


The plastid genome of *Klainedoxa gabonensis* Pierre ex Engl. (Malpighiales)

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ABSTRACT

Klainedoxa gabonensis Pierre ex Engl. is an important tropical tree species. In this study, its complete plastome sequence was determined. This is the first reported complete plastome sequence in the family Irvingiaceae. The plastome is totally 160,118 bp in length, containing a pair of 26,963-bp-long inverted repeat regions (IRs), a large single copy region of 88,157 bp, and a small single copy region of 18,035 bp. A total of 112 unique genes were identified in *K. gabonensis* plastome, of which 78 are protein-coding genes, 30 are tRNA genes, and four are rRNA genes. Phylogenetic analysis confirmed the close relationship between *K. gabonensis* and *Irvingia malayana*.

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Klainedoxa gabonensis Pierre ex Engl. belongs to the genus *Klainedoxa*, one of the three genera in family Irvingiaceae. Irvingiaceae is a small family containing approximately 11 species, all of them are important tropical tree species. *Klainedoxa gabonensis* is a large tropical tree species widely distributed in the forested regions of West and Central Africa. Its spreading evergreen crown makes it one of the largest trees of the rainforest. The fruits of it and other *Irvingia* species are swallowed whole by elephants (Kubitzki 2014). This plant is used as a rain-forest medicinal plant in Cameroon and Congo (Wansi et al. 2010). Moreover, it may serve as an alternative engineering material to widen the raw material base for timber industry (Boadu et al. 2017). Being the first complete plastome data for the family Irvingiaceae, it will aid us in further research of this family and provide useful genomic information for tropical tree species. It will also be a useful reference for the phylogenomics and evolutionary studies of Malpighiales. In this study, we determined the complete plastome of *K. gabonensis* based on the whole-genome Illumina sequencing dataset. The annotated plastome of *K. gabonensis* has been deposited in the GenBank with the accession number MK814480.

Fresh leaves of a single individual of *K. gabonensis* were sampled from Woleu-Ntem, Gabon (00°37'02"N 010°24'49"E). Voucher specimen (SIMAB 011703) was deposited in Missouri Botanical Garden. Total DNA was extracted using the DNeasy Plant Mini Kit, then fragmented to construct short-insert (400 bp) library following manufacturer's manual (Illumina).

Paired-end (PE) sequencing was performed on Illumina HiSeq X TEN at Plant Germplasm and Genomics Center (Kunming Institute of Botany). The paired-end reads were filtered and assembled into a complete plastome using GetOrganelle v1.5.1c (Camacho et al. 2009; Bankevich et al. 2012; Langmead and Salzberg 2012; Jin et al. 2018), with final assembly graph checked with Bandage (Wick et al. 2015). The plastome was automatically annotated using PGA (Qu et al. 2019), then manually adjusted in Geneious 9.0.5 (Kearse et al. 2012). The plastome of *K. gabonensis* is 160,118 bp in length, containing a large single copy (LSC) region of 88,157 bp and a small single copy (SSC) region of 18,035 bp separated by a pair of 26,963-bp-long IR regions. The overall GC content was 35.3% and the plastome includes 112 unique genes (78 protein-coding genes, 30 tRNA genes, and four rRNA genes). Six protein-coding, seven tRNA, and four rRNA genes are duplicated in the IR regions, the *rps16* gene was lost.

To validate the phylogenetic relationships of *K. gabonensis* in Malpighiales, we constructed a maximum-likelihood (ML) tree of eight taxa within Malpighiales with *Averrhoa carambola* and *Vitis rotundifolia* as outgroup species (Figure 1). Phylogenetic analysis was performed on a data set including 82 gene sequences using RAXML version 8.2.11 with 1000 bootstrap replicates (Stamatakis, 2014). Our results were congruent with previous studies, except for one low-supported node (Xi et al. 2012; Angiosperm Phylogeny Group 2016). *Klainedoxa gabonensis* and *Irvingia malayana* from another genus of Irvingiaceae formed a strongly supported clade.

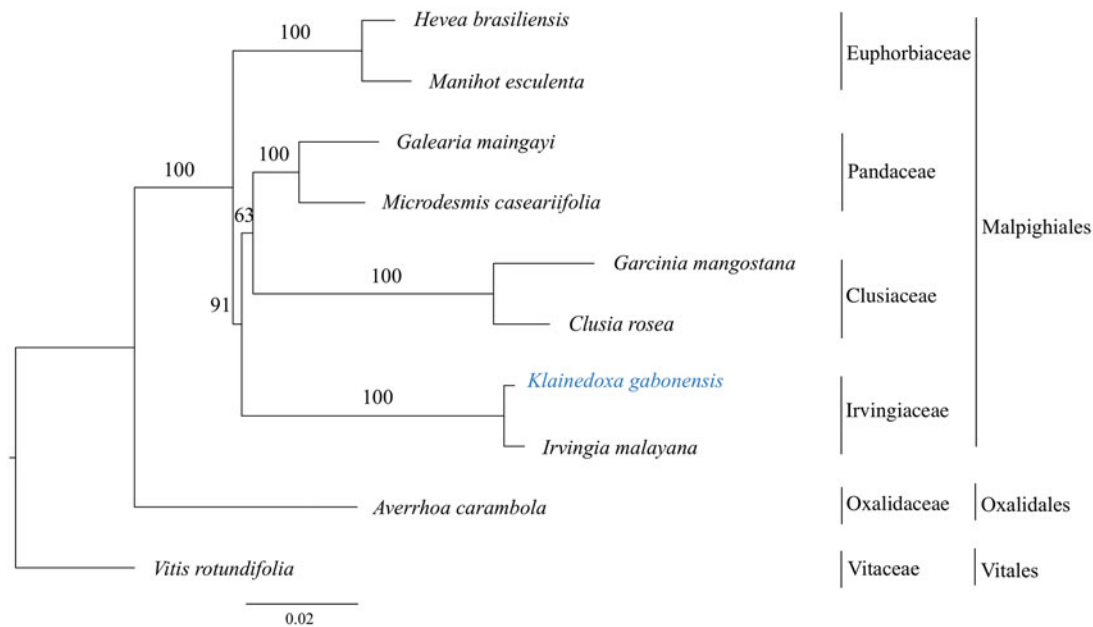


Figure 1. Maximum-likelihood (ML) tree inferred from the 82-gene (76 protein-coding and 4 rRNA genes) matrix. The number at each node indicate the ML bootstrap values. Genbank accession numbers of five taxa (*Clusia rosea*, *Galearia maingayi*, *Garcinia mangostana*, *Irvingia malayana*, *Microdesmis caseariifolia*) referred to the previous plastid phylogenetic study of Malpighiales (Xi et al. 2012), other 4 taxa are shown below, *Hevea brasiliensis* (NC_015308), *Manihot esculenta* (NC_010433), *Averrhoa carambola* (NC_033350), and *Vitis rotundifolia* (NC_023790).

Disclosure statement

No potential conflict of interest was reported by the authors.

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