

RINGKASAN

Nepenthes adalah tanaman karnivora dengan kantong unik yang digunakan untuk menangkap serangga sebagai sumber nutrisi tambahan. Populasinya semakin terancam akibat kerusakan habitat, perubahan iklim, dan eksploitasi, sehingga upaya identifikasi dan konservasi menjadi sangat penting. Selain morfologi, pendekatan molekuler berbasis DNA, seperti marka IGS *atpB-rbcL*, diperlukan untuk identifikasi yang lebih akurat dan mendukung strategi pelestarian.

Penelitian ini mengkaji keanekaragaman genetik delapan sampel *Nepenthes* (*N. ampullaria*, *N. rafflesiana*, *N. gracilis*, *N. reinwardtiana*, *N. sumatrana*, *N. mirabilis* var. *globosa*, *N. mirabilis* var. *mirabilis*, dan *N. maxima*) dengan pendekatan morfologi dan molekuler menggunakan IGS *atpB-rbcL*. Penelitian dilaksanakan dengan metode eksploratif. Pohon filogenetik dibuat untuk menunjukkan hubungan kekerabatan.

Analisis morfologi menunjukkan variasi pada bentuk kantong, daun, batang, *peristome*, dan *operculum*. Secara molekuler, keanekaragaman *haplotype* sebesar $1,000 \pm 0,0625$ dan keanekaragaman *nucleotide* sebesar $0,125098 \pm 0,068675$. Hasil dendrogram menunjukkan spesies *N. ampullaria* sebagai cabang awal evolusi, diikuti *N. maxima* sebagai kelompok wilayah Wallaceae, kemudian *N. mirabilis*, *N. gracilis*, *N. reinwardtiana*, *N. sumatrana*, dan *N. rafflesiana* sebagai kelompok *Sundaland*. Hasil ini mendukung strategi konservasi berbasis data genetik dan morfologi, serta menyoroti urgensi pengayaan database genom *Nepenthes*.

Kata Kunci: *atpB-rbcL*, filogenetik, keanekaragaman genetik, morfologi, *Nepenthes*

SUMMARY

Nepenthes, known for their unique pitcher structures that ensnare insects as an additional nutrient source, are experiencing growing population declines. Their populations are increasingly threatened by habitat destruction, climate change, and exploitation, making identification and conservation efforts critically important. Beyond morphology, DNA-based molecular approaches, such as the *atpB-rbcL* IGS marker, are required for more accurate identification and to support preservation strategies.

This study examined the genetic diversity among eight *Nepenthes* samples (*N. ampullaria*, *N. rafflesiana*, *N. gracilis*, *N. reinwardtiana*, *N. sumatrana*, *N. mirabilis* var. *globosa*, *N. mirabilis* var. *mirabilis*, and *N. maxima*) using both morphological and molecular approaches with the *atpB-rbcL* IGS marker. The study was conducted using an exploratory method. A phylogenetic tree was constructed to illustrate taxonomic relationships.

Morphological analysis revealed variations in pitcher, leaf, stem, peristome, and operculum shapes. Molecular analysis showed a haplotype diversity of 1.000 ± 0.0625 and a nucleotide diversity of 0.125098 ± 0.068675 . The resulting dendrogram indicated *N. ampullaria* as the earliest evolutionary branch, followed by *N. maxima* as a member of the Wallacea group, and then *N. mirabilis*, *N. gracilis*, *N. reinwardtiana*, *N. sumatrana*, and *N. rafflesiana* as part of the Sundaland group. These findings support the development of conservation strategies based on genetic and morphological data and highlight the urgent need for the enrichment of the *Nepenthes* genomic database.

Keywords: *atpB-rbcL*, genetic diversity, morphology, *Nepenthes*, phylogenetic