Chloroplast genome structure and phylogenetic analysis of Glycosmis parviflora (Sims) Little 1948, a folk medicinal plant featured in Lingnan Region, China

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ABSTRACT
Glycosmis parviflora is the most widely spread and the most morphologically varied species of Chinese Glycosmis, and its roots and leaves serve as folk medicines. We sequenced the complete chloroplast (cp) genome of G. parviflora. The cp genome obtained was a circular DNA molecule of 159,825 bp in length, containing one large and one small single copy region (LSC and SSC) of 87,517 and 18,352 bp separated by a pair of 26,978 bp inverted repeat regions (IRs). The overall GC content of the cp genome was 38.4%. The phylogenetic analysis revealed that Glycosmis was strongly supported as a monophyletic group belonging to Clauseneae, and G. parviflora was closely related to G. pentaphylia. The results will provide the basis for the further study of molecular markers and phylogeny of G. parviflora.
overall chloroplast genome, IR regions, LSC and SCC are 38.40, 42.9, 36.7, 32.9%, respectively.

In order to gain insight into its phylogenetic position, a phylogenetic analysis was performed using the complete cp genomes of *G. parviflora* and other 19 species of Rutaceae. The cp genomes of the 19 species were downloaded from GenBank (species names and accession numbers shown in Figure 1). All the cp genomes were aligned with MAFFT (Rozewicki et al. 2019), and then edited manually by MEGA X (Kumar et al. 2018). The maximum likelihood (ML) tree was inferred in RAxML (Stamatakis 2014) with the best fitting substitution model (GTR + F + R2) determined by the Akaike information criteria (AIC). The bootstrap support was calculated with 1000 replications.

In the phylogenetic tree with *Phellodendron chinense* as an outgroup species, two clades were clearly recognized, which corresponded to Clauseneae and Aurantieae respectively. *Glycosmis* was a strongly supported monophyletic group (PP = 100) in Clauseneae, and was the sister group to *Micromelum*. *G. parviflora* was closely related to *G. pentaphylla* (Figure 1).

**Author contributions**

Z C conceived the study, reviewed and revised the drafts of the paper. AM C analyzed data, wrote and revised the manuscript. F L performed the genome assembly and annotation. XN X conducted the molecular experiments, and assisted with data analysis. RH assisted in manuscript revision. EW T collected plant materials and assisted with the molecular experiments. All authors read and approved the final manuscript.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

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**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov/](https://www.ncbi.nlm.nih.gov/) under the accession no. MW714375. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA820442, SRX14636471, and SAMN27006371, respectively.

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