

Low genetic diversity and significant pedigree differentiation characterize the evolutionary history of *Camellia drupifera* in China

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Abstract

Camellia drupifera is a main tea-oil *Camellia* species, and understanding its genetic variation, origin and evolution will facilitate protection and utilization of its genetic resources. However, the differentiation, genetic variation, origin and evolution of *C. drupifera* remains unknown. Here, SRAP markers and chloroplast sequences of 32 *C. drupifera* populations were used to determine genetic variation and differentiation and infer the origin and evolutionary history of the species. Genetic diversity is low ($H=0.200$, $H_d=0.861$, $P_i=0.00238$), with obvious pedigree geographical structure among populations ($N_{st}=0.612$, $G_{st}=0.117$). Genetic differentiation is high ($G_{st}=0.400$, SRAP; $F_{st}=0.68080$, cpDNA), but gene exchange is low ($N_m = 0.749$ for nrDNA, $N_m = 0.358$ for cpDNA). The phylogenetic tree and PCA showed that this differentiation is mainly due to separation of the Hainan Island and mainland populations. Geographical isolation and island effects caused the pedigree structure, with large genetic differentiation, and reduced genetic diversity. STRUCTURE analysis revealed that compared with the Hainan Island population, the mainland population has a single genetic background. The TCS network showed that H17 was the original haplotype on Hainan Island; the H41 haplotype was important in the expansion of *C. drupifera* from Hainan Island to mainland China. Haplotype historical dynamics revealed expansion of the Hainan Island populations (Tajima's $D=-2.31467^{**}$, Fu's $F_s=-2.45270^{*}$). Comprehensive analysis suggests that *C. drupifera* originated on Hainan Island and expanded its range to mainland China. These results provide a scientific basis for the protection, development and utilization of *C. drupifera* resources and a good example of how geographic isolation and island effects can drive plant lineage differentiation.

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