



Abstract Cycas taitungensis C. F. Chen as A Synonym of C. revoluta Thumb. ⁺

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Abstract: The incipient species is the interesting part to study speciation. However, the species boundary would be ambiguous for their admixed genetic structure and similar morphology. The features are resulted from recent gene flow and ancestral polymorphism and may further challenge the taxonomy. Cycas sect. Asiorientales, including Cycas taitungensis and C. revoluta mainly in Taiwan and the Ryukyu Archipelago, diverged recently with reciprocal paraphyletic relationship. Previous evolutionary studies were questioned by few genetic markers and incomprehensive population samplings. Also, the morphological comparisons were incomplete due to long-term taxonomy misunderstanding of C. taitungensis. Here, we used genome-wide SNP with comprehensive population samplings to infer the geographic mode of speciation by approximate Bayesian computation (ABC) in two species. Individual tree was also reconstructed for species delimitation and gene flow inferences. Additionally, the morphometrics of diagnostic traits were incorporated for taxonomy reappraisal. The morpho-genetic data rejected the allopatric speciation by continuous gene flow and overlapped morphological variations. The individual tree further implied spatially heterogenous gene flow from Taiwan to northern Ryukyu islands possibly by transoceanic vegetative dispersal and pollen flow. With evolutionary inference and morphometrics, C. taitungensis was treated as a synonym to C. revoluta. Our study highlighted the importance of Kuroshio for species evolution and the judgement on species as the conservation unit.

Keywords: continental island; cycad; ddRAD-seq; Kuroshio; speciation; species delimitation

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