

# 板栗线粒体基因组的组装与比较分析

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**摘要:**【目的】板栗 (*Castanea mollissima* Blume), 壳斗科, 是原产于中国和朝鲜的一种坚果树种, 也是食用栗属品种改良的重要遗传资源, 在了解栗属物种起源和进化方面具有重要地位。板栗叶绿体基因组已被测序, 而线粒体基因组迄今尚未被探索。【方法】使用 BGI 的二代测序数据和 Nanopore 的三代测序数据, 采用混合组装的策略组装板栗线粒体基因组, 并与其相关物种的线粒体基因组进行比较分析。【结果】板栗线粒体基因组是一个多环结构, 有两个长度分别为 363,232 bp 和 24,806 bp 的环状分子。该基因组包括 35 个蛋白质编码基因、19 个 tRNA 基因和 3 个 rRNA 基因。在整个板栗线粒体基因组中共鉴定了 139 个 SSRs。叶绿体和线粒体基因组之间同源片段的总长度为 5,766 bp, 占线粒体基因组的 1.49%。共预测到 484 个 RNA 编辑位点, 均为出 C-U 的编辑。【结论】系统发育分析发现, 板栗与木姜叶柯 (*Lithocarpus litseifolius*) 和麻栎 (*Quercus acutissima*) 的亲缘关系较近。板栗、麻栎、木姜叶柯、欧洲水青冈 (*Fagus sylvatica*) 和胡桃楸 (*Juglans mandshurica*) 的线粒体基因组序列在排列顺序上极度不保守, 经历了极其频繁的基因组重组。本研究首次报道了板栗的线粒体基因组, 作为栗属重要经济植物的参考基因组, 为分子育种研究提供一定的信息。

**关键词:** 板栗; 线粒体基因组; 重复序列; 系统发育关系

## Assembly and comparative analysis of the complete mitochondrial genome of *Castanea mollissima* Blume

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**Abstract:** 【Objective】The Chinese chestnut, *Castanea mollissima* Blume, is a nut-bearing tree belonging to the Fagaceae family and is native to China and North Korea. *C. mollissima* is an important genetic resource for the improvement of edible chestnut varieties and occupies an important position in understanding the origin and evolution of chestnut species. The *C. mollissima* chloroplast genome has been sequenced; however, the mitochondrial genome (mitogenome) is to date unexplored. 【Method】We characterized the *C. mollissima* mitogenome, assembling it using reads from BGI and Nanopore sequencing platforms, and analyzed in comparison with mitochondrial genomes of closely related species. 【Result】The *C. mollissima* mitogenome is a polycyclic structure with two circular molecules of 363,232 bp and 24,806 bp in length. The genome comprises 35 unique protein-coding genes, 19 tRNA genes and 3 rRNA genes. We identified 139 SSRs across the whole *C. mollissima* mitogenome. The total length of homologous fragments between the chloroplast and mitochondrial genomes was 5,766 bp, accounting for 1.49 % of the mitogenome. A total of 484 RNA editing sites were predicted in *C. mollissima*, all exhibiting C-to-U RNA editing. 【Conclusion】Phylogenetic analysis of the mitogenomes of related species revealed that *C. mollissima* was closely related to *Lithocarpus litseifolius* (Hance) Chun and *Quercus acutissima* Carruth. The mitogenome sequences of *C. mollissima*, *L. litseifolius*, *Q. acutissima*, *Fagus sylvatica* L., and *Juglans*

*mandshurica* Maxim. are not conserved in their alignments, suggesting they have undergone frequent genome reorganization. In this study, we report for the first time the mitogenome of *C. mollissima*, which serves as a reference genome for economically important plants of the genus *Castanea* and also provides information to inform molecular breeding.

**Key words:** *Castanea mollissima*; mitogenome; repeated sequences; phylogenetic relationship.