

Chloroplast genome variation and phylogenetic insights across Moraceae with the complete chloroplast genome of *Streblus asper*

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The present study presents a comparative analysis of 76 Moraceae chloroplast genomes, including a chloroplast genome for *Streblus asper* and an independent assembly for *Ficus hispida*. We identified notable structural variations, particularly significant gene truncations in *ndhD* and *yef1* in *S. asper*. Our 76-species phylogenetic analysis robustly places *S. asper* in a clade with *Trophis caucana* and *Antiaris toxicaria*, resolving a key taxonomic uncertainty. The placement of *F. hispida* within the *Ficus* clade is also confirmed. These findings provide crucial genomic resources, clarify evolutionary relationships, and deepen our understanding of genomic evolution in Moraceae.

Keywords: Chloroplast genome, Moraceae, nucleotide diversity, phylogenetics, *Streblus asper*.

to improve phylogenetic resolution and taxonomic clarity within the family⁴.

Chloroplast genomes, due to their conserved gene content, maternal inheritance, and relatively small size, have become indispensable in plant phylogenetic and evolutionary studies⁵. Recent advances in next-generation sequencing (NGS) have allowed the accurate assembly of complete chloroplast genomes, providing powerful insights into plant evolution and lineage diversification⁶. In Moraceae, these genomic approaches are especially valuable for resolving relationships among closely related genera and species where morphological convergence is common⁷.

Recent studies have significantly advanced Moraceae phylogenomics, including foundational work by Zeng *et al.*⁸ on *Morus* and a comprehensive analysis of *Ficus* by Huang *et al.*⁹ which included the report of the *F. hispida* plastome. However, genomic representation remains uneven across the family with several genera still lacking