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MITOGENOME ANNOUNCEMENT

Characterization of the complete chloroplast genome of *Handroanthus chrysanthus* (Bignoniaceae)

Hong-Ze Liao[a,b], Man-Man Sun[a], Hao Zhou[a] and Xiu Liu[b]

[a]Key Laboratory of Protection and Utilization of Marine Resources, Guangxi Minzu University, Nanning, China; [b]Guangxi Key Laboratory of Special Non-wood Forest Cultivation and Utilization, Guangxi Forestry Research Institute, Nanning, China

ABSTRACT

Handroanthus chrysanthus is a deciduous broadleaved species with ecological and medicinal value. Here, the complete chloroplast genome of *H. chrysanthus* is characterized to investigate its phylogenetic position in Bignoniaceae. The chloroplast genome is 159,437 bp in size with GC content of 38.1%, including a large single copy region of 85,659 bp, a small single copy region of 12,824 bp and a pair of inverted repeats of 30,477 bp. It encodes 132 genes, including 87 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. Based on current available chloroplast genome sequences, the phylogenetic analysis indicated that *H. chrysanthus* is closely related to *Tabebuia nodosa*.

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Handroanthus chrysanthus (Jacq.) S. O. Grose (synonym *Tabebuia chrysantha* (Jacq.) G. Nicholson, 1877) is the species of the genus *Handroanthus* within the family Bignoniaceae (Grose and Olmstead 2007). As a deciduous broadleaved tree with brilliant yellow flowers, it is widely used in gardening in tropical and subtropical areas, and its stem extract possesses antimicrobial, anti-inflammatory and anticancer properties (Panda et al. 2019). In this study, we described and characterized the complete chloroplast genome of *H. chrysanthus* to better understand its genomic structure and phylogenetic relationship in Bignoniaceae.

The fresh leaves of *H. chrysanthus* were collected from Guangxi Forestry Research Institute, Nanning, China (N22.92°, E108.35°), and the specimens were conserved in Guangxi Minzu University (Hao Zhou, zhou.hao.gxun@foxmail.com) under the voucher number LCY20190606. The total genomic DNA was extracted following a modified CTAB protocol (Allen et al. 2006) and sequenced using NovaSeq 6000 system (Illumina, San Diego, CA, USA). In total, about 4.4 Gb of raw reads with 14,491,668 clean paired-end reads were generated. The chloroplast genome was assembled using SPAdes v3.13.1 (http://cab.spbu.ru/software/spades/) (Bankevich et al. 2012) and annotated with PGA software (https://github.com/quxiaojian/PGA) (Qu et al. 2019), then deposited into GenBank under the accession number ON243876.

The chloroplast genome of *H. chrysanthus* is 159,437 bp in length, with an overall GC content of 38.1%. It comprises a large single copy region of 85,659 bp and a small single copy region of 12,824 bp, which were separated by a pair of inverted repeats of 30,477 bp. A total of 132 genes were predicted, including 87 protein-coding genes, 37 tRNA genes, and 8 rRNA genes.

There was only one complete chloroplast genome of *Handroanthus* species (*Handroanthus impetiginosus*) well-characterized before (Sobreiro et al. 2020), and it might share a close relationship with *H. chrysanthus*. Unfortunately, the chloroplast genome sequence of *H. impetiginosus* was unavailable in public database. To reveal the phylogenetic position of *H. chrysanthus*, the complete chloroplast genomes of 16 other species from Bignoniaceae and one species (*Aloysia citrodora*) from Verbenaceae served as an outgroup were introduced for phylogenetic analysis. The sequences were aligned by MAFFT v7.490 (https://mafft.cbrc.jp/alignment/software/) (Katoh and Standley 2016) and a maximum-likelihood tree was constructed by IQ-TREE 2 (http://www.iqtree.org) using the TVM + F + I + G4 model with 1000 bootstrap replications (Minh et al. 2020). Based on current available chloroplast genome sequences, the phylogenetic analysis showed that *H. chrysanthus* was closest to *Tabebuia nodosa* (Figure 1).

Author contributions

X. L. and H. Z. L. conceived and designed the experiments; H. Z. L., M. M. S., and H. Z. performed the experiments and analyzed the data; H.Z.L. and X. L. wrote the paper. All authors have read and approved the final manuscript to be

CONTACT Xiu Liu xiuliu1010@126.com Guangxi Key Laboratory of Special Non-wood Forest Cultivation and Utilization, Guangxi Forestry Research Institute, Nanning, China

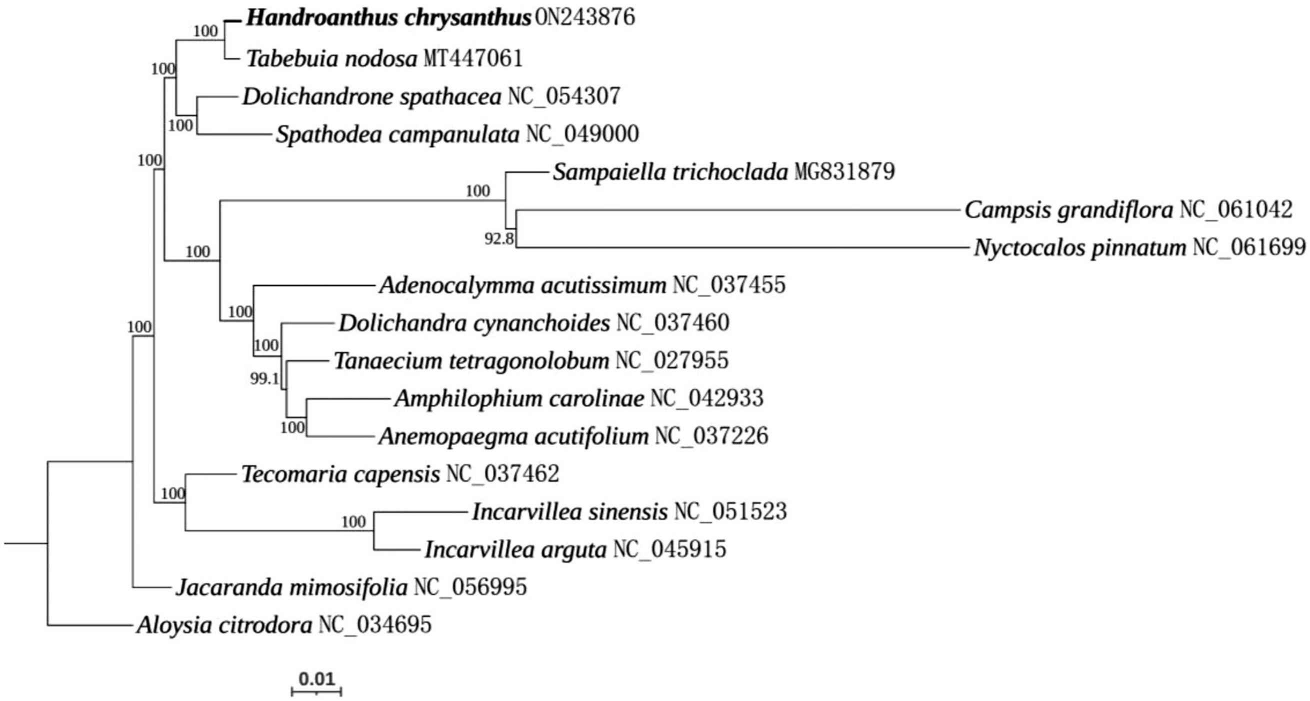

Figure 1. The maximum-likelihood phylogenetic tree based on the 16 chloroplast genomes of Bignoniaceae. *Aloysia citrodora* (Verbenaceae) served as an outgroup.

published, and agree to be accountable for all aspects of the work.

Disclosure statement

No potential conflict of interest was reported by the author(s).

Data availability statement

The data support the findings of this study are openly available in NCBI GenBank (https://www.ncbi.nlm.nih.gov) under the accession number ON243876. The associated BioProject, SRA, and Bio-Sample numbers of the raw sequencing data of *Handroanthus chrysanthus* are PRJNA826917, SRR18765829, and SAMN27591411, respectively.

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ORCID

Hong-Ze Liao http://orcid.org/0000-0002-3546-3713

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