

DNA 甲基转移酶基因的表达分析表明 GhDMT6 触发了棉花对干旱和盐胁迫的反应中的 C5-MTase

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摘要: DNA 甲基化是基因组 DNA 修饰的重要表观遗传模式, 是维持表观遗传含量和调控基因表达的重要组成部分。胞嘧啶-5 DNA 甲基转移酶(C5-MTase)是 DNA 甲基化过程中的关键酶。迄今为止, 还没有对棉花中 C5-MTase 进行分析的研究。本研究利用棉花基因组信息, 采用生物信息学方法对棉花 C5-MTase 编码基因进行全基因组鉴定和分析。鉴定了 33 个 C5-MTase, 其中 8 个属于雷蒙德氏棉(D 基因组)、9 个属于亚洲棉(A 组)、16 个属于陆地棉(AD 组)。系统进化分析将 33 个基因分为 4 个亚家族, 包括 4 个 MET 同源蛋白、18 个 CMT 同源蛋白、8 个 DRM 同源蛋白和 3 个 DNMT2 同源蛋白。对棉花 C5-MTase 蛋白结构域进行比对发现, 33 个参与甲基化修饰的蛋白 C 末端有 6 个保守基序, 表明 C5-MTase 具有基本的甲基化催化功能。N 末端差异将蛋白质分为 4 类, 其中 DNMT2 缺乏 N 末端调控结构域。不同胁迫处理下棉花不同部位编码 C5-MTase 的基因的表达模式不同, 说明棉花 C5-MTase 基因家族的功能多样性。VIGS 沉默 *GhDMT6* 的棉花幼苗在不同胁迫处理下表现出明显的表型差异。与野生型的棉苗相比, 沉默 *GhDMT6* 的棉苗表现出明显的抗逆性。研究结果表明, C5-MTase 可能参与了棉花对非生物胁迫的响应, 为进一步研究 C5-MTase 调控非生物胁迫下细胞周期的机制奠定了基础。

关键词: C5-MTase; 雷蒙德氏棉; 亚洲棉; 陆地棉; 非生物胁迫

Expression analysis of DNA methyltransferase gene implies GhDMT6 triggers C5-MTases involved responding to drought and salt stress in cotton

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Abstract: DNA methylation is an important epigenetic mode of genomic DNA modification that is an important part of maintaining epigenetic content and regulating gene expression. Cytosine-5 DNA methyltransferases (C5-MTase) are the key enzymes in the process of DNA methylation. From now, there has been no systematic analysis the C5-MTase found in cotton. In this study, the whole genome of cotton C5-MTase coding genes were identified and analyzed using a bioinformatics method based on information from the cotton genome. Thirty-three C5-MTases were identified, of which 8 belonged to *Gossypium raimondii* (D genome), 9 belonged to *G. arboreum* L. (A genome), and 16 belonged to *G. hirsutum* L. (AD genome). Systematic evolutionary analysis divided the 33 genes into four subfamilies, including 4 MET homologous proteins, 18 CMT homologous proteins, 8 DRM homologous proteins and 3 DNMT2 homologous proteins. After the protein domain alignment of C5-MTases in cotton, there are 6 conserved motifs involved in methylation modification in the C-terminus of 33 proteins, indicating that C5-MTases have basic catalytic methylation function. The N-terminal difference divides proteins into four classes, of which DNMT2 lacks the N-terminal regulatory domain. The expression of C5-MTases in different parts of cotton were different

under different stress treatments, indicating the functional diversity of cotton C5-MTase gene family. *GhDMT6*-silenced by VIGS cotton seedlings under different stress treatments showed significant phenotypic differences. Compared with wild type cotton seedlings, *GhDMT6*-silenced cotton seedlings showed significant stress resistance. Our results suggest that C5-MTases may be involved in response to abiotic stress in cotton, which lays a foundation for further study on the mechanism of C5-MTases regulating cell cycle under abiotic stress.

Keywords: C5-MTase; *Gossypium raimondii*; *Gossypium arboreum*; *Gossypium hirsutum*; abiotic stress