乌拉尔甘草*HMGR*基因cDNA的克隆与序列分析

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中文摘要:目的: 对乌拉尔甘草3-羟基-3-甲基戊二酰辅酶A还原酶(3-hydroxy-3methylglutary CoA reductase,HMGR) 的cDNA克隆并进行序列分析。 方法 :根据NCBI数据库中的豆科其他物种HMGR的cDNA保守区设计引物,利用同源扩增和cDNA末端快速扩增技术从甘草根中获得目的基因;利用BLAST进行序列比对,ORF Finder寻找开发阅读框,Prosite分析蛋白质的基本结构域,Clustal x比对已有HMGR的氨基酸序列,并构建进化树。 结果 :得到1个全长为1 842 bp的*HMGR*的cDNA序列,含有1 722 bp的开放阅读框(open reading frame,ORF),编码573个氨基酸,具有HMGR家族的特异序列,推测的氨基酸序列与豌豆、菠萝苜蓿的氨基酸序列一致性分别为84%,76%。 结论 :对甘草*HMGR*基因的cDNA进行了克隆,为进一步研究3-羟基-3-甲基戊二酰辅酶A在甘草酸生物合成途径中的作用提供了理论依据。

中文关键词:甘草 *HMGR* RACE

Cloning and characterization of 3-hydroxy-3-methylglutary CoA reductase cDNA of *Glycyrrhiza uralensis*

Abstract: Objective : To clone and analysis the sequence of 3-hydroxy-3-methylglutary CoA reductase (HMGR) cDNA from *Glycyrrhiza uralensis*. Method : The primers were designed based on the conservative region of *HMGR* nucleic acids sequence from public database. The target gene was obtained from root of *G. uralensis* by use of homologous cDNA amplificati on and RACE technologies. The sequence alignment was performed using BLAST. The open reading frame was identified by use of the ORF Finder. The protein domains were defined by use of Prosite software. Clustal was used to conduct multiple amino acid sequence alignment and MEGA 5.0 was used to conduct the phylogenetic tree. Result : The *GuHMGR* cDNA sequence was obtained contains 1 842 bp contains a 1 722 bp ORF, encoding 573 amino acids with 3-hydroxy-3-methylglutary CoA reductases family profile. Deduced amino acid sequence had 84% and 76% homology to the amino acid sequence of *Pisum sativum*, *Medicago truncatula*. Conclusion : The cloning of 3-hydroxy-3-methylglutary CoA reductase (HMGR) cDNA will provide a foundation for exploring the function of *HMGR* in glycyrrhizin biosynthesis.

keywords:*Glycyrrhiza uralensis* *HMGR* RACE

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