

## 棉花叶绿体基因RNA编辑位点的测定及分析

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## Identification and Analysis of RNA Editing Sites in Chloroplast Transcripts of *Gossypium hirsutum*

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摘要

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**摘要** 陆生植物叶绿体RNA编辑是转录后基因表达调控的一种重要方式。该文在预测棉花(*Gossypium hirsutum*)叶绿体基因RNA编辑位点的基础上, 选取中棉10 (CRR1 10)为实验材料, 采用PCR、RT-PCR及测序等方法, 确定CRR1 10的27个叶绿体蛋白编码基因共有55个编辑位点, 均是C→U的转换。与棉种柯字310(C310)的编辑位点对比后发现, CRR1 10多出*accD*-468和*rpoC1*-163两个编辑位点, 同时缺失*psbN*-10。利用生物信息学分析这3个位点, *rpoC1*-163和*psbN*-10的编辑可能会改变各自蛋白的二级结构。对CRR1 10中55个编辑位点上游的顺式作用元件(-30~-1)分析显示, 共有8组顺式作用元件的相似性达到60%或以上, 推测各组中的编辑位点可能由相同的反式作用因子来识别。

**关键词:** 叶绿体 顺式作用元件 棉花 RNA编辑

**Abstract:** RNA editing is one of the post-transcriptional modification processes in which the bases of a RNA molecule are altered by the addition, deletion and alteration of nucleotides. In most higher plants, RNA editing mainly occurs in mitochondria and plastids and converts from C to U, very rarely from U to C. We investigated RNA editing sites in chloroplasts of *Gossypium hirsutum* 'CRR1 10' by PCR, RT-PCR and sequence alignment. We identified 55 editing sites in 27 protein-coding genes all of which were C-to-U conversion. By comparing editing sites between CRR1 10 and Coker310FR, CRR1 10 had two novel editing sites, *accD*-468 and *rpoC1*-163, whereas site *psbN*-10 was absent. Bioinformatics analysis of the 3 sites revealed that *rpoC1*-163 and *psbN*-10 editing might affect the secondary structure of the corresponding protein. Comparison among upstream regions (-30 to -1) of the 55 editing sites of CRR1 10 revealed that 8 pairs share more than 60% sequence similarity suggesting that the sites in each pair may be recognized by the same trans-acting factors.

**Keywords:** chloroplast *cis*-elements cotton RNA editing

Received 2010-11-18; published 2011-07-01

Fund:

转基因生物新品种培育

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引用本文:

江媛, 范术丽, 宋美珍等. 棉花叶绿体基因RNA编辑位点的测定及分析[J] 植物学报, 2011, V46(4): 386-395

Yuan Jiang, Shuli Fan, Meizhen Song etc. Identification and Analysis of RNA Editing Sites in Chloroplast Transcripts of *Gossypium hirsutum*[J], 2011, V46(4): 386-395

链接本文:

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