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慈竹*C3H*基因克隆及其生物信息学分析

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摘要

香豆酸-3-羟化酶(*C3H*)是调控植物木质素生物合成的关键酶，本文以慈竹为材料，利用RT-PCR技术克隆慈竹*C3H*基因，并对其进行生物信息学分析，为通过基因工程手段降低工业用竹木质素含量奠定基础。结果表明，该cDNA序列全长为1 581 bp，编码区为1 539 bp，编码512个氨基酸，蛋白分子量为58.33KD，等电点为9.09；氨基酸序列和结构分析显示*C3H*有一个保守区域，即P450结构域。系统进化分析表明,该基因与毛竹和水稻的*C3H*基因具有很高的同源性。慈竹与毛竹和水稻*C3H*基因编码蛋白为亲水性蛋白，这三种编码蛋白很可能定位在内质网(膜)上，其编码蛋白的二级结构及三级结构都含有丰富的α-螺旋和无规卷曲，β-转角和延伸链的含量较少，都含有2个相对保守的无序化区域。该基因已在GenBank上注册,基因序列登录号为JF693629,可能与慈竹木质素的生物合成有关。

关键词 慈竹；*C3H*基因；克隆；生物信息学分析

分类号 S718.46

Cloning and Bioinformation Analysis of *C3H* Gene in *Neosinocalamus affinis*

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Abstract

p-Coumarate 3-hydroxylase plays an important role in the biosynthesis pathways of plant lignin. The full-length sequence of *C3H* in *Neosinocalamus affinis*(*NaC3H*) was successfully cloned by RT-PCR, and its bioinformation analysis was carried out. It aims to provide theoretical basis for decreasing the content of lignin in bamboo for making-pulp through engineering technique. The sequence is 1 581 bp in length. The bioinformation analysis showed that the CDS region of the nucleotide sequence was 1 539 bp, encoding 512 predicted amino acids. The protein molecular weight was 58.33 kD and theoretical pI was 9.09. According to the amino acid sequence and structural analysis, it showed that the protein encoding by *C3H* contained one conserved domain, viz. P450 domain. Phylogenetic analysis showed that *NaC3H* was most similar to *C3H* from *P.edulis* and *Oryza sativa*. The proteins encoded by *C3H* genes were hydrophilic ones. Subcellular localizations of these three proteins were in the endoplasmic reticulum (membrane). The secondary structures and tertiary structures were abundant in alpha helixs and random coils, beta turns and extended strains were less. Two relative conserved disordered domains were found in amino acid sequences encoded by *C3H* genes from *N.affinis*, *P.edulis* and *O.sativa*. The full-length sequence of *NaC3H* has been submitted to GenBank with the accession number JF693629.

Key words *Neosinocalamus affinis* *C3H* gene cloning bioinformation analysis

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