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_.
(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 \textit{B. cochinchinensis} was sister to \textit{Barthea barthei} with strong bootstrap support.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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