

The complete chloroplast genome sequence of *Elsholtzia densa*, a herb with volatile aroma component

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ABSTRACT

The complete chloroplast genome sequence of *Elsholtzia densa* was analysed. The results indicated that the size of the chloroplast genome was 149,095 bp in length with a large single-copy region (LSC) of 81,497 bp, a small single-copy region (SSC) of 17,364 bp, and a pair of inverted repeat (IR) regions of 25,117 bp. The overall GC content of the cpDNA genome was 37.86%, while the corresponding values of the LSC, SSC, and IR regions were 35.96%, 31.92%, and 43.16%, respectively. A total of 132 functional genes were identified, including 84 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. The maximum likelihood phylogenetic tree suggested that *E. densa* was closely related to the species in the family Labiatae.

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Elsholtzia densa belongs to the *Elsholtzia* genus of the family Labiatae. It is widely spread throughout the warm zone of Eurasia. It grows mainly in the north of China in Hebei, Shanxi, QTP (The Qinghai-Tibetan Plateau) and adjacent areas, including Gansu, Qinghai, and Tibet, West Sichuan, etc. (Sun et al. 1996). Although *E. densa* is considered a weed, it was also used as a medicine because of its rich nutrients and bioactive substances, especially the herb has essential oil containing bioactive compounds. 73 volatile compounds in the volatile oil have been reported (Xue et al. 2016; Zhang et al. 2019). A new study also reported the presence of 40 constituents comprising 83.3–83.7% of essential oil composition. Essential oil extracted from the leaf of *E. densa* was characterized by citral (52.2%), geranyl acetate (3.3%), and geraniol (3.1%) (Chauhan et al. 2018). So, *Elsholtzia* species are commonly used in traditional medicine to treat colds, fever, dysentery, digestion disorders, and heat stroke, among others (Liu et al. 2007). So far, the researches on the genome of *E. densa* have not been reported. Here, to develop and utilize the herbal plants better, the complete chloroplast genome sequence (Genbank accession number: MN793319) has been detected and phylogenetic analysis was also conducted, which provide more genome data information for its genetic and evolution in the family Labiatae.

In this study, the specimen *E. densa* was sampled from Qinghai lake Erlangjian scenic, Gonghe County, China (36.5785°E, 100.4911°N). A voucher specimen (FGE20197201) was stored in the Qinghai Nationality University, Qinghai, China. Total DNA was extracted from freshly collected leaf tissue using the modified CTAB method described by Rofers

and Bebdich (1998). The complete chloroplast was sequenced by Illumina Hiseq 4000 (Illumina, San Diego, CA) in Genepioneer Biotechnologies Inc., Nanjing, China. The trimmed reads were mainly assembled by SPAdes (Bankevich et al. 2012), with that of its congener *Pogostemon cablin* (GenBank accession number: MF287372.1) (Zhang et al. 2019) and approximately 5.3 Gb clean data were assembled.

The 149,095 bp length circular chloroplast genome of *E. densa* was obtained, which comprised of two inverted repeats (IRs) of 25,117 bp, a large single-copy (LSC) region genome of 81,497 bp, and a small single-copy (SSC) region of 17,364 bp. The total GC content is 37.92% while the corresponding value of the LSC, SSC, and IR regions was 35.96%, 31.92%, and 43.16%, respectively. A total of 129 genes was identified, which included 84 unique protein-coding genes, 37 unique tRNA genes, and 8 unique rRNA genes.

Alignment for cpDNA *E. densa* sequences was conducted using MAFFT (<https://mafft.cbrc.jp/alignment/server/>). Phylogenetic relationships were evaluated based on cpDNA sequences using the maximum likelihood (ML) method. RA × ML v8.2.10 software (<https://cme.h-its.org/exelixis/software.html>) was used to reconstruct the phylogenetic tree with 1000 bootstraps under the GTRGAMMAI substitution model. The tree was reconstructed including *E. densa*, and 31 published complete chloroplast sequences of Labiatae and *Sesamum indicum* (Pedaliaceae) was chosen as an outgroup. Based on the phylogenetic analysis, the species from identical family were clubbed together as a monophyletic clade and all nodes showed strong support (>95%). Meanwhile, a monophyletic clade was formed including *E. densa* and

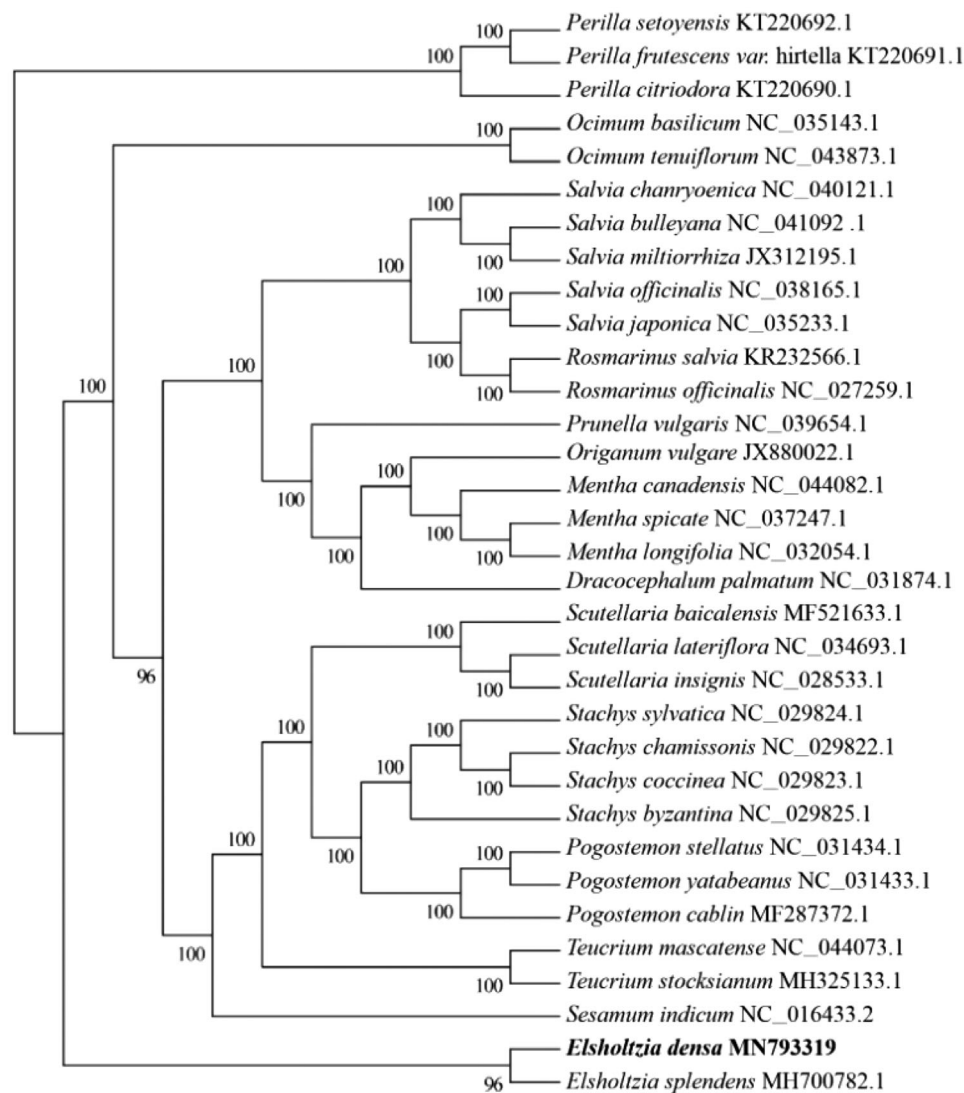


Figure 1. The maximum likelihood (ML) tree inferred from 31 representative chloroplast genomes of Labiatae and Pedaliaceae. The bootstrap value based on 1000 replicates is marked on each node and species accession numbers are shown in the figure.

Elsholtzia splendens (MH700782.1). A close relationship was revealed between *E. densa* and *E. splendens* (Figure 1). The results in this study will provide a useful foundation for further investigation of genetic and phylogenetic studies for the family Labiatae.

Disclosure statement

No potential conflict of interest was reported by the authors.

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