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PLASTOME REPORT

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The complete chloroplast genome sequence of *Arytera littoralis* (Sapindoideae, Sapindaceae)

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ABSTRACT

Arytera littoralis Blume 1847 is an evergreen small tree belonging to the Sapindaceae family. It is distributed in South China to SE Asia and the Solomon Islands. However, the chloroplast genome of *A. littoralis* has yet to be reported. In this study, the complete chloroplast genome of *Arytera littoralis* was determined. The total genome size was 161,091 bp in length, consisting of two inverted repeats (IRs) (28,432 bp) separated by the large single-copy (LSC) (85,737 bp) and small single-copy (SSC) (18,490 bp) regions. The genome contained 133 genes, including 87 protein-coding genes, 37 tRNA genes, and eight rRNA genes. The GC content of the complete chloroplast genome was 37.8%. A maximum-likelihood (ML) phylogenetic tree of *A. littoralis* and 13 related species from the family Sapindaceae indicated that *A. littoralis* was close to a clade composed of *Sapindus*, *Nephelium*, *Litchi*, and *Dimocarpus*. This study will offer essential genetic resources of *A. littoralis* and provide insights into the phylogeny and evolution of Sapindaceae.

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Arytera littoralis; chloroplast genome; phylogenetic analysis; Sapindaceae

Introduction

Arytera littoralis Blume 1847 is an evergreen small tree belonging to the Sapindaceae family. This species usually grows in primary and secondary forests and is distributed from South China (Guangdong, Guangxi, Hainan, and Yunnan) to SE Asia and the Solomon Islands. It is 3–10 m tall, rarely 13 m tall. The branches are terete, striate, and pubescent when young, with many dense and yellowish-white lenticels. Leaves are 15–35 cm, with 2 or 3 (or 4) pairs of sub-opposite leaflets; petiolules are less than 1 cm; blades are oblong-lanceolate to lanceolate-ovate, 8–18 cm long, 2.5–7.5 cm wide, thinly leathery, base broadly cuneate to nearly obtuse, apex cuspidate, and mucronate (Figure 1). Inflorescences are compact and multiflowered. Flowers are bisexual and fragrant, having five pilose sepals and five petals, with villous scales and lobed disks. Fertile schizocarps are red or orange, ellipsoid to orbicular. Its tough, resilient wood was used in China's farm tool production (Xia and Gadek 2007). Recently, some scholars evaluated the potential bioactivity of *A. littoralis* and found that the methanol extract of different parts of this species had powerful antioxidants (Praptiwi et al. 2022). *A. littoralis* has high prospects to be a potent source of natural antioxidants.

Despite its economic values and potentialities, *Arytera littoralis* has been neglected and underutilized (Praptiwi et al. 2022). The plant chloroplast genome is helpful for population genetics study, species-level identification, and phylogenetic analysis (Lyu et al. 2020). So far, little data are available about the complete chloroplast genome of *A. littoralis*. In this study, we assembled the complete chloroplast genome of *A. littoralis* herein to explore the reasonable further relationships among this species and other Sapindaceae members.

Figure 1. Photograph of *Arytera littoralis*. Yihua Tong took the picture in the South China Botanical Garden, Chinese Academy of Sciences. Branches are terete, striate, and pubescent when young, with many dense and yellowish-white lenticels. Leaves are 15–35 cm, with 2 or 3 (or 4) pairs of sub-opposite leaflets; petiolules are less than 1 cm; blades are oblong-lanceolate to lanceolate-ovate, 8–18 cm long, 2.5–7.5 cm wide, thinly leathery, base broadly cuneate to nearly obtuse, apex cuspidate, and mucronate.

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Materials and methods

The fresh silica-dried leaves of *Arytera littoralis* (Figure 1, Yihua Tong, yh-tong@scbg.ac.cn, accession no. Tong 20210701) were collected from South China Botanical Garden, Chinese Academy of Sciences (23.18794°N, 113.373781°E), Guangdong Province, China. The voucher specimens were deposited in HYNU (Hengyang Normal University Herbarium, Limin Cao, limincaohn@126.com). The total genomic DNA was extracted for the following operation. Sequencing was conducted on the Illumina NovaSeq system (Illumina, San Diego, CA). After comparing with all existing chloroplast genomes of Sapindaceae in GenBank, chloroplast genome-related reads of *A. littoralis* were obtained. The raw reads were assembled using NOVOPlasty 3.7 (Dierckxsens et al. 2017) with ribulose-1,5-bisphosphate carboxylase/oxygenase (*rbc*L) gene from *Sapindus mukorossi* Gaertn 1788 (GenBank accession no. KM454982) as seed. After that, the complete genome sequence was annotated by the online annotation tool GeSeq (https://chlorobox.mpimp-golm.mpg.de/geseq.html) (Tillich et al. 2017) and adjusted manually if necessary. To ascertain the phylogenetic relationship between *Arytera littoralis* and other species of Sapindaceae, 13 cp genome sequences were achieved from the NCBI (Figure 2). All sequences were aligned by the MAFFT program (Katoh et al. 2005). Phylogenetic analysis was conducted by

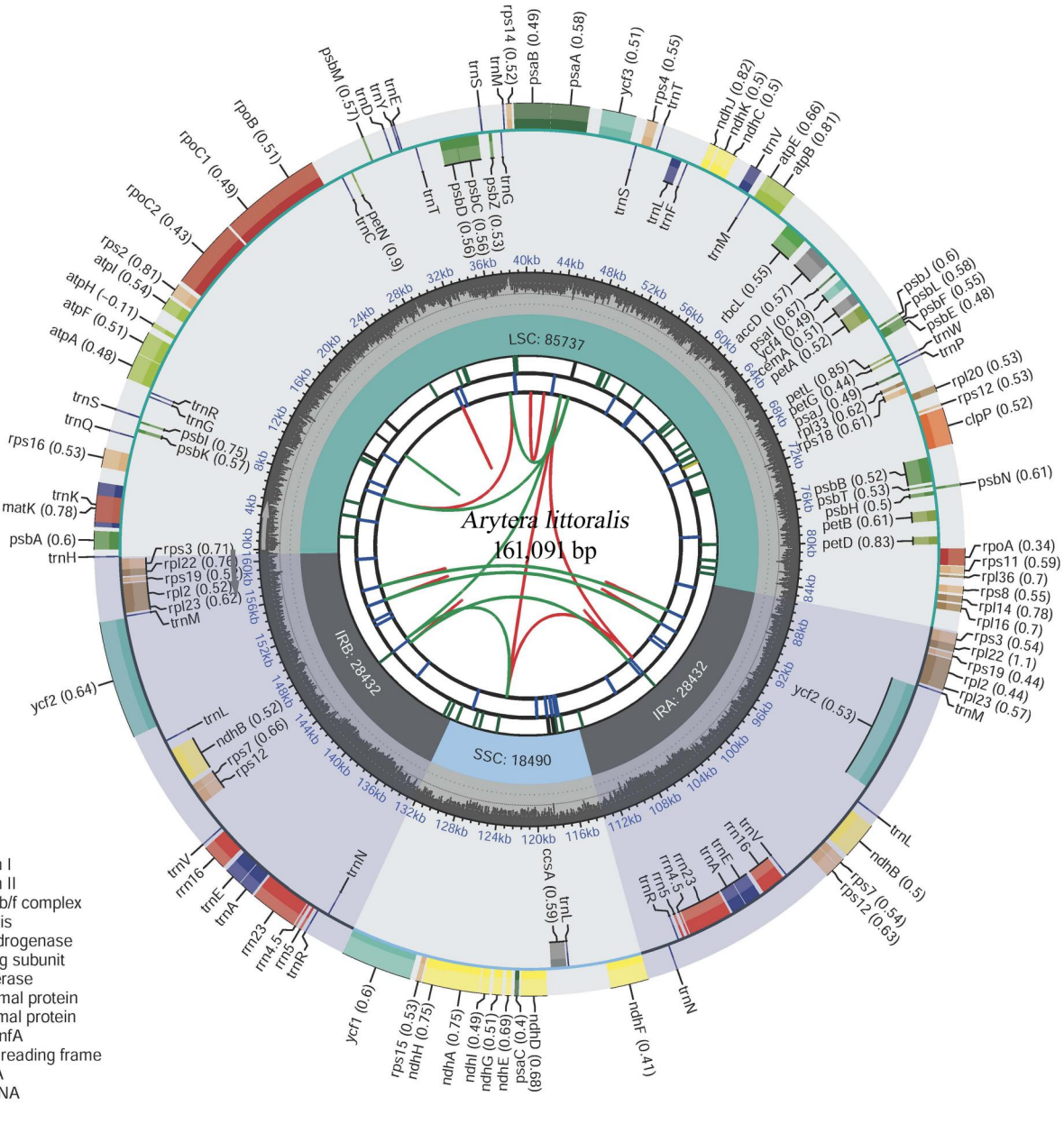

Figure 2. The maximum-likelihood (ML) phylogenetic tree with evolutionary distances for *Arytera littoralis* and 13 related species from the family Sapindaceae. *Acer davidii*, *Acer palmatum*, *Dipteronia sinensis*, *Aesculus chinensis*, and *Aesculus assamica* are outgroups. The bootstrap support values were shown at the branches. The following sequences were used: *Dimocarpus longan* (MG214255, Wang et al. 2017), *Litchi chinensis* (MW067100, Areces-Berazain et al. 2020), *Nephelium lappaceum* (MT884002, Liu et al. 2021), *Sapindus mukorossi* (KM454982, Yang et al. 2014), *Arytera littoralis* (ON098015, this study), *Koelreuteria paniculata* (KY859413, Kim et al. 2018), *Koelreuteria bipinnata* (MT675915, Lyu et al. 2020), *Eurycorymbus cavaleriei* (MG813997, Du et al. 2019), *Dodonaea viscosa* (MF155892, Saina et al. 2018), *Acer davidii* (KU977442, Jia et al. 2016), *Acer palmatum* (KY457568), *Dipteronia sinensis* (KT878501, Zhou et al. 2015), *Aesculus chinensis* (MK737939, Zhang et al. 2019), and *Aesculus assamica* (MW067097, Areces-Berazain et al. 2020).

the maximum-likelihood (ML) method using raxmlGUI (Silvestro and Michalak 2012) with rapid bootstrap (1000 replicates) and the GTRGAMMA model selected.

Results

There were 37,718,630 Illumina short reads generated. The read coverage plot is shown in Supplementary Figure S1. *Arytera littoralis* had two large inverted repeats (IRs), separated by large single-copy (LSC) and small single-copy (SSC) regions, which were similar to its Sapindaceae allies. The complete chloroplast genome of *A. littoralis* (GenBank accession no. ON098015) was 161,091 bp in length, consisting of two IRs (28,432 bp) separated by the LSC (85,737 bp) and SSC (18,490 bp) regions (Figure 3). The genome contained 133 genes, including 87 protein-coding genes, 37 tRNA genes, and eight rRNA genes. Of these, nine genes (*rps*16, *atp*F, *rpo*C1, *ycf*3, *clp*P, *rpl*2, *ndh*B, *ndh*A, and *ycf*1) are cis-spliced (Supplementary Figure S2), and rps12 is a trans-spliced gene (Supplementary Figure S3). The GC content of the complete chloroplast genome was 37.8%.

The results of the phylogenetic analysis indicated that *A. littoralis* was close to a clade composed of *Sapindus*, *Nephelium*, *Litchi*, and *Dimocarpus* (Figure 2).

Discussion and conclusions

Studying chloroplast genomes is important for understanding chloroplast DNA structure, origin, plant molecular markers, and species relationships (Tang et al. 2011). In this study, the complete chloroplast genome of *Arytera littoralis* was sequenced, exhibiting a total length of 161,091 bp, consisting of two IRs of 28,432 bp separated by a LSC and a SSC of 85,737 bp and 18,490 bp, respectively. A total of 133 genes were annotated, comprising 87 PCGs, 37 tRNA genes, and eight rRNA genes. The chloroplast genome structure and genome size of *A. littoralis* were similar to those of other species in the family Sapindaceae, which have a typical quadripartite structure and genome size between 155,212 bp and 163,863 bp (e.g. Yang et al. 2014; Jia et al. 2016; Wang et al. 2017; Zhang et al. 2019; Areces-Berazain et al. 2020; Lyu et al. 2020). Phylogenetic analysis of the cp genome sequences indicated a close genetic relationship between *A. littoralis* and a clade composed of *Sapindus*, *Nephelium*, *Litchi*, and *Dimocarpus*. Therefore, it is reasonable to place this species in the subfamily Sapindoideae. The results presented here will offer essential genetic resources of *A. littoralis* and provide insights into the phylogeny and evolution of Sapindaceae.

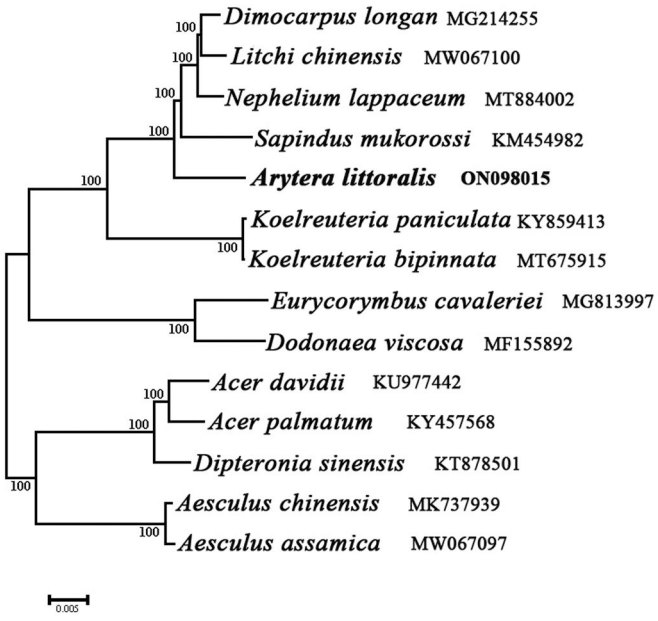

Figure 3. Schematic map of the complete chloroplast genome of *Arytera littoralis* generated by CPGview. The boxes of different sizes and colors on the outermost circle represent genes and their lengths. The transcription directions for the genes outside and inside the outermost circle are counter-clockwise and clockwise, respectively. The grey area in the middle circle represents the changes in GC content at different positions. The large single-copy (LSC), small single-copy (SSC), and inverted repeat (IRa and IRb) regions are shown in various colors on the inner circle. The functional classification of the genes is shown in the bottom left corner.

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Author contributions

Limin Cao designed the study and wrote the main manuscript text; Zhixin Wang analyzed the molecular data and prepared Figures 2 and 3, Figures S1, S2, and S3. Shuai Wang wrote the introduction and conducted an investigation; Yanfen Chang analyzed the phylogenetic data and revised the manuscript. All the authors read and approved the manuscript.

Ethical approval

The plant materials used in this study are not included in the IUCN Red List of Threatened Species, and the sampling site is not located in any protected area. The research was conducted with permission from Hengyang Normal University.

Disclosure statement

No potential conflict of interest was reported by the author(s).

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Data availability statement

The data supporting this study's findings are available in NCBI at https://www.ncbi.nlm.nih.gov/ under accession no. ON098015. The associated BioProject, Sequence Read Archive, and BioSample numbers are PRJNA837695, SRR19182469, and SAMN28227742, SAMN28227743.

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