The complete chloroplast genome of *Sonneratia griffithii* Kurz (Lythraceae)

Duangjai Sangsakrua, Chutima Sonthirod, Wanapinun Nawae, Chutintorn Yundaeng, Waraththaya Promchoo, Wirulda Pootakhama, and Sithichoke Tangphatsornruanga

**National Omics Center, National Science and Technology Development Agency (NSTDA), Pathum Thani, Thailand;**
**Department of Marine and Coastal Resources, Royal Thai Government Ministry of Natural Resources and Environment, Bangkok, Thailand**

**CONTACT**
Sithichoke Tangphatsornruang, Email: panyavut.aum@nstda.or.th

**ARTICLE HISTORY**
Received 25 February 2022
Accepted 27 August 2022

**KEYWORDS**
Chloroplast genome; phylogeny; mangrove; *Sonneratia griffithii*

*Sonneratia griffithii* (Kurz 1871) is a true mangrove in the family Lythraceae. It is categorized as a rare and critically endangered species under the International Union for Conservation of Nature (IUCN) (Duke et al. 2010). *Sonneratia griffithii* can be found along the coasts of Bengal and the Andaman Sea in India, Myanmar, Malaysia, and Thailand (Kathiresan and Rajendran 2005). In Thailand, *S. griffithii* is distributed near the western coast in Ranong, Phang-nga, Krabi, and Trang provinces. *Sonneratia* variations have been reported by a natural hybridization between *S. griffithii* and *Sonneratia alba* (Qiu et al. 2008). Understanding genetic diversity is important for *Sonneratia* conservation and for clarifying the evolution of this mangrove species. In this paper, we report the complete chloroplast genome of *S. griffithii*, which provide a useful resource for genetic diversity studies. We also performed a phylogenetic analysis to demonstrate the relationships between *S. griffithii* and other mangrove species.

*Sonneratia griffithii* leaves were collected from a mature plant in the Ranong Mangrove Forest Research Center, Ranong Province, Thailand (10°10’20.3”N, 98°42’31.4”E), following the guidelines on the implementation of the ‘IUCN Policy Statement on Research Involving Species at Risk of Extinction’ (June 1989). Sample collection for this study was permitted by the Department of Marine and Coastal Resources, Ministry of Natural Resources and Environment, Thailand (project number 1952261). The analysis of chloroplast DNA was followed protocols in Ruang-Areerate et al. (2021). Leaf tissues were frozen in liquid nitrogen after being collected and genomic DNA was extracted from young leaves using the MagAttract HMW DNA Kit (Qiagen, Germany). The DNA sample was deposited in the National Biobank of Thailand (NBT), Thailand Science Park, Pathum Thani, Thailand (contact person: Panyavut Aumpuchin; Email: panyavut.aum@nstda.or.th) under the voucher number NBTG000002. Paired-end (PE) reads of 150 bp were conducted on an Illumina HiSeq X Ten platform (Illumina, USA). After quality assessment, the 101,166,742 raw reads were used to assemble the chloroplast genome using GetOrganelle v1.7.3.5 (Jin et al. 2020), and the assembly was annotated with GeSeq (Tillich et al. 2017). The complete chloroplast genome sequence of *S. griffithii* was submitted to the GenBank database with accession number OL628854.

The complete chloroplast genome of *S. griffithii* contained 152,730 nucleotides with a GC content of 37.31%. The genome had a large single copy (LSC) region with a length of 87,226 bp and a small single copy (SSC) region of 17,764 bp. These single-copy regions were separated by a pair of 23,870-bp inverted repeats (IRs). In total, 113 unique genes were predicted, including 79 protein-coding genes, 30 tRNA genes, and 4 rRNA genes. There were 16 genes (atpF, ndhA, ndhB, petB, petD, rpl16, rpoC1, rps12, rps16, rrm23, trnA-UGC, trnG-UCC, trnL-UAA, trnK-UUU, trnL-1UA, and trnV-UAC) containing one intron and 2 genes (cspP1 and pafI) having two introns.

A phylogenetic tree was constructed from 15 species in the family Lythraceae (including 5 *Sonneratia* species and 3 inter-specific hybrids) and 8 other mangrove species. *Vistis vinifera* was used as an outgroup species. The complete chloroplast sequences were downloaded from the NCBI (www.ncbi.nlm.nih.gov). A total of 76 conserved orthologs were identified, and the maximum-likelihood phylogenetic
The bootstrap support values in the phylogenetic tree were between 83 and 100% (except for the Sonneratia group), suggesting a confident species grouping in the tree. Based on our phylogenetic tree, S. griffithii was closely related to S. alba and was placed in a monophyletic group with Sonneratia species, while Trapa species were placed in a sister group (Figure 1). The data reported in this study are useful for genetic conservation as well as for phylogenetic studies of mangrove species.

**Disclosure statement**

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

**Funding**

This study was supported by the National Science and Technology Development Agency (NSTDA), Thailand under [grant number 1952261].

**ORCID**

Chutintorn Yundaeng [http://orcid.org/0000-0002-4654-4201](http://orcid.org/0000-0002-4654-4201)

Wirulda Pootakham [http://orcid.org/0000-0001-6721-6453](http://orcid.org/0000-0001-6721-6453)

Sithichoke Tangphaatsornruang [http://orcid.org/0000-0003-2673-0012](http://orcid.org/0000-0003-2673-0012)

**Data availability statement**

The data that support the findings of this study are openly available in the GenBank database [https://www.ncbi.nlm.nih.gov/genbank/](https://www.ncbi.nlm.nih.gov/genbank/) under the accession number OL628854. The associated BioProject, SRA, and Biosample numbers are: PRJNA783371, SRR17035265, and SAMN23429313 respectively.
References

Duke N, Kathiresan K, Salmo SG, III Fernando ES, Peras JR, Sukardjo S, Miyagi T. 2010. Sonneratia griffithii, The IUCN Red List of Threatened Species. 2010:e.T178799A7609832.

Fan X, Wang W, Wagutu GK, Li W, Li X, Chen Y. 2022. Fifteen complete chloroplast genomes of Trapaceae: insight into genome structure, comparative analysis and phylogenetic relationships. BMC Plant Biol. 22(1):230.

Gu C, Tembrock LR, Li Y, Lu X, Wu Z. 2016. The complete chloroplast genome of queen’s crape-myrtle (Lagerstroemia macrocarpa). Mitochondrial DNA B Resour. 1(1):408–409.

Gu C, Dong B, Xu L, Tembrock LR, Zheng S, Wu Z. 2018. The complete chloroplast genome of Heimia myrtifolia and comparative analysis within Myrtales. Molecules. 23(4):846.

Jansen RK, Kaittanis C, Lee SB, Saski C, Tomkins J, Alverson AJ, Daniell H. 2006. Phylogenetic analyses of Vitis (Vitaceae) based on complete chloroplast genome sequences: effects of taxon sampling and phylogenetic methods on resolving relationships among rosids. BMC Evol Biol. 6:32.

Jian S, Ren H. 2019. The complete chloroplast genome sequence of Pemphis acidula (Lythraceae). Mitochondrial DNA Part B. 4(1):912–913.

Jin JJ, Yu WB, Yang JB, Song Y, DePamphilis CW, Yi TS, Li DZ. 2020. GetOrganelle: a fast and versatile toolkit for accurate de novo assembly of organelle genomes. Genome Biol. 21(1):1–31.

Kathiresan K, Rajendran N. 2005. Mangrove ecosystems of the Indian Ocean region. Indian J Marin Sci. 34:104–113.

Qiu S, Zhou RC, Li YQ, Havannon S, Jaengjai C, Shi SH. 2008. Molecular evidence for natural hybridization between Sonneratia alba and S. griffithii. J Systemat Evol. 46(3):391–395.

Rabah SO, Lee C, Hajarah NH, Makki RM, Alharby HF, Alhebshi AM, Sabir J, Jansen RK, Ruhlman TA. 2017. Plastome sequencing of ten nonmodel crop species uncovers a large insertion of mitochondrial DNA in cashew. Plant Genom. 10(3). doi: 10.3835/plantgenome2017.03.0020.

Ruang-Areeate P, Kongkachana W, Naktang C, Somtiroid C, Narong N, Jomchai N, Maprasop P, Maknual C, Phormsin N, Shearman JR, et al. 2021. Complete chloroplast genome sequences of five Bruguiera species (Rhizophoraceae): comparative analysis and phylogenetic relationships. PeerJ. 9:e12268.

Ruang-Areeate P, Yoocha T, Kongkachana W, Phetchawang P, Maknual C, Meepol W, Jiiumjamrassil D, Pootakham W, Tangphatsornruang S. 2022. Comparative analysis and phylogenetic relationships of Ceriops species (Rhizophoraceae) and Avicennia lanata (Acanthaceae): insight into the chloroplast genome evolution between middle and seaward zones of mangrove forests. Biology. 11(3):383.

Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics. 30(9):1312–1313.

Tillich M, Lehward P, Pellitzer T, Ulbricht-Jones ES, Fischer A, Bock R, Greiner S. 2017. GeSeq – versatile and accurate annotation of organelle genomes. Nucleic Acids Res. 45(W1):W6–W11.

Wang SQ, Ren F. 2022. The chloroplast genome of Sonneratia ovata: genome structure and comparative analysis. Mitochondrial DNA B Resour. 7(1):226–227.

Xue QZ, Xue JH, Victorovna KM, Ma KP. 2017. The complete chloroplast DNA sequence of Trapa maximowiczii Korsh. (Trapaceae), and comparative analysis with other Myrtales species. Aquat Bot. 143:54–62.

Yan M, Zhao X, Zhou J, Huo Y, Ding Y, Yuan Z. 2019. The complete chloroplast genomes of Pumica granatum and a comparison with other species in Lythraceae. JUAMS. 2012(2):2886.

Zhou QJ, Chen YM, Wu W, Zhou RC, Zhang Y. 2018. The complete chloroplast genome sequence of an Endangered mangrove tree Luminitzera littorea (Combretaceae). Conservation Genet Resour. 10(4):911–913.