中国中药杂志
China Journal of Chinese Materia Medica

高良姜1-脱氧-*D*-木酮糖5-磷酸还原异构酶cDNA克隆与表达调控

投稿时间： 2012-07-16 责任编辑： 点此下载全文

引用本文：张春荣,杨全,陈虎彪,庞玉新,唐晓敏,程轩轩,吴文雅,陈诗敏.高良姜1-脱氧-*D*-木酮糖5-磷酸还原异构酶cDNA克隆与表达调控[J].中国中药杂志,2012,37(21):3208.

DOI：10.4268/cjcmm20122110

作者中文名	作者英文名	单位中文名	单位英文名	E-Mail
张春荣	ZHANG Chun-rong	广东药学院 中药学院,广东 广州 510006	School of Traditional Chinese Medicines, Guangdong Pharmaceutical University, Guangzhou 510006, China	
杨全	YANG Quan	广东药学院 中药学院,广东 广州 510006	School of Traditional Chinese Medicines, Guangdong Pharmaceutical University, Guangzhou 510006, China	yangquan7208@vip.163.com
陈虎彪	CHEN Hu-biao	香港浸会大学 中医药学院,香港	School of Chinese Medicine, Hong Kong Baptist University, Hong Kong, China	
庞玉新	PANG Yu-xin	中国热带农业科学院 热带作物品种资源研究所,海南 儋州 571737	Tropical Crops Genetic Resources Institute, Chinese Academy of Tropical Agricultural Sciences, Danzhou 571737, China	
唐晓敏	TANG Xiao-min	广东药学院 中药学院,广东 广州 510006	School of Traditional Chinese Medicines, Guangdong Pharmaceutical University, Guangzhou 510006, China	
程轩轩	CHENG Xuan-xuan	广东药学院 中药学院,广东 广州 510006	School of Traditional Chinese Medicines, Guangdong Pharmaceutical University, Guangzhou 510006, China	
吴文雅	WU Wen-ya	广东药学院 中药学院,广东 广州 510006	School of Traditional Chinese Medicines, Guangdong Pharmaceutical University, Guangzhou 510006, China	
陈诗敏	CHEN Shi-min	广东药学院 中药学院,广东 广州 510006	School of Traditional Chinese Medicines, Guangdong Pharmaceutical University, Guangzhou 510006, China	

基金项目：农业部热带作物种质资源利用重点开放实验室开放基金项目(KFKT-2011-02);国家科技基础性工作专项重点项目(2007FY110600);广东省科技计划项目(2009B060700076);广东省大学生创新实验项目(1057310024)

中文摘要：目的：克隆高良姜1-脱氧-*D*-木酮糖5-磷酸还原异构酶(DXR)的全长cDNA,分析其组织表达模式及茉莉酸甲酯(MeJA)的调控模式,为高良姜有效成分的基因调控及基因工程育种奠定基础。 方法：应用简并引物RT-PCR和RACE技术从高良姜根茎中克隆DXR全长cDNA,运用生物信息学解析其编码的蛋白质结构,实时荧光定量PCR法分析其组织表达模式和MeJA的调控模式。 结果：克隆了高良姜DXR全长cDNA序列(*AoDXR*),开放读码框长1 419 bp,编码的蛋白质含472个氨基酸残基、相对分子质量约51.48 kDa。推导的AoDXR氨基酸序列与其他高等植物的 DXR具有高度的序列一致性(73%~99%)。*AoDXR*在高良姜叶片中表达量最强,而在根茎中表达量较弱。外源茉莉酸甲酯(MeJA)处理提高了根茎*AoDXR*的转录水平和1, 8-桉油精含量。 结论：*AoDXR*在高良姜根茎中的表达水平与1, 8-桉油精的积累不一致,反应了AoDXR催化的终产物的多样性和表达调控的复杂性。外源MeJA可促进根茎*AoDXR*的表达和1, 8-桉油精的积累,对提高药材品质有应用价值。

中文关键词：高良姜 单萜生物合成 1-脱氧-*D*-木酮糖5-磷酸还原异构酶 茉莉酸甲酯

Cloning and expression regulation of 1-deoxy-*D*-xylulose-5-phosphate reductoisomerase cDNA from *Alpinia officinarum*

Abstract: The rhizome of *Alpinia officinarum* is a widely used Chinese herbal medicine. The essential oil in *A. officinarum* rhizome is mainly composed of 1, 8-cineole and other monoterpenes, as the major bioactive ingredients. In plants, monoterpenes are synthesized through the methylerythritol phosphate (MEP) pathway in the plastids, and 1-deoxy-*D*-xylulose 5-phosphate reductoisomerase (DXR) is an enzyme catalyzing a committed step of the MEP pathway. In the present study, the full-length cDNA encoding DXR was cloned from the rhizome of *A. officinarum*, using homology-based RT-PCR and rapid amplification of cDNA ends (RACE) techniques. The new cDNA was designated as AoDXR and submitted to GenBank to be assigned with an accession number HQ874658. The full-length cDNA of AoDXR was 1 670 bp containing a 1 419 bp open reading frame encoding a polypeptide of 472 amino acids with a calculated molecular mass of 51.48 kDa and an isoelectric point of 6.15. Bioinformatic analyses revealed that AoDXR showed extensive homology with DXRs from other plant species and contained a conserved plastids transit peptide, a Pro-rich region and two highly conserved NADPH-binding motifs in its N-terminal region characterized by all plant DXRs. The phylogenetic analysis revealed that AoDXR belonged to angiosperm DXRs. The structural modeling of AoDXR showed that AoDXR had the typical V-shaped structure of DXR proteins. The tissue expression pattern analysis indicated that AoDXR expressed strongly in leaves, weak in rhizomes of *A. officinarum*. Exogenous methyl jasmonate (MeJA) could enhance the expression of AoDXR and the production of 1, 8-cineole in *A. officinarum* rhizomes. The cloning and characterization of AoDXR will be helpful to reveal the molecular regulation mechanism of monoterpene biosynthesis in A. officinarum and provides a candidate gene for metabolic engineering in improving the medicinal quality of *A. officinarum* rhizome.

keywords: *Alpinia officinarum* monoterpene biosynthesis 1-deoxy-*D*-xylulose 5-phosphate reductoisomerase methyl jasmonate

查看全文 查看/发表评论 下载PDF阅读器