loss, risk of extinction of native species due to competition for resources, and other public safety concerns.

We compared the chloroplast rbcL DNA of five species, the Native Cattail Reed and its invasive counterpart Common Reed; The Native Northern Bush-honeysuckle; As well as the Invasive species Japanese Knotweed and Bittersweet. Our team met with Carlos Martinez -the head of operations of Building, Trail, and Animal Care at the Alley Pond Environmental Center [APEC] in Queens- and discussed the destructive impact invasive plant species have upon APEC's ecosystem. Mr. Martinez told us about how he has spent over 20 years fighting the growth of the invasive species within the APEC facilities, but they continue to survive every year. He taught us about the species we had chosen to compare for this study and only allowed us to collect samples on the condition that we did not intend to plant the invasive species directly into any open ground. Researchers have already looked into environmental factors that affect invasive species growth, but our plan was to look at the chloroplast DNA of each species and see if there was a genetic reason for invasive dominance over their native counterparts. We hypothesized that there would be no special chloroplast DNA distinction that allowed the invasive plants to survive better.

# Materials & Methods

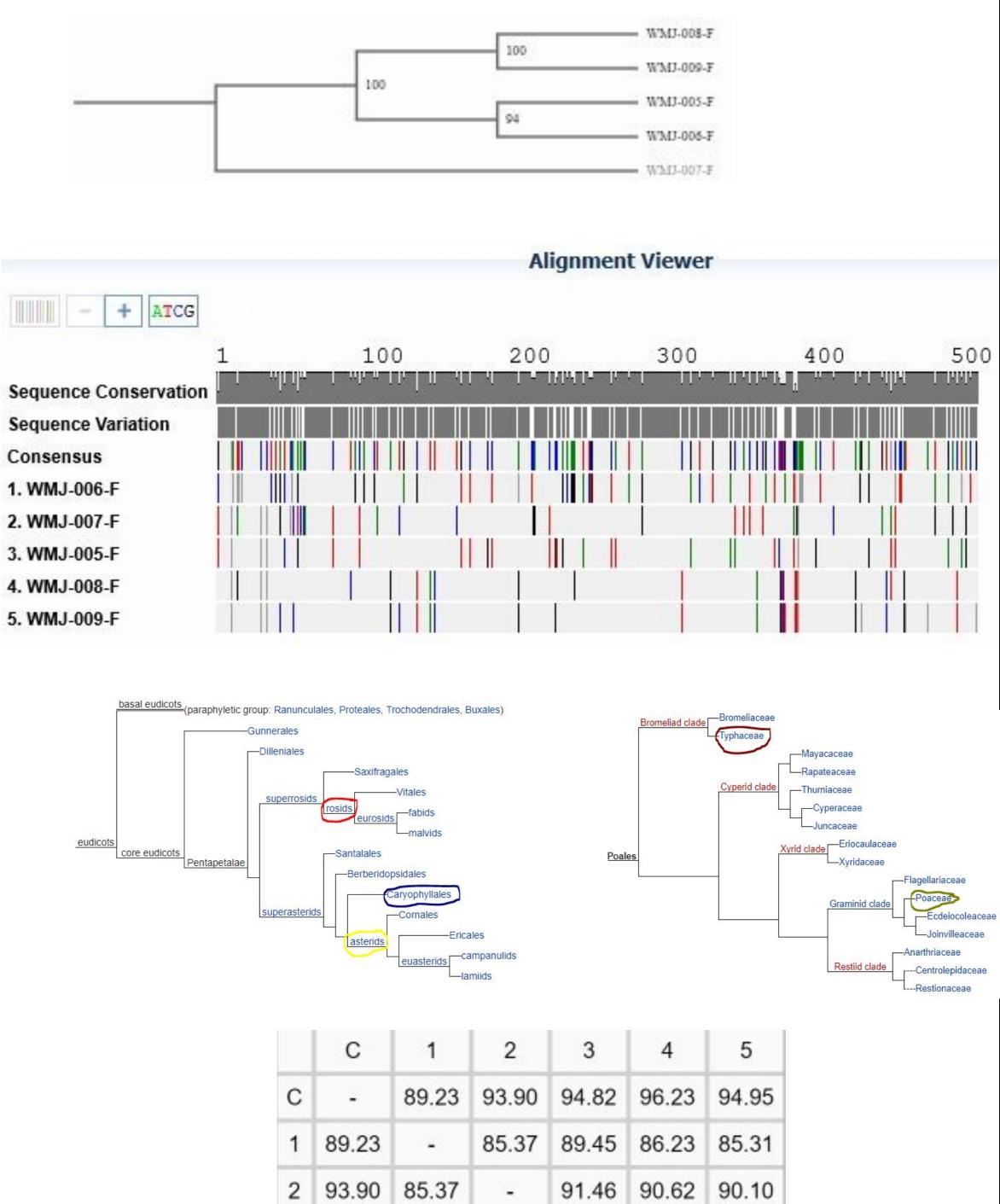
We used a total of 5 plants in our experiment, all gathered from the APEC in Queens, New York. The collection took place on Monday, March 11th with written permission from Mr. Carlos Martinez. We chose to collect from APEC as they have diverse native and invasive species growing naturally in their preserved environment. APEC staff also spent time with our team highlighting a few of the incredibly invasive species APEC is home to and the impact they have on their ecosystem. Mr. Martinez even took our team around APEC, helping us identify which plants we were looking for, as well as recommending additional invasive species to analyze. Samples were chosen based on the availability of a species within APEC and its state of being a known native or invasive species. For example, Cattail Reed a well known native plant to New York has a highly invasive counterpart known as the Common Reed. The Common Reed is known for being aggressively invasive and altering entire habitats due to its ability to outcompete native species. Whereas, Honeysuckle is a thriving native plant, and Japanese knotweed and Oriental Bittersweet are invasive species. We collected two samples from each species, either leaves, roots, buds, or branches depending on the plant and what we were allowed to collect.

We used the silica DNA isolation method to isolate the rbcL gene in the chloroplast DNA which allowed for PCR and DNA sequencing. This method involves using lysis solution and silica resin. In the presence of lysis solution, silica resin will bind to the DNA, which forms a pellet that clings to the walls of the tube. The supernatant is then discarded, distilled water is added to the tube, and once centrifuged, the supernatant can be utilized for PCR, and DNA sequencing. Gel electrophoresis is conducted in order to test if DNA isolation and PCR functioned properly. Silica DNA isolation worked for every sample except for the Japanese Knotweed, which was surprising for us given that we had used roots and a formed bud as our collected samples. Therefore we conducted a second DNA isolation method for Japanese Knotweed using the Promega Wizard Genomic DNA Purification kit. This method utilized nuclei lysis solution, along with RNase solution, and a protein precipitate solution. The Silica Isolation method causes the DNA to concentrate and form a pellet as it bonds to the silica resin and lysis solution, the supernatant that forms is waste materials that gets discarded. In the Wizard method every pellet that forms is waste materials that gets discarded, and it is the supernatant contains the DNA. Then the supernatant is mixed with DNA rehydration solution, and incubated before PCR can be conducted. All samples were successfully isolated and showed results when conducting gel electrophoresis. The DNA is then sequenced and DNA Subway is used to compare the chloroplast DNA between the samples.

After completing the sequencing of our DNA, we found that the closest related species, in relation to chloroplast DNA, seemed to be the Northern Bush-honeysuckle and the Oriental Bittersweet which had a 97% sequence similarity. Where as, the Common Reed and the Oriental Bittersweet share the least percentage of genetic similarities between the tested plants with a score of 83.31%. The three invasive species we tested, Common Reed, Oriental Bittersweet, and Japanese Knotweed, shared 90.10%, 83.31%, and 85.37% of their DNA with each other, respective of the order given above. The two non-invasive species of plant to the northeastern region of the United States, the Cat-Tail Reed and the Northern Bush Honeysuckle, shared 91.46% of their chloroplast DNA with each other. The invasive species shared more DNA with native species than they did with each other. Key:

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Consensus 1. WMJ-006-F 2. WMJ-007-F 3. WMJ-005-F 4. WMJ-008-F 5. WMJ-009-F



94.82 89.45 91.46

96.23 86.23 90.62 91.54

5 94.95 85.31 90.10 89.66 97.00 -

91.54 89.66

- 97.00

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# Results

- WMJ-006 / 1. Common Reed (Phragmites australis)
- WMJ-007 / 2. Japanese Knotweed (Reynoutria japonica)
- WMJ-005 / 3. Cat-tail reed (Typha latifolia)
- WMJ-008 / 4. Northern Bush-honeysuckle (Diervilla lonicera)
- WMJ-009 / 5. Oriental Bittersweet (Celastrus orbiculatus)

Native species exhibited a higher percentage of shared chloroplast DNA than the invasive species did with each other; with native species sharing 91.46% comparative to the invasive average of 86.26%. Given that the greatest genetic similarities were between a native and invasive plant that were not even from the same Order, we believe that the chloroplast DNA similarities and differences are not what give invasive plants a competitive edge over natives. The results we found suggest that there is no distinct divergences between our samples' chloroplast DNA sequences that would corroborate the idea that chloroplast DNA would be the cause of invasive species greater fitness. This fits our initial hypothesis that there is no specific genetic difference that would separate invasive species from native species in their fight to grow and survive. A major problem that may have occurred in our experiment took place in the collection phase. Due to the fact that we collected our samples from the wild, it is possible that incorrect plants were sampled in the stead of the plants we intended to gather. This error would invalidate all of our data collection and make it unusable. However, due to the fact that we did receive help from a park ranger it is relatively safe to presume that our plants were what we believed them to be. If this topic is expanded upon by other scientists, such as through the sequencing of nuclear DNA and not just chloroplast DNA, then this data can be used to help support the ecosystem. By determining what is or is not involved in the dominance of a species over another, we can better protect native environments from harm by invaders.

**CSH** Cold Spring Harbor Laboratory DNA LEARNING CENTER

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### Discussion

### References

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New York State Department of Environmental Conservation, www.dec.ny.gov/in

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