

The complete chloroplast genome of *Pholidota imbricata* (Orchidaceae)

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ABSTRACT

Pholidota imbricata belongs to tribe Coelogninae in Orchidaceae distributed in Sichuan, Xizang, and Yunnan. Here, we report the first complete chloroplast (cp) genome and the cp genome features of *P. imbricata*. The complete cp genome sequence of *P. imbricata* is 159,292 bp in length and presented a typical quadripartite structure including one large single-copy region (LSC, 87,515 bp), one small single-copy region (SSC, 20,999 bp), and two inverted repeat regions (IRs, 25,389 bp each). The cp genome encoded 141 genes, of which 108 were unique genes (80 protein-coding genes, 24 tRNAs, and 4 rRNAs). The phylogenetic relationships show that *P. imbricata* is sister to the species of the genus *Pleione* in tribe Coelogninae.

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Pholidota imbricata; chloroplast genome; phylogenetic; Coelogninae; Orchidaceae

The genus *Pholidota* belongs to the tribe Coelogninae (Orchidaceae: Epidendroideae) with 12 species, ranging through mainland and SE Asia, Australia, New Guinea, and the Pacific islands. (Chen et al. 2009; Pridgeon et al. 2014). Plants of *Pholidota* are widely used in Chinese traditional medicine (Zou et al. 2017; Fu et al. 2018; Huang et al. 2018;

Zhang et al. 2018). The complete chloroplast (cp) genome sequence of *P. imbricata* was assembled in this study.

Specimens of *P. imbricata* were deposited in the National Orchid Conservation Centre herbarium (NOCC; specimen code Z.J.Liu 3524; geospatial coordinates N22°36'1" E114°10'42"). Total genomic DNA was extracted from fresh material using

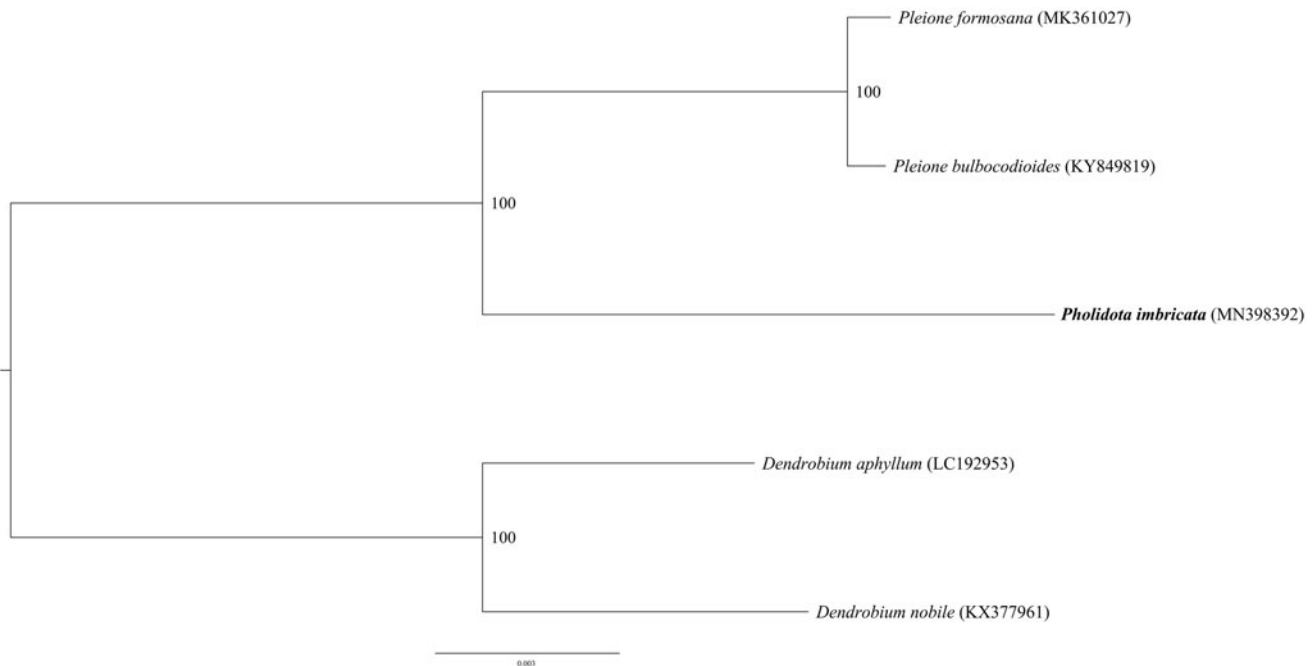




Figure 1. Phylogenetic position of *Pholidota imbricata* inferred by maximum-likelihood (ML) of complete cp genome. The bootstrap values are shown next to the nodes.

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the modified CTAB procedure of Doyle and Doyle (1987). Sequenced on Illumina Hiseq 2500 platform (Illumina, San Diego, CA). Genome sequences were screened out and assembled with MITObim v1.8 (Hahn et al. 2013), which resulted in a complete circular sequence of 159,292 bp in length. The cp-genome was annotated with CpGAVAS (Liu et al. 2012).

The cp genome sequence of *P. imbricata* (GenBank accession MN398392) is 159,292 bp long and presented a typical quadripartite structure including one large single-copy region (LSC, 87,515 bp), one small single-copy region (SSC, 20,999 bp), and two inverted repeat regions (IRs, 25,389 bp each). The cp genome encoded 141 genes, of which 108 were unique genes (80 protein-coding genes, 24 tRNAs, and 4 rRNAs).

Three accessions of Coelogninae species and two outgroups were used for the molecular analysis. The phylogenetic tree was constructed based on the maximum-likelihood (ML) methods. The ML analysis was performed using the CIPRES Science Gateway web server (RAxML-HPC2 on XSEDE 8.2.10) with 1000 bootstrap replicates and settings as described by Stamatakis et al. (2008). The result showed that *P. imbricata* is mostly distinguished from *Pleione* species (Figure 1). This newly reported cp genome will be helpful for further phylogenetic study, species identification, and genetic engineering.

Disclosure statement

No potential conflict of interest was reported by the authors.

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