

## Complete plastome sequence of *Torenia benthamiana* Hance (Linderniaceae), an endemic herb in South China

Xia-Lan Cheng<sup>a</sup>, Yi-Ming Liu<sup>b</sup>, Hong-Xin Wang<sup>c</sup>, Hai-Li Li<sup>a</sup>, Yan Chen<sup>a</sup> and Li-Yun Wang<sup>a</sup>

<sup>a</sup>School of Life Science and Technology, Lingnan Normal University, Zhanjiang, Guangdong, China; <sup>b</sup>Administrative Bureau of Guangdong, Zhanjiang Mangrove National Nature Reserve, Zhanjiang, Guangdong, China; <sup>c</sup>Institute Arts, Sanya University, Sanya, Hainan, China

### ABSTRACT

*Torenia benthamiana* Hance is an endemic plant species distributed in southern China. In this study, we report and characterize the complete plastid genome sequence of *T. benthamiana* in order to provide genomic resources helpful for promoting its conservation and garden utilization. The complete plastome is 153,526 bp in length and contains the typical quadripartite structure of angiosperm plastome, including two inverted repeat (IR) regions of 24,638 bp, a large single-copy (LSC) region of 85,417 bp, and a small single-copy (SSC) region of 18,833 bp. The plastome contains 114 genes, consisting of 80 unique protein-coding genes, 30 unique tRNA gene, and 4 unique rRNA genes. The overall A/T content in the plastome of *T. benthamiana* is 62.40%. The complete plastome sequence of *T. benthamiana* will provide a useful resource for the conservation and garden utilization of this species as well as for the phylogenetic studies of Linderniaceae.

### ARTICLE HISTORY

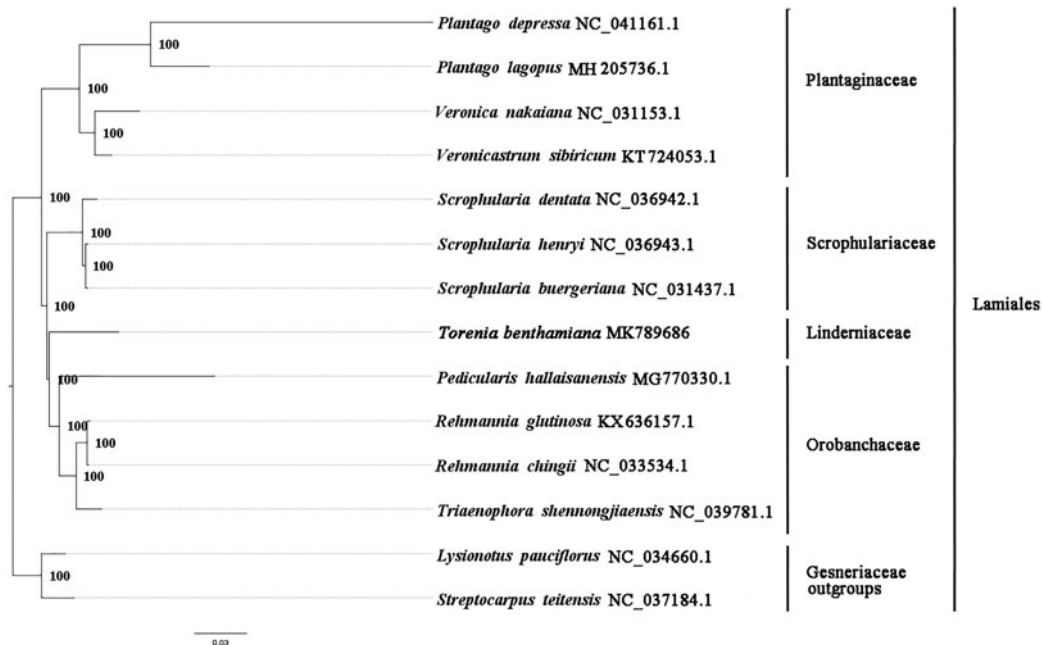
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### KEYWORDS

*Torenia benthamiana* Hance; plastome; phylogeny; genome structure; Linderniaceae

*Torenia benthamiana* Hance is a plant of family Linderniaceae. It is a creeping herb with showy purple flowers and distributed in southern China, including Fujian, Guangdong, Guangxi, Hainan, Taiwan (China ECoFo, 2013).

*Torenia benthamiana* could be used as ornamental plants due to its aesthetic value. So far, no studies on the genome of *T. benthamiana* have been published. Here, we determined the complete plastid genome sequence of *T. benthamiana*



**Figure 1.** The best ML phylogeny recovered from 14 complete plastome sequences by RAxML. Accession numbers: *Torenia benthamiana* MK789686, *Plantago depressa* NC\_041161.1, *Plantago lagopus* MH205736.1, *Veronica nakaiana* NC\_031153.1, *Veronicastrum sibiricum* KT724053.1, *Scrophularia dentata* NC\_036942.1, *Scrophularia henryi* NC\_036943.1, *Scrophularia buergeriana* NC\_031437.1, *Pedicularis hallaisanensis* MG770330.1, *Rehmannia glutinosa* KX636157.1, *Rehmannia chingii* NC\_033534.1, *Trienophora shennongjiaensis* NC\_039781.1, *Lysionotus pauciflorus* NC\_034660.1, *Streptocarpus teitensis* NC\_037184.1.

(GenBank accession number: MK789686) to provide genetic and genomic information to promote its systematics research and garden utilization.

In this study, *T. benthamiana* was sampled from Heishiyong, Gaozhou County, China (111°11'05"E, 21°56'36"N). A voucher specimen (LNH180702030) was deposited in the Herbarium of Lingnan Normal University, Zhanjiang, China.

The experiment procedure is as reported in Gao et al. (2017). Around 6Gb clean data were assembled against the plastome of *Trachelospermum asiaticum* (MG\_963252.1) using MITO bim v1.8 (Natural History Museum, University of Oslo, Oslo, Norway) (Hahn et al. 2013). The plastome was annotated using Geneious R8.0.2 (Biomatters Ltd., Auckland, New Zealand) against the plastome of *T. asiaticum* (MG\_963252.1). The annotation was corrected with DOGMA (Wyman et al. 2004).

The plastome of *T. benthamianas* was found to possess a total length 153,526 bp with the typical quadripartite structure of angiosperms, containing two inverted repeats (IRs) of 24,638 bp, a large single-copy (LSC) region of 85,417 bp, and a small single-copy (SSC) region of 18,833 bp. The plastome contains 114 genes, consisting of 80 unique protein-coding genes, 30 unique tRNA genes, and 4 unique rRNA genes. The overall A/T content in the plastome of *T. benthamianas* is 62.40%, for which the corresponding value of the LSC, SSC, and IR region were 64.50, 68.00, and 56.40%, respectively.

We used RAxML (Stamatakis 2006) with 1000 bootstraps under the GTRGAMMAI substitution model to reconstruct a maximum likelihood (ML) phylogeny of *T. benthamianas* and 13 published complete plastomes of Plantaginaceae, Scrophulariaceae, Orobanchaceae, Gesneriaceae, using

*Lysionotus pauciflorus* and *Streptocarpus teitensis* (Gesneriaceae) as outgroups. The phylogenetic analysis indicated that *T. benthamiana* is closer to *Pedicularis hallaisanensis*, *Rehmannia glutinosa*, *Rehmannia chingii*, *Triaenophora shennongjiaensis* (Figure 1). Most nodes in the plastome ML trees were strongly supported. The complete plastome sequence of *T. benthamiana* will provide a useful resource for its conservation and garden utilization as well as the phylogenetic studies of Linderniaceae.

## Disclosure statement

No potential conflict of interest was reported by the authors.

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