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大豆种子Em基因 (LEA1) 启动子的克隆与序列分析

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摘要: 根据已公布的大豆种子Em基因 (LEA1) 的5' 末端序列设计二个基因特异反向引物 (EmS1, EmS2)。以大豆基因组DNA为模板, 利用染色体步行 (Chromosome Walking) 法, 获得了Em基因起始密码子上游836bp 的特异DNA片段。进行序列测定和生物信息学分析。结果表明, 这段DNA序列为一尚未在基因数据库登录的DNA片段。该序列含有启动子的基本元件TATA-box和CAAT-box, 因此可能具有启动子活性。含有1个DRE1和2个ABRE。该启动子可能受到ABA和干旱等条件的诱导。含有1个AG-motif 和1个ELRE-motif, 该启动子可能参与创伤和诱导子等胁迫因素的应答。含有2个RY-repeat和1个TGTCACA-Motif, 该启动子片段可能具有种子特异性。结果表明, 所克隆到的片段可能为Em基因的诱导型启动子, 并且很可能是种子特异性启动子。

Abstract: According to the sequence of soybean seed Em gene from Genebank, two reverse primer was designed and synthesized. A DNA fragment of 836bp upstream of the coding sequence of Em gene was amplified by chromosome walking with the genomic DNA of Glycine max as the template. Sequence analysis showed that the fragment was a novel DNA sequence. Using Bioinformatics software, it was found the fragment contained the core elements of promoter including TATA-box and CAAT-box, so that it could be possibly the promoter sequence of Em gene. In addition, the fragment contained some putative cis-elements, such as a DRE1-motif, two ABRE-motifs, an AG-motif and an ELRE-motif etc, constituting the drought/salt-induced promoter activity. Then, it is found that the fragment contained two RY-repeat motifs and a TGTCACA-Motif, indicating the potential seed-specific promoter activity. Based on above preliminary analysis, it is suggested that the fragment might be the promoter of Em gene with induced promoter activity and seed-specific promoter activity.

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