

研究论文

野败型育性恢复基因在AA基因组野生稻中的分布与遗传

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摘要 分析了野败型恢复基因在AA基因组野生稻的分布。结果表明: (1) 在31份野生稻中, 有16份含有恢复基因, 分布频率达51.6%。(2) 6个AA基因组野生稻种中有4个种存在恢复基因, 但主要集中于O. rufipogon和O. nivara。(3) 在所鉴定的16份野生稻恢复系中, 对野败型花粉育性恢复力大于80%和50%~80%的各6份, 小于50%的4份; 强恢复源主要来自印度次大陆的一年生野生稻O. nivara中。(4) 在随机选择的8份野生稻中, 除w15含双基因外, 其他的都只含有1对野败型恢复基因; 对其中的6份野生稻的等位性分析表明, 至少涉及3个恢复基因位点。

关键词 [AA基因组野生稻](#) [野败细胞质雄性不育](#) [恢复基因](#) [分布与遗传](#)

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Distribution and Inheritance of the Fertility Restorer Genes for WA-CMS in Wild Rice with AA Genome

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Abstract It is very important to research the fertility restorer genes (Rf) for cytoplasmic male sterility (CMS) in wild rice for our better understanding the origin of the Rf, the interaction between cytoplasm and nuclear, and the development of new restorer lines. For such an end, the distribution and inheritance of the Rf for Wild-abortive (WA) CMS in wild rice with AA genome were investigated. The results showed that: (1) Sixteen out of the 31 test-crossed wild rice accessions were identified having Rf genes, and the frequency of the Rf in wild rice accessions was 51.6%. (2) The wild rice accessions with Rf fell into four species of genus *Oryza*, and majority of them belonged to the species of *O. nivara* and *O. rufipogon*. (3) The fertility of the microspores in the spikelets of the hybrid F1 between Yuetai A and wild rice accessions ranged from 10%—90%, of which, six wild restorer accessions' F1 were over 80%, six accessions 50%—80%, and the other four accessions' lower than 50%. Majority of the accessions with complete restoring ability belong to the annual specie of *O. nivara*. (4) The distribution of the wild rice accessions with Rf were imbalance in geography, 14 accessions from Asia and two wild rice accessions from Africa carried restorer genes, the wild rice accessions from Oceania and Latin America all contained no Rf for WA-CMS. (5) Apart from one out of the randomly selected eight accessions having two pairs of restorer genes, the other seven accessions all possessed only one pair of restorer allele. Further allelic analysis showed that among of the six randomly selected accessions, the Rf alleles in w15, w29 and w34 were all un-allelic to that of Milyang 23, and whereas the Rf between w15 and w34 was also un-allelic. Therefore, we speculate that there are at least three restorer alleles in the six tested wild restorer lines.

Key words [Distribution and inheritance](#) [Fertility restorer gene](#) [WA-CMS](#) [Wild rice with AA genome](#)

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