

油茶酰基 CoA 合成酶家族基因的鉴定及当归酰基 CoA 合成酶基因筛选

摘要 【目的】油茶是我国特有的木本食用油料树种, 其次生代谢物三萜类皂苷具有抗癌活性, 而当归酰基修饰能增强三萜皂苷的抗炎抗癌等药理功能, 体内的皂苷生物合成过程以当归酰基 CoA 作为当归酰基修饰供体。油茶酰基 CoA 合成酶 (acyl-coenzyme A synthetase, ACS) 基因家族鉴定及当归酰基 CoA 合成酶基因筛选对于油茶三萜皂苷合成研究具有重要意义。【方法】本研究从全基因组水平鉴定油茶酰基 CoA 合成酶家族基因, 以 Pfam 中 AMP 结合结构域隐马尔可夫模型 (hidden markov model, HMM) 和拟南芥 ACS 基因, 南欧大戟 *EpCCL1*、*EpCCL2*、*EpCCL3*, 啤酒花 *HlCCL4* 及马铃薯 *StCCL* 具有当归酰基 CoA 合成酶功能的基因作为参考, 鉴定油茶 ACS 基因, 根据油茶 ACS 基因和参考基因的蛋白序列比对, 构建系统进化树; 对相关基因在染色体上分布、基因结构、蛋白结构域、理化性质预测、亚细胞定位及组织特异性表达进行分析, 筛选油茶当归酰基 CoA 合成酶候选基因。【结果】鉴定到油茶基因组中含有 35 个 ACS 家族基因, 分布在油茶 9 条染色体上, 其中 23 个基因在基因组上有串联关系; 系统发育树将 35 个基因分为 5 个亚家族, 其中有 10 个油茶 ACS 基因与当归酰基 CoA 合成相关, 均含有 AMP 结合结构域及 ACS 特征保守基序; 转录水平表达分析表明, *Co02g005016*、*Co10g155733*、*Co10g015711* 基因在果实中特异高表达, 可作为油茶中当归酰基 CoA 合成酶候选基因。【结论】鉴定得到 35 个油茶 ACS 基因, 系统进化分析将其分为 5 个分支, 并最终筛选得到 *Co02g005016*、*Co10g155733*、*Co10g015711* 3 个油茶当归酰基 CoA 合成酶关键候选基因。

关键词 油茶; 酰基 CoA 合成酶; 当归酰基 CoA; 基因家族鉴定

Identification of Acyl CoA Synthetase Family Genes in *Camellia oleifera* and Screening of Angelicae Acyl CoA Synthetase Genes

Abstract 【Objective】*Camellia oleifera* is a unique woody edible oil tree species in China. The secondary metabolite triterpenoid saponins have anticancer activity, and Angelica acyl modification can enhance the anti-inflammatory and anticancer pharmacological functions of triterpenoid saponins. The biosynthesis process of saponins in vivo uses Angelica acyl CoA as an Angelica acyl modification donor. The identification of acyl-coenzyme A synthetase (ACS) gene family and the screening of Angelica acyl-CoA synthetase gene are of great significance for the study of triterpenoid saponin synthesis in *Camellia oleifera*. 【Method】In this study, the acyl-CoA synthetase family genes of *Camellia oleifera* were identified at the genome-wide level. The AMP binding

domain hidden markov model (HMM) in Pfam and *Arabidopsis thaliana* ACS gene, *EpCCL1*, *EpCCL2*, *EpCCL3* in *Euphorbia peplus*, *HICCL4* in *Humulus lupulus* and *StCCL* in *Solanum tuberosum* with the function of Angelica acyl-CoA synthetase were used as reference genes to identify the ACS gene of *Camellia oleifera*. According to the protein sequence alignment of the *Camellia oleifera* ACS gene and the reference gene, the phylogenetic tree was constructed. The distribution of related genes on chromosomes, gene structure, protein domain, physical and chemical properties prediction, subcellular localization and tissue-specific expression were analyzed to screen the candidate genes of Angelica acyl-CoA synthetase in *Camellia oleifera*. **【Result】** It was identified that the genome of *Camellia oleifera* contained 35 ACS family genes, which were distributed on 9 chromosomes of *C.oleifera*, of which 23 genes had a tandem relationship on the genome. According to the phylogenetic tree, 35 genes were divided into 5 subfamilies. Among them, 10 ACS genes were related to the synthesis of Angelica acyl CoA, all of which contained AMP binding domain and ACS characteristic conserved motif. Transcriptional expression analysis showed that *Co02g005016*, *Co10g155733* and *Co10g015711* genes were specifically highly expressed in fruits, which could be used as candidate genes for angeloyl CoA synthetase in *Camellia oleifera*. **【Conclusion】** Thirty-five ACS genes were identified and divided into five branches by phylogenetic analysis. Finally, three key candidate genes of Angelica acyl-CoA synthetase in *Camellia oleifera*, *Co02g005016*, *Co10g155733* and *Co10g015711*, were screened.

Keywords *Camellia oleifera* ; acyl-CoA synthetase ; angelica acyl CoA ; gene family identification