

The complete chloroplast genome sequence of *Kandelia obovata* (Rhizophoraceae)

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ABSTRACT

The complete plastid genomic data will be helpful to study the origin, evolution and the relationship between the phenotype and environment of *Kandelia obovata*. In this study, we determined the complete chloroplast genome sequence for *K. obovata* using Illumina sequencing data. The complete chloroplast sequence is 168,046 bp, including large single-copy (LSC) region of 94,755 bp, small single-copy (SSC) region of 19,953 bp, a pair of invert repeats (IR) regions of 26,669 bp. Plastid genome contains 119 genes, 79 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. Phylogenetic analysis base on 13 plastid genomes indicates that *K. obovata* is sister to *Rhizophora stylosa*, which forms a base clade of Myrtales in Rhizophoraceae.

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Kandelia obovata belongs to Rhizophoraceae, which is shrub or small tree, and mainly distributed in the interface between land and sea in tropical and subtropical (Chen and Long 2006; Donato et al. 2011). The habitats of *K. obovata* are stressful in multiple dimensions including high salinity, hypoxia, strong UV light and anaerobic soils (Giri et al. 2011). All these stresses fluctuate daily as the tides ebb and flow. In order to adapt to this extremely harsh environment, *K. obovata* has evolved a highly specialized trait, vivipary, which is key to adapting to intertidal habitats (Ma et al. 2013; Olsen et al. 2016). The *K. obovata* community can accelerate the natural deposition of the beach and promote soil growth (Wang et al. 2010). It also has the ecological functions of maintaining coastal ecological balance and can effectively reducing pollutants into the sea (Yu et al. 2013). The complete plastid genomic data will be helpful to study the origin, evolution and the relationship between the phenotype and environment of *K. obovata*. Herein, we report the complete plastid genome of *K. obovata* based on Illumina pair-end sequencing technology. The plant material of *K. obovata* was collected from Minjiang Wetland Protection Park, Mawei District, Fuzhou City, Fujian province, China (119°14'11.5"E, 26°02'17.8"N). The voucher specimen is kept at the Herbarium of College of Forestry, Fujian Agriculture and Forestry University (specimen code FAFU08018).

DNA extraction was conducted by using fresh leaf tissue, with 500 bp randomly interrupted by the Covaris ultrasonic breaker for library construction. The constructed library was

sequenced PE150 by Illumina HiSeq Xten platform, approximately 2GB data was generated. Illumina data was filtered by script in the cluster (default parameter: -L 5, -p 0.5, -N 0.1). Using the complete plastid genome of *Rhizophora stylosa* (GeneBank accession: NC_042819) as reference, plastid genome of *K. obovata* was assembled by GetOrganelle pipe-line (<https://github.com/Kinggerm/GetOrganelle>). We obtain plastid-like reads, and the reads were viewed and edited by Bandage (Wick et al. 2015). Assembled plastid genome annotation was conducted base on comparison with *R. stylosa* by Geneious v 11.1.5 (Biomatters Ltd., Auckland, New Zealand) (Kearse et al. 2012). The annotation result was drawn with the online tool OGDRAW (<http://ogdraw.mpimp-golm.mpg.de/>) (Lohse et al. 2013).

The complete plastid genome sequence of *K. obovata* (GenBank accession: MN313722) was 168,046 bp in length, with a large single-copy (LSC) region of 94,755 bp, a small single-copy (SSC) region of 19,953 bp, and a pair of inverted repeats (IR) regions of 26,669 bp. Complete plastid genome contains 119 genes, there were 79 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. The complete genome GC content was 34.7%. To reveal the phylogenetic position of *K. obovata* with other members of Rhizophoraceae, a phylogenetic analysis was performed based on 11 complete plastid genomes of Myrtales, and two species (*Haloxylon ammodendron*, *H. persicum*) as outgroups. The genome data were downloaded from NCBI GenBank. The sequences were aligned by MAFFT v7.307 (Katoh and Standley 2013), and

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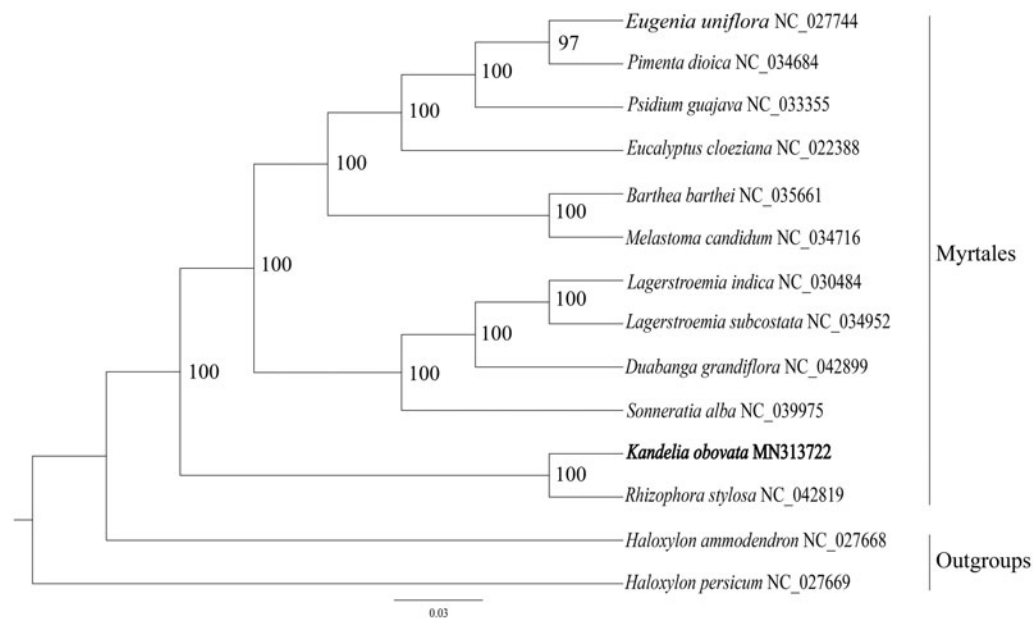


Figure 1. Phylogenetic analysis of 11 species of Myrtales and two taxa (*Haloxylon ammodendron*, *H. persicum*) as outgroup based on plastid genome sequences by RAxML, bootstrap support value near the branch.

phylogenetic tree constructed by RAxML (Stamatakis 2014). The phylogenetic tree showed that *K. obovata* is sister to *R. stylosa*, which forms a base clade of Myrtales with strong support (Figure 1).

Disclosure statement

No potential conflict of interest was reported by the authors.

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References

- Chen TY, Long SJ. 2006. Chemical constituents and pharmacological effects of *Kandelia obovata*. *J Northwest Pharm J.* 03:137–138.
- Donato DC, Kauffman JB, Murdiyarso D, Kurnianto S, Stidham M, Kanninen M. 2011. Mangroves among the most carbon-rich forests in the tropics. *Nat Geosci.* 4:293–297.
- Giri C, Ochieng E, Tieszen LL, Zhu Z, Singh A, Loveland T, Masek J, Duke N. 2011. Status and distribution of mangrove forests of the world using earth observation satellite data. *Global Ecol Biogeogr.* 20: 154–159.
- Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Mol Biol Evol.* 30:772–780.
- Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics.* 28: 1647–1649.
- Lohse M, Drechsel O, Kahlau S, Bock R. 2013. Organellar Genome DRAW—a suite of tools for generating physical maps of plastid and mitochondrial genomes and visualizing expression data sets. *Nucleic Acids Res.* 41:W575–W581.
- Ma T, Wang J, Zhou G, Yue Z, Hu Q, Chen Y, Liu B, Qiu Q, Wang Z, Zhang J, et al. 2013. Genomic insights into salt adaptation in a desert poplar. *Nat Commun.* 4:2797.
- Olsen JL, Rouzé P, Verhelst B, Lin Y-C, Bayer T, Collen J, Dattolo E, De Paoli E, Dittami S, Maumus F, et al. 2016. The genome of the seagrass *Zostera marina* reveals angiosperm adaptation to the sea. *Nature.* 530: 331–335.
- Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics.* 30:1312–1313.
- Wang TS, Li XJ, Cai JB, Zhang DQ, He DJ, Liu C, Wang QB, Zheng KJ, Zheng KJ. 2010. Comparison of biomass of natural and artificial forests of *Kandelia obovata* along the coast of Fujian Province. *J Southwest Forest Coll.* 30:16–20.
- Wick RR, Schultz MB, Zobel J, Holt KE. 2015. Bandage: interactive visualization of de novo genome assemblies. *Bioinformatics.* 31:3350–3352.
- Yu RL, Hu GR, Zhao JX, Han Z. 2013. Distribution, migration and reserves of heavy metals in *Kandelia obovata* mangrove forests in Quanzhou Bay Estuary Wetland. *Environ Chem.* 32:125–131.