

Characterization of the chloroplast genome of *Styrax* (Styracaceae) species and comparative analysis

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Abstract

Chloroplasts are pivotal organelles in plant cells and serve as crucial sites for photosynthesis. Their sequences are typically conserved and stable, making chloroplasts important subjects for studying the adaptive evolution of angiosperms. The development of the APG IV system and DNA barcoding technology has gradually unraveled many mysteries regarding species relationships. However, research on *Styrax* is extremely limited, therefore, we conducted an analysis and reconstruction of the five chloroplast genomes of *Styrax* based on phylogenetic analysis. The results revealed copy number variation of *rps12* gene in *S. faberi* and *S. dasyanthus*. Ka/Ks analysis demonstrated positive selection for *rbcL*, *rpoC1*, and *ycf3* genes, indicating that *Styrax* is undergoing adaptive evolution. Furthermore, phylogenetic trees constructed using *rpl32* and *ycf15* exhibited strong support, suggesting that these two genes can also be utilized as specific DNA barcodes for identifying interspecific relationships within *Styrax*.