

香榧种仁油脂合成遗传结构和分子机制解析

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摘要:【目的】香榧 (*Torreya grandis* cv. *Merrillii*) 属于裸子植物门红豆杉科榧属植物。香榧是我国特产的经济树种, 其种仁可食用, 并且富含不饱和脂肪酸。然而, 在不同地方品种的香榧种仁中, 脂肪酸和油含量存在差异。作为裸子植物, 香榧是否具有特殊的油脂代谢机制? 本研究旨在解析脂肪酸和油脂含量的遗传结构及其潜在分子调控机制。【方法】我们构建了一个高质量的香榧参考基因组, 并对 170 个不同香榧地方品种的种仁的 10 个脂肪酸和油脂性状进行了转录组参考关联分析 (TRAS)。为了验证 TRAS 结果, 我们对与油脂显著相关的基因进行了功能验证和分子生物学实验。【结果】我们通过 TRAS ($-\log_{10}(P) > 6.0$) 鉴定了与 7 个性状显著相关的 34 个转录本中的 41 个 SNP 位点。结果表明, LOB domain-containing protein 40 (LBD40) 和 surfeit locus protein 1 (SURF1) 可能分别间接参与了植物油脂和金松酸的生物合成调控。过表达 *TgLBD40* 能显著提高种子含油量。TRAS 结果显示, *TgLBD40* 编码区的非同义变异可以改变其含油量。皮尔逊相关性分析和双荧光素酶瞬时调控实验分析表明, *TgLBD40* 通过影响油脂合成途径基因 (如 *TgDGATI*) 的表达来促进油脂积累。【结论】我们的研究为香榧油脂合成的遗传基础提供了新的见解, 并表明了整合转录组测序和 TRAS 作为一个强大的关联分析手段, 可以有效地独立于参考基因组解析香榧的重要性状。

关键词: 油脂合成; 香榧; 转录组参考关联分析; 单核苷酸多态性; 转录组测序

Transcriptome-referenced association study provides insights into the regulation of oil and fatty acid biosynthesis in *Torreya grandis* kernel

Abstract: 【Objective】*Torreya grandis* is a gymnosperm belonging to Taxodiaceae. As an economically important tree, its kernels are edible and rich in oil with high unsaturated fatty acids, such as sciadonic acid. However, the kernels from different *T. grandis* landraces exhibit fatty acid and oil content variations. As a gymnosperm, does *T. grandis* have special regulation mechanisms for oil biosynthesis? The aim of this study was to dissect the genetic architecture of fatty acid and oil content and the underlying mechanism in *T. grandis*. 【Method】 We constructed a high integrity reference sequence of expressed regions of the genome in *T. grandis* and performed transcriptome-referenced association study (TRAS) for 10 fatty acid and oil traits of kernels in the 170 diverse *T. grandis* landraces. To confirm the TRAS result, we performed functional validation and molecular biology experiments for oil significantly associated genes. 【Result】 We identified 41 SNPs from 34 transcripts significantly associated with 7

traits by TRAS ($-\log_{10}(P) > 6.0$). Results showed that LOB domain-containing protein 40 (LBD40) and surfeit locus protein 1 (SURF1) may be indirectly involved in the regulation of oil and sciadonic acid biosynthesis, respectively. Moreover, overexpression of *TgLBD40* significantly increased seed oil content. The nonsynonymous variant in the *TgLBD40* coding region discovered by TRAS could alter the oil content in plants. Pearson's correlation analysis and dual-luciferase assay indicated that *TgLBD40* positively enhanced oil accumulation by affecting oil biosynthesis pathway genes, such as *TgDGATI*. **【Conclusion】** Our study provides new insights into the genetic basis of oil biosynthesis in *T. grandis* and demonstrates that integrating RNA sequencing and TRAS is a powerful strategy to perform association study independent of a reference genome for dissecting important traits in *T. grandis*.

Key words: Oil biosynthesis; *Torreya grandis*; Transcriptome-referenced association study; single nucleotide polymorphism; RNA sequencing.