MITOGENOME ANNOUNCEMENT

The complete chloroplast genome of *Blastus auriculatus* (Melastomataceae)

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**ABSTRACT**

*Blastus auriculatus*, a shrub sparsely distributed in Yunnan, China, occurs only in bamboo forests at an elevation of below 200 m. It is categorized as “Critically Endangered (CR)” in China Biodiversity Red List. In addition, the phylogenetic position of *Blastus* within the Melastomataceae family is still unclear. This study generated the complete chloroplast genome sequence of *B. auriculatus* with aims to provide genetic resources for conservation genetics and to resolve the phylogenetic position of *Blastus*. The size of the chloroplast genome of *B. auriculatus* is 155,981 bp, including a large single-copy (LSC) region of 85,955 bp and a small single-copy (SSC) region of 16,434 bp, separated by a pair of identical inverted repeat regions (IRs) of 26,796 bp each. The chloroplast genome contains a total of 125 genes, including 80 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. Phylogenetic analysis showed that *B. auriculatus* is closest to *Barthea barthei* among species in Melastomataceae with available chloroplast genome sequences.

After quality filtering, approximately 5.97 Gb high-quality reads were used to assemble the chloroplast genome using NOVOPlasty (Dierckxsens et al. 2017) with the *rbcl* sequence of *Melia toba candium* (GenBank accession GQ436728) as the seed sequence. The chloroplast genome sequence of *B. auriculatus* was annotated using the DOGMA (Wyman et al. 2004) and submitted to GenBank with the accession number MK335944.

The complete chloroplast genome of *B. auriculatus* has a circular molecular structure of 155,981 bp in length with 37.03% of GC content. It has a large single copy (LSC) region of 85,955 bp and a small single copy (SSC) region of 16,434 bp, separated by a pair of identical inverted repeat regions (IRs) of 26,796 bp each. The chloroplast genome contains a total of 125 genes, including 80 protein-coding genes, 37 tRNA genes, and 8 rRNA genes.

To clarify the phylogenetic position of *Blastus* within Melastomataceae, phylogenetic analyses were performed based on 20 species in Melastomataceae (Reginato et al. 2016; Ng et al. 2017; Zhou et al. 2018) as well as *Eucalyptus globulus* (Myrtaceae) as an outgroup. These sequences were aligned using MAFFT (Katoh and Standley 2013). The ML tree was produced by RAxML (Stamatakis 2014) using 1000 bootstrap replicates. As shown in the phylogenetic tree (Figure 1), *B. auriculatus* is closest to *Barthea barthei* in the family Melastomataceae among closely related species with available chloroplast genome sequences. The chloroplast genome reported here offers a useful resource for conservation genetics and phylogenetic studies.
Disclosure statement

No potential conflict of interest was reported by the authors.

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Figure 1. Maximum likelihood tree based on complete chloroplast genome sequences of 20 species of Melastomataceae with Eucalyptus globulus as an outgroup showing the phylogenetic position of Blastus auriculatus. The bootstrap support values shown next to the nodes were based on 1000 replicates. Scale in substitutions per site.