

# 大豆细胞质雄性不育系与保持系 *atp6* 基因的 RNA 编辑比较研究

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**摘要:** 对大豆细胞质雄性不育系 NJCMS1A 与其保持系 NJCMS1B 的 *atp6* 基因的 RNA 编辑进行比较研究。结果在不育系 NJCMS1A 与保持系 NJCMS1B 的 *atp6-3* 基因保守区中均发现 2 个编辑位点, 但互不相同, 并且导致了氨基酸的不同变化; mtDNA 序列分析显示, *atp6-3* 基因转录本保守区在不育系 NJCMS1A 与保持系 NJCMS1B 间存在 1 个碱基的差异; 另外还发现 *atp6-1*、*atp6-2* 和 *atp6-3* 的表达在不育系 NJCMS1A 与保持系 NJCMS1B 间存在明显差异。

**关键词:** 大豆; 细胞质雄性不育; *atp6* 基因; RNA 编辑

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## Comparative Studies of RNA Editing of *atp6* Gene between Cytoplasmic Male Sterile Line and Its Maintainer Line in Soybean (*Glycine max* L. Merr.)

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**Abstract:** The *atp6* gene is an important mitochondrial functional gene. The studies on some plant species showed that RNA editing of *atp6* gene was related to the cytoplasmic male sterility. In this paper, the comparative studies of RNA editing of *atp6* gene between the cytoplasmic male sterile line NJCMS1A and its maintainer line NJCMS1B in soybean (*Glycine max* L. Merr.) were conducted. The results showed that two editing sites were found on the conservative region of the *atp6* gene of NJCMS1A and NJCMS1B, but the two editing sites of the *atp6* gene of NJCMS1A were different from those of NJCMS1B, and led to the different changes of amino acid. The results of the mtDNA sequence comparison showed that one base difference was found in the conservative region of *atp6-3* gene between NJCMS1A and NJCMS1B. In addition, the obvious difference was found on the expression of *atp6-1*, *atp6-2* and *atp6-3* between NJCMS1A and NJCMS1B.

**Key words:** Soybean; Cytoplasmic male sterility(CMS); *Atp6* gene; RNA editing

RNA 编辑是 RNA 成熟化的一种重要加工方式, 普遍存在于真核生物的线粒体中<sup>[1-2]</sup>。在高等植物的线粒体中, RNA 编辑一般优先选择转录本的蛋白质编码区, 且主要作用于密码子的第 1 及第 2 位点上, 所造成的核苷酸的改变通常会改变编码氨基酸的种类, 因此, RNA 的正常编辑对线粒体功能的正常发挥起着重要作用<sup>[3]</sup>。

*atp6* 基因是重要的线粒体功能基因, 它的正常表达与 ATP 合成酶功能的正常行使有着本质的联系。多个物种的研究结果表明 *atp6* 基因的 RNA 编辑与植物细胞质雄性不育有关, Hemould 等<sup>[4]</sup> 把编辑和未编辑 *atp6* 基因转入烟草, 结果显示导入编辑 *atp6* 基因的烟草植株全部可育, 而导入未编辑 *atp6* 基因的烟草植株表现雄性不育; Iwabuchi 等<sup>[5]</sup> 报告

BT 型水稻不育系的 *atp6* 基因的 RNA 编辑水平比恢复系低; Howad 等<sup>[6]</sup> 报道高粱 A3 不育系 *atp6* 基因的编辑表现出花药专一性降低, 不具有恢复基因的任何核背景均不能恢复 *atp6* 基因的正常编辑, 其表达产物没有 2 个保守位点的 Leu 残基, 很可能影响了 ATP 合成酶的活性, 导致花粉败育; HL 型水稻不育系, *atp6* 基因的编辑在不育系、恢复系和有核恢复基因存在条件下, 不发生改变, 但各位点的编辑频率在核恢复基因作用下均有较大提高<sup>[7]</sup>。迄今为止, 在大豆上尚未见到 *atp6* 基因 RNA 编辑的相关报道, 现以大豆细胞质雄性不育系 NJCMS1A 与其保持系 NJCMS1B 为材料, 探讨 *atp6* 基因的 RNA 编辑与大豆细胞质雄性不育之间的关系。

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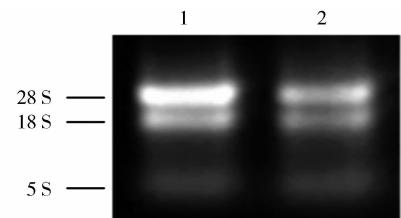
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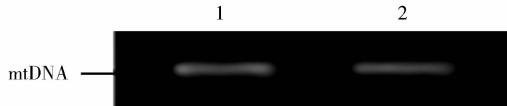
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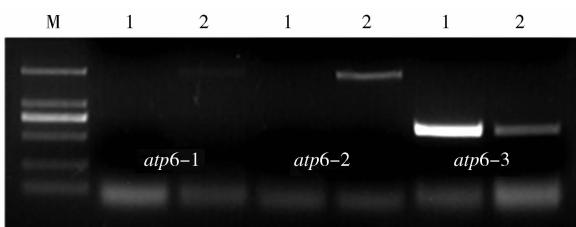


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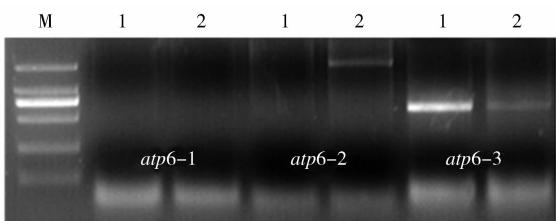
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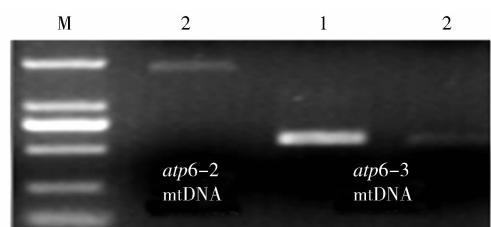


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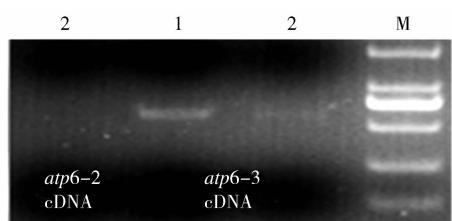
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育植株之间的差异很可能就是导致不育的原因。该研究对大豆 *atp6* 基因的 3 个拷贝 *atp6-1*、*atp6-2* 和 *atp6-3* 在大豆细胞质雄性不育系 NJCMS1A 与其保持系 NJCMS1B 中的表达进行了比较研究,结果显示 *atp6-1*、*atp6-2* 和 *atp6-3* 在不育系 NJCMS1A 与保持系 NJCMS1B 中的表达存在较大差异。*atp6-1*、*atp6-2* 和 *atp6-3* 的互相协调作用决定 ATP 亚基 6 的结构变化,在保持系 NJCMS1B 中,*atp6-1*、*atp6-2* 和 *atp6-3* 均正常表达,而在不育系 NJCMS1A 中,*atp6-1* 和 *atp6-2* 不表达或者表达量很少,*atp6-3* 表达量则较保持系中高很多,这样在不育系 NJCMS1A 中 3 个拷贝的协调作用与保持系 NJCMS1B 中存在很大的变化,可能导致不育系 NJCMS1A 中 ATP 亚基 6 的结构发生异常,ATP 合成酶的功能受到影响,从而导致不育系 NJCMS1A 中的能量供应比保持系 NJCMS1B 中要少,引起雄性不育的发生,具体机理尚需进一步研究证实。

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