


Complete plastid genome sequence of a medical herb, *Anisomeles indica* (L.) Kuntze (Lamiaceae)

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ABSTRACT

The species *Anisomeles indica* is used medicinally and widely distributed from India, to China and the Indo-China Peninsula. The first complete plastid genome sequence of *A. indica* reported here was 151,900 bp long, with the large single copy (LSC) region of 83,144 bp, the small single copy (SSC) region of 17,556 bp and two inverted repeats (IRa and IRb) of 25,600 bp. The plastome contained 113 genes, including 79 protein-coding genes, 4 ribosomal RNA genes and 30 transfer RNA genes. The overall GC content was 38.26%. Result from phylogenetic analysis suggests that *Anisomeles* is closely related to the genus *Pogostemon*.

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Anisomeles R. Brown belongs to the tribe Pogostemoneae, subfamily Lamioideae, family Lamiaceae (Li et al. 2016; Yao et al. 2016). It consists of about five or six species of herbs (Li and Hedge 1994), among which the species *Anisomeles indica* (L.) Kuntze is a strong-scented herb, occurring widely from India to China and the Indo-China Peninsula, and it is found usually growing along forest margins, roadsides and waste areas (Li and Hedge 1994; Batish et al. 2012). The species is used medicinally for rheumatism, colds, fevers, liver disease and protection, and snake bites (Li and Hedge 1994; Rao et al. 2009).

Samples of *Anisomeles indica* were collected from Guangdong province (China; N23°11'7", E113°21'53"). Voucher specimen (G. Yao 448) was deposited in the Herbarium of South China Botanical Garden, Chinese Academy of Sciences (IBSC). Total DNA was isolated using the CTAB method (Doyle and Doyle 1987) and sequenced on the Illumina HisSeq 2500 Sequencing System. Reads were assembled with the pipeline GetOrganelle (Jin et al. 2018), and the genome obtained was annotated using software PGA (Qu et al. 2019). The annotated plastid genome sequence has been deposited into the GenBank with the accession number MN115836.

The whole plastid genome of *Anisomeles indica* was 151,900 bp in length, with a large single-copy (LSC) region (83,144 bp), a small single-copy (SSC) region (17,556 bp), and a pair of inverted repeats (IRa and IRb; 25,600 bp). The annotated genome comprised 113 genes, including 79 protein-coding genes, four ribosomal RNA genes (rrn 16, rrn23,

rrn4.5, rrn5), and 30 transfer RNA genes. Seventeen genes were duplicated in the IR regions, including six protein-coding genes (*ndhB*, *rpl2*, *rpl23*, *rps12*, *rps7*, *ycf2*), four ribosomal RNA genes (rrn16, rrn23, rrn4.5, rrn5), and seven transfer RNA genes (trnA-UGC, trnI-CAU, trnI-GAU, trnL-CAA, trnN-GUU, trnR-ACG, trnV-GAC). The overall GC content of *A. indica* plastid genome is 38.26% (LSC, 36.38%; SSC, 32.29%; IRs, 43.37%).

The maximum likelihood (ML) phylogenetic tree was constructed using RAxML-HPC2 (8.1.24) (Stamatakis 2014) on the CIPRES cluster (Miller et al. 2010), employing the GTR + G model and the default number of rate categories (C = 25). We conducted a rapid bootstrap analysis using the GTR + G model with 1000 bootstrap replicates. Phylogenetic analysis based on 79 protein-coding genes of 24 representative plastomes within the family Lamiaceae suggests that *Anisomeles* is closely related to the genus *Pogostemon* (Figure 1).

Disclosure statement

No potential conflict of interest was reported by the authors.

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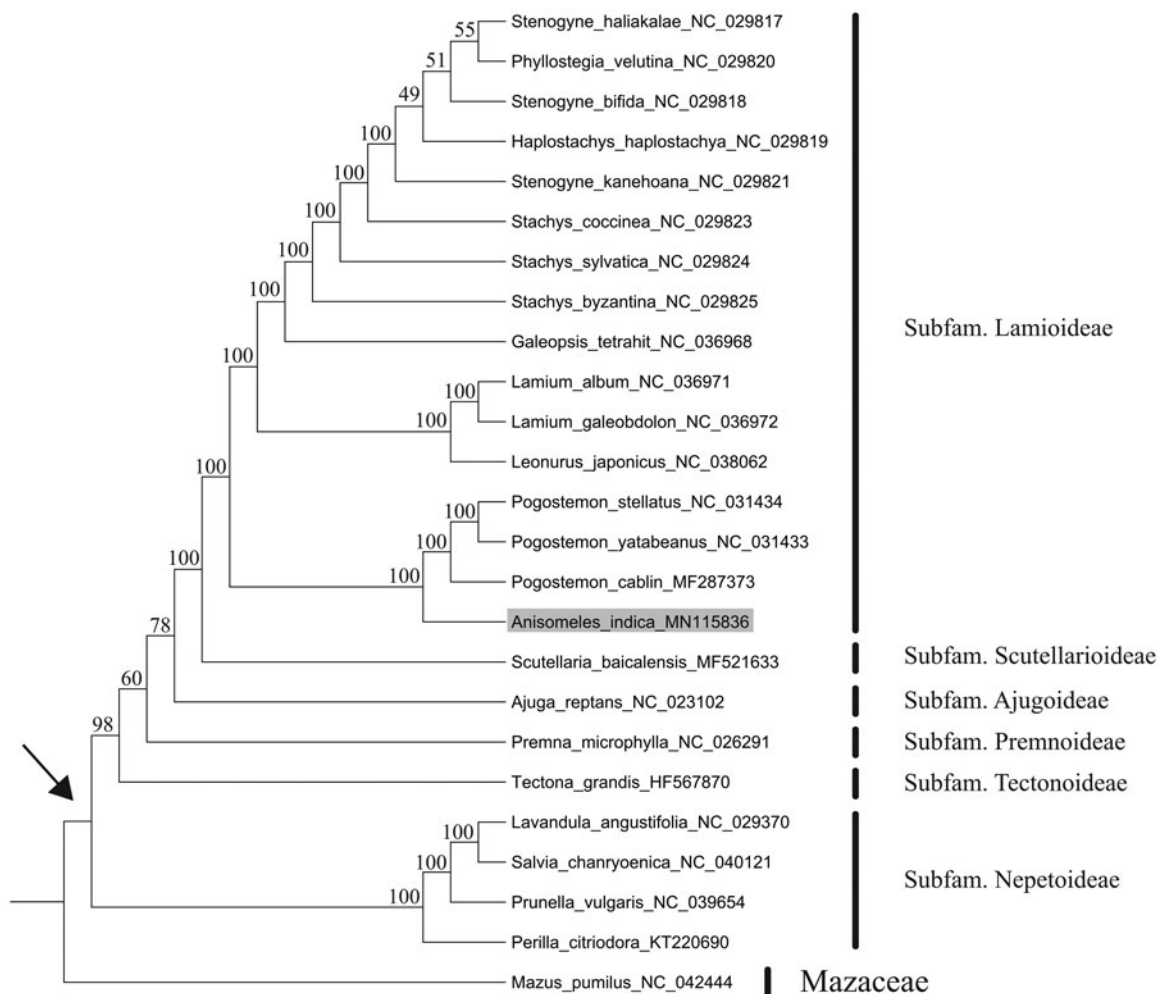


Figure 1. Maximum likelihood tree of Lamiaceae inferred from 79 protein-coding genes of 25 plastomes (including the outgroup *Mazus pumilus* from Mazaceae). Bootstrap values are indicated above branches. The crown node of Lamiaceae is shown by an arrowhead. The species *Anisomeles indica* is marked with gray background.

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