Complete chloroplast genome of a wild-type Gardenia jasminoides ellis (rubiaceae) adapted to island climate

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Gardenia jasminoides Ells is a traditional aromatic and medicinal plant in China. Here, the complete chloroplast genome of a wild-type gardenia adapted to island climate was assembled. The assembled genome was 155,247 bp in length, with four typical regions, i.e., a large single-copy (LSC) region (85,414 bp), a small single-copy (SSC) region (18,235 bp) and two inverted repeats (IRs) regions (25,799 bp each). In total, 138 genes were predicted, including 90 protein-coding genes, 40 tRNA genes and eight rRNA genes. The overall GC content of the chloroplast genome was 37.5%. The chloroplast genome would provide more information for the phylogeography and phylogeny study of G. jasminoides.

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conducted by MAFFT 7.158 (Katoh and Standley 2013). Then phylogenetic inference was performed in RAxML-VI-HPC (Stamatakis 2006) software under the GTR-gamma model. To assess the confidence of each internal node, rapid bootstrap method was applied with 1000 replications. The result showed that phylogenetic positions of all the taxa were successfully resolved (Figure 1). *Gardenia jasminoides* was placed in Rubiaceae clade and classed together with *Coffea arabica*, which indicated that *Gardenia* is more closely related to *Coffea* than other studied genera.

**Disclosure statement**

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

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**Data availability statement**

The raw sequence data supporting this study are deposited in the National Center for Biotechnology Information Short Read Archive under BioProject ID PRJNA678106 (accession number SRP292439). The assembled genome and its annotation are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov](https://www.ncbi.nlm.nih.gov), reference number MW160432.

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![Figure 1.](image) Maximum-likelihood tree based on the sequences of 21 chloroplast genomes from Gentianales. Numbers at tree nodes represent bootstrap values for 1000 replications. Number after ‘j’ shows the accession number in GenBank for each accession. The position of the wild-type *Gardenia jasminoides* reported in this study is marked in bold.