

超量表达PMADS20-SRDX的矮牵牛花瓣和雌蕊出现异位表皮毛和气孔

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Over-expressing PMADS20-SRDX Repressor Leads to the Formation of Ectopic Trichome and Stoma on Petals and

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摘要 以矮牵牛 (*Petunia hybrida*) 花序cDNA 为模板, 利用EST 数据库信息, 克隆了一个MADS-box 基因编码区序列, GenBank 登录为PMADS20 (GU129907)。进化树分析表明, PMADS20 属StMADS11 亚家族SVP 分支, 与番茄和辣椒的JOINTLESS 基因氨基酸序列相似性最高。定量PCR 检测结果表明, PMADS20 在矮牵牛营养器官中的表达量高, 在花中的表达量低。构建了PMADS20 的超量表达载体 (35S : PMADS20) 和CRES-T (Chimeric Repressor Gene Silencing Technology) 载体 (35S : PMADS20-SRDX)。

35S : PMADS20 和35S : PMADS20-SRDX 转基因矮牵牛的花器官表型变化相似, 花萼增大, 花瓣和雌蕊出现营养器官特征, 但35S : PMADS20-SRDX 的变化更为明显。扫描电镜观察显示, 35S : PMADS20-SRDX 转基因花瓣下表皮的表皮毛增多, 并有气孔分布; 子房和花柱表面为表皮毛覆盖, 呈现超量表达UNHAVEN 的矮牵牛心皮的特征, 并且有气孔分布。35S : PMADS20 转基因植株株形无明显变化, 35S : PMADS20-SRDX 植株花序的节间较野生型短。

关键词: 矮牵牛 StMADS11 亚家族 PMADS20 花器官发育

Abstract: Based on EST sequence data analysis, PMADS20 (GU129907) was cloned from *Petunia hybrid* by PCR using inflorescence cDNA as template. Phylogenetic analysis shows that PMADS20 belongs to SVP clade of StMADS11 subfamily and is most closely related to tomato and pepper JOINTLESS. qRT-PCR analysis indicated that PMADS20 mRNA accumulated high level in vegetative organs, and low level in flowers. Vectors of over-expressing PMADS20 and PMADS20-SRDX were constructed. When they were introduced into *petunia* using *Agrobacterium*-mediated transformation method, both 35S : PMADS20 and 35S : PMADS20-SRDX transgenic floral organs exhibited leaf-like characteristics. However, the alterations of 35S : PMADS20-SRDX flowers were more severe than that of the 35S : PMADS20 flowers. The 35S : PMADS20-SRDX petals and pistils showed the unshaven floral phenotype which characterized by ectopic trichome and stoma formation on adaxial side of petals and the surface of ovaries and styles. The results suggest that PMADS20 functions in flower development by transcriptional suppression. Constitutive expression of PMADS20 did not lead to obvious changes in plant stature, while the internodes of 35S : PMADS20-SRDX transgenic inflorescences were shorter than that of the wild type. These results suggest that PMADS20 may function differently between in *petunia* inflorescence internode and flower development.

Keywords: *petunia*, StMADS11 subfamily, PMADS20, floral organ development

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