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大豆 gma-miR1508a 靶基因预测及功能分析

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摘要: microRNA(miRNA)是生物中广泛分布的、内源性的、由21~25个核苷酸大小的非编码单链小分子RNA。miRNA与靶基因mRNA具有互补关系,能够介导降解靶基因和转录后水平的基因沉默,引起目的基因表达的下调。通过利用PlantCARE、PMRD、BAR等数据库对 gma-miR1508a 启动子顺式调控元件和靶基因进行了生物信息学分析,启动子分析结果表明gma-miR1508a含有多种非生物胁迫响应元件,其表达受ABA、低温、干旱等胁迫诱导。利用PMRD软件预测获得7个gma-miR1508a的靶基因,分别参与了细胞凋亡、开花调控、逆境胁迫、细胞壁修饰等调控,最终通过拟南芥同源基因分析获得了Glyma10g03840.1、Glyma16g27800.1、Glyma17g07280.1等5个与低温反应相关的候选靶基因。

Abstract: microRNA(miRNA) is widely distributed RNA regulatory genes, endogenous and 21-25nt noncoding single-stranded small molecule RNA. miRNA has a complementary relationship with its target gene mRNA, and mediates the degradation of target genes. The transcriptional gene silencing causes the down-regulation of the expression of the target gene. In the present study, the promoter and the target gene of gma-miR1508a gene were predicted by bioinformatics methodology in PlantCARE, PMRD and BAR databases. Analysis results showed that many important abiotic stress cis-acting regulatory elements were found in the promoter sequence and gene expression may induce by ABA, low temperature and drought stresses. Seven gma-miR1508a target genes were identified by PMRD software, which involved in cell apoptosis, regulation of flowering, stress responses, cell wall modification. Finally, Glyma10g03840.1, Glyma16g27800.1, Glyma17g07280.1 totally five of them may be the target genes of gma-miR1508a under low temperature stress.

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