

蒺藜苜蓿花器官特异基因的表达分析

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摘要 蒺藜苜蓿(*Medicago truncatula* G.)花器官特异表达基因是参与其花器官形成与发育的重要基因。筛选蒺藜苜蓿的花器官特异表达基因,寻找这类基因在其他模式植物中的直系同源基因,并将其表达模式在不同植物间进行比较,有利于深入的理解这类基因在蒺藜苜蓿花器官发育中的功能。根据蒺藜苜蓿表达谱,并以其*PISTILLATA(PI)*基因为模板,文章筛选了97个蒺藜苜蓿花器官特异表达基因($\text{Ratio} \geq 10$, 且 $\text{Z} \geq 7.9$)。通过同源比对,确定了这类基因在拟南芥(*Arabidopsis thaliana* L.)、大豆(*Glycine max* L.)、百脉根(*Lotus japonicus* L.)和水稻(*Oryza sativa* L.)中的直系同源基因。对这类基因在5种植物中的表达量、表达部位和功能进行比较,发现进化关系较近的植物,直系同源基因的表达变异较小,而进化关系较远的植物,直系同源基因的表达变异较大。进一步对表达分化较大的直系同源基因进行启动子分析,发现不同植物中直系同源基因表达模式的变化与启动子中调控元件的特性有关。

关键词: 蒺藜苜蓿 花器官 同源基因 表达模式

Abstract: The expression of genes specific to floral organ is important for the floral organ formation and development in *Medicago truncatula*. Screening of the genes specifically expressed in *M. truncatula* flowers and comparing the expression patterns of their orthologous homologous genes among different model plants can provide novel insights into the functions of these genes in controlling the floral organ development in *M. truncatula*. According to the expression profile data of *PISTILLATA (PI)*, we screened 97 genes specifically expressed in *M. truncatula* floral organs ($\text{ratio} \geq 10$ and $\text{Z} \geq 7.9$). Their homolog genes were also identified in *Arabidopsis thaliana*, soybean (*Glycine max* L.), *Lotus japonicus*, and rice (*Oryza sativa* L.). The results of comparing the gene expression levels, the gene expression patterns, and the gene functions among these species indicated that the expression variation of the orthologous homolog genes was small in the kindred species and was great in distant species. Furthermore, we compared the *cis*-acting regulatory elements of the genes, which had large expression variation among different plants. These results suggest that the great discrepancy of the orthologous homolog gene expression caused by the different character of *cis*-element in the promoter region.

Keywords: *Medicago truncatula*, floral organ, orthologous homolog gene, expression pattern

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