

MITOGENOME ANNOUNCEMENT



The complete chloroplast genome sequence of *Horsfieldia kingii* (Myristicaceae)

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ABSTRACT

Horsfieldia kingii is a member of Myristicaceae. The *H. kingii* chloroplast genome is found to be 155,655 bp in length and has a base composition of A (30.03%), G (19.52%), C (19.72%), and T (30.73%). The genome contained two short inverted repeat (IRa and IRb) regions (48,052 bp) which were separated by a large single copy (LSC) region (86,912 bp) and a small single copy (SSC) region (20,691 bp). The genome encodes 123 unique genes, including 85 protein-coding genes, 27 transfer RNA (tRNA) genes, and 8 ribosomal RNA (rRNA) genes. Further, complete chloroplast sequence of *H. kingii* was aligned together with other 2 species of Myristicaceae and other 5 basal angiosperms species which have reported the complete chloroplast sequence. This complete chloroplast genome will provide valuable information for the development of DNA markers for future species resource development and phylogenetic analysis of *H. kingii*.

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KEYWORDS

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Genus *Horsfieldia*, belonging to Myristicaceae, include about 5 genera (Editorial Committee of Chinese Academy of Sciences Flora 1979). For this genus, it is mainly studied on species classification (Wu et al. 2015), fatty acid ingredients (Xue and Fang 2012; Hu et al. 2010; Peng 2017), seed propagation (Hu et al. 2011), leaf traits variation (Hu et al. 2017), and rarely reported in molecular biology. *Horsfieldia kingii* is a species of genus *Horsfieldia*, it is mainly reported in chemical composition (Liu, Chen, et al. 2019; Liu, Du, et al. 2019), chlorophyll contents (Yang et al. 2018), but there is no reported in molecular biology else. In this study, we characterized the complete chloroplast genome sequence of *H. kingii* for phylogenetic analysis. The annotated genome sequence has been deposited Genbank under the accession number MK285562.

The fresh leaves of *H. kingii* was collected in 2017 from plantation base of Yunnan Institute of Tropical Crops (YITC), Jinghong, China (10°47'E, 22°00'N), and its genome DNA was extracted using the DNeasy Plant Mini Kit (QIAGEN, Valencia, CA), the remaining DNA was stored in an ultra-low temperature freezer. A specimen of this tree was conserved in YITC and the number of voucher specimen is 20140434. Genome sequencing was performed using Roche/454, sequencing libraries were prepared by the GS Titanium library preparation kit. The chloroplast genome assembled using CLC Genomic Workbench v3.6 (<http://www.clcbio.com>). The genes in the chloroplast genome were predicted using the DOGMA program (Wyman et al. 2004).

The circular genome is 155,655 bp in size, and comprises a large single copy (LSC) region (86,912 bp), a small single copy (SSC) region (20,691 bp), and two short inverted repeat (IRa and IRb) regions (48,052 bp). The base composition of the circular chloroplast genome is A (30.03%), G (19.52%), C (19.72%), and T (30.73%). The GC content of whole *H. kingii* chloroplast genome was 39.24%. The *H. kingii* chloroplast genome encodes a total of 123 unique genes, including 85 protein-coding genes, 27 transfer RNA genes, and 8 ribosomal RNA genes. There were 43 genes duplicated in the IR regions. The LSC region contained 64 genes, which including 43 protein-coding genes, 18 tRNA genes, and 2 rRNA genes, whereas 12 protein-coding genes and 2 tRNA gene were included in the SSC region. The introns were detected in 10 genes, *psbB*, *rpoB*, *rps7*, *atpH*, *ndhI*, *rpl23*, *rps19-fragment*, *trnQ-UUG*, *trnS-GGA*, *trnL-CAA* and they all have 1 intron.

To study *H. kingii* phylogenetic relationship with the angiosperms, *Horsfieldia pandurifolia*, *Myristica yunnanensis* of Myristicaceae (Changli, Fenglian, Tian et al. 2019; Changli, Fenglian, Xiaoqin et al. 2019) and other complete chloroplast genome sequences of angiosperms were download for analyses. The maximum likelihood phylogenetic was performed using MEGA X (Kumar et al. 2018) (Figure 1). A bootstrap analysis was performed on the resulting phylogenetic tree, and values were obtained after 1000 replications. The result shows that *H. kingii* was clustered with other species and closely to *Horsfieldia pandurifolia* and *Myristica yunnanensis* chloroplast complete genome.

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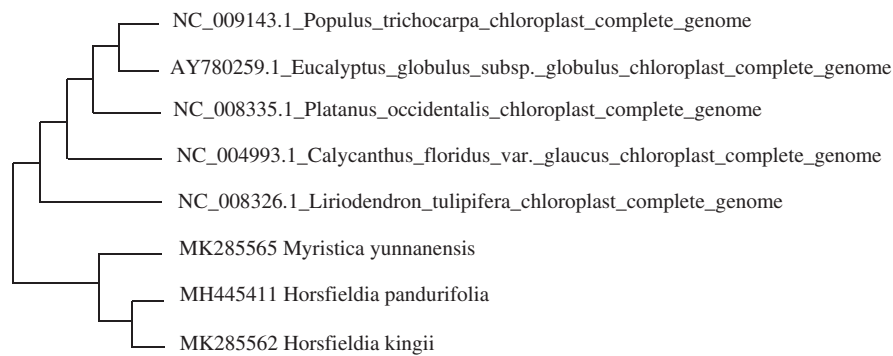


Figure 1. Maximum-likelihood phylogenetic tree of *H. kingii* with 7 species based on complete chloroplast genome sequences. The gene's accession number is list in figure and the data of *H. pandurifolia* and *M. yunnanensis* come from author.

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of this article.

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References

- Changli M, Fenglian Z, Tian Y, Xiaoqin L, Yu W. 2019. The complete chloroplast genome sequence of *Myristica yunnanensis* (Myristicaceae). Mitochondrial DNA B Res. 4:1871–1872.
- Changli M, Fenglian Z, Xiaoqin L, Tian Y, Jin L, Yu W. 2019. The complete chloroplast genome sequence of *Horsfieldia pandurifolia* (Myristicaceae). Mitochondrial DNA B Res. 4:949–950.
- Editorial Committee of Chinese Academy of Sciences Flora. 1979. Floral reipublicae popularis sinicae. Vol. 30(2). Beijing: Science Press.
- Hu YH, Wu Y, Mao CL, Zhang JH, Duan AA. 2011. Testing for seed propagation of oil tree *Horsfieldia amygdalina*. Trop Agric Sci Technol. 34(02):26–27. +34.
- Hu YH, Wu Y, Xu YL, Zhang JH, Duan AA. 2010. Fatty acids components of seed oil in *Horsfieldia amygdalina*. Trop Agric Sci Technol. 33(04): 27–28.
- Hu YH, Yang XL, Li XQ, Zhang FL, Mao CL, Yang T, Zhang H, Wu Y. 2017. Variation analysis on leaf traits of *Horsfieldia amygdalina*. Trop Agric Sci Technol. 40(1):28–32.
- Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. Mol Biol Evol. 35(6):1547–1549.
- Liu B, Chen YG, Tian XJ, Zhan R. 2019. Diarylpropanes from *Horsfieldia kingie*. Nat Prod Res. 19:1–7.
- Liu B, Du SZ, Kuang F, Liu Y, Tian XJ, Chen YG, Zhan R. 2019. Two new lignans from *Horsfieldia kingie*. Nat Prod Res. 33(1):95–100.
- Peng W. 2017. Studies on the chemical constituents of *Horsfieldia glabra*. Yunnan: Yunnan Normal University.
- Wu Y, Mao CL, Zhang FL, Yang XL, Zeng JS, Duan AA. 2015. Taxonomic position of *Horsfieldia pandurifolia* Hu (Myristicaceae). Bull Bot Res. 35: 652–659.
- Wyman SK, Jansen RK, Boore JL. 2004. Automatic annotation of organellar genomes with DOGMA. Bioinformatics. 20(17):3252–3255.
- Xue BZ, Fang Z. 2012. Extraction of *Horsfieldia amygdalina* seed oil and analysis of its fatty acids. Nat Prod Res Dev. 24(S1):110–113.
- Yang XL, Hu YH, Li XQ, Zhang FL, Mao CL, Yang T, Zhao Q, Zhang H, Wu Y. 2018. Comparative analysis for chlorophyll contents of *Horsfieldia amygdalina* and *Horsfieldia kingie*. Agric Sci Technol. 41(02):37–42.