


## Complete plastome sequence of *Aspidopterys obcordata* (Malpighiaceae), a traditional Dai medicinal plant from Xishuangbanna, Yunnan, China

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### ABSTRACT

We reported the first complete plastid genome of *Aspidopterys* (Malpighiaceae) in this study. The complete plastome of *Aspidopterys obcordata* is 160,453 bp in length with a base composition of A (31.4%), G (18.5%), C (18.2%), and T (32.0%). Structurally, the genome contains two short inverted repeats (26,905 bp for each), which are separated by a large single copy region (88,491 bp) and a small single copy region (18,152 bp). The plastome contained 113 unique genes, including 79 protein-coding genes, 30 transfer RNAs, and 4 ribosomal RNAs. Phylogenetic analyses showed that *A. obcordata* was sister to *Bunchosia argentea* in the monophyletic Malpighiaceae. This study provided a high-quality plastome sequence for future studies in *Aspidopterys*, as well as Malpighiaceae.

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*Aspidopterys obcordata* Hemsl. (Malpighiaceae) is a woody liana and distributes in Hainan and South Yunnan, China (Chen and Funston 2008). The whole plant contained some important biochemical compounds having effects on anti-phlogistic and diuresis treatments, which could be used to cure urinary infection and calculus, cystitis, rheumatism, and bone pain, as well as postpartum weak health and children's digestion diseases (e.g., Wu et al. 2001; Li et al. 2016; Hu et al. 2018; Li et al. 2019). Plants of this species are important ingredients in some ancient prescriptions of the traditional Dai medicine (State Administration of Traditional Chinese Medicine 2005). To date, there had four complete chloroplast genomes reported representing three genera in Malpighiaceae, but none of them belongs to *Aspidopterys* A. Juss. ex Endl. In this study, we reported the complete plastome sequence of *A. obcordata* in the first time, which can be used to develop DNA markers for molecular authentication and conservation genetics of *Aspidopterys*.

Fresh leaves of *A. obcordata* (W.-B. Yu et al. DAI-159 (KUN)) were collected at Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences (21°55'18.66"N 101°16'32.09"E), Mengla, China, then was dried using silica-gel. Genomic DNA was extracted using a modified CTAB method (Doyle and Doyle 1987). The 150 bp pair-end reads were generated by Illumina Hi-Seq 2500 using 500 bp insert size library. Around 7.25 Gb clean data with 20,455,554 reads were *de novo* assembled using GetOrganelle toolkit (Jin et al. 2020).

The plastome was annotated using GeSeq (Tillich et al. 2017), then manually adjusted in Geneious (Kearse et al. 2012).

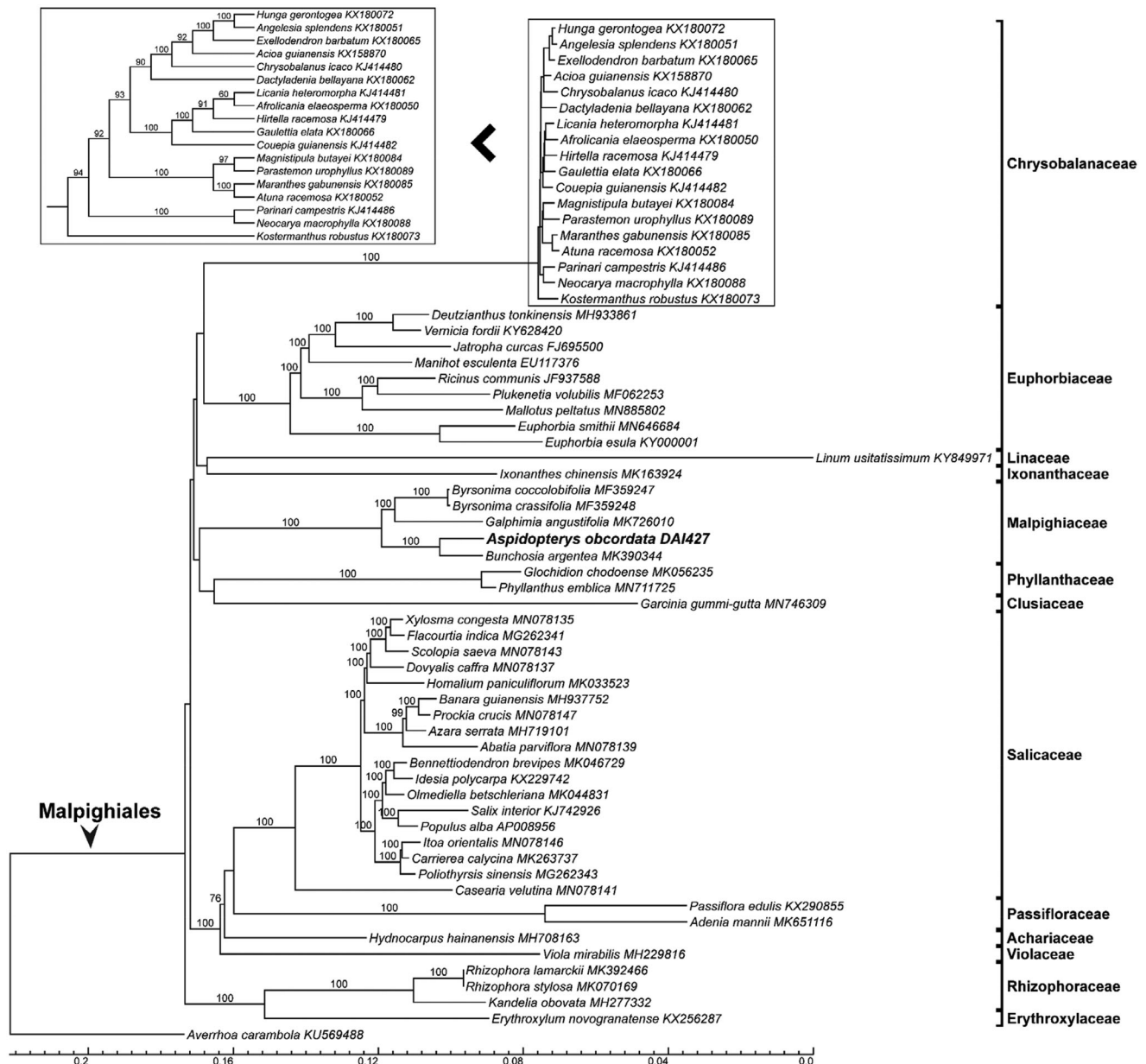
The whole plastome of *A. obcordata* was 1,60,453 bp (MT590775) in length with two inverted repeats (IRs, 26,905 bp for each) that were separated by a large single-copy (LSC, 88,491 bp) and a small single-copy (SSC 18,152 bp) regions. The plastome contained 131 genes in total, including 113 unique genes in 79 protein-coding, 30 tRNA, and four rRNA genes. There are nine protein-coding (three are partial), seven tRNA, and four rRNA genes in IR regions. The overall GC content was 36.6%.

The whole sequences with one IR region of 62 taxa of Malpighiales and an outgroup *Averrhoa carambola* L. (Oxalidales, KU569488) were aligned using MAFFT (Katoh and Standley 2013), then the gaps were trimmed by trimAl (Capella-Gutiérrez et al. 2009) using the command '-gt 0.9 -cons 60.' For Maximum Likelihood analyses, we used RAxML (Stamatakis et al. 2008) using GTRGAMMAI model with 1000 bootstraps to reconstruct phylogeny of Malpighiales. Phylogenetic analysis showed that the backbone of Malpighiales was not resolved, and *A. obcordata* was sister to *Bunchosia argentea* (Jacq.) DC. (MK390344) in the monophyletic Malpighiaceae (Figure 1). This new plastome sequence will be valuable for investigations on systematics and conservation genetics of *Aspidopterys*.

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**Figure 1.** Plastome phylogenomics of Malpighiales based on Maximum-likelihood (ML) estimation. *Aspidopterys obcordata* was highlighted by bold and blue style. ML bootstrap values of nodes indicated above the branch. The bottom scale bar represents the number of substitutions per site.

## Disclosure statement

The authors report no conflicts of interest and responsible for the content and writing of this article.

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## Data availability statement

The complete plastome was deposited at GenBank with accession number MT590775, which was also available at Figshare (doi: 10.6084/m9.figshare.12497900). The data was collected without violation of the protection of human subjects, or other valid ethical, privacy, or security concerns.

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