



Chicago Botanic Garden

Research Experiences for Undergraduates

Plant Biology & Conservation: From Genes to Ecosystems

Poster Symposium

August 18, 2023





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1) **Caroline Leung** is majoring in Biosciences with a concentration in Integrative Biology at Rice University and is expecting to graduate in 2024.

Title: Analyzing Differences in Soil Health Subsequent to Kernza Planting Across Intercropping Sites



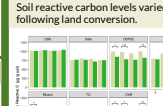
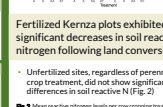
Abstract: Modern agricultural practices have been found to negatively impact soil health, decreasing soil stability, microbiome diversity, and carbon storage capacity. Prior work has shown that planting perennial crops in polyculture – such as Kernza, a deep-rooted perennial grass – can potentially restore soil health in degraded agroecosystems. Most studies describe the impact of these strategies at a single site; few have compared responses between sites across a geographic range. This study quantified reactive soil carbon levels before and after planting perennial monocultures and polycultures at seven sites across the United States. The response of soil reactive nitrogen levels to the perennial treatments was measured at one of the sites. Reactive carbon exhibited varying responses to planting between sites and treatments. Soil reactive nitrogen levels significantly decreased in fertilized plots - a pattern that did not appear in their non-fertilized counterparts. These results suggest that site characteristics which vary by location, such as soil type and climate, may influence observed effects of perennialization and polyculture on soil health, and that fertilization could negatively impact the efficacy of soil restoration efforts, though more long-term data is needed to optimize the use of perennialization and polyculture in restoration.



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Analyzing Differences in Soil Health Subsequent to Kernza Planting Across Intercropping Sites


Caroline Leung^{1,2}, Leila Rquib^{3,4}, Louise Egerton-Warburton^{3,4}
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BACKGROUND	MATERIALS & METHODS	RESULTS
<ul style="list-style-type: none"> Intensive agricultural practices degrade soil health (i.e. loss of stability, decreased carbon storage) Soil restoration practices involving perennial crops and polycultures have the potential to restore soil health <ul style="list-style-type: none"> Specifically, Kernza, a deep-rooted perennial grass, has been shown to greatly aid land regeneration within first year of planting Reactive carbon is a form of processed soil C that is closely correlated with the total soil organic C pool Reactive nitrogen is a glycoconjugate largely produced by the llyphases of arbuscular mycorrhizal fungi (AMF) Both reactive carbon and nitrogen have been identified as useful metrics of soil health 	<div style="display: flex; justify-content: space-between;"> <div style="width: 30%;"> <p>Study Sites</p>  </div> <div style="width: 40%;"> <p>Experimental Design</p>  </div> <div style="width: 30%;"> <p>Soil Analyses</p> <ul style="list-style-type: none"> Soil samples taken before and after row cropping treatments were analyzed using spectroscopy Reactive C – all sites Reactive N – all sites¹ </div> </div>	<p>Soil reactive carbon levels varied between sites and treatments following land conversion.</p>  <p>We found that soil reactive carbon:</p> <ul style="list-style-type: none"> Increased significantly → UVM Decreased significantly → DDPSC, Mizou, TI Did not change significantly → CBG, Cella, KU (Fig. 1) <p>Fig. 1 Row cropping treatments produced various responses in soil reactive carbon levels per site. Columns marked with stars have significant differences ($F^* = p < 0.05$, $** = p < 0.01$, $*** = p < 0.001$).</p>
<p>QUESTION</p> <p>How do perennialization and polyculture affect soil health across varying geographic regions?</p>	<p>RESULTS</p> <p>Fertilized Kernza plots exhibited significant decreases in soil reactive nitrogen following land conversion.</p>  <p>Fig. 2 Mean reactive nitrogen levels per row-cropping treatment at CBG. Columns marked with stars have significant differences ($F^* = p < 0.05$, $** = p < 0.01$, $*** = p < 0.001$).</p>	<p>DISCUSSION</p> <ul style="list-style-type: none"> Site characteristics that vary by location could have influenced inconsistent soil reactive C responses across sites In Variations in soil type, soil texture, land use history, and climate Fertilization negatively impacts reactive nitrogen levels Plant mycorrhizal relationships that benefit soil health do not form in presence of fertilizer? <p>FUTURE DIRECTIONS</p> <ul style="list-style-type: none"> Future inquiries into the effectiveness of perennial polycultures in restoration could consider other site traits Consider interactive effects of soil type, soil texture, land use history, and climate on results Restoration-focused land management strategies should avoid fertilization, regardless of crop treatment
<p>HYPOTHESIS</p> <p>If we subject seven intercropping sites to various crop treatments, then we will observe the greatest increase in soil health in plots where perennial polycultures have been planted</p>	<p>REFERENCES</p> <p>Carroll, D., & Leung, C. (2023). Investigating the above and below ground traits of plants to help meet restoration goals. We can improve restoration outcomes by understanding the above and below ground traits of plants to help meet restoration goals. We can improve restoration outcomes by understanding the above and below ground traits of plants to help meet restoration goals.</p>	<p>ACKNOWLEDGEMENTS</p> <p>Support for this work was provided by the National Science Foundation (NSF) grant 2108188 (LE) and the Chicago Botanic Garden (CBG) (LE). We thank the following individuals for their assistance: ...</p>

2) **Kiera Carpenter** is majoring in Sustainability Studies with a minor in Environmental Science at Roosevelt University and is expecting to graduate in 2023.

Title: Exploring Plant Interactions for Restoration: A Focus on Above and Belowground Traits

Abstract: The restoration of ecosystems relies on native plant species to survive, especially after damage and land degradation. It is important that we understand above and below ground traits to aid restoration. Investigating root traits enhances restoration insights by allowing us to understand plant behavior. Our hypotheses were that root length can be predicted using easily obtainable shoot measurements and that the growth of our plants (Silphium and Dalea) would vary across Little Blue Stem Densities. We conducted an interactive experiment with 202 plants across 80 pots, observing interactions over a six week period. Statistical methods and predictive models were employed to assess root traits. Linear regression and Random Forest algorithms predicted length using plant height, shoot mass, leaves and density. Our hypotheses were partially supported by the results of our experiment. While we need more information to confirm this, initial results indicate that we can possibly predict root length from easy-to-measure aboveground traits.



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Exploring Plant Interactions for Restoration: A Focus on Above and Belowground Traits

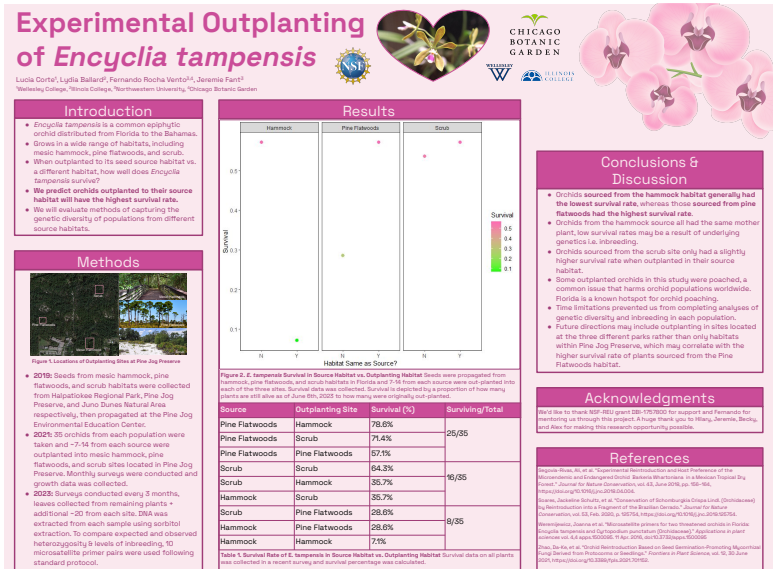
Kiera Carpenter¹, Kiera Carpenter¹, Kiera Carpenter¹
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INTRODUCTION	RESEARCH / FINDINGS
<p>Restoring land following damage and degradation through the implementation of native plant species is a vital part of keeping our ecosystems healthy (Jiang et al., 2020). Investigating the above and below ground traits of plants can help meet restoration goals. We can improve restoration outcomes by understanding the above and below ground traits of plants to help meet restoration goals.</p>	<p>4. Little Blue Stem plants grew taller than the other species (see Fig. 1)</p> <p>5. Dalea showed more growth under density two conditions than under density one conditions. (Fig. 2)</p> <p>6. Silphium showed more growth under density one conditions than under density two conditions. (Fig. 3)</p>
<p>2. HYPOTHESES</p> <p>Additionally, we hypothesized that root length can be predicted using easily obtainable shoot measurements.</p>	<p>7. MACHINE LEARNING</p> <p>We conducted an in-depth assessment of above-ground characteristics, including shoot height and leaf and above biomass, to predict below-ground traits of root length.</p> <p>Model Performance Comparison:</p> <ul style="list-style-type: none"> Linear Regression: RMSE: 3.74, MAE: 1.7 Random Forest: RMSE: 2.38, MAE: 1.7 SGD: RMSE: 3.04, MAE: 1.2
<p>3. METHODOLOGY</p> <p>Plant Selection: Three plant species: Little Blue Stem (<i>Phlox pilularis</i>), Black-eyed Susan (<i>Rudbeckia hirta</i>), and Prairie Flower (<i>Chamaenerion lanceolatum</i>).</p> <p>Experimental Set Up: 80 pots were set up with 202 plants across 80 pots, observing interactions over a six week period.</p>	<p>CONCLUSIONS</p> <p>There is evidence that we can possibly predict root length from easy-to-measure aboveground traits, but more data is needed to improve this prediction.</p> <p>We also discovered that overall, plants with higher density of the species showed less growth amongst other plants. Dalea had reduced growth with more Little Blue Stem density.</p>

3) **Lucia Corte** is majoring in Biological Sciences with a minor in Statistics at Wellesley College and is expecting to graduate in 2026.

Title: Experimental Outplanting of *Encyclia tampensis*

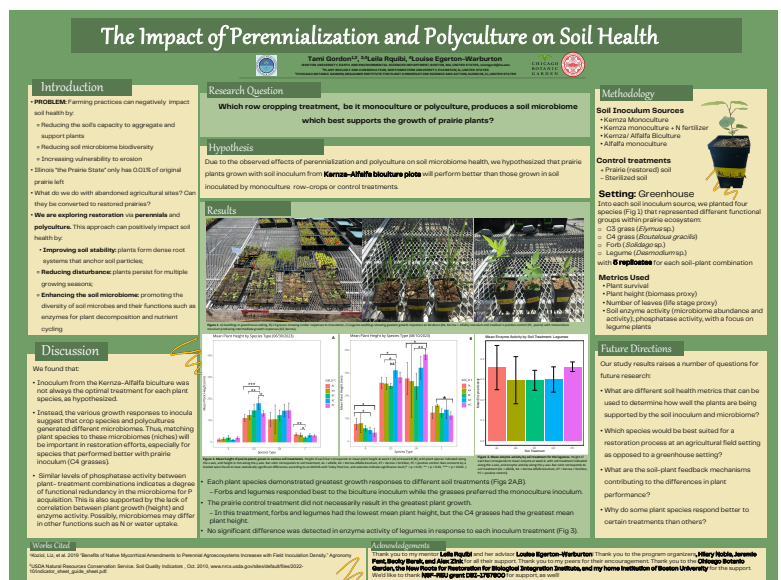
Abstract: *Encyclia tampensis* is a common epiphytic orchid distributed from Florida to the Bahamas. *E. tampensis* lacks habitat specialization and is capable of growing in a variety of habitats that exist in Florida, from areas with sparse vegetation, such as scrub, to areas with dense vegetation, such as mesic hammock and pine flatwoods. This study seeks to determine if matching seed source habitat to outplanting site habitat leads to a higher survival rate for reintroduced individuals. In 2019, seeds from mesic hammock, pine flatwoods, and scrub habitats were collected from Halpatiokee Regional Park, Pine Jog Preserve, and Juno Dunes Natural Area respectively, then propagated at the Pine Jog Environmental Education Center. 35 orchids from each population were taken and ~7-14 from each source were outplanted into mesic hammock, pine flatwoods, and scrub sites located in Pine Jog Preserve. Surveys were conducted every 1-3 months to collect growth and survival data. Leaves from surviving plants and an additional 20 from each site were collected to extract DNA and compare expected heterozygosity, observed heterozygosity, and levels of inbreeding. As of August 2020, Orchids sourced from the hammock habitat generally had the lowest survival rate, whereas those sourced from pine flatwoods had the highest survival rate.



4) **Tami Gordon** is majoring in Earth and Environmental Sciences with a minor in Ecosystems at Boston University and is expecting to graduate in 2025.

Title: The Impact of Perennialization and Polyculture on Soil Health

Abstract: Intensive agriculture practices have contributed to degradation of soil health and the loss of natural prairie ecosystems. Previous work suggests that the use of perennial crops can improve the health of degraded soil, with benefits to soil biodiversity and nutrient cycling. It is not yet established which combinations of perennial crops most effectively restore soil health, or whether these gains in soil health are sufficient to support the restoration of degraded sites to natural ecosystems. This study explored whether several different row cropping treatments produced a soil microbiome that could support the growth of prairie plants. Sterilized soil was inoculated with soil taken from plots planted with one of four different row crop treatments. Four species of native prairie plants were planted in pots with the inoculated soil. Plant height was measured weekly. At six weeks, an enzyme analysis was run to determine the activity of phosphatase enzymes. After eight weeks, each species demonstrated the greatest amount of growth under a different soil treatment. The enzyme analysis found no significant differences in activity between treatments. These findings suggest that the use of perennialization and polyculture could be an effective step towards restoring former agricultural sites to native prairie ecosystems.



5) **Erica Cao** is majoring in Biology at Northwestern University and is expecting to graduate in 2026.

Title: Unearthing the evolutionary history of the Pawpaw, *Asimina triloba*, using Next Generation Sequencing (NGS)

Abstract: The pawpaw (*Asimina triloba*), is a small deciduous tree native to eastern North America. They are part of a tropical family of fruits, and bear a fruit that tastes like a combination of bananas and mango. At its most northern range are the Ontario and New York pawpaws. Previous analysis on pawpaw populations has been done but those did not include pawpaws in the northernmost areas. This study uses genotyping-by-sequencing (GBS), a next generation sequencing technique, to find genetic similarity between different pawpaw individuals. First the DNA is extracted, then GBS libraries are constructed, then the libraries are sent out for sequencing, and lastly the libraries are processed. The processed DNA is then analyzed by creating dendrograms and PCA plots in R Studio to visualize the clustering. DNA from New York pawpaws were extracted using the DNAeasy Plant Mini Kit (Qiagen). As of August 16, 2023 GBS libraries of the New York pawpaws are currently in construction. The data processing protocol was refined from a previous protocol and tested on another collection of samples with geographic origins from various states. That data was analyzed and visualized in R Studio.

6) **Teagan LeVar** is majoring in Biology at Northwestern University and is expecting to graduate in 2024.

Title: Effects of Light Availability and Order of Arrival on Oak Woodland Species' Competitive Interactions

Abstract: In the Midwest U.S., oak woodlands provide a significant source of plant biodiversity, but many of these woodlands have been degraded. A common restoration tactic is the addition of native plants through seed mixes, and it is necessary to understand competitive interactions between species of seed mixes to effectively restore woodlands. In this experiment, 12 species from local seed mixes were used in experimental communities where arrival order and light availability were manipulated. Plant leaf count was taken at planting and two weeks later to determine growth rates during this time. Analysis focused on four graminoid species: conservative *Bromus kalmii* and *Diarrhena obovate* and non-conservative *Panicum virgatum* and *Glyceria striata*. Conservatism relates to species' responses to environmental disturbance, with non-conservative species showing higher tolerance. Non-conservative species had higher growth rates than conservative, and late arrival for these non-conservative species led to significantly reduced growth rates. Conservative species' establishment was not impacted by arrival order, and light availability did not significantly impact any species' growth. Additional research covering other life history strategies for these species may provide more insight into the impact of arrival order.

7) **Jay An** is majoring in Biology at Stanford University and is expecting to graduate in 2024.

Title: Collection inspection: extracting DNA from cycads in living collections for phylogenetic analysis and detection of hybrids

Abstract: Cycads are an ancient lineage of plants that is highly threatened in the wild. Because cycad seeds become inviable in seed bank conditions, cycad conservation is performed through living collections. In these collections, cycads of multiple genera and species are housed together in a conservatory setting. Despite the absence of obligate pollinators, natural pollination has been observed in collection cycads, indicating that hybridization is also possible. Since living collections may be used for reintroduction efforts, hybridization can risk genetic swamping, where introduced hybrid genotypes replace local genotypes in the wild. We investigated methods to extract DNA from cycads in living collections in order to generate sequence data that will be used to identify unknown individuals and determine whether hybridization occurs in cycad collections. DNA extraction was performed via a modified CTAB protocol, and resulting DNA yield and purity was assessed. We found that the extraction protocol yielded sufficient quantities of DNA from cycad tissue, however extracted DNA was often of substandard purity. Sequencing results will be needed to further assess the efficacy of the modified CTAB protocol to generate DNA of sufficient quantity and quality for phylogenetic analysis and hybrid identification.

Background

- Cycads are highly threatened, over half of species are critically endangered (Dutilleul et al. 2004)
- Seeds become inviable in seed banks, making living collections necessary for conservation (Griffith et al. 2005)
- Pollination occurs in collections despite lack of obligate pollinators, indicating that hybridization is possible
- Hybridization in collections can harm reintroduction efforts by causing genetic swamping, where local genotypes are replaced by introduced hybrid genotypes (Levin et al. 1988)

Objectives

- Verify methods to extract cycad DNA of sufficient quality for sequence analysis
- Sequence cycads from various collections and compare with existing phylogenetic and sequence data to:
 - Identify unknown and mislabeled individuals
 - Detect hybrid individuals and identify whether hybridization occurs in collections

Methods

Leaf tissue sampled from cycads at Lincoln Park and Garfield Park Conservatories, Chicago Botanic Garden

desiccate tissue

Extract DNA via modified CTAB protocol

Quantify DNA concentration via Qubit fluorometer (see Results)

Quantify DNA purity (A260/280) via Nanodrop (see Results)

re-extract

insufficient yield

sufficient yield

Prepare DNA for sequencing via Illumina TruSeq Nano library prep protocol

Sequence DNA via Illumina TruSeq Nano library prep protocol

Target sequences used for phylogenetic analysis and hybrid identification

Capture target sequences via hybridization with MYbaits probes

Results

DNA Concentration by Genus

DNA Purity by Genus

Conclusions

- Modified CTAB extraction yielded DNA of sufficient quantity for sequencing
- In cases of insufficient yield, repeated extraction produced sufficient DNA
- DNA extracted from cycads via modified CTAB protocol is often of substandard purity
- Sequence data (in progress) needed to further assess the effectiveness of modified CTAB protocol

References

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8) **Anabelle Manrique** is majoring in Plant Biology with a minor in Environmental Science and Terrestrial Resource Management at the University of Washington and is expecting to graduate in 2024.

Title: Influence of Drought Stress on *Castilleja Coccinea*

Abstract: This study investigates the response of *Castilleja coccinea* (Orobanchaceae) to changing abiotic conditions caused by climate change, specifically focusing on the impact of drought stress on the two color variants (red and yellow) across distinct populations. This research aims to understand how drought stress influences foliar anthocyanin production and growth/survival rates, shedding light on the adaptive strategies of these plant populations.

Through a controlled greenhouse experiment, four populations of *Castilleja coccinea* were subjected to well-watered and drought conditions. Various morphological traits and physiological measurements were taken, including: rosette diameter, leaf length, number of leaves, and anthocyanin content. Results indicate that yellow variants exhibit reduced rosette diameters under drought stress, while red populations show higher anthocyanin levels regardless of treatment. These findings raise questions regarding genetic and population-level factors impacting physiological resilience and drought tolerance. Furthermore, extending the study period and integrating biomass measurements could provide a more comprehensive understanding of *Castilleja coccinea*'s adaptive mechanisms in the face of changing environmental conditions. Overall, this study highlights the intricate connection between abiotic stresses, floral color polymorphism, and plant fitness in the context of climate change.

1. Introduction

Climate change has brought about shifts in precipitation patterns, including heightened mid-season drought and notable fluctuations in both average temperatures and extreme temperature events, altering the abiotic environments of many plant communities.

To investigate how mesicstem plant species may respond to changes in abiotic conditions and the possible implications on fitness, our study centers *Castilleja coccinea* (Orobanchaceae), a perennial, hemiparasitic, fire-widely distributed species from the Midwest and eastern United States. *Castilleja coccinea* maintains a fixed color polymorphism consisting of a red and a yellow variant, with the red coloration being a result of the stress compound and pigment known as anthocyanin. Beyond its visual significance, foliar anthocyanin and its derivatives also serve in UV protection, thermal stress tolerance, and defense against herbivory. Yellow populations are more commonly found in prairie ecosystems, and red is more common in exposed rocky outcrops, with varying drought tolerances likely due to local adaptation.

Our investigation involves a drought experiment designed to evaluate how abiotic drivers such as drought differentially impact the morphological and physiological stress tolerances of the two variants of *Castilleja coccinea* across distinct populations.

2. Research Question

How does drought stress impact both foliar anthocyanin production and growth/survival rates across red and yellow populations?

3. Methods

Greenhouse Setup

- Three red populations (R1, R2) and two yellow populations (Y1, Y2)
- 20 plants per bin with 10 plants from each population
- 20 plants per bin with 10 plants from each population
- 20 plants per bin with 10 plants from each population

Measurements

- Rosette diameter
- Number of leaves
- Leaf length
- Soil moisture

Anthocyanin Extraction

Foliar anthocyanin content was quantified for 60 plants from the R2 population and 60 plants from the Y2 population

500mg of leaf material was collected from each plant

Leaf tissue was then used to extract anthocyanin and the color was measured using a spectrophotometer

The tissue was combined with an extraction solution and incubated overnight

Samples were applied into 96 well plates and absorbance was measured using a spectrophotometer at 530nm and 630nm

4. Results

Figure 1A: Anthocyanin content (mg/g) in well-watered and drought conditions for R2 and Y2 populations. R2 populations show significantly higher anthocyanin content in drought conditions compared to Y2 populations.

Figure 1B: Rosette diameter (cm) in well-watered and drought conditions for R2 and Y2 populations. Y2 populations show significantly reduced rosette diameters in drought conditions compared to R2 populations.

Figure 1C: Leaf length (cm) in well-watered and drought conditions for R2 and Y2 populations. Y2 populations show significantly reduced leaf lengths in drought conditions compared to R2 populations.

5. Discussion

Under drought stress, yellow variants exhibited smaller rosette diameters than the control treatment groups.

We found no significant difference in rosette diameter between treatment groups in R1 and R2.

Yellow variants are significantly dependent on anthocyanin accumulation during the drought and well-watered conditions.

A genetic and population dynamics analysis is necessary to determine if the use of identifying within populations and its contribution to the results and if genetic divergence between populations exists from anthropogenic selection or other evolutionary processes.

Research could provide a more accurate measure of growth, and assessing the sampling period, increasing sample size could yield a more accurate measure of growth.

Future Directions

- Explore other anthocyanin-containing rosette plants to determine whether anthocyanin accumulation is linked to drought tolerance.
- Investigate the effects of other climate change-related variables, such as salinity, CO₂ levels, and higher temperatures on plant response.
- Explore genetic connections between population genetics, dynamics, and functional traits across different populations.

Literature Cited

Griffith, M. Andrew, Colman, Michael, Matthews, Alan, et al. of the Chicago Botanic Garden Cycad Collection Curators. 2005. Living Collections of Cycads. *Journal of the American Botanical Society* 118(1): 1-10.

9) **Eva Murillo** is majoring in Ecology and Sociology at Swarthmore College and is expecting to graduate in 2026.

Title: How Distance from a Public Greenspace Impacts Private Lawn Biodiversity

Abstract: Private lawns make up a significant portion of land use in the United States, and their management can damage the environment. Specifically, turfgrass lawns can diminish biodiversity, which reduces beneficial ecosystem services (i.e., pollination, flood mitigation) and worsens environmental problems (i.e., habitat fragmentation). Understanding which factors influence lawn biodiversity could aid in conserving ecosystems across the United States; this study investigates the public parks as one potential factor. To determine the influence of public parks over private lawn biodiversity, we surveyed ten private lawns at varying distances from park by 1. Counting the number of plant species and number of individuals per species, 2. Estimating % grass cover, and 3. Calculating the species diversity of each lawn. We then used regression analyses to model the relationship between distance from the park and species richness, species diversity, and % grass cover. Our data revealed a significant relationship between distance and species diversity, indicating that lawns closer to public parks are more likely to have higher species diversity. Future work might examine how homeowners interact with parks, and whether parks influence their planting practices.

10) **Julia Lemos** is majoring in Integrative Biology and Anthropology at the University of Florida and is expecting to graduate in 2026.

Title: Species and Functional Trait Diversity Across Soil Nutrient Gradients

Abstract: Oak ecosystems across the Midwestern U.S. have been almost completely lost, and what remains has been heavily degraded. Ecological restoration efforts aim to restore the biodiversity and ecosystem quality found in pre-degraded oak ecosystems. This study aims to look at how both species diversity and functional traits (morphological, physiological, and phenological characteristics of plants) change across soil nutrient gradients. Total and native species richness were used as metrics of species diversity, and serve as indicators of ecosystem quality in this study. The functional traits measured were specific leaf area (SLA), leaf nitrogen content (LNC), and seed mass. Metrics of species diversity and functional trait community-weighted mean values were analyzed across gradients of ammonium (NH₄), nitrate (NO₃), and phosphate (PO₄). There was an increase in both overall and native species richness with increasing soil nutrient availability. However, there was no relationship between functional traits and soil nutrients.

By establishing the relationships between both native species richness and functional traits with soil nutrient gradients, we are able to assess the ability of functional traits to serve as an indicator of environmental quality. Our results suggest that species diversity metrics, and not functional trait values, remain the better indicator of ecosystem quality in restorations.

11) **Xitlali Ramirez** is majoring in Environmental Science and Policy with a minor in Earth and Climate Sciences at Duke University and is expecting to graduate in 2024.

Title: Towards culturally-informed urban conservation practices: An Evanston pilot study

Abstract: Lawns constitute a large part of both public and private urban greenspaces, therefore making their management an essential component of urban biodiversity. Homeowners outwardly express their aesthetic and cultural values with the plant and management strategies they utilize on their lawns. While lawns are recognized as essential for maintaining urban biodiversity, the effect of cultural and racial background on plant diversity has yet to be studied as a tool for urban conservation. In my pilot study, I identified 3 neighborhoods with different racial majorities in Evanston, IL and found that each neighborhood had popular and distinct plants found in all studied houses. More homes in Evanston must be surveyed to increase the accuracy of these results. Additionally, homeowner interviews are required to identify the cultural drivers behind plant choices. Once plant preferences and the cultural drivers behind them are identified, native and beneficial alternatives to these popular plants can help increase biodiversity and ecosystem health while maintaining homeowners' aesthetic preferences.

Towards culturally-informed urban conservation practices: An Evanston pilot study

REU Site: Plant Biology & Conservation Research Experience for Undergraduates - From Genes to Ecosystems (Sponsored by NSF award DBI-2149888)

Xitlali Ramirez, Eva Murillo, Brian Lovejoy, Brianna Vargas
Duke University, Swarthmore College, Northwestern University

INTRODUCTION

- Lawns constitute a large part of both public and private urban greenspaces, therefore making their management an essential component of urban biodiversity (Chollet et al 2018).
- Homeowners outwardly express their aesthetic and cultural values with the plant and management strategies they utilize on their lawns (Galluzzi et al 2010).
- Understanding homeowner's landscaping choices and their unique cultural drivers is essential to inform the design of effective urban conservation programs (Uren et al 2015).

OBJECTIVES

- Determine plant genera that are popular within and between racial groups in Evanston
- Determine if racial differences across neighborhoods influence front lawn plant biodiversity in Evanston

METHODS

- I used U.S. census data and bestneighborhood.org to identify census tract 8103.01 in Evanston, IL as the area of focus for this study due to the presence of majority Black, Latino, and White neighborhoods of similar lawn size
- I identified and counted every plant genus on the front lawn of 3 single-family detached homes in each neighborhood. I used the Shannon-Wiener Diversity Index to calculate plant biodiversity of each neighborhood on the genus level.

RESULTS

The Latino-majority neighborhood showed a statistically significant difference in front lawn biodiversity compared to Black ($p = 0$) and White ($p = 0.001$) majority neighborhoods (Fig. 1, t-test).

Each neighborhood had unique non-"weed" plants found in all houses surveyed (Table 1).

Table 1 - Popular plant genera in Evanston across racial groups

Majority race in neighborhood	Popular genus	# Houses Present
Black	Buxus*, Poa**, Taraxacum*, Ribus, Pilea, Buxus*, Medicago*, Pilea*	3
Black	Poa**, Hibiscus*	2
Latino	Buxus**, Medicago*	2
White	Poa**, Hibiscus*, Equisetum, Leucantherum, Echium	3

* = May be considered "weedy" by homeowners
** = seen in all houses regardless of racial group

Figure 1 - Front lawn plant biodiversity in Evanston across racial groups

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12) **Evelin Munoz** is majoring in General Biology with a minor in Earth and Environmental Sciences at the University of Illinois at Chicago and is expecting to graduate in 2024.

Title: A Comparative Analysis of the Genetic Diversity of *Amsonia kearneyana*

Abstract: Endemic species with small population sizes are at risk of extinction. Conservation genetics can be used to assess the genetic health of threatened populations and inform future management projects. *Amsonia kearneyana* is endemic to a single mountainside in southern Arizona and has been listed under the Endangered Species Act since 1989. This study aims at informing the conservation management of *A. kearneyana* by understanding its population genetics and evaluating its relatedness to other *Amsonia*. DNA was extracted from three subpopulations of *A. kearneyana* (UBC, LBC, and South), *A. kearneyana* herbarium specimen, and sister *Amsonia* species. The genetic diversity of *A. kearneyana* was assessed via a comparative analysis of observed heterozygosity (Ho) and inbreeding coefficient (FIS). The genetic structure of *A. kearneyana* was also evaluated to estimate gene flow. Our results suggest that *A. kearneyana* is monophyletic and sister species to *A. palmeri*. Structure plots indicate that gene flow is occurring across all subpopulations, and the genetic diversity of *A. kearneyana* is not significantly lower than that of other larger sister populations. This research can be taken a step further by comparing the effective population size (Ne) of all of the *A. kearneyana* subpopulations to sister species for a better comparison of overall genetic health.

A Comparative Analysis of the Genetic Diversity of *Amsonia kearneyana*

Evelin Munoz¹ & Dylan Cohen²
¹University of Illinois Chicago, ²Chicago Botanic Garden

Introduction

Endemic species with small population sizes are at risk of extinction. Conservation genetics can be used to assess the genetic health of threatened populations. *Amsonia kearneyana* is endemic to a single mountainside in southern Arizona and has been listed under the Endangered Species Act since 1989. This study aims at informing the conservation management of *A. kearneyana* by understanding its population genetics and evaluating its relatedness to other *Amsonia*. DNA was extracted from three subpopulations of *A. kearneyana* (UBC, LBC, and South), *A. kearneyana* herbarium specimen, and sister *Amsonia* species. The genetic diversity of *A. kearneyana* was assessed via a comparative analysis of observed heterozygosity (Ho) and inbreeding coefficient (FIS). The genetic structure of *A. kearneyana* was also evaluated to estimate gene flow.

Objectives

- Assess the genetic diversity and inbreeding for *Amsonia kearneyana*
- Determine if there is gene flow across subpopulations
- Construct a phylogeny of *A. kearneyana* and determine if it is monophyletic

Methods

Sample Collection

- Leaves were dried on silica or collected from herbarium vouchers
- Amsonia palmeri* (50 ind.), *A. kearneyana* (50 ind.)
- UBC, LBC, and South

DNA Extractions

- DNA extractions were done using a modified CTAB procedure and quantified using a Qubit DNA Library Prep & Sequencing
- Library prep was done following a modified ABR-ADseq protocol. Libraries were sequenced at the NUSCA Core facility at Northwestern University

Analyses

- SNPs were called using the STACKS VCFtools was used to filter SNPs for population genetic analyses
- We used the R programs HeterDist and Dnapars to estimate observed heterozygosity (Ho) and inbreeding coefficients (FIS). ADMIXTURE was used to detect if gene flow was occurring across *A. kearneyana* populations. The best K was chosen based on the lowest cross-validation value

Results

Figure 1: (A) Distribution map of *Amsonia kearneyana* populations (purple) in southern Arizona. (B) Map of the *A. kearneyana* subpopulations (UBC, LBC, and South) and sister species *A. palmeri* (red) in the study area. (C) Phylogenetic tree showing relationships between *A. kearneyana* subpopulations and sister species.

Figure 2: (A) Observed heterozygosity (Ho) by *Amsonia* species. (B) Inbreeding coefficient (FIS) by *Amsonia* species. (C) Genetic diversity (Ho) by subpopulation. (D) Genetic diversity (Ho) by subpopulation. (E) Genetic diversity (Ho) by subpopulation. (F) Genetic diversity (Ho) by subpopulation.

Figure 3: Phylogenetic reconstruction for sister species *Amsonia*. Shaded areas indicate bootstrap support and values >90 indicate strongly supported clades. Several *Amsonia* accessions were used to test the phylogeny of *A. kearneyana* (purple) and *A. palmeri* (red).

Discussion and Conclusion

Phylogeny

- Amsonia kearneyana* is monophyletic and sister species to *A. palmeri*. Together they are sister to *Amsonia* and *A. longifolia*.

Genetic diversity

- Genetic diversity (Ho) of *A. kearneyana* is not significantly lower than that of other larger *Amsonia* species populations (Fig. 2A).
- This suggests that genetic diversity is not a conservative metric for measuring genetic health or extinction risk.
- Intraspecific assessment of genetic diversity (Ho) revealed that larger subpopulations are correlated with higher genetic diversity (Fig. 2B).
- Herbarium and LBC subpopulations have lower genetic diversity due to their very small population size.
- Large populations of *Amsonia* in general have a lower Fis value, suggesting higher rates of outbreeding.

Gene flow

- ADMIXTURE suggested K = 2 for the three subpopulations (UBC, LBC, and South). Individuals appear to be moving pollen across the entire distribution of *A. kearneyana*.

Future Research

This research can be taken a step further by comparing the effective population size (Ne) of all of the *A. kearneyana* subpopulations to sister species. Genotyping the offspring generations can also be used to understand how much genetic diversity has been lost over time.

Acknowledgments

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13) **Ana Pineda** is majoring in Biology and Data Analytics at Denison University and is expecting to graduate in 2026.

Title: Combing molecular and morphological studies to explore the fungal diversity of Costa Rican Oak Forests

Abstract: Research on neotropical fungi has increased substantially in the last decade. As result, several new species have been described but fungal diversity and distribution in neotropics are unknown yet. In this project, we explore the fungal diversity in a Neotropical Quercus Forest in Costa Rica. We used dried specimens collected in 2022 to extract DNA, amplify the rDNA ITS and perform molecular analysis to identify the species. *Lactarius*, *Amanita*, and *Russula* were the most abundant genera. We focused on *Lactarius* species to perform phylogenetic analysis. Our results show that there are 5 new potential species of *Lactarius* inhabiting the *Quercus* forest in Costa Rica. These species are different from *Lactarius* species previously described in *Quercus* forests in America.

Background
Fungi are the second most species-rich organism group after insects. However, they are a very much understudied and underexplored group with more than 90% of them still unknown to science. In this project, we explored the fungal diversity in a neotropical Quercus forest in Costa Rica using molecular studies as the first step. Is the fungal diversity in a Neotropical Quercus Forest in Costa Rica similar to other Quercus Oak Forests in America?
Hypothesis: The fungal diversity in Costa Rica Quercus Forest will be different from other Oak Forests

Methods
DNA extraction, PCR and sequencing
DNA was extracted from dried specimens harvested from the San Gerardo de Dota, Quercus (Oak) forest in Costa Rica using a DNeasy Extraction Process. The nuclear DNA ITS region was amplified using primers ITS1-ITS4. PCR products were purified and then sequenced with a 3750xl DNA Analyzer (Thermo Fisher) at the Pritzker Lab of Molecular Systematics and Evolution (Field Museum). The obtained sequences were assembled and edited using BioEdit.
Phylogenetic analysis
From all our sequences we selected *Lactarius* species to perform phylogenetic analysis to understand the phylogenetic relationships and identify potential new species, as it was the most abundant genus found. The obtained sequences were assembled and edited using Sequencher. Reference sequences were downloaded from GenBank and included in the analysis. Separate data sets for the two markers were aligned using MAFFT, and maximum likelihood (ML) was performed using IQ-TREE.

Results & Discussion
The overall fungal diversity after completing DNA sequencing consisted of *Lactarius*, *Amanita*, *Russula*, and 22 other genera. Our preliminary results from the phylogenetic tree show that there are 5 potentially new species of *Lactarius* highlighted in green. The *Lactarius* species collected in Costa Rica haven't been previously found in other Quercus forests. Furthermore, they seem to be phylogenetically close with American and Caribbean sequences. Moving further in this study, morphological studies would have to be done to propose the new *Lactarius* species found in this project.

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14) **Melissa Patino-Martinez** is majoring in Biology and Spanish with a minor in Latin American, Latinx and Caribbean Studies at Dickinson College and is expecting to graduate in 2024.

Title: Population genetics of *Impatiens* endemic to Tanzania's Eastern Arc

Abstract: *Impatiens* is a genus of flowering plant that has species all over the world, these plants tend to prefer moist, tropical climates and often migrate up mountain sides to avoid fluctuation of environment. Our focus was on species endemic to the Eastern Arc Mountains, as they are known to be a biodiversity hotspot, with a large portion of endemic flora and fauna. Interestingly though, they are not as very studied, so this work is an effort to fill in the gaps in our knowledge and to understand how gene flow, inbreeding and environmental and human factors might affect. We analyzed a SNP dataset for multiple populations of *Impatiens engleri*, which is a primarily butterfly pollinated flowering plant, and *Impatiens keilii*, which is a primarily bird pollinated flowering plant. Due to the differences in primary pollinator species, we hypothesized that there would be less gene flow, genetic variation, and more structure for *I. engleri* over *I. keilii*. Through a double digest restriction-site associated (ddRAD) method, DNA was extracted, digested, barcoded, and pooled into sublibraries to be amplified. After this, through the use of STACKS and other programs we were able to analyze the dataset for loci, heterozygosity, homozygosity, Fis and then Principle Component Analysis (PCA) to visualize the results. Ultimately, our results found that our hypothesis that gene flow is higher in bird pollinated *Impatiens* such as *I. keilii* was correct. It was also found that gene flow did occur between populations of the same mountain block.

Introduction
Impatiens is a genus of flowering plant that has species throughout the world, these plants tend to prefer moist, tropical climates and often migrate up mountain sides to avoid fluctuation of environment. Our focus was on species endemic to the Eastern Arc Mountains, as they are known to be a biodiversity hotspot, with a large portion of endemic flora and fauna. Interestingly though, they are not as very studied, so this work is an effort to fill in the gaps in our knowledge and to understand how gene flow, inbreeding and environmental and human factors might affect. We analyzed a SNP dataset for multiple populations of *Impatiens engleri*, which is a primarily butterfly pollinated flowering plant, and *Impatiens keilii*, which is a primarily bird pollinated flowering plant. Due to the differences in primary pollinator species, we hypothesized that there would be less gene flow, genetic variation, and more structure for *I. engleri* over *I. keilii*. Through a double digest restriction-site associated (ddRAD) method, DNA was extracted, digested, barcoded, and pooled into sublibraries to be amplified. After this, through the use of STACKS and other programs we were able to analyze the dataset for loci, heterozygosity, homozygosity, Fis and then Principle Component Analysis (PCA) to visualize the results. Ultimately, our results found that our hypothesis that gene flow is higher in bird pollinated *Impatiens* such as *I. keilii* was correct. It was also found that gene flow did occur between populations of the same mountain block.

Methods
DNA Extraction - Library Prep
Library prep was completed with a double digest restriction-site associated DNA (ddRAD) method. Total DNA was extracted using a modified CTAB DNA extraction protocol using alkaline lysis (Doak & Davis 1973). The extracted DNA was then digested by EcoRI and MspI enzymes, barcodes were added, and samples pooled into 3 sub-libraries. These fragments were amplified. Fragments were size selected for 350 base pair (bp) inserts for sequencing on NextSeq.

Results
The ddRAD assembly pipeline for *I. engleri*. 200 loci were retained after filtering 9175 loci were retained after filtering the 4000 markers by repeat from 1000. 6222 with a median of 128.7 marker sequences. The final dataset had 12.2 - 0.78 with a median of 10.1.

Discussion
Pairwise Fis was overall higher in *I. engleri* compared to *I. keilii*, indicating that population structure is overall higher in this butterfly pollinated species. This supports the hypothesis that gene flow is higher in bird pollinated *Impatiens* such as *I. keilii*.
Gene flow is occurring in populations that occur on the same mountain block, such as Tengeru & Likipinga, Ngara 1 & 2, and Makishi & Mikungu.
Even for bird pollinated *Impatiens* populations have moderate to pronounced structure, indicating that Eastern Arc mountains do not have strong gene flow between blocks.

15) **Marian Arevalo** is majoring in Elementary Education with a minor in Middle School Science at Northeastern Illinois University and is expecting to graduate in 2024.

Title: How the plant's microbiome affects its health

Abstract: Plants' health is greatly determined by its microbiome. A plant's microbiome consists of 3 sections. These sections are called the phyllo sphere, the endosphere, and the rhizosphere. However the most important section is the rhizosphere as it's the area around a plant root that is inhabited by a unique population of microorganisms that can either positively or negatively impact a plant's development. We learned a lot of insightful information regarding the different rhizosphere organisms and how they impact plant immunity and growth. For example, we learned that there are both beneficial and harmful rhizosphere organisms. Beneficial rhizosphere bacteria that promote plant growth include pseudomonas, bacillus, as well as fungi from the deuteromycetes (Trichoderma and Gliocladium).

Rhizosphere bacteria that are deleterious to plant growth include pathogenic fungi (eg: parasites) and oomycetes. Pathogenic fungi, oomycetes, and nematodes. These types of bad bacteria rob plants from important minerals such as magnesium. A lack of minerals leads to malabsorption in the plant. This can be deadly for the plant as malabsorption does not allow the plant to receive the nutrients needed to survive and grow. Furthermore, we learned about a technique that Botany professionals use in their plant nurseries. This technique is known as AMF colonization. This technique consists of inoculating the plant with the friendly fungi known as mycorrhizal fungi to restore a healthy soil microbiome. This type of fungi is considered friendly bacteria because they give plants an enormous boost in immunity and growth by protecting their host from harmful bacteria such as parasites.

HOW THE PLANT'S MICROBIOME AFFECTS ITS HEALTH
BY MARIAN AREVALO AND ALICIA FOX

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School: Northeastern Illinois University

INTRODUCTION
Plant's health is greatly impacted by its microbiome. A plant's microbiome consists of three sections. These sections are called the phyllo sphere, the endosphere, and the rhizosphere. However the most important section is the rhizosphere as it's the area around a plant root that is inhabited by a unique population of microorganisms that can either positively or negatively impact a plant's growth.

DISCUSSION
We found that there are many types of Rhizosphere organisms. These rhizosphere organisms can either be beneficial or damaging to a plant's growth. Rhizosphere organisms that are damaging to a plant's growth include pathogenic fungi eg: parasites and oomycetes. Pathogenic fungi, oomycetes, and nematodes can result in major stresses in plants. The reason for this is these types of harmful bacteria lead to malabsorption among plants, which does not allow plants to effectively absorb nutrients, water, and carbohydrates. As a result, plants can become deficient in important minerals such as magnesium. A deficiency of magnesium in plants results in a disease called chlorosis. Chlorosis refers to a plant being unable to produce an adequate amount of chlorophyll. The main symptom of chlorosis is plants developing yellow leaves instead of green leaves. A lack of chlorophyll impedes plants from partaking in the process of photosynthesis. Just as there is harmful rhizosphere microorganisms, there are also friendly rhizosphere microorganisms. Examples of friendly rhizosphere microorganisms that promote plant growth include pseudomonas, bacillus, as well as fungi from the deuteromycetes (Trichoderma and Gliocladium). Pseudomonas promotes plant growth in various ways. For example, Pseudomonas suppresses pathogenic microorganisms by producing cell wall degrading enzymes. Cell wall degrading enzymes impede pathogenic fungi from invading the plant. In addition, pseudomonas help with regulating plant hormones. Plant hormones include ethylene, gibberellins, cytokinins, abscisic acid, and auxins. It's essential that these hormones are synthesized as they help with promoting increased plant disease resistance. Similarly to pseudomonas Bacillus also promotes plant growth. However, Bacillus does this differently. Bacillus promotes plant growth by producing stress-tolerant spores. Bacillus spores combat abiotic stress. Examples of abiotic stresses that plants may experience include excessive drought and parasite infestations. Additionally, abiotic spores maintain the ionic balance of plants. Plant ionic balance refers to plants receiving an adequate amount of crucial minerals such as nitrogen, phosphorus, potassium and magnesium, and sulfur. Combined, these plant nutrients are key to healthy plant growth. Nitrogen boosts photosynthesis. Phosphorus facilitates root growth. Potassium helps plants form enzymes which are necessary for several metabolic functions such as photosynthesis and respiration. Magnesium results in the production of chlorophyll which allows plants to absorb sunlight and convert it to energy. Sulfur ensures that plants are forming amino acids such as phenylalanine, tyrosine, and tryptophan which are vital for chlorophyll formation. Moreover, Bacillus spores ensure that water moves effectively through a plant. This is essential as water carries nutrients back and forth between roots and leaves resulting in healthy plant growth and development. As mentioned, pathogenic fungi are the type of fungi that are detrimental to the health of all organisms including plants. However, there are beneficial fungi. Examples of beneficial fungi include mycorrhizal fungi. They form a symbiotic relationship with plants. This symbiotic relationship is known as Mycorrhizal fungi. The study called "Effect of arbuscular mycorrhizal fungi on the physiological functioning of maize under zinc-deficient soils" proves mycorrhizal fungi effectiveness among maize inoculants. According to the study, an increase in chlorophyll uptake was seen in inoculated maize with Mycorrhizal fungi. On the other hand, non-inoculated maize experienced a decrease in chlorophyll uptake (Saboor et al., 2021). This further proves how mycorrhizal fungi positively impact the growth of plants by acting like a sponge for important nutrients.

MYCORRHIZAL FUNGI
We predict that the type of rhizosphere microorganisms found in a plant's rhizosphere will determine whether the plant will survive and grow.

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-Betsy Barak
-Leticia Riquiri
-Julia Lenos

16) **Manya Srivastava** is studying at Oswego East High School.

Title: Using ecological niche models in GIS to predict the occurrence of the hybrid gentian, *Gentiana x billingtonii*

Abstract: Natural hybridization involves successful mating in nature between individuals from two populations. For rare species, hybridization may accelerate extinction rates through the loss of traits that make that species unique, but paradoxically, it can also allow a species to gain traits to adapt to changing conditions. This research aims to identify the mechanisms promoting hybridization in rare species to understand the potential risk of extinction better. This process was investigated in two species that can hybridize, *Gentiana puberulenta*, a species considered rare in some of its range, and *Gentiana andrewsii*, a more common species. Ecological niche models in GIS (geographic information system) software were used to predict the occurrence of hybrid species at study sites.

Using ecological niche models in GIS to predict the occurrence of the hybrid gentian, *Gentiana x billingtonii*
Manya Srivastava¹, Melissa Duda²
¹Oswego East High School ²Northwestern University

Introduction:
The rare congener *Gentiana puberulenta* (Downy Gentian) and the common congener *Gentiana andrewsii* (Closed Bottle Gentian) hybridize under specific circumstances to form *Gentiana x billingtonii*. This project examines the circumstances that allows the congeners to hybridize and if it will increase the risk of extinction for the Downy Gentian.

Objectives:
- What conditions cause hybridization?
- To create a species distribution model to predict the occurrence of *Gentiana x Billingtonii*

Acknowledgements:
We would like to thank Sophie Taddeo for all of her guidance. Thank you to the Chicago Botanic Gardens for hosting this research and the NSF-REU grant DBI-1757800 for support.

Methods:
- Created a species distribution model (SDM) for both gentian species to layer them and find where the hybrid occurs
- Conducting field research to see if there are common pollinators that promote hybridization

Discussion:
As climate change shifts the natural range of species, the Downy Gentian and Closed Bottle Gentian may start to inhabit more of the same areas. This causes more hybridization occur and the Downy Gentian may face extinction if the hybrids have stronger seedlings and pollen. SDMs were used in a study by Ding et al. (2020) to determine the potential distribution of *Betula microphylla*, a species declining toward potential extinction due to climate change and human activities, and two common congeners, *Betula tianshanica* and *Betula platyphylla*.

Results:
Although field research is still ongoing, we are looking to find more on the following:
- If there are shared pollinators between the two species
- How strong are the hybrid seedlings compared to the downy seedlings
- Will the rare downy gentian become extinct as the hybrid becomes more common

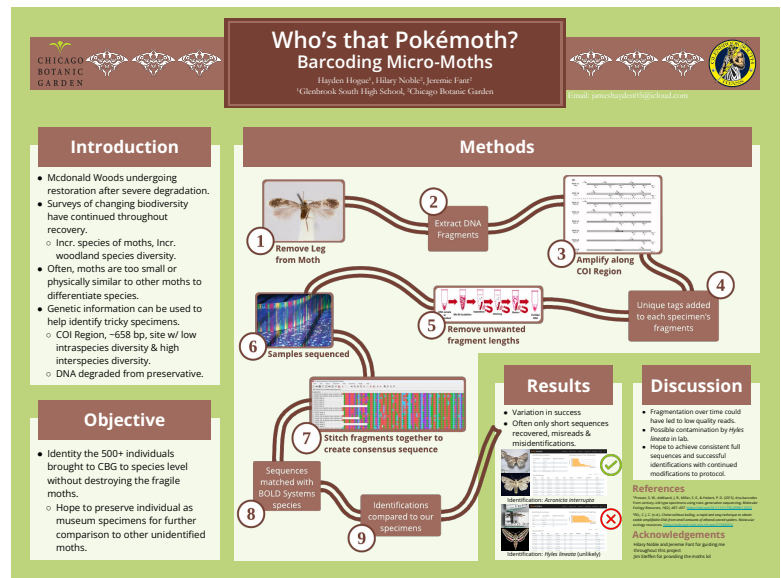
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CHICAGO BOTANIC GARDENS

17) **Hayden Hogue** is studying at Glenbrook South High School.

Title: Who's that Pokémoth? Barcoding Micro-Moths

Abstract: The McDonald Woods, once severely degraded post-European colonization, has ongoing efforts to restore it to its pre-settlement condition. Ecologist Jim Steffen has led the endeavor to document the forest's moths, pollinators which can indicate broader species diversity. However, due to interspecific physical similarity and small size, over 500 specimens remain unidentified. In response to this challenge, we have turned to genetic analysis using the COI region, a genetic "barcode" approximately 650 base pairs in length, characterized by high interspecific diversity and low intraspecific diversity. We extracted the DNA with a Chelex protocol, and amplification along the COI region created fragments we stitched together to reference to the online species database BOLD Systems. However, since the moths in our collection have been preserved in Dichlorvos, a pesticide that denatures DNA, fragment quality is unpredictable. Our most recent data yielded varied success, with both plausible and unlikely identifications. Despite this, we hope to see more consistent, quality results with modifications we have made this summer.



PROGRAM INFORMATION:

The Chicago Botanic Garden has hosted a Research Experiences for Undergraduates (REU) Site, supported in-part by NSF, since 2003. This year 27 students participated in our ten-week summer undergraduate research experience, which is one of only a few programs in the country that offers undergraduate students an opportunity to explore a diverse array of scientific fields related to plant biology and conservation. Students are mentored by faculty and graduate students from the joint Chicago Botanic Garden–Northwestern University Graduate Program in Plant Biology and Conservation and other graduate programs as well as staff from the Garden. Their research projects are based at the Daniel F. and Ada L. Rice Plant Conservation Science Center, and they receive training in all aspects of the research process, from hypothesis formulation through experimental design, data collection, analysis, and ultimately presentation of results through this public research symposium. REU interns also serve as research mentors for high school students participating in the Garden’s College First program, and participate in field trips, workshops, and professional development activities. Additionally, students and their mentors often pursue opportunities to present at national scientific meetings or publish findings in peer-reviewed journals following completion of the program.

REU Coordinators: Jeremie Fant, Becky Barak, Hilary Noble, and Alex Zink

BIG THANKS TO:

Mentors: This science training program would not be possible without your dedication. We appreciate all the time and effort you have put into these students and hope that it has been as rewarding for you as it was for the students.

College First: Your partnership allowed for a richer growth of our students through mentorship and science communication.

Institutional Partners: The Morton Arboretum and UIC CIM²AS Program for fostering a network of institutions that seek to train the next generation of scientists. Thank you in particular to the Biology department of UIC for hosting the lunch and poster symposium.

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