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genomic DNA was extracted from fresh leaves using a modified Cetyltrimethylammonium Ammonium Bromide (CTAB) method (Doyle and Doyle 1987) and sequenced by the BGISEQ-500 platform. The samples were collected from Jinan district, Fujian, China (26°38'N, 119°27'E) and the voucher specimen deposited at Herbarium of Fujian Agriculture and Forestry University (specimen code FJFC 0411). The clean reads were used to assemble the complete chloroplast genome by the GetOrganelle pipe-line (Jin et al. 2018), with the chloroplast genome of *Goodyera procera* (GenBank accession KT886429) as the reference sequences. The assembled chloroplast genome was annotated using the Geneious R11.15 (Kearse et al. 2012).

The total chloroplast genome of *Ch. chinensis* (GenBank accession MN641483) was 147,218 bp in length, consisting of a large single-copy region (LSC) of 81,081 bp, a small single-copy region (SSC) of 14,769 bp, and two inverted repeat regions (IRA and IRB) of 25,684 bp. The GC content of the chloroplast genome was 36.79%, while the corresponding values of the LSC, SSC, and IR regions are 34.32%, 29.00%, and 42.93%, respectively. The complete chloroplast genome contains 131 genes, including 38 transfer RNA (tRNA) genes, 8 ribosomal RNA (rRNA) genes and 85 protein-coding genes.

To confirm the phylogenetic position of *Ch. chinensis*, a phylogenetic analysis was performed based on 12 species of Orchidoideae and two outgroup species of Cypripedioideae. All sequences were aligned with the HomBlock pipeline (Bi et al. 2018), and the phylogenetic tree constructed by RAxML (Stamatakis 2014) with 1000 ultrafast bootstrap (UFBoot) replicates (Minh et al. 2013; Chernomor et al. 2016). The results showed that *Ch. chinensis* nested within Goodyerinae (Figure 1).

Disclosure statement

No potential conflict of interest was reported by the authors.

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