

茶树肌动蛋白基因（CsActin1）全长cDNA克隆与生物信息学分析

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摘要

以茶树 (*Camellia sinensis*) 萌动芽为材料, 根据茶树萌动芽芽抑制消减杂交文库中分离得到的肌动蛋白 (actin) 基因的5' -片段设计引物, 利用3' -RACE技术克隆了其cDNA全长序列, 该基因cDNA全长 1 470 bp, 命名为*CsActin1* (GenBank登录号HQ235647)。序列分析表明, *CsActin1*开放阅读框长1 134 bp, 编码377个氨基酸, 5' 非编码区100 bp, 3' 非编码区236 bp。推测的蛋白质分子量为41.70 kD, 等电点约为5.31, 具有肌动蛋白家族的特征信号序列 (YVGDEAqS. KRG和WIAKaEYDE) 和肌动蛋白相关蛋白的特征信号序列 (LLTEApLNPkaNR)。 *CsActin1*与GenBank中注册的其它植物肌动蛋白核苷酸序列的相似性在80%以上, 氨基酸序列相似性在95%以上。与其它植物肌动蛋白的进化树分析结果表明, 茶树肌动蛋白与杨树的两个肌动蛋白间的亲缘关系最为密切。并对推导的蛋白结构进行了分析。

关键词 茶树; 肌动蛋白基因 *CsActin1* ; RACE; 序列分析

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Cloning and Bioinformatics Analysis of Full-length cDNA of Actin Gene(*CsActin1*) from Tea Plant (*Camellia sinensis*(L.) O. Kuntze)

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Abstract

Two suppression subtractive hybridization (SSH) libraries of tea plant(*Camellia sinensis*(L.) O. Kuntze) were constructed using cDNA from the dormant buds and sprouting buds. A cDNA fragment, which was homologous to the 5'-end of actin gene family, was identified from the sprouting bud SSH library. Using one primer designed on the basis of the fragment, its full length cDNA sequence was cloned through 3'-rapid amplification of cDNA ends (3'-RACE). The full length of the actin gene, named *CsActin1*, was 1 470 bp (GenBank accession No. HQ235647) and contained a 1134 bp open reading frame (ORF) encoding a 377 amino acid residues, a 5'-UTR of 100 bp and a 3'-UTR of 236 bp. The deduced protein molecular weight was 41.70 kD and its theoretical isoelectric point was 5.31. It contained the characteristic actin family signature sequence (YVGDEAqS.KRG and WISKgEYDE) and actin-related proteins signature (LLTEApLNPkaNR). Homologous alignment showed that it shared over 80% nucleotide sequence similarity and over 95% amino acid sequences similarity with actins in other plants. The phylogenetic tree reconstructed on the basis of amino acid sequences suggested that the relationship between *C.sinensis* and *Populus trichocarpa* is the most intimate.

Key words tea plant(*Camellia sinensis*(L.) O. Kuntze) actin gene(*CsAtin1*) RACE sequence analysis

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