

## Characterization of the complete chloroplast genome sequence of *Blastus cochinchinensis* (Melastomataceae)

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### ABSTRACT

*Blastus* Lour. belongs to tribe Sonerileae (Melastomataceae), comprising about 18 species worldwide. Herein, we presented, assembled, and annotated the first complete chloroplast genome of *Blastus* (*B. cochinchinensis*). The complete chloroplast genome (cp) size of *B. cochinchinensis* was 156,005 bp in length, containing a pair of 26,812 bp inverted repeat (IR) regions, which were separated by a large single-copy region (LSC) 85,926 bp and a small single-copy (SSC) region 16,455 bp. The overall GC content of the genome was 37.0%. The whole genome contained 129 unique genes, including 81 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. The phylogenetic analysis showed that *B. cochinchinensis* was sister to *Barthea barthei*. The present study provided *B. cochinchinensis* genomic information that may be found useful in conservation and molecular phylogenetic studies on *Blastus*.

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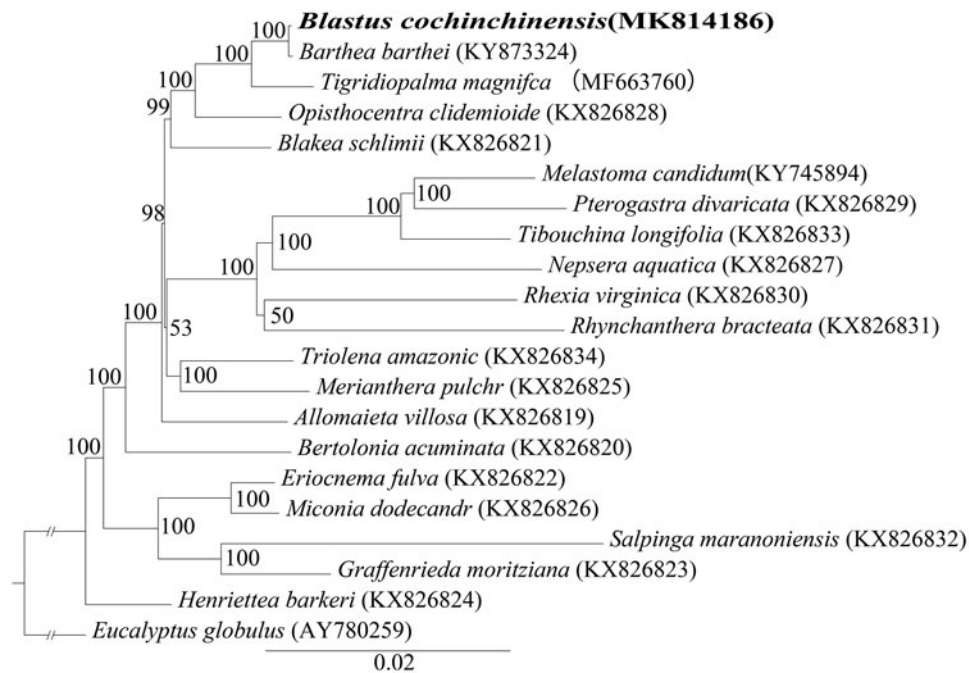
*Blastus cochinchinensis*;  
chloroplast genome;  
Melastomataceae; phylogenetic relationships

*Blastus* Lour. belongs to tribe Sonerileae (Melastomataceae), comprising about 18 species worldwide, distributed in eastern India to southeast Asia, southwestern China to Taiwan and the Japanese Ryukyu Islands (Chen 1984; Chen and Renner 2007). China including about 14 species, accounting for 77.8% of the world, is the distribution center of this genus. Previous studies had performed the phylogenetic position of genus (Clausing et al. 2000; Clausing and Renner 2001; Fritsch et al. 2004; Zeng, Huang, et al. 2016; Zeng, Zou, et al. 2016; Zhou, Ng, et al. 2018; Zhou, Zhou, et al. 2018; Zhou, Lin, et al. 2018), while interspecific relationship within the genus have not been investigated with molecular tools. In this study, we reported the first complete chloroplast genome of *Blastus cochinchinensis* based on Illumina sequencing technology, commonly found in southern China, as a resource for future studies of the genus. To explore the evolution status and genomic information of *B. cochinchinensis*, we inferred the phylogenetic relationships based on 19 other species complete chloroplast genomes of Melastomataceae.

The fresh leaf sample was taken from HongKong, China, where was the type locality. And the voucher specimen was deposited in herbarium CANT (specimen code SJ440). Total genomic DNA was isolated from fresh leaves tissue using Plant Tissues Genome DNA Extraction Kit (TianGen DP305, Beijing, China), and sequenced using the Illumina pair-end technology, with 350 bp randomly interrupted by the Covaris ultrasonic breaker for library construction. The chloroplast

genome was assembled using the software CLC Genomics Workbench v8.0 (CLC Bio, Aarhus, Denmark) and annotated using the online tool DOGMA (Wyman et al. 2004). Then, GENEIOUS R10 (Biomatters Ltd., Auckland, New Zealand) (Kearse et al. 2012) was used to correct the annotation by comparing the sequence of *Opisthocentra clidemioides* (GenBank accession number: KX826828). The annotation result was drawn with the internet tool OGDRAW (<https://chlorobox.mpimp-golm.mpg.de/OGDraw.html>) (Lohse et al. 2013). Finally, the accurate new annotated complete chloroplast genome of *B. cochinchinensis* was submitted to the GenBank (accession number: MK814186). The whole complete chloroplast genome of *B. cochinchinensis* was a circular with 156,005 bp in length and comprised a large single-copy (LSC) region of 85,926 bp, a small single-copy (SSC) region of 16,455 bp, and two inverted repeat (IRA and IRB) regions of 26,812 bp each. The genome contained 129 unique genes, including 81 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. The overall GC content was 37.0%.

In order to study the phylogenetic relationship of *B. cochinchinensis* with 19 other members of Melastomataceae (Reginato et al. 2016; Ng et al. 2017; He et al. 2017; Zhou, Lin, et al. 2018), a species (*Eucalyptus globulus*, GenBank Accession Number: AY780259) from Myrtaceae was selected as an outgroup. The sequences were firstly aligned using HomBlocks pipeline (Bi et al. 2018). Using RAXML-HPC2 on XSEDE version 8.2.10 (Stamatakis 2014) on CIPRES cluster



**Figure 1.** Maximum likelihood tree based on the complete chloroplast genome sequences of 20 species from Melastomataceae, and *Eucalyptus globulus* (Myrtaceae) as outgroup. Shown next to the nodes are bootstrap support values based on 1000 replicates.

(<https://www.phylo.org/>) to construct a maximum likelihood tree (Figure 1), the branch support was computed with 1000 bootstrap replicates. The phylogenetic analysis showed that *B. cochinchinensis* was sister to *Barthea barthei* with strong bootstrap support.

## Disclosure statement

No potential conflict of interest was reported by the authors.

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