

Systematic investigations of plastid genomes and nuclear integrants of plastid DNA in cupressophytes (Conifers II)

Chih-Yao Hsu^{1,2}, Chung-Shien Wu¹, Hui-Ling Hsieh¹ and Shu-Miaw Chaw¹

¹Biodiversity Research Center, Taiwan

²National Taiwan University & Academia Sinica, Taiwan

Previously, investigating nuclear plastid DNAs (nupts) are limited in the plants whose nuclear and plastid genomes have been completely sequenced. However, to elucidate the nupts of conifers, it is impractical to completely sequence their huge nuclear genomes that range from 10 to 30 GB. Here, we proposed a cost-effective strategy that enables us to obtain the nupts of conifers and understand their molecular evolution in nuclear genomes. We sampled the completely sequenced plastomes from nine cupressophytes species, including *Wollemia nobilis* (Araucariaceae), *Dacrycarpus imbricatus* (Podocarpaceae), *Sciadopitys verticillata* (Sciadopityaceae), *Taxus mairei*, *Amentotaxus formosana* (Taxaceae), *Cephalotaxus wilsoniana* (Cephalotaxaceae), *Chamaecyparis formosensis*, *Cryptomeria japonica*, and *Taiwania cryptomerioides* (Cupressaceae). We used the cpDNA of *Cycas taitungensis* as an outgroup reference. We found nine specific gene-clusters of cupressophytes that are reasonable to be the products of plastomic rearrangements. We assumed that before these rearrangements occurred, the ancient plastomes of cupressophytes had been similar to that of *Cycas* in their gene-order, and some ancient plastomic fragments of cupressophytes had been transferred to the nuclear genomes and become nupts. Therefore, specific primer pairs based upon the gene-order of the *Cycas* plastome might enable us to amplify these ancient nupts and avoid contaminants in cupressophytes. Our tree analyses placed all nupts we found in odd placements that are disagree with recent phylogenetic studies, suggesting that these nupts should have lost phylogenetic information and be under different genetic condition from their plastomic counterparts. Our proposed methods provide a novel and alternative avenue for investigation of nupts in plants with huge nuclear genomes.

Biography

Chih-Yao Hsu is a Ph.D. student in National Taiwan University and his major is genome and systems biology. He has completed his master degree from the department of horticulture, National Taiwan University. His research interests include plant plastid evolution and plant secondary metabolisms.

ivanhsu@gate.sinica.edu.tw