

转录组和代谢组联合解析香榧中榧黄素生物合成通路

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摘 要:【目的】明确香榧中特有双黄酮类物质榧黄素的生物合成途径及其组织特异性积累的分子机制。【方法】以不同组织根、茎、叶、种仁、假种皮为对象,分别进行转录组测序和代谢物质检测。通过各个组织中差异基因表达量与榧黄素含量的相关性分析,筛选到榧黄素生物合成中关键候选基因,并结合酿酒酵母实验进行功能验证。【结果】榧黄素含量具有明显的组织特异性分布,在假种皮、叶和茎中含量最高,而在根和种仁中几乎检测不到。通过转录组和榧黄素含量的相关性分析,筛选到榧黄素生物合成中关键的氧甲基转移酶,进一步的酿酒酵母实验鉴定出 TgOMT1。此外,通过共表达分析对参与 TgOMT1 基因调控的转录因子进行了筛选,提示它们可能调控榧黄素的生物合成。【结论】以芹菜素为底物的 4'-O-甲基转移酶可能作为关键步骤在榧黄素的积累中发挥重要作用,为后续榧黄素提取和生物合成提供理论基础。

关键词: 香榧; 榧黄素; 氧甲基转移酶; 生物合成

Integrated metabolomic and transcriptional analysis reveals mechanisms of tissue specificity in xiangfei kayaflavone biosynthesis

Abstract: 【Objective】To elucidate the biosynthetic pathway of kayaflavone and its molecular mechanism of tissue-specific accumulation in xiangfei (*Torreya grandis*). 【Methods】The roots, stems, leaves, seeds and arils of different tissues were selected for transcriptome sequencing and metabolic substances detection. Through the correlation analysis of differential gene expression and kayaflavone content in each tissue, the key candidate genes in kayaflavone biosynthesis were screened, and their functions were verified by *Saccharomyces Cerevisiae* experiment. 【Results】The content of kayaflavone in arils, leaves and stems was the highest, but hardly detected in roots and seeds. Through the correlation analysis between the transcriptome and the content of kayaflavone, the key O-methyltransferase in the biosynthesis of kayaflavone was screened, and further experiments on yeast identified TgOMT1. In addition, transcription factors involved in TgOMT1 gene regulation were screened by co-expression analysis, suggesting that they may regulate the biosynthesis of kayaflavone in *T. grandis*. 【Conclusion】4'-O-methyltransferase with apigenin as the substrate may play an important role in the accumulation of kayaflavone, providing a theoretical basis for subsequent extraction and biosynthesis of kayaflavone.