An investigation of plants with epiphytic algae growing on in Urban lakes in Suzhou

冷泉港亚洲DNA学习中心
Cold Spring Harbor Asia DNA Learning Center

Edward JIxiao Wu Noah Yinzhe Xu Qiqi Yuqi Pu

Abstract:

Epiphytic algae can grow on a large variety of aquatic plants, this relationship have both positive and negative effects on the environment. The effects of removing a species in the system is not predictable. To understand this interaction, we use DNA barcode (a way of identify species via comparing their similarity of genetic sequence) to identify the aquatic plant species and invested their mutualism or competition.

Introduction & Hypothesis:

Epiphytic algae influence its host in many different ways, studies have shown that they can despoil its hosts' phosphate as its nutrient source [1] but also present as the main producer in an aquatic food web [2]. Which means its hosts might greatly differ cording to identify its hosts in the two main lakes (Jinji lake and Tai lake) in Suzhou:

1. Collect and store the sample in dark at 4C with dH2O overnight.
2. Transfer the sample to the petri dish with dH2O in darkness, tape the dish with black tape, leaving only one opening on the edge of the dish.
3. Put the taped dish under light for 3 min.
4. Carefully take out the sample form the other side of the dish, dry it using a paper tower
5. Take taxonomy photos under microscope.
6. Isolate DNA using Qiagen DNeasy plant kit.
7. Amplify RBCL gene using PCR.
8. Analyze the PCR results using gel electrophoresis.
9. DNA sequencing and BLAST the result.

Fig1

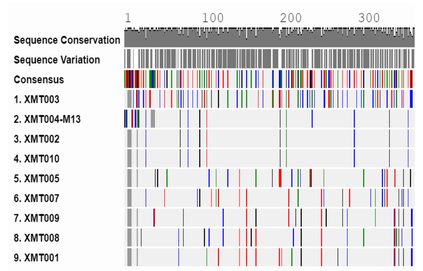

Fig2

Fig3

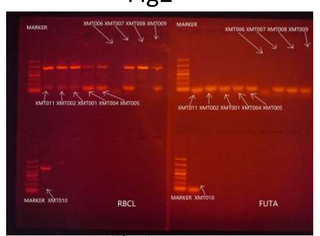

Fig4

Results:

The results of electrophoresis show only 8 samples out of 10 were successfully amplified and we can perceive that except XMT-006 all the other sample appear the aim stripes with different luminance on RBCL gel but FUTA gel has no target stripes but primer sprites through the amplification and electrophoresis of RBCL and FUTA gene order by PCR .Thus we can find that our samples are not algae. The result of sequencing comes out and we were able to identify 7 out of 8 species using DNA barcode by BLAST with the standard sequence on Genbank.com or uniport.org. The result come out are listed in Fig5，the barcode shows that sample XMT-002 collect in the Jinji Lake is identical to XMT-010 that collected in the Tai lake, so we can judge that they are the same species. Further on we can infer that there are similarities between the aquatic species in Jinji Lake and Tai lake.

Sample picture	Sample ID	DNA subway ID	Genebank ID	% idententy
	XMT001	azolla sp.	azolla sp.	100%
	XMT002	Ceratophyllum demersum	Ceratophyllum demersum	100%
	XMT003			
	XMT004	Spirogyra sp.	Spirogyra sp.	
	XMT005	Nymphoides peltata	Nymphoides peltata	99.80%
	XMT006	not set	not set	
	XMT007	Myriophyllum spicatum	Myriophyllum spicatum	100%
	XMT008	Vallisneria natans	Vallisneria natans	97.40%
	XMT009	hydrocharis dubia	hydrocharis dubia	
	XMT010	Ceratophyllum demersum	Ceratophyllum demersum	99.90%
	XMT011	Najas marina	Najas marina	100%

Fig5

Methods' detail:

The two lakes are both in drainage of Tai lake, But In comparing to Tai, Jinji lake is near to the CBD and take a smaller area (detailed on the map) Sampling location was chosen near the bank for convenience. Location 1 and 2 are both in Jinji lake, sample 3 was taken from Tai hu. Step 1-4 was taken to remove any contaminants (planktons) in the water using "light baiting". This attract the planktons near light source, and the waste liquid was removed.

Fig1:The map of the sampling site.
Fig2 :The DNA barcode.
Fig3:A photo taken of the sampling location in Tai Lake, which shows that the water contains a lot of sediment.
Fig4:The results of electrophoresis.
Fig5: The results of gel electrophoresis.

Discussion:

In general, the result supported our hypothesis, there are same species with epiphytic algae growing on in both lakes, but surprisingly, there is a certain type of hosted plant that only fond in Jinji lake, where is more developed area. This may because of the sample we collected was not enough for a wider conclusion which means we need more investment in future.

Reference：

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