

陆地棉 BAM(β -淀粉酶)基因家族的全基因组鉴定及在棉纤维发育中的功能分析

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摘要: β -淀粉酶(β -amylase, BAM)是植物体内催化淀粉水解转化为麦芽糖的重要酶,在调控多种植物的生长发育过程中发挥重要作用。迄今为止,BAM已经在拟南芥中得到了广泛的研究,但在重要经济作物棉花中BAM基因家族的特征尚未见报道。为了解陆地棉 *GhBAM* 基因家族的结构和表达特征,对 *GhBAM* 进行了全基因组鉴定和进化分析,并研究了 *GhBAM* 在不同纤维发育时期的表达模式。通过全基因组鉴定了陆地棉基因组中的 27 个 *GhBAM* 基因,根据序列相似性和系统发育关系将其划分为 3 个组。对陆地棉基因组中鉴定出的所有 *GhBAM* 基因进行了基因结构、染色体分布和共线性分析。进一步应用葡萄糖基水解酶核心结构域的序列进行比对,结果显示,所有 *GhBAM* 蛋白均存在 Glycosyl hydrolase family 14 结构域。系统发育分析表明,4 个棉种和拟南芥的 BAM 基因家族分为 3 组。这一系统分析为陆地棉 BAM 基因的特性提供了新的见解,并为进一步研究这些基因的功能奠定基础。

关键词: β -淀粉酶基因家族;陆地棉;全基因组鉴定;纤维发育;淀粉代谢

Genome-wide identification of the BAM (β -amylase) gene family in *Gossypium hirsutum* and its function in cotton fiber development

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Abstract: The β -amylase (BAM) is an important enzyme that catalyzes the conversion of starch to maltose in plants, and plays an important role in regulating the growth and development of various plants. So far, BAMs have been extensively studied in *Arabidopsis thaliana*, but the characteristics of the BAM gene family in the important economic crop, cotton have not been reported. In order to understand the structure and expression characteristics of *GhBAM* gene family in *Gossypium hirsutum*, the whole genome identification and evolutionary analysis of *GhBAM* were carried out, and the expression pattern of *GhBAM* in different fiber development stages were studied. In this study, 27 *GhBAM* genes of *G. hirsutum* were identified by genome-wide identification, and they were divided into three groups according to sequence similarity and phylogenetic relationship. The gene structure, chromosome distribution and collinearity of all *GhBAM* genes identified in *G. hirsutum* were analyzed. Further sequence alignment of the core domain of glucosyl hydrolase showed that all *GhBAM* proteins had Glycosyl hydrolase family 14 domain. Phylogenetic analysis showed that the BAM gene families of four cotton species and *Arabidopsis thaliana* were divided into three groups. This systematic analysis provides new insights into the characteristics of BAM genes in *G. hirsutum*, and lays the foundation for further study of the function of these genes.

Keywords: β -amylase gene family; *Gossypium hirsutum*; genome-wide identification; fiber development; starch metabolism

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