

菜薹抽薹相关基因BrcuDFR-like/BrcuAXS 的克隆与表达特性分析

肖旭峰¹, 王恒, 王义林, 曹必好, 雷建军

(¹江西农业大学农学院, 南昌 330045; ²华南农业大学园艺学院, 广州 510642; ³江西生物科技职业学院, 南昌 330200)

Cloning and Expression Analysis of BrcuDFR-like/BrcuAXS Gene in Flowering Chinese Cabbage

XIAO Xu-Feng¹, WANG Heng, WANG Yi-Lin, CAO Bi-Hao, LEI Jian-Jun

(¹College of Agriculture, Jiangxi Agricultural University, Nanchang 330045, China; ²College of Horticulture, South China Agricultural University, Guangzhou 510642, China; ³Jiangxi Biotech Vocational College, Nanchang 330200, China)

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摘要 为了预测抽薹相关基因BrcuDFR-like/BrcuAXS 的功能, 通过PCR 和RACE 的方法克隆了菜薹BrcuDFR-like/BrcuAXS 基因的cDNA 和gDNA 全长序列。结果表明: 该基因编码区全长1 332 bp, 编码312 个氨基酸残基。对应的gDNA 全长为2 460 bp, 含有8 个外显子和7 个内含子, 内含子总长为1 042bp, 其中第3 个内含子最长, 为401 bp。内含子中含有多个基本转录元件和顺式作用元件, 如光应答元件、赤霉素响应元件、参与抗性和胁迫应答元件、热响应元件、WRKY 转录因子的结合位点及干旱胁迫元件MYB 转录因子结合位点等。利用半定量RT-PCR 分析表达模式, 发现BrcuDFR-like/BrcuAXS 随菜薹花芽形态逐步建成直至抽薹开花, 其表达量逐渐增强, 与其它物种DFR-like 基因的表达模式更吻合, 由此预测该基因在菜薹生长发育阶段编码DFR-like 酶的可能性大于编码AXS 的可能性, 其功能可能与菜薹营养分生组织向花分生组织转变有关。

关键词: 菜薹 抽薹 基因结构 表达

Abstract: In order to predict the function of BrcuDFR-like/BrcuAXS, both the full-length of cDNA and genomic DNA were cloned with the method of PCR and RACE and expression pattern was investigated in flowering Chinese cabbage (*Brassica rapa* syn. *campestris* L. ssp. *chinensis* var. *utilis* Tsen et Lee). The results indicated that the cDNA with the complete coding region was 1 332 bp in length which encoded 312 putative amino acids. The corresponding gDNA was 2 460 bp in length which harbored eight exons and seven introns. The longest intron was the third intron with 401 bp in length. A computer scan disclosed that the introns harbored light-responsive element, gibberellin-responsive element, defense and stress responsiveness element, heat stress responsiveness element, WRKY and MYB binding site and so on. The semi-quantitative RT-PCR analysis revealed that no detectable levels were expressed during the first stage of sampling, then transcripts were detected during the two true-leaf, the four true-leaf, the five true-leaf and the flowering stages. Based on expression analysis, it is more likely to encode DFR than AXS, and it may play a role of transition from vegetative growth to reproductive growth in flowering Chinese cabbage.

Keywords: flowering Chinese cabbage, bolting, gene structure, expression

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