

## Abstract

Integrative data from plastid and nuclear loci are increasingly utilized to resolve species boundaries and phylogenetic relationships within major angiosperm clades. *Debregeasia* (Urticaceae), an economically important genus, presents challenges in species delimitation due to its overlapping morphological traits and unstable taxonomic assignments. Here, we analyzed 14 morphological traits and generated 12 data matrices from the plastomes and nrDNA using genome skimming from the nine recognized morphospecies to clarify species boundaries and assess barcode performance in *Debregeasia*. We also used a universal set of 353 nuclear genes to explore reticulate evolution and biogeographic history of *Debregeasia*. Plastomes of *Debregeasia* exhibited the typical quadripartite structure with conserved gene content and marginal independent variations in the SC/IR boundary at inter- and intra-specific levels. Three *Debregeasia* species were non-monophyletic and could not be discerned by any barcode; however, ultra-barcodes identified the remaining six (67%), outperforming standard barcodes (56%). Our phylogenetic analyses placed *Debregeasia wallichiana* outside the genus and suggested six monophyletic clades in *Debregeasia*, although the placement between *Debregeasia hekouensis* and *Debregeasia libera* varied. There was extensive trait overlap in key morphologically diagnostic characters, with reticulation analysis showing potentially pervasive hybridization, likely influenced by speciation patterns and overlaps between species ranges. We inferred that *Debregeasia* crown diversification began at ca. 12.82 Ma (95% HPD: 11.54–14.63 Ma) in the mid-Miocene within Australia, followed by vicariance and later longdistance dispersal, mainly out of southern China. Our findings highlight the utility of genomic data with integrative lines of evidence to refine species delimitation and explore evolutionary relationships in complex plant lineages.