Camellia osmantha is a new species discovered in Nanning, Guangxi, China, in 2012. It can be used as an excellent woody oil crop. There is little related research on this species in China and abroad, and its genome information is still lacking. In this study, the complete chloroplast genome sequence of C. osmantha was first reported (GenBank number: MZ128138). The whole chloroplast genome is 156,981 bp in length with a GC content of 37.28%, and it is composed of a large single copy (LSC) region of 86,647 bp, a small single copy (SSC) region of 18,284 bp, and a pair of inverted repeat (IR) regions of 26,025 bp each. The genome contains a total of 135 functional genes, including 37 transfer RNA genes, 90 protein-coding genes, and 8 ribosomal RNA genes. The maximum likelihood analysis based on 21 chloroplast genomes showed that C. osmantha and C. oleifera (MF541730.2) were the most closely related.

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The complete chloroplast genome of Camellia osmantha, an edible oil Camellia

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ABSTRACT
Camellia osmantha is a new species of the Camellia genus discovered in Nanning, Guangxi, China, in 2012. It can be used as an excellent woody oil crop. There is little related research on this species in China and abroad, and its genome information is still lacking. In this study, the complete chloroplast genome sequence of C. osmantha was first reported (GenBank number: MZ128138). The whole chloroplast genome is 156,981 bp in length with a GC content of 37.28%, and it is composed of a large single copy (LSC) region of 86,647 bp, a small single copy (SSC) region of 18,284 bp, and a pair of inverted repeat (IR) regions of 26,025 bp each. The genome contains a total of 135 functional genes, including 37 transfer RNA genes, 90 protein-coding genes, and 8 ribosomal RNA genes. The maximum likelihood analysis based on 21 chloroplast genomes showed that C. osmantha and C. oleifera (MF541730.2) were the most closely related.

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C. osmantha and C. oleifera (MF541730.2) was found to be the closest.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

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**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at (https://www.ncbi.nlm.nih.gov/) under the accession No. MZ128138. The associated BioProject, Bio-Sample, and SRA numbers are PRJNA725044, SAMN18928057, and SRR14469701 respectively.

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