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Genomics of the critically endangered monotypic genus *Sinopora*: the plastome of *S. hongkongensis* (Lauraceae)

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ABSTRACT

Sinopora hongkongensis is a critically endangered endemic tree species restricted to Hong Kong. Here we report its plastome sequence. The *S. hongkongensis* plastome was 158,612 bp in length, with a large single-copy (LSC) region of 89,405 bp and a small single-copy (SSC) region of 18,205 bp, separated by two inverted repeat (IR) regions of 25,498 bp. It contained 126 genes, including 89 coding genes, 29 tRNA genes, and 8 rRNA genes. The overall GC content was 39.0%, and 43.0%, 37.7%, and 34.0%, in the IRs, LSC, and SSC regions, respectively. A phylogenetic analysis combining a subset of Lauraceae plastomes with closely related outgroup families confirms the placement of *S. hongkongensis* in Lauraceae and explores relationships with other genera in the family.

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Lauraceae; complete chloroplast genome; Critically Endangered; *Sinopora hongkongensis*; genomics

Lauraceae are a major plant family in Magnoliids, consisting of more than 55 genera distributed worldwide (Oliveira-Filho et al. 2015; Zhao et al. 2018). Its species are distributed mainly in subtropical or tropical warm temperate regions consisting of woody elements ranging from small treelets to large canopy elements (Lim 2012). Species in the family form an important ecological and economic component of Asian forests, providing valuable sources of medicine, timber, spices, nutritious fruits, and perfumes. In China, Lauraceae are represented by more than 400 species from nearly all Asian genera (25; sensu Li, Li, et al. 2008), in addition to two monotypic endemic Chinese genera (*Sinopora* J. Li et al. and *Sinosassafras* H. W. Li). Despite the importance of the family, the evolutionary relationships in Lauraceae are still poorly understood (Rohwer 2000; Huang et al. 2016; Liu et al. 2017). Availability of genomic resources is steadily increasing in the family (e.g. Liang et al. 2019; Song et al. 2019), but for most genera, such data are still lacking, hindering a clear evaluation of their taxonomic and evolutionary status (Rohwer et al. 2014; Hinsinger and Strijk 2017a; Zhao et al. 2018).

Sinopora hongkongensis (Xia et al. 2006; Li, Xia, et al. 2008), the only species in the genus *Sinopora*, is restricted to the evergreen broad-leaved forests of Hong Kong. The species is here classified under the IUCN Red List Assessment criteria as Critically Endangered B1 + 2ab,C2a(i),D. Although the habitat in which the last remaining individuals are found is

under protective legislation (and exact locality details are restricted), the species is balancing on the brink of extinction without the development of ex-situ approaches such as micropropagation.

Here, we report the plastome sequence of *S. hongkongensis* to provide resources in support of further genomic and conservation genetic studies on this exceptionally rare species.

Supported by staff from the Agriculture, Fisheries and Conservation Department (AFCD, HK), we visited one individual of *S. hongkongensis* and collected leaves which were field preserved in dry ice. We extracted genomic DNA as described before (Cvetković et al. 2019), from 0.1 g of frozen fresh leaves. Voucher material was deposited at the herbarium of the Agriculture, Fisheries and Conservation Department (AFCD, HK) and the Biodiversity Genomics Team tissue bank (BGT; Strijk 3723). Library construction and sequencing were performed by Novogene (Beijing, China) using the NEBNext Ultra II DNA Library Prep Kit (Ipswich, Massachusetts, USA), as described elsewhere (Hinsinger and Strijk 2017a, 2017b, 2017c). *De novo* assembly of the cp genome was conducted using org.asm v0.2.05 (ORG.ASM 2016) and annotated using cpGAVAS (Liu et al. 2012).

The plastome of *S. hongkongensis* (GenBank accession number MN722652) was 158,612 bp in length, with a large single-copy (LSC) region of 89,405 bp and a small single-copy (SSC) region of 18,205 bp, separated by two inverted repeat

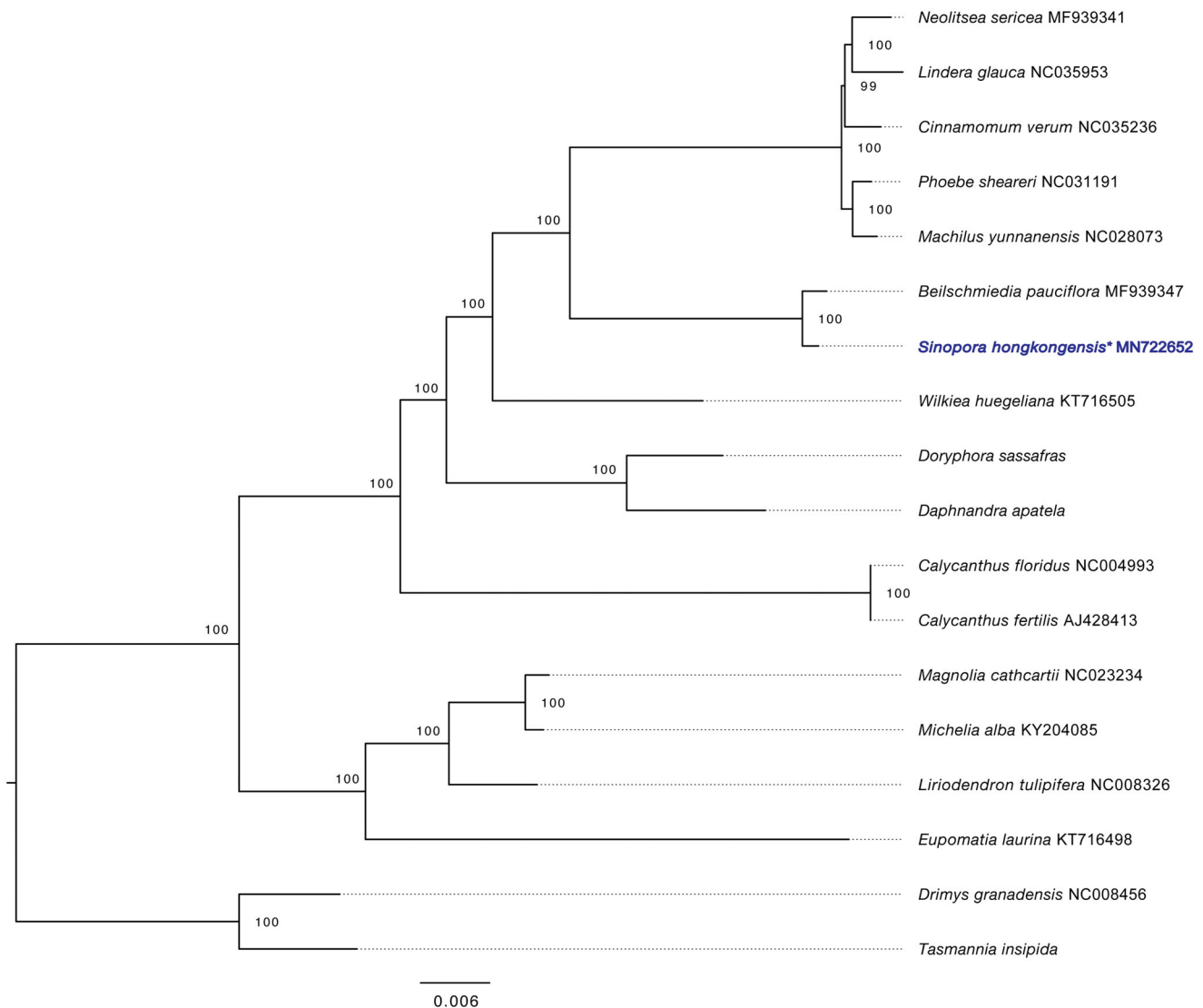


Figure 1. ML phylogenetic tree based on plastome data showing relationships between representative genera in Lauraceae and selected outgroup taxa. The position of *S. hongkongensis* is highlighted with an asterisk. Bootstrap support values (1000 replicates) are indicated on branches. Plastomes of *Doryphora sassafras*, *Daphnandra apatela*, and *Tasmannia insipida* were obtained from Dryad (doi.org/10.5061/dryad.j64j0).

regions (IRs) of 25,498 bp. The genome contained 126 genes, including 89 coding genes, 29 tRNA genes, and 8 rRNA genes. The overall GC content was 39.0%, and 43.0%, 37.7%, 34.0%, in the IRs, LSC, and SSC regions, respectively.

We reconstructed a maximum-likelihood phylogenetic tree including representative species in Lauraceae and other families using RaxML-NG v0.8.1 (Kozlov et al. 2019), with 1000 bootstrap replicates and the GTR + I + G4 substitution model, as selected by ModelTest-NG v0.1.5 (Darriba et al. 2019). This phylogenetic analysis indicated that *S. hongkongensis* is sister to *Beilschmiedia pauciflora* (Figure 1). All nodes in the plastome ML trees were strongly supported. The complete plastome sequence of *S. hongkongensis* will provide a useful resource for its conservation as well as future phylogenetic studies in this genus.

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Disclosure statement

No potential conflict of interest was reported by the authors.

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