

MITOGENOME ANNOUNCEMENT



The complete chloroplast genome sequence of *Phlegmariurus carinatus*

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ABSTRACT

The first complete chloroplast genome (cpDNA) sequence of *Phlegmariurus carinatus* was determined from Illumina HiSeq pair-end sequencing data in this study. The cpDNA is 150,349 bp in length, contains a large single-copy region (LSC) of 100,582 bp and a small single-copy region (SSC) of 19,455 bp, which were separated by a pair of inverted repeat (IR) regions of 15,156 bp. The genome contains 120 genes, including 79 protein-coding genes, 8 ribosomal RNA genes, and 33 transfer RNA genes. The overall GC content of the whole genome is 34.0%, and the corresponding values of the LSC, SSC, and IR regions are 31.6%, 30.4%, and 44.2%, respectively. Further phylogenomic analysis showed that *P. carinatus* and *Huperzia serrata* clustered in a clade in family Lycopodiaceae.

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Phlegmariurus carinatus (Desv.) Ching [synonymous with *Lycopodium carinatum* Desv. ex Poir.] is a representative species of the *Phlegmariurus* genus within Huperzioidae in the family of Lycopodiaceae (Zhang and Kong 2000). *P. carinatus* was used as a traditional herbal medicine in China for long time (Liu et al. 2014). It has significant curative effect on rheumatoid arthritis, rheumatoid arthritis, muscle and bone pain (Zhang et al. 2016). It contains lycopodium alkaloids, triterpenes, phenolic acids, and flavones (Kogure et al. 2016). Therefore, *P. carinatus* has valuable for pharmaceutical applications (Luo et al. 2010). However, there have been no genomic studies on *P. carinatus*.

Herein, we reported and characterized the complete *P. carinatus* plastid genome (MN566837). One *P. carinatus* individual (specimen number: 5309270453) was collected from Cangyuan, Yunnan Province of China (23°16'17"N, 99°1'15"E). The specimen is stored at Yunnan Academy of Forestry Herbarium, Kunming, China and the accession number is YAFM20180401. DNA was extracted from its fresh leaves using DNA Plantzol Reagent (Invitrogen, Carlsbad, CA, USA).

Paired-end reads were sequenced by using Illumina HiSeq system (Illumina, San Diego, CA, USA). In total, about 21.1 million high-quality clean reads were generated with adaptors trimmed. Aligning, assembly, and annotation were conducted by CLC de novo assembler (CLC Bio, Aarhus,

Denmark), BLAST, GeSeq (Tillich et al. 2017), and GENEIOUS v 11.0.5 (Biomatters Ltd., Auckland, New Zealand). To confirm the phylogenetic position of *P. carinatus*, the other four species of family Lycopodiaceae from NCBI were aligned using MAFFT v.7 (Katoh and Standley 2013) and maximum likelihood (ML) bootstrap analysis was conducted using RAxML (Stamatakis 2006); bootstrap probability values were calculated from 1000 replicates. *Isoetes yunguiensis* (MK047605) and *Isoetes malinverniana* (MH549640) were served as the out-group.

The complete *P. carinatus* plastid genome is a circular DNA molecule with the length of 150,349 bp, contains a large single-copy region (LSC) of 100,582 bp and a small single-copy region (SSC) of 19,455 bp, which were separated by a pair of inverted repeat (IR) regions of 15,156 bp. The overall GC content of the whole genome is 34.0%, and the corresponding values of the LSC, SSC, and IR regions are 31.6%, 30.4%, and 44.2%, respectively. The plastid genome contained 120 genes, including 79 protein-coding genes, 8 ribosomal RNA genes, and 33 transfer RNA genes. Phylogenetic analysis showed that *P. carinatus* and *Huperzia serrata* clustered in a unique clade in family Lycopodiaceae (Figure 1). The determination of the complete plastid genome sequences provided new molecular data to illuminate the Lycopodiaceae evolution.

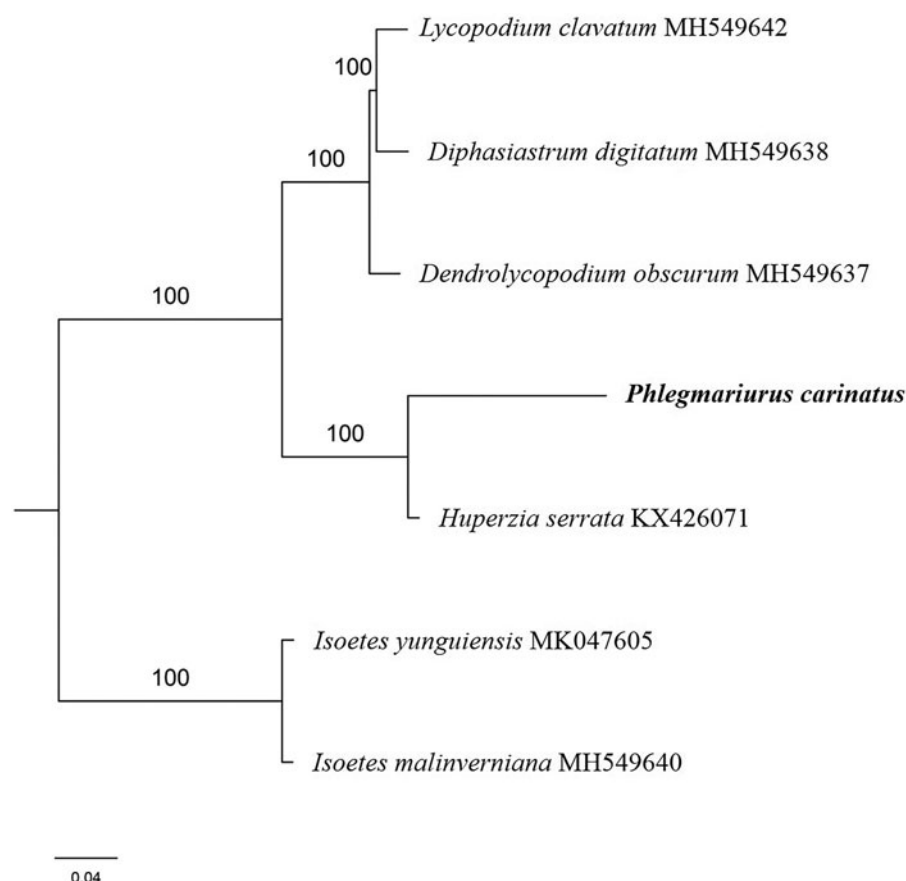


Figure 1. The maximum-likelihood tree based on the five chloroplast genomes of *Lycopodiaceae*. The bootstrap value based on 1000 replicates is shown on each node.

Disclosure statement

No potential conflict of interest was reported by the authors.

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