Mangroves are a taxonomically diverse group of plants that have undergone genome-wide convergent evolution to adapt to coastal conditions with fluctuating salinity and inundation (Xu et al. 2017). The genus Sonneratia, one of the major components of mangrove ecosystems, comprises six species distributed from East Africa to the West Pacific Ocean (Spalding et al. 2010), with S. alba being the most widely distributed species. Due to the overlapping distribution of congeneric species, natural hybridization is common in Sonneratia (Zhou et al. 2005). At the same time, the genus contains rare species of high conservation status; S. griffithii and S. ovata are listed as critically endangered and near threatened on the IUCN Red List, respectively (Duke et al. 2010; Salmo et al. 2010). Natural hybridization of S. alba and S. griffithii (Qiu et al. 2008) could threaten the species integrity of the latter and complicate current conservation efforts. Phylogeographic studies on S. alba revealed low genetic diversity in this species, especially at the outer edge of its distribution range, suggesting genetic erosion from repeated range contraction and expansion (Wee et al. 2017; Yang et al. 2017). Here, we report the complete chloroplast genome of S. alba to provide genomic resources for conservation and for investigating convergent evolution of mangrove species (e.g. Xu et al. 2017).

Leaf material was collected from one individual of S. alba (sah11) in Hainan province (19° 37’ 40”, 110° 50’ 22”; China; voucher AKSW_SACH01 deposited in the herbarium of the Biodiversity Genomics Team (BGT), Guangxi University, Nanning, China). Genomic DNA extraction followed by library construction and sequencing on the Illumina hiSeq2500 (genome skimming) was performed by Novogene (Beijing, China). The chloroplast genome was assembled de novo using org.asm (ORG.ASM. 2016) and annotated using cpGAVAS (Liu et al. 2012).

The chloroplast genome of S. alba (GenBank accession MH105772) was 153,061 bp in length, consisting of a large single copy (LSC) with 87,226 bp, a small single copy (SSC) region of 18,033 bp, separated by two inverted repeats (IRs) regions of 23,901 bp. The overall GC content was 37.3%, and 43.1%, 35.4%, and 31.1% in the IRs, LSC, and SSC regions, respectively. It contained 106 genes, including 79 coding genes, 24 tRNA genes, and four rRNA genes. A phylogenetic analysis confirmed that S. alba was clustered with Trapa maximowiczii within the family Lythraceae.
convergent evolution in photosynthetic genes among species frequently exposed to ecophysiological stress.

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**Disclosure statement**

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**References**


Figure 1. Maximum likelihood (ML) phylogenetic tree based on complete chloroplast genome sequences of Sonneratia alba and other nine species from the order Myrtales using Monsonia marlothii of Geraniaceae as an outgroup. Numbers on branches are bootstrap support value based on 100 iterations.

