

研究报告

## 水稻CMS相关基因在稻属AA基因组中的分布及其单核苷酸多态性

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### 摘要

水稻线粒体基因组嵌合基因orf79 和 orfH79分别被认为与BT-型和HL-型水稻CMS有关, 两者具有98%的同源性, 并且其DNA序列只存在4核苷酸的差异。对于这两个嵌合基因, 前者来源于栽培稻 (*Oryza sativa* L.), 而后者则来源于普通野生稻 (*O. rufipogon* Griff.)。这意味着orf79/ orfH79可能在广泛分布于稻属AA基因组中。为了调查orf79/ orfH79在稻属物种中的分布和变异, 190份栽培稻品系[包括156份亚洲栽培稻 (*O. sativa* var. *landrace*) 和34份非洲栽培稻 (*O. glaberrima*)]以及104份稻属AA基因组野生稻品系(包括*O. rufipogon*、*O. nivara*、*O. glumaepatula*、*O. barthii*、*O. longistaminata*和*O. meridionalis* 6个种), 被用于PCR扩增检测。31份具有控制粤泰A和籼锦A的特异片段的稻属AA基因组水稻品系被检测出。所有特异片段均被回收并测序, 基于DNA 序列的聚类结果显示31份水稻材料被分成了两组, 分别代表为BT-型和HL-型水稻不育细胞质组群。结果也进一步表明: HL-型水稻CMS胞质主要分布于一年生的*O. nivara*中; BT-型水稻CMS胞质可能来源于栽培稻变种或多年生野生稻*O. rufipogon*。

关键词 [细胞质雄性不育](#) [orf79和orfH79](#) [稻属](#) [AA基因组](#) [单核苷酸多态性](#)

分类号

## Distribution and SNPs of the rice CMS-related gene in AA-genome of *Oryza* species

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### Abstract

<P>The moiety of a chimeric gene in mitochondrial genome, <EM>orf79 </EM>and <EM>orfH79</EM>, probably related to BT-type and HL-type CMS of rice respectively, has 98% homology and only 4 nucleotide variation in DNA sequence. Of which, the former comes from <EM>Oryza</EM> sativa L., and the latter originates from *Oryza rufipogon* Griff. That means the <EM>orf79/ orfH79</EM> may widely exist in <EM>Oryza</EM> <EM>species with</EM> AA genome. In order to investigate the distribution and difference of <EM>orf79/ orfH79</EM> in the <EM>Oryza</EM> species, 190 cultivated rice accessions<EM> (including *O. sativa* and *O. glaberrima*)</EM> and 104 accessions of AA-genome <BR><BR>*Oryza* wild species<EM> (including *O. nivara*, *O. rufipogon*, *O. barthii*, *O. longistaminata*, *O. glumaepatula*, and *O. meridionalis*)</EM> were detected with PCR amplification. Of which, 31 accessions mainly from AA-genome <EM>Oryza </EM>species were found to share the special amplified fragment with the control of Yueta<EM>i</EM> A and Shijin A. The special amplified fragments were all recovered and sequenced. Phylogenetic analysis based on DNA sequences showed that the 31 accessions were fallen into two groups, correspondingly representing HL-type and BT-type cytoplasm group. Further, the results revealed that the HL-type cytoplasm distributed mainly in annual *O. nivara*,</EM> and the BT-type cytoplasm centered in cultivated varieties or perennial *O. rufipogon*.</EM>

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**Key words** [cytoplasmic male sterility](#) [orf79 and orfH79](#) [Oryza](#) [AA-genome](#) [single nucleotide polymorphisms](#)

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