**The complete mitochondrial genome of *Osmanthus fragrans* (Lamiales, Oleaceae) from China**

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*Osmanthus fragrans* Lour. (sweet osmanthus, Oleaceae) is a well-known evergreen ornamental tree that produces small white, yellow, or orange flowers with a sweet, rich fragrance (Xiang and Liu 2008). It is also edible and has medicinal values (Zhou et al. 2017). In previous phylogenetic studies, *O. fragrans* was clustered with *Chionanthus retusus* based on nuclear ribosomal DNA sequences (Bensard et al. 2009), which is inconsistent with the results based on plastid sequences (Bensard et al. 2009; Duan et al. 2019). In this study, the complete mitochondrial genome sequence of *O. fragrans* was assembled and characterized to reveal the evolutionary history of *O. fragrans* based on a mitochondrial phylogenomic analysis.

The fresh leaves were collected from a tree in the Shijiazhuang People’s Medical College (Hebei, China) (N 37.99°; E 114.45°). The voucher specimen (accession no. PMC160614) was deposited in the Shijiazhuang People’s Medical College (http://www.sjzmyz.com/, Jie Guo, 876538268@qq.com). Genomic DNA was extracted using a modified CTAB method (Doyle and Doyle 1987). The extracted DNA was fragmented for Illumina library construction by Illumina TruSeq DNA sample prep kit and then sequenced on the HiSeq X Ten platform (Illumina Inc., San Diego, CA, USA). The complete mitochondrial genome sequence of *O. fragrans* was assembled with GetOrganelle v.1.6.2e (Jin et al. 2020) and annotated with the OGAP pipeline using the default settings (https://github.com/zhangren gang/OGAP). The draft annotations were then adjusted manually with the assistance of BLAT (Kent 2002).

The complete mitochondrial genome of *O. fragrans* was assembled as a circular molecule 563,202 bp in length (GenBank accession no. MW645067), with an overall GC content of 44.58%. Sixteen chloroplast-derived segments with an average length of 1260 bp were identified. The complete mitochondrial genome contained 74 genes in total, including 44 protein-coding, three rRNA, and 27 tRNA genes, among which seven protein-coding and six tRNA genes were chloroplast-derived. Phylogenetic analysis showed that *O. fragrans* was closely related to *Chionanthus rupicola* within the Oleaceae. This study could provide genomic resources for a better understanding of *O. fragrans* and further studies on the evolution of Oleaceae.
Lamiales were consistent with previous chloroplast-based studies (Duan et al. 2019; Zhu et al. 2020). In summary, this study extended our knowledge to *O. fragrans* and provided a reference for further research on the phylogeny and evolution of the family Oleaceae as well as the order Lamiales.

**Disclosure statement**

No potential conflict of interest was declared by the authors.

**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at http://www.ncbi.nlm.nih.gov/ under the accession no. MW645067. The associated BioProject, SRA, and BioSample numbers are PRJNA713943, SRR13948793, and SAMN18275439, respectively.

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**Figure 1.** Phylogenetic tree inferred by maximum-likelihood method based on mitochondrial protein-coding gene sequences of *O. fragrans* and other 12 species within the order Lamiales. *Solanum lycopersicum* was served as the outgroup. Numbers in the nodes are the bootstrap values from 1000 replicates. The branch of *Ajuga reptans* was truncated as it was too long.