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PLASTOME REPORT

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The complete chloroplast genome of *Tabebuia rosea* (Bignoniaceae)

Guihong Xu, Wei Zeng, Xiaofeng Zhang, Jiayu Hu and Jiangli Lei

Key Laboratory of Southern Subtropical Plant Diversity, Fairy Lake Botanical Garden, Shenzhen, China

ABSTRACT

Tabebuia rosea is a world-renowned woody plant with colorful flowers in full bloom. In addition to its high ornamental value, it also has ecological and medicinal value. In this study, the complete circular chloroplast genome of *T. rosea* was reconstructed and annotated using Illumina sequencing. The chloroplast genome was 158,919 bp in size with GC content of 38.21%, including a large single-copy region of 85,823 bp, a small single-copy region of 12,816 bp, and a pair of inverted repeats of 30,140 bp. It encoded 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 *T. rosea* was clustered with *T. nodosa* and *H. chrysanthus*. This study provided insights into the evolutionary relationships among different species of Bignoniaceae.

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Chloroplast genome; *Tabebuia rosea*; Bignoniaceae; Phylogenetic analysis

Introduction

Tabebuia rosea is a species of the genus *Tabebuia* within the family Bignoniaceae (Grose and Olmstead 2007). It is native to America distributed from Brazil to Mexico, including Central America and the Antilles. *T. rosea* is found in commercial plantations mainly for high quality timber production and in urban and peri-urban plantations due to its colorful blossoms and ecosystemic services (Ruiz-González et al. 2023). *T. rosea* is widely cultivated in southern China due to its high ornamental value (Meng et al. 2023). *T. rosea* seed oil is a satisfactory feedstock for biodiesel production (Sirigeri et al. 2019). In addition, the seeds or bark have medicinal value because of the antibacterial, antioxidant, and antiproliferative activities of their extracts (Devika et al. 2022; Muruganandham et al. 2023).

To our knowledge, the complete chloroplast genome of Handroanthus species (*Handroanthus impetiginosus, Handroanthus chrysanthus*) and Tabebuia species (*T. nodosa*) have been characterized (Fonseca and Lohmann 2020; Sobreiro et al. 2020; Liao et al. 2022). However, the complete chloroplast sequence of *T. rosea* and its phylogenetic position in Bignoniaceae are still unknow. Therefore, in this study, the whole-genome information of *T. rosea* chloroplast was measured by Illumina sequencing. Using bioinformatics software, we also analyzed the sequence characteristics, gene composition, and phylogenetic relationship of this species.

Materials and methods

The fresh leaves of *T. rosea* were collected from a natural population (Figure 1) situated in Luohu District, Shenzhen,

Figure 1. *Tabebuia rosea* plant and its inflorescence. The photo was taken by Guihong Xu in Fairy Lake Botanical Garden, Shenzhen, China. Tree. Flowers bisexual, racemose inflorescence. The calyx is tubular and bell shaped, with a shallow slit at the tip and no hair on the surface.

CONTACT Guihong Xu xuguihong1985@outlook.com; Jiangli Lei wy521lxw@163.com Key Laboratory of Southern Subtropical Plant Diversity, Fairy Lake Botanical Garden, Shenzhen, China

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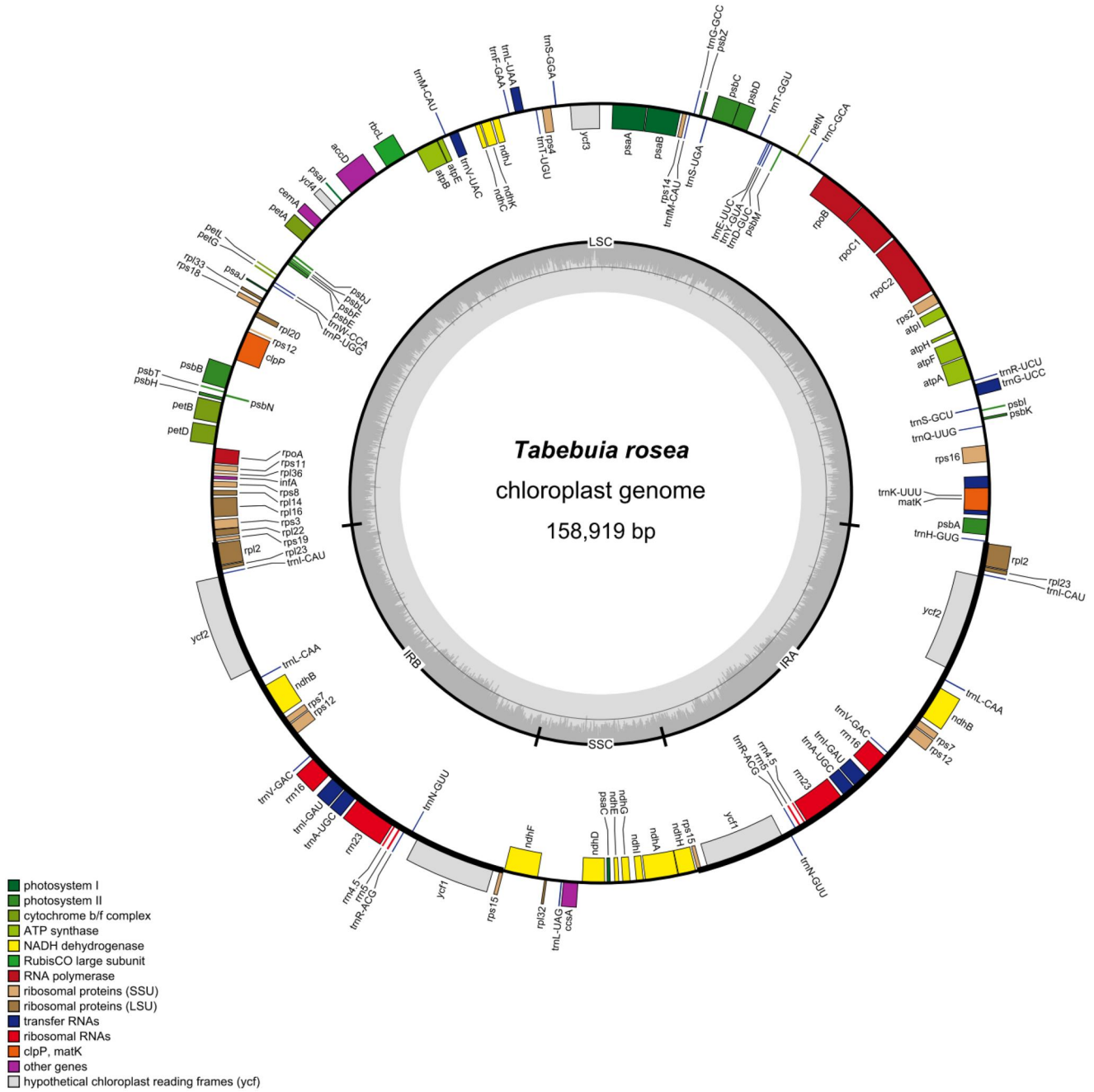

Figure 2. Circular map of the *Tabebuia rosea* chloroplast genome. Genes shown inside the circle are transcribed clockwise, those outside the circle are counterclockwise transcribed. The light grey and the darker grey in the inner circle represent at and GC content, respectively. Different functional groups of genes are signed according to the colored boxes. LSC: large single copy; SSC: small single copy; IRA/IRB: Inverted repeat regions.

China (coordinates N 22.5864, E 114.1738). A voucher specimen with the collection number SZG20240606 has been stored at the Herbarium of the Fairy Lake Botanical Garden (contact person: Wei Zeng, wuhuanzi@126.com).

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, approximately 6.21 Gb of raw reads and 6.17 Gb of clean paired-end reads were generated. The complete chloroplast genome was *de novo* assembled using SPAdes v3.14.1 (http://cab.spbu.ru/software/spades/) (Bankevich et al. 2012) and annotated with PGA software (https://github.com/quxiaojian/PGA) (Qu et al. 2019) based on chloroplast genome of *Chilopsis linearis* (MW148797), then deposited into GenBank under the accession number PP706415.

To infer the phylogenetic placement of *T. rosea* within the Bignoniaceae (Tubiflorae), 54 common protein-coding genes (Supplementary Table 1) in each complete cp genome of 28 species were aligned with the genes in *T. rosea* using MAFFT 7.037 (Katoh and Standley 2016) with the FFT-NS-2 strategy. *Verbena officinalis* in Verbenaceae (Tubiflorae) was selected as outgroups. Finally, iqtree 2.0 was used to construct a

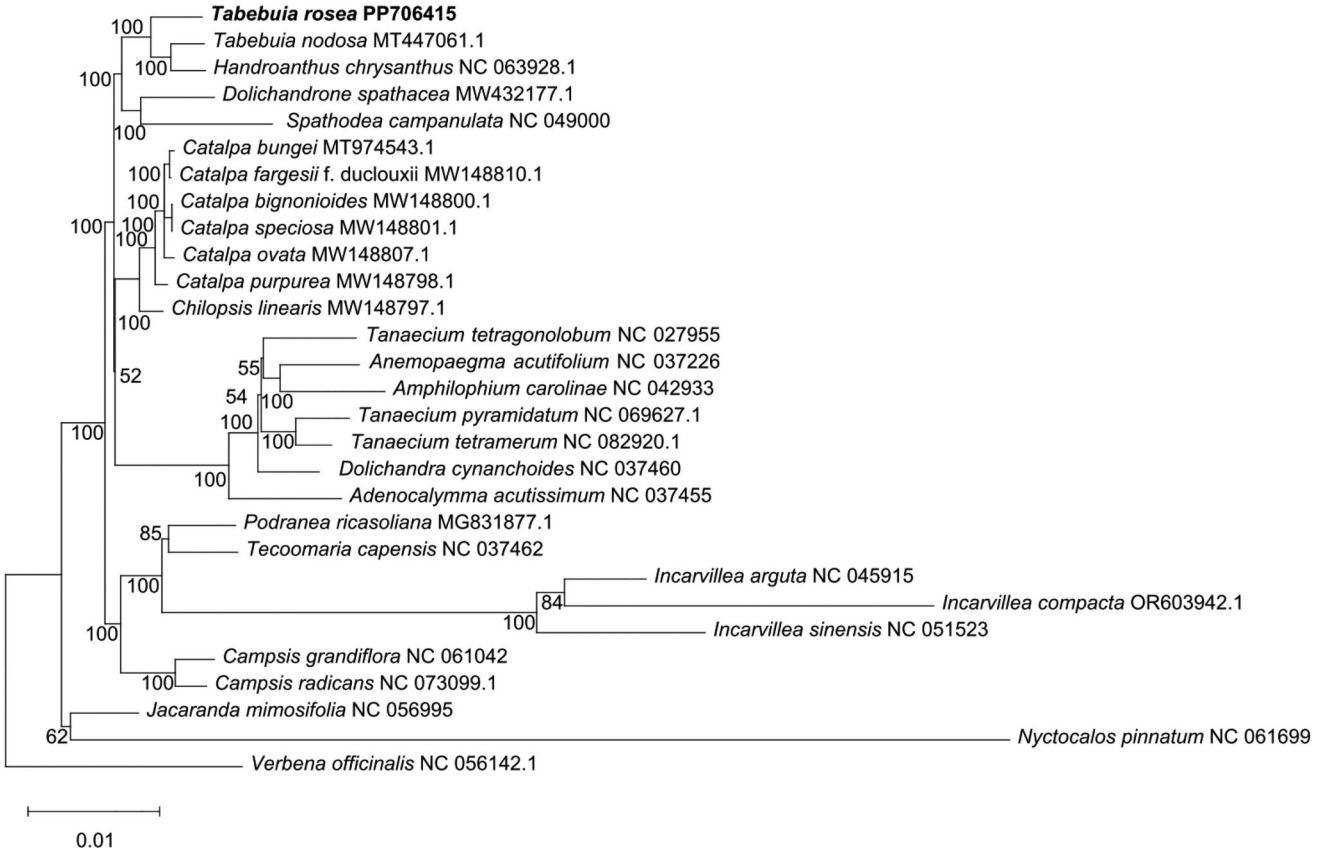

Figure 3. Phylogenetic tree of *Tabebuia rosea* and 28 species in the order Lamiales using maximum likelihood (ML) analyses based on 54 common protein-coding genes in the complete chloroplast genome sequences. *Verbena officinalis* in Verbenaceae (Tubiflorae) was selected as outgroups. The numbers at nodes of the phylogenetic tree show the bootstrap support values. GenBank accession numbers: *Handroanthus chrysanthus* NC 063928.1 (Liao et al. 2022), *Tabebuia nodosa* MT447061.1 (Fonseca and Lohmann 2020), *Podranea ricasoliana* MG831877.1 (Fonseca and Lohmann 2018), *Dolichandrone spathacea* MW432177.1 (Yu et al. 2021), *Spathodea campanulata* NC 049000 (Wang et al. 2019), *Campsis grandiflora* NC 061042 (Chen et al. 2022), *Nyctocalos pinnatum* NC 061699 (Fan et al. 2022), *Adenocalymma acutissimum* NC 037455 (Fonseca and Lohmann 2018), *Dolichandra cynanchoides* NC 037460 (Fonseca and Lohmann 2018), *Tanaecium tetramerum* NC 082920.1 (Frazão et al. 2023), *Tanaecium tetragonolobum* NC 027955 (Nazareno et al. 2015), *Amphilophium carolinae* NC 042933 (Thode and Lohmann 2019), *Anemopaegma acutifolium* NC 037226 (Firetti et al. 2017), *Amphilophium carolinae* NC 042933 (Thode and Lohmann 2019), *Tecoomaria capensis* NC 037462 (Fonseca and Lohmann 2018), *Incarvillea sinensis* NC 037462 (Wu et al. 2021), *Incarvillea arguta* NC 045915 (Ma et al. 2019), *Jacaranda mimosifolia* NC 056995 (Zhao et al. 2019), *Incarvillea compacta* OR603942.1 (Wu et al. 2019), *Campsis radicans* NC 073099.1 (Li et al. 2023), *Tanaecium pyramidatum* NC 069627.1 (Frazão et al. 2023), *Chilopsis linearis* MW148797.1 (Dong et al. 2022), *Catalpa purpurea* MW148798.1 (Dong et al. 2022), *Catalpa speciosa* MW148801.1 (Dong et al. 2022), *Catalpa bignonioides* MW148800.1 (Dong et al. 2022), *Catalpa fargesii* MW148810.1 (Dong et al. 2022), *Catalpa bungei* MT974543.1 (Yang et al. 2020), *Catalpa ovata* MW148807.1 (Dong et al. 2022), *Verbena officinalis* NC 056142.1 (Yue et al. 2021).

phylogenetic tree with 1,000 bootstraps based on the ML method (Minh et al. 2020). Iqtree 2.0 is based on an internal model selector, and the best model to select is TVM+F + I + G4.

Results

The minimum and average read mapping depths were 496× and 7987×, respectively (Supplementary Figure 1). The chloroplast genome of *T. rosea* exhibited a typical quadripartite structure, which was 158,919 bp in length. The chloroplast genome consisted of a pair of inverted repeat (IR) regions of 30,140 bp that separated the large single-copy (LSC) region (85,823 bp) and the small single-copy (SSC) region (12,816 bp) (Figure 2). A total of 132 genes were annotated, including 87 protein-coding, 37 transfer RNA, and 8 ribosomal RNA genes. Among the CDS genes, 17 were cis splicing, of which 15 genes (*trn*K-UUU, *rps*16, *trn*G-UCC, *atp*F, *rpo*C1, *trn*L-UAA, *trn*V-UAC, *pet*B, *pet*D, *rpl*16, *rpl*2, *ndh*B, *trn*I-GAU, *trn*A-UGC, *ndh*A) contain one intron, while *clp*P, *ycf*3 have two introns. The placement of the exon regions of the trans-splicing gene, *rps*12, was also identified (Supplementary Table 2; Supplementary Figure 2-3). The total GC content of the chloroplast genome was 38.21%. In this study, the phylogenetic relationship was determined using 54 common protein-coding genes within the complete chloroplast genome sequence, based on the 29 taxa were well resolved, the bootstrap support value, which this paper care about, was greater than 80%. *T. rosea* was clustered with the other two species of *T. nodosa* and *H. chrysanthus* (Figure 3).

Discussion and conclusion

The intracellular organelle chloroplast has its own genome, which encodes a number of chloroplast-specific components (Tang et al. 2004). The size of chloroplast circular genome varies from 39.4 to 200.8 kb among photosynthetic plant species (Köhler et al. 1997). The chloroplast genome of *T. rosea*

was 158,919 bp in size with GC content of 38.21%, including a large single-copy region of 85,823 bp, a small single-copy region of 12,816 bp and a pair of inverted repeats of 30,140 bp (Figure 2). The genome structure and gene content of the complete chloroplast genome of *T. rosea* are similar to those of *T. nodosa* (Fonseca and Lohmann 2020), *H. impetiginosus* (Sobreiro et al. 2020), and *H. chrysanthus* (Liao et al. 2022), suggesting that the chloroplast genome of Bignoniaceae could be highly conserved.

Bignoniaceae is one of the most species rich family of woody plants in Neotropical seasonally dry forests (Sobreiro et al. 2020). The phylogenetic analysis indicated that *Tabebuia nodosa* is strongly supported as sister to a clade composed of *Handroanthus umbellatus* and *Crescentia cujete* (Fonseca and Lohmann 2020), and *H. chrysanthus* is closely related to *Tabebuia nodosa* (Liao et al. 2022). To infer the phylogenetic placement of *T. rosea* within the Bignoniaceae, Here we reported the evolutionary comparative analyses of 28 Bignoniaceae species representing the genera for which whole-genome chloroplast sequences were available. *T. rosea* was supported as sister to a clade composed of two Bignoniaceae species: *T. nodosa* and *H. chrysanthus* (Figure 3).

To better understand its phylogenetic relationships, additional chloroplast genomes from the littoral Bignoniaceae clade are urgently needed. This study has contributed to the enlargement of the chloroplast genome database for Bignoniaceae and has provided valuable insights into the evolutionary relationships among various Bignoniaceae species.

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Author contributions

Guihong Xu and Jiangli Lei conceived the study. Guihong Xu, Wei Zeng, and Xiaofeng Zhang collected the sample. Wei Zeng and Jiayu Hu conducted the molecular experiment and analyzed the data. Guihong Xu, Wei Zeng, and Jiangli Lei wrote the paper. All authors have approved the final version of this manuscript.

Ethical approval

This study includes no human, animal, or endangered plant species, and the sampling site was not in the natural reserve. No permissions are needed during the collection of plant material.

Disclosure statement

No potential conflict of interest was reported by the authors.

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Data availability statement

The chloroplast genome assembly of *T. rosea* was deposited into the NCBI GenBank database with accession number PP706415. The associated BioProject, Bio-Sample, and SRA numbers are PRJNA1105126, SAMN41096169, and SRR28816935, respectively.

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