Invasion of Plants in An Urban Garden:Using DNA Barcodes of Plants in Bailu Garden,Suzhou to Assess Potential Invasive Species

Author： Siqi Hu

Mentors： David Micklos, Xinyue Wang, Cold Spring Harbor Asia DNA Learning Center

Abstract

Urban parks often contain a mix of native and introduced plant species, some of the introduced species may threaten local biodiversity. This project aims to assess whether widely distributed plants in Suzhou Bailu Garden pose a potential risk of invasion to the park's ecosystem. During the process, we use Chelex DNA isolation,Silica DNA isolation (for samples that failed the first PCR) and PCR. The samples are sequenced by GENEWIZ and Oxford Nanopore Technology. I expect to identify the species and origin of the samples and assess their risk of invasion by using PHYLIP to explore their relationship with known invasive species. It turns out that the park is being invaded. Among the 13 samples, 10 are non-native.Cuscuta campestris,Verbena bonariensis and Compositae plants such as Conyza bonariensis and Oligoneuron have great potential for being invasive.

Introduction

Invasive plant can easily spread in urban green spaces. Lin et al. (2012) found that compositae plants dominate invasive plants in Suzhou. Specifically, Erigeron annuus and Solidago canadensis are found widely distributed in urban green spaces. However,compositae plants share similar physical features, making them difficult for government to distinguish, leading to missed or misidentified cases that hinder early control of invasive species. DNA barcoding has recently became a solution for accurate identification, regardless of plants' growth stage. Wilson et al. (2024) confirmed that ITS and psbA-trnH combined barcode effectively resolves herbaceous invasive plants. However, systematic DNA barcoding surveys in Suzhou's urban parks is scarce, and the invasive plant composition of Bailu Garden, an urban green space, is still unclear. This study uses DNA barcoding to identify 15 plant species from Bailu Garden and access their risk of invasion .

Materials & Methods

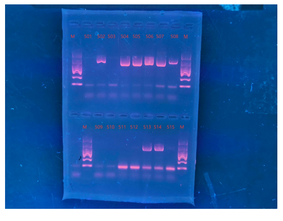
Collect samples:

I collected 15 plant samples,which were visibly abundant or occured in totally different environment(for example,some Conyza bonariensis occurs near the pond and some occurs in the bushes, shown in figure 1), as these were most likely to be established populations or their .

My route

DNA isolation and sequencing:

For the first round of DNA isolation, I use Chelex DNA isolation, perform PCR ,and use gel electrophesis to check. Out of the 15 samples, 8 successful samples are sent to GENEWIZ for sequencing. For the failed ones,I use Silica DNA isolation to remove more impurities and 5 out of 7 samples are successful. Oxford Nanopore Technology is used for a fast sequencing.



The first gel result(not too bad :))

Species identification and analysis:

Species identification and geographic origin (shown in Figure 2) were determined by BLAST searches against the NCBI database using DNA Subway 2.0. To assess invasion risk, I made phylogenetic trees (shown in figure)with PHYLIP to compare our sequences with known invasive species according to Lin M, Hao J H, Chen G Q.'s Composition and distribution of invasive alien plants in Suzhou area.

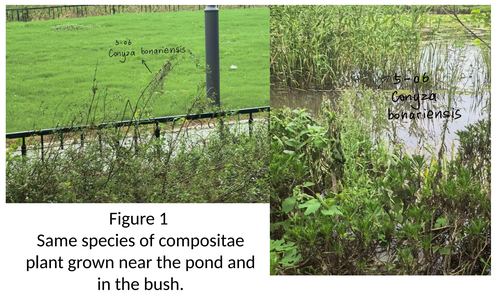


Figure 1
Same species of compositae plant grown near the pond and in the bush.

Number	Name	Origin	Native or non-native
5-01	Cosmos parviflorus	Central and south America	Non-native
5-02	Coreopsis leavenworthii	Southeastern US	Non-native
5-03	Oligoneuron	North America	Non-native
5-04	Mazus pumilus	Tropical Asia	native
5-05	Torenia crustacea	Tropical Asia	native
5-06	Conyza bonariensis	South America	Non-native
5-07	Salvia corrugata	South America	Non-native
5-08	Othonna daucifolia	South Africa	Non-native
5-11	Thalia dealbata	Southern US and Mexico	Non-native
5-12	Verbena bonariensis	South America	Non-native
5-13	Celtis sinensis	China	native
5-14	Cuscuta campestris	North America	Non-native

Figure 2

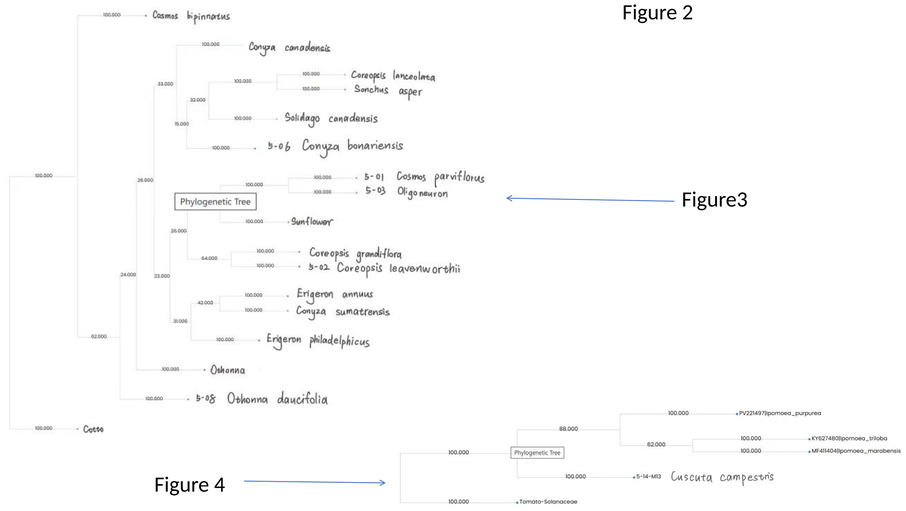


Figure3

Figure 4

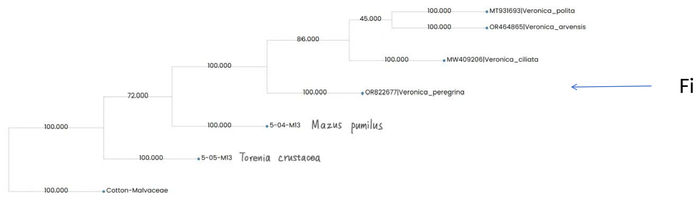


Figure 5

Result

Of the 15 samples, we identified 12 plant species, 10 of which are non-native(shown in figure 2)
Compared with the known invasive plants :

1.**Sample 5-06 (Conyza bonariensis): Highest risk**
Nests within the invasive Erigeron clade, closely related to known invaded species (e.g., C. canadensis).
2.**Sample 5-01 (Cosmos parviflorus,): Moderate risk**
Clusters with 5-02 and 5-03 in a genus that contains recorded invasive species (e.g., Coreopsis).
3.**Sample 5-02 (Coreopsis leavenworthii): Moderate risk**
Belongs to the same genus as the invasive C. lanceolata; the genus includes multiple invasive taxa.
4.**Sample 5-03 (Oligoneuron): Moderate risk**
Same as 5-01 and 5-02; grouped within a genus with documented invasives.
5.**Sample 5-08 (Othonna daucifolia): Cannot be assessed**
Bootstrap support is low; this single phylogeny provides insufficient evidence for risk evaluation.
6.**Sample 5-14 (Cuscuta campestris): low to moderate risk**
Forms a sister branch to the Ipomoea clade (which contains invasive I. triloba), though belonging to a different family.
7.**Sample 5-04 (Mazus pumilus): low to moderate risk**
Sister to the Veronica clade; has some phylogenetic proximity to groups with invasive members.
8.**Sample 5-05 (Torenia crustacea): Low risk**
Deep divergence and distant relationship from all known invasive clades in the tree.

Note: 5-01, 5-02, 5-03, 5-06, 5-08 's relationship with known invasive species shown in figure 3
5-14's is shown in figure 4
5-04, 5-05's are shown in figure 5

Discussion

First,our results show that 10 of the 12 identified species are non-native, with several,including Cuscuta campestris, Verbena bonariensis, Conyza bonariensis, and Oligoneuron, showing phylogenetic proximity to known invasive species. This raises an important concern for urban green spaces. Many of these non-native plants, particularly compositae species, have been intentionally introduced as ornamentals due to their bright flowers While they may not currently cause observable ecological damage within the urban park environment, their seeds may carried by wind or birds and small mammals into real natural habitats.Probably they will establish feral populations and compete with native plants. Thus, the presence of these species in urban parks should not be dismissed as benign; our result represents a potential invasion front that help withpark manager's work.

Second,as a Bioblitz, our study demonstrates that DNA barcoding provides an efficient and scientifically robust tool for early detection of invasive species. By sequencing standard markers (e.g., ITS or rbcL) and comparing our samples against both global reference databases and phylogenies of known invaders, we can rapidly assess invasion risk even without full morphological kwoledge. Thus,our result represents a potential invasion list that help with park manager's work for early intervention. In this way, Bioblitz projects caneffectively complementing traditional surveys and contributr to protection of local ecosystem.

Third,I hope to set up a more recent standard to identify invasive speicies according to the changing climate because the most recent classification is in 2018, 7 years ago.As Hill, A. P., & Hadly, E. A.'s study shows that the defination of "native vs. invasive" is no longer sufficient in the Anthropocene, and a new standard should be established to classify species.

References

[1] Lin M, Hao J H, Chen G Q. Composition and distribution of invasive alien plants in Suzhou area[J]. Journal of Plant Resources and Environment, 2012, 21(3): 98-104.

[2] Tian X F, Qu B. Application progress of DNA barcoding in identification of invasive plants[J]. Journal of Biosafety, 2016, 25(2): 99-105.

[3] Zhao Y F, Zhao C Y, Zhu J F, et al. Distribution pattern of invasive alien plants in typical parks of Beijing[J]. Acta Ecologica Sinica, 2022, 42(9): 3656-3665.

[4] Wilson E, et al. DNA barcoding of terrestrial invasive plant species in Southwest Michigan[J]. Plant Direct, 2024, 8(7): e4127. DOI:10.1002/pld3.4127.

[5] Hill A P, Hadly E A. Rethinking "Native" in the Anthropocene[J]. Frontiers in Earth Science, 2018, 6: 96.

Acknowledgements

I successfully completed my research and finally had my project presented with the help of everyone who supported me. First of all, I give sincere thanks and appreciation for our tutor Dave who patiently help and encourage me. It is a pleasure to study under his guidance. I am also extremely grateful to our classmates who have kindly assistance and companionship in the course of preparing this project.