A Preliminary Study of Applying DNA Barcoding to the Ecology of Electric Power Industry

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I. Research Background and Purposes

DNA barcoding is a commonly used technique in biological researches. By means of sequencing specific DNA fragments, it can help identify different species. The concept is similar to barcoding of supermarket products or ISBN universal code of books. Consequently, it is widely used in biological researches in species identification, biodiversity and phylogenetic analysis.

Recently, Taipower has devoted a lot of effort in ecological protection. There are many important ecological issues no matter in land areas (e.g., hydroelectric power plants) or sea areas (e.g., offshore wind farms). It is urgent to introduce professional biological techniques for such studies. In this research, we applied DNA barcoding technique to ecological studies conducted at Datan and Linkou Power Plants to explore the feasibility of this technique.

II. Methods

W used coralline algae and fish larvae as the research materials for species identification. The coralline algae samples were collected from drift bottles in Guan Xin algal reef, and fish larvae from thermal discharge channel of Linkou Power Plant. Samples were preserved in 95% ethanol to avoid DNA degeneration. The DNA extraction kit (Qiagen) was used for DNA extraction, followed by polymerase chain reaction (PCR) to amplify two specific molecular markers. The ribosome SSU (the small subunit of the ribosomal rDNA) and chloroplast psbA (Photosystem II protein D1 coding gene) were used in coralline algae, while the mitochondrial COI (cytochrome c oxidase I) in fish larvae. The PCR products were sequenced to obtain specific DNA sequences.

Phylogenetic analyses were conducted by using MEGA X software. Additional DNA sequences of closely related species were downloaded from GenBank of National Center for Biotechnology Information (NCBI) for comparison purposes. Phylogenetic trees were constructed by using neighbor-joining (NJ) and maximum likelihood (ML) methods. The bootstrap algorithm was used to test the feasibility of clustering.

III. Results and Application

(i) Results of coralline algae

Phylogenetic analysis results (Fig. 1, 2) showed that all the coralline algae samples in this study were genetically closed to *Phymatolithon* sp. 1 in Liu et al. (2018), and certain genetic divergences between *Phymatolithon margoundulatus* and *Phymatolithon* sp. 2.

(ii) Results of fish larvae

Phylogenetic analysis results (Fig. 3) showed that 37 fish larvae samples could be clustered to 7 taxonomic units, including 6 species (*Chelon affnis*, *Chelon* haematocheilus, Elops machnata, Nematalosa japonica, Encrasicholina punctifer, Acanthopagrus schlegelii). Among the samples, *Chelon affnis* accounted for the largest proportion (70%, 26/37), the remaining 5 species 3~8%.

(iii) Future application

The results showed that DNA barcoding could be applied to ecological research of electric power industry, and provide tremendous help without background knowledge. Morphological identification of coralline algae and fish larvae was difficult in the past. In this study, the results showed DNA barcodingwas useful for species identification. Under ecological protection policy devoted by Taipower company, we believe that DNA barcoding will be widely used in different ecological topics of electric power industry in the future.



Fig. 1 The Phylogenetic analysis results of SSU showed that the coralline algae samples (red dots) in this study should be the same species as *Phymatolithon* sp. 1 in Liu et al. (2018)



Fig. 2 The Phylogenetic analysis results of psbA showed that the coralline algae samples (red dots) in this study should be the same species as *Phymatolithon* sp. 1 in Liu et al. (2018)



Fig. 3 The Phylogenetic analysis results showed that 37 fish larvae samples could be clustered to 7 taxonomic units, including 6 species and 1 unknown species.