

研究论文

# 蜀恢527抗水稻白叶枯病改良系的遗传背景和农艺性状分析

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**摘要** 利用336个SSR标记和100个RAPD引物, 对分子标记辅助选择获得的10个蜀恢527抗水稻白叶枯病改良系的遗传背景、白叶枯病的抗性和抗谱及农艺性状进行了研究。结果表明, 10个改良株系在Xa21和Xa4位点纯合, 抗我国7个病原型代表菌系C I ~CVII和菲律宾小种1和6 (P1和P6)。在遗传背景分析检测的位点中, 改良系与蜀恢527表现差异的SSR位点仅为1~5个, RAPD位点的相似率在92.1%~97.5%之间。在考察的改良系及其与D62A和G46A所配制的杂交组合的8个农艺性状中, 除与G46A所配杂交组合在千粒重、每穗颖花数和产量性状方面与对照差异显著外, 其余均无显著差异, 但是所得改良系的抗性得到了提高, 其余性状与轮回亲本相似, 其中以Line 9和Line 10的遗传背景和农艺性状与蜀恢527最为相似。表明分子标记改良蜀恢527对白叶枯病的抗性是成功的, 是一种有效的育种方法。

**关键词** [Xa21和Xa4](#) [遗传背景分析](#) [抗白叶枯病](#) [农艺性状分析](#)

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## Analysis of Genetic Background and Agronomic Traits in Improved Restoring Lines Shuhui 527 with Resistance to Bacterial Blight

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**Abstract** The genetic background, resistance spectrum to bacterial blight and agronomic traits were evaluated in 10 ‘Shuhui 527’ improved restoring lines with resistance to Bacterial blight, which were bred by Molecular Marker-assisted Selection (MAS). Results showed that these lines were homozygous in loci Xa21 and Xa4 and resistant to the representative strains of 7 Chinese pathotypes C I —CVII in China, and Philippine race 1 and 6, P1 and P6. Comparison of genetic background showed that there were only 1—5 differential SSR loci, the similarity of RAPD bands was 92.1%—97.5%. The variation of the 8 agronomic traits observed between the improved restoring lines and combinations released from the each lines crossed with D62A was not significant. The agronomic traits investigated between the restoring line and the combinations of these lines crossed with G46A, respectively, had no significant difference except the 1 000-grain weight, spikelets per panicle and yield. But the resistance to Bacterial blight of these lines was improved and the other traits were similar to the recurrent parent. The genetic background and agronomic traits of line 9 and line 10 were more similar to Shuhui 527, it indicated that improvement of resistance to Bacterial blight of Shuhui 527 by using MAS was successful, and the MAS method used in rice breeding was a effectiveness approach.

**Key words** [Xa21 and Xa4](#) [Genetic-background analysis](#) [Bacterial blight resistance](#) [Agronomic traits evaluation](#)

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