

实验简报

超级杂交水稻 TIR1 类似基因 cDNA 的克隆与生物信息学分析

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摘要 生长素受体TIR1通过形成SCFTIR1复合体与生长素直接结合,即为Aux/IAA在26S蛋白酶降解过程中的关键蛋白质。在BLAST检索和生物信息学分析的基础上设计特异引物,以超级杂交水稻(Oryza sativa)亲本株1S为材料,通过RT-PCR扩增并经T-A克隆后测序,获得一条长度为2 219 bp的序列,其开放阅读框长度为1 764 bp,编码含587个氨基酸残基的肽链。该序列经生物信息学分析发现,其与拟南芥TIR1相似性为77%,同样具有2个保守的结构域,即F-box和亮氨酸富集重复区域(LRR),且都不具有跨膜结构域和信号肽。该cDNA序列命名为OsTIR1。

关键词 生长素受体 生物信息学 超级杂交水稻 TIR1**Cloning and Bioinformatics Analysis of TIR1 cDNA from Super Hybrid Rice Parental Line 1S**

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Abstract The auxin receptor TIR1, which can directly bind to auxin through the formation of the SCFTIR1 complex, is the key protein in the Aux/IAA degradation pathway of the 26S proteasome. In this research, we designed a specific primer according to the results of a BLAST search of bioinformatics data; the super hybrid rice parental line 1S was used as the plant material. After RT-PCR and T-A cloning, a 2 219 bp cDNA sequence was obtained through sequencing. Its open reading frame (ORF) was 1 764 bp long and coded for a polypeptide of 587 amino acids. Bioinformatics analysis revealed that the polypeptide shares 77% similarity with AtTIR1. Both polypeptides contain an F-box motif and a leucine-rich repeat domain but no transmembrane helices or signal peptide. The cDNA sequence was designated as OsTIR1 and submitted to GenBank.

Keywords auxin receptor bioinformatics super hybrid rice TIR1

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