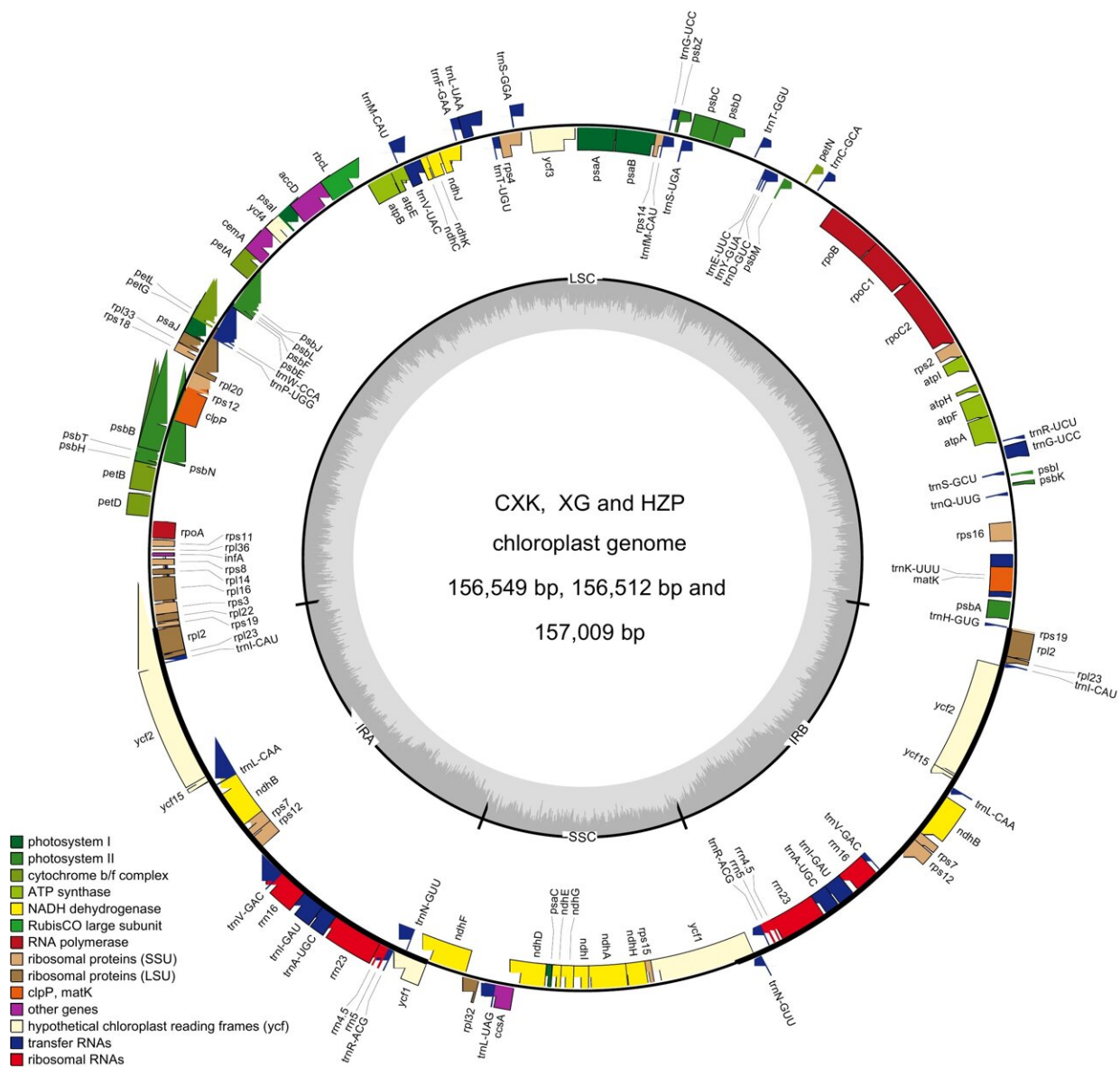


# Chloroplast genome study separates *C. meiocarpa* and *C. oleifera* to enhance tea-oil camellia breeding

August 19 2024



Chloroplast genome map of *C. meiocarpa* and *C. oleifera*. Credit: *Tropical Plants* (2024). DOI: 10.48130/tp-0024-0022

A research team sequenced and analyzed the complete chloroplast genomes of *C. oleifera* and *C. meiocarpa*, uncovering significant differences that clarified their phylogenetic relationship. This study developed 17 chloroplast DNA primers for distinguishing between them, contributing valuable tools for assessing genetic diversity in tea-oil *Camellia*.

These findings hold significant potential for future research and practical applications in germplasm resource assessment, molecular phylogenetic analysis, and the innovation and utilization of tea-oil *Camellia* in agricultural and industrial practices.

Tea-oil *Camellia*, known for its high oil content and health benefits, is a key woody oil crop with significant cultivation value, especially in China. Despite its importance, the phylogenetic relationships among tea-oil *Camellia* [species](#), particularly between *C. meiocarpa* and *C. oleifera*, remain controversial due to complex nuclear genomes and interspecific hybridization.

Moreover, no reports exist on the chloroplast genome of *C. meiocarpa*, and no [comparative analysis](#) has been done between *C. oleifera* and *C. meiocarpa*. These unresolved issues hinder effective breeding and production.

A [new study](#), published in *Tropical Plants* on 24 July 2024, aims to clarify these relationships by analyzing the chloroplast genomes of *C. oleifera* and *C. meiocarpa* and developing molecular markers for variety

identification and resource utilization.

The research employed [comparative genomics](#) to analyze the chloroplast genomes of *C. meiocarpa* (CKX/XG) and *C. oleifera* (HZP), focusing on genome structures, repetitive sequences, IR region variations, nucleotide diversity, and phylogenetic relationships.

The chloroplast genomes exhibited a typical circular tetrameric structure with slight size differences among the species. Repetitive sequences and simple sequence repeats (SSRs) were distributed unevenly, with distinct patterns observed between the species. The expansion and contraction of the IR regions revealed genomic adaptations, particularly between HZP and CKX/XG.

Nucleotide diversity analysis highlighted the *ycf1* gene as having the most mutations, and intergenic regions showed significant variation. Phylogenetic analysis confirmed that CKX and XG is not closely related to HZP.

Additionally, 56 pairs of primers were designed based on polymorphic sites, with 17 primers successfully validated for assessing polymorphic sites, providing essential tools for the identification and genetic study of tea-oil *Camellia* species.

According to the study's senior researcher, Daojun Zheng, "The present study provided high-quality chloroplast genomes and reliable molecular marker resources for future tea-oil *Camellia* research."

This study primarily investigated the chloroplast genomes of *C. meiocarpa* and *C. oleifera*, revealing significant genetic differences that support *C. meiocarpa* as an independent species. The development of 17 primers enhances species identification and resource assessment, benefiting breeding programs and production practices. These findings

provide high-quality [chloroplast](#) genomes and reliable molecular marker resources for future tea-oil *Camellia* research.

**More information:** Heng Liang et al, Comparative chloroplast genome analysis of *Camellia oleifera* and *C. meiocarpa*: phylogenetic relationships, sequence variation and polymorphic markers, *Tropical Plants* (2024). [DOI: 10.48130/tp-0024-0022](https://doi.org/10.48130/tp-0024-0022)

Provided by Chinese Academy of Sciences

Citation: Chloroplast genome study separates *C. meiocarpa* and *C. oleifera* to enhance tea-oil camellia breeding (2024, August 19) retrieved 20 August 2024 from <https://phys.org/news/2024-08-chloroplast-genome-meiocarpa-oleifera-tea.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.