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陆地棉MADS-box基因GhMADS13的功能分析

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Analysis of Transgenic *Arabidopsis thaliana* with the *Gossypium hirsutum* L. MADS- box Gene *GhMADS13*

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摘要 为了研究*GhMADS*13的功能，利用NCBI上提交的序列设计引物进行PCR扩增，扩增序列与提交序列的ORF (Open reading frame)的一致性为100%。qRT-PCR结果表明：棉花的各个组织中，*GhMADS*13在花中的表达量最高，是表达量低的根的几百倍；花器官中*GhMADS*13在萼片、花瓣、雄蕊、心皮和胚珠中都有表达，表达量虽有差异，但差异不大，其在胚珠中的表达量最高。将*GhMADS*13插入到pBI121载体上，构建了植物超表达载体。通过浸花法转化拟南芥，获得了2个转基因株系，分子检测和表型数据统计的结果表明*GhMADS*13的转录水平越高植株越矮小，角果的长度越短，种子的数目越少。根据*GhMADS*13的qRT-PCR结果和异位表达分析，推测*GhMADS*13主要抑制胚珠的发育。

关键词： 陆地棉 MADS-box GhMADS13 转基因

Abstract: *GhMADS*13, whose primer designed according to submitted sequence, was obtained by PCR with the 100% identity to explore its function. qRT-PCR in different tissues revealed that *GhMADS*13 had the highest expression level in the flower, and this was hundreds of times greater than root with the lowest expression level. *GhMADS*13 was expressed in all floral organs, and expression levels in the sepal, petal, stamen, carpel, ovule were little different, and ovule had the highest expression level. *GhMADS*13 was inserted into a pBI121 vector, and a plant over-expression vector was constructed successfully. Two lines of transgenic Arabidopsis were obtained by floral-dipping. The results of the molecular detection and phenotypic data showed that the Arabidopsis plants with high expression levels of *GhMADS*13 were shorter, and produced less seeds and siliques. Based on the qRT-PCR results and the analysis of ectopic expression, we deduce *GhMADS*13 mainly negatively regulates ovule development.

Keywords: *Gossypium hirsutum* L. MADS-box GhMADS13 transgenic gene

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