

樟科植物萜类化合物多样性形成机制

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摘要: 植物作为优秀的化学家, 可合成百万种结构功能多样的天然化合物。其中, 谱系特异性萜类化合物通常限定与特定的生态位或单一物种, 参与植物对环境的适应。已有研究表明, 谱系特异性萜类化合物往往诞生于物种进化中产生的新基因, 特别是可通过聚合合成酶、修饰酶、转运蛋白或转录因子形成基因簇以进行特异萜类化合物的高效合成。樟科 (*Lauraceae*) 植物是我国重要的香料、医药原料的重要来源。其中樟树、山苍子和油樟等规模化种植面积超过2000万亩, 年产值近200亿元。樟科植物富含芳樟醇、柠檬醛和桉叶油醇等近百种萜类化合物, 不同种不同化学型所含的萜类化合物种类及数量丰富、功效多样。但是, 樟科萜类化合物多样性形成机理尚不清楚, 限制了其生物合成和代谢精准调控研究。本研究基于比较基因组鉴定了一个樟科特有的柠檬醛生物合成基因簇MYB-ADHs, 该基因簇包含醇脱氢酶ADH28和ADH29以及转录因子MYB44, 其中, ADH为柠檬醛合成途径中最后也是最关键的修饰酶。MYB-ADHs通过樟科特异性的串联和近端重复事件形成。酶活性和酶动力学分析表明, 山苍子、樟树、牛樟的ADH28和29在催化底物和酶活性上发生了分化, 山苍子ADH28和29对香叶醇和橙花醇的催化活性显著高于樟树和牛樟。同时, MYB44可通过直接结合ADH28和29启动子中的CAGTTG和CTTAGGTTT元件调控ADHs在果实中特异性高表达, 为山苍子中柠檬醛的大量合成提供了遗传基础。基于MYB-ADHs基因簇, 我们利用遗传转化体系创制了柠檬醛提高20%的山苍子转基因株系。本研究揭示了樟科萜类化合物多样性的特征和合成机制, 并提出了基于樟科特有基因簇进行良种选育的新策略。

The mechanism underlying diversification of Lauraceae terpenoids

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Abstract: Lineage-specific terpenoids appear and enrichment during the evolution of green plants are often believed to play a role in the ecological interactions. Species-specific gene clusters in plants have provided new perspectives on the evolution of secondary metabolism. Lauraceae is an important economic and ecological tree family, with members of the family having considerable value because they are rich in monoterpenes. However, the gene cluster responsible for the biosynthesis of monoterpenes have yet to be elucidated. Here, a Lauraceae-specific citral gene cluster (CGC) was identified and investigated using a multifaceted approach combining phylogenetic, collinearity, biochemical analyses. The CGC comprises MYB44 as a regulator and two alcohol dehydrogenases (ADHs) as the modified enzyme, which is derived from species-specific tandem and proximal duplication. The divergency of ADHs enzyme activity and substrate has led to the fruit of *Litsea cubeba*, a core Lauraceae species, containing more than 80%

of citral. In addition, MYB44 negatively regulated citral biosynthesis by directly binding to the *ADHs* promoters. Aggregation of specific citral biosynthetic pathways suggests they may form the basis of important characteristics that enhance adaptability. Findings from this study provide new insights into the evolution and regulation mechanism of plant terpene biosynthesis.