

## Complete chloroplast genome sequence of *Petrocodon jingxiensis* (Gesneriaceae)

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### ABSTRACT

The complete chloroplast genome of *Petrocodon jingxiensis* (Yan Liu, H.S. Gao, and W.B. Xu) A. Weber and Mich. Möller was determined in this study. The cp genome was 153,056 bp in length including two inverted repeats (IRs) of 25,405 bp, which were separated by LSC and SSC of 84,154 bp and 18,092 bp, respectively. The GC content was 41.9%. The genome encoded 112 functional genes, including 79 protein-coding genes, 29 tRNA genes, and four rRNA genes. This plastid genome is the first report for the *Petrocodon* in Gesneriaceae which will be useful data for developing markers for further studies on resolving the relationship within the genus.

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*Petrocodon* Hance (Gesneriaceae), is a small genus growing in mountainous karst habitats of S China, N Vietnam and NE Thailand (Hance 1883; Wang et al. 1998; Li and Wang 2004; Wei et al. 2010). Based on the latest molecular phylogenetic analyses, *Petrocodon* has been expanded to now include more than 30 species (Wang et al. 2011; Weber et al. 2011; Möller et al. 2016; IPNI 2019), and include all species previously referred to the genera *Calcareaoboea* C. Y. Wu ex H. W. Li, *Paralagarosolen* Y. G. Wei, *Dolicholoma* D. Fang and W. T. Wang, *Tengia* Chun, and *Lagarosolen* W. T. Wang, and four species from *Didymocarpus* Wall., one species from *Wentsaiboea* D. Fang and D. H. Qin and one species from *Primulina* Hance (Weber et al. 2011). Despite Möller et al. (2016) reconstructed the phylogenetic relationship of Gesneriaceae, the relationships within *Petrocodon* still remain poorly resolved.

The DNA sequence of the chloroplast genome can be used as a super barcode or a resource for research in phylogeography, genetic diversity and evolution. For *Petrocodon*, however, no complete chloroplast sequence has been published to date.

In the present study, mature and healthy leaves of *Petrocodon jingxiensis* were collected from natural population in Jingxi County, Baise City, Guangxi, China (N 106°21'24", E 23°1'32") and immediately dried by silica gel for DNA extraction. Voucher specimen (WF046) of this collection was deposited at IBK. The total genomic DNA was extracted using the CTAB method (Doyle and Doyle 1987) with minor modification and we sequenced the complete chloroplast genome of *Petrocodon jingxiensis* with Illumina HiSeq 4000 sequencing platform (Novogene, <http://www.novogene.com>, Beijing,

China). We used Map to Reference function in Geneious R11 (Kearse et al. 2012) to exclude nuclear and mitochondrial reads using published plastid genome of *Primulina huajieensis* (MF472012) as reference. The cp genome was manually adjusted to remove ambiguous sites. The annotation process was performed following Liu et al. (2018) using *Primulina huajieensis* (MF472012) as the reference. The complete chloroplast genome of *Petrocodon jingxiensis* was 153,056 bp in length (MK887172), the GC content was 41.9%. LSC and SSC contained 84,154 bp and 18,092 bp respectively, while IR was 25,405 bp in length. The plastid genome encoded 112 functional genes, including 79 protein-coding genes, 29 tRNA genes, and four rRNA genes.

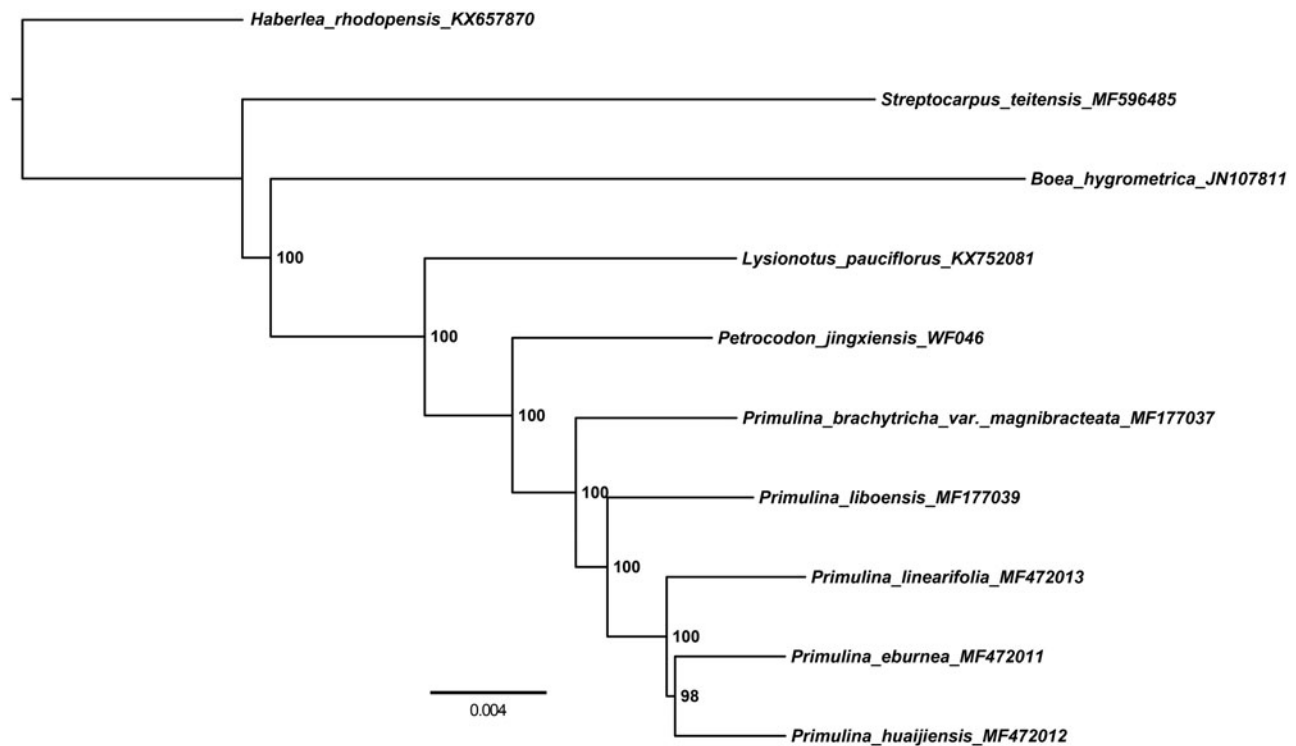
The maximum likelihood phylogenetic analysis of 10 chloroplast genomes showed that *Petrocodon jingxiensis* was most closely related to the members of *Primulina* (Figure 1). The newly characterized cp genome of *Petrocodon jingxiensis* will provide essential data for further study on the phylogeny and evolution of the genus *Petrocodon* and of the family Gesneriaceae.

### Disclosure statement

No potential conflict of interest was reported by the authors.

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**Figure 1.** Phylogenetic tree reconstructed by maximum-likelihood (ML) analysis based on chloroplast genome sequences from 10 species of Gesneriaceae, numbers next to nodes are assessed by ML bootstrap.

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