Bailu Park Bioblitz: Habitat and Species Diversity

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Abstract

A two-hour BioBlitz was conducted at Bailu Park, during which 9 plant and insect samples were collected. This experiment focus on explore whether species diversity in the park is associated with habitat type. Species were identified through DNA barcoding, and each species was linked to its corresponding habitat (water vs. land). The results suggest an association between habitat type and species diversity: the water group consisted of wetland plants and a damselfly, while the land group included garden plants, a butterfly, and a moth. This pattern indicates that species composition corresponds to habitat type. Overall, these preliminary findings suggest that differences between water and land habitats are associated with local species diversity.

Introduction

In recent years, China has paid more attention to biodiversity consercation in cities. National policies encourage the protection and restoration of urban wetlands and urban biodiversity. In Suzhou, the government revised the Wetland Protection Regulation in 2025 to protect wetland ecosystems and their biodiversity.

Different species have different life cycle requirements. Some insects have aquatic immature stages (e.g., damselflies), while butterflies and moths complete their entire life cycle on land. Based on this reasoning, I expected that water-associated and land-based areas in Bailu Park would support different species assemblages.

Materials & Methods

1. Plant leaf samples were collected from multiple locations within Bailu Park, Suzhou, on August 13, 2026. Photos were taken when collecting. Flying insects were captured using nets, and high-resolution images were taken using a Digital USB Microscope Camera.
2. DNA was extracted from plant tissues using a Rapid DNA extraction kit following the Rapid protocol in “Using DNA Barcodes to Identify and Classify Living Things”.
3. PCR for plant samples was performed using the rbcL primer set (rbcLaF / rbcLa rev) following the protocol described in “Using DNA Barcodes to Identify and Classify Living Things”. For insect samples, PCR amplification was conducted using the invertebrate primer cocktail (LCOI1490 / HC02198 / FormCOI_F / FormCOId_R)

Table 1

Species	Sample ID	Egg	Larva	Naiad	Adult	Habitat association
Cephonodes hylas	MZT-821	land	land	-	land	all stages on land
Ceriagrion nipponicum	MZT-822	water	water	water	land	immature stages in water, adult on land
Argynnis hyperbius	MZT-823	land	land	-	land	all stages on land

Fig. 1 Plants I collected

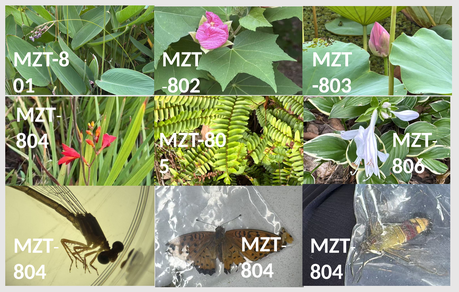

Fig. 2 Insects I collected

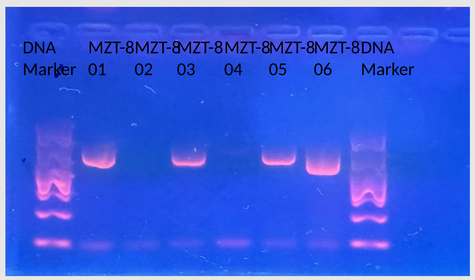

Fig. 3 Gel Electrophoresis results for plants

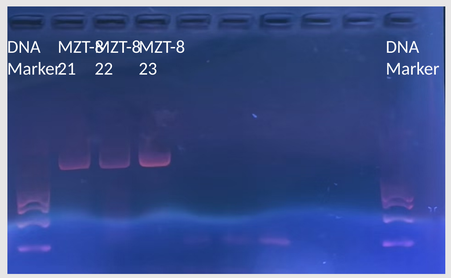

Fig. 4 Gel Electrophoresis results for insects

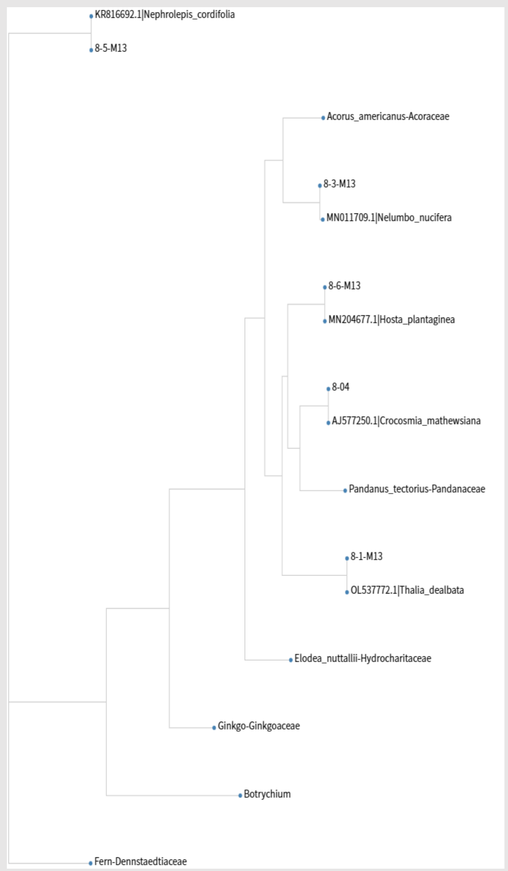

Fig. 5 Tree for Plants

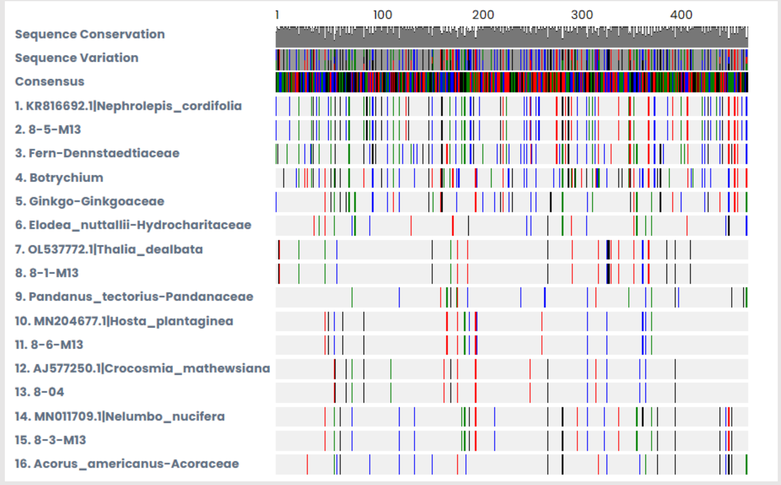

Fig. 6 DNA Barcode for Plants

Results

A total of 9 species were recorded during the 2-hour BioBlitz at Bailu Park. The water-associated group contained 3 species: two aquatic plants (Nelumbo nucifera and Thalia dealbata) and one damselfly (Ceriagrion nipponcum). The land-based group contained 6 species: four terrestrial plants (Hibiscus mutabilis, Nephrolepis cordifolia, Thalia dealbata, Nelumbo nucifera, Hosta plantaginea)

Discussion

1. I found that the species collected from water-associated areas and land-based areas in Bailu Park were different. The water group contained aquatic plants and a dameslfly, while the land group contained terrestrial plants, a butterfly, and a moth. No species were shared between the two habitat types.
2. My hypothesis was supported. I predicted that water-associated and land-based areas would support different species assemblages, and my results confirmed this prediction. This pattern is likely explained by species life cycle requirements. For example, the damselfly (Ceriagrion nipponicum) has aquatic immature stages, which means it must live near water to complete its life cycle. In contract, the butterfly and hawk moth depend on land plants for food and reproduction, so they are found mainly in terrestrial areas.
3. My evidence comes directly from our field observations and species identification. The species list and habitat distribution clearly show the separation between the two groups.
4. One difficulty I encountered was the DNA barcoding result for Hibiscus mutabillis. DNA extraction from this plant was less efficient compared to other samples, and the PCR amplification gave weak products. As a result, the number of usable reads obtained from sequencing was limited.

References

Using DNA Barcodes to Identify and Classify Living Things
Suzhou Municipal Government. (2025). Wetland Protection Regulation of Suzhou

Acknowledgements

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