

研究论文

利用回交重组自交群体检测水稻条纹叶枯病抗性位点

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摘要 利用98个家系组成的Nipponbare/Kasalath//Nipponbare回交重组自交系 (backcross inbred lines, BIL) 群体 (BC1F10), 采用苗期强迫饲毒和田间重病区自然接种的方法, 以病情指数作为条纹叶枯病的表型值, 鉴定了两亲本及98个BILs对条纹叶枯病的抗性。利用QTL Cartographer软件复合区间作图的方法, 对水稻条纹叶枯病抗性基因进行了QTL检测分析。苗期强迫饲毒鉴定, 检测到2个水稻抗条纹叶枯病QTL, 分别位于第7、第11染色体上, LOD值分别为2.77、8.58, 贡献率分别为8.96和31.79%。田间自然接种在第11染色体上也检测到抗条纹叶枯病QTL, 贡献率达22.49%。表明第11染色体上存在一个稳定表达的主效抗条纹叶枯病QTL, 该主效抗性QTL及其相应标记, 可望在条纹叶枯病抗性分子标记辅助选择育种中加以应用。

关键词 [水稻](#) [抗水稻条纹叶枯病](#) [重组自交系群体](#) [抗性基因](#) [QTL分析](#)

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Detection and Analysis of QTL for Resistance to the Rice Stripe Disease in Rice, Using Backcross Inbred Lines

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Abstract Rice stripe disease transmitted by small brown planthopper (*Laodelphax striatellus* Fall.) is one of the most serious viral diseases in East Asia. The disease is severely epidemic in most rice growing areas where the main cultivars are susceptible or moderately susceptible to rice stripe virus (RSV). A mapping population, the backcross inbred lines (BIL) derived from a cross of Nipponbare/ Kasalath// Nipponbare by the single seed descent method, was used to detect quantitative trait loci (QTL) conferring resistance to RSV. Reactions of the two parents and 98 RILs to RSV were investigated by both artificial inoculation at laboratory and natural infection methods in the field attached the virus, and scored by disease index. The quantitative trait loci for resistance to RSV were analyzed by QTL Cartographer software. By feeding the healthy seedlings with viruliferous small brown planthoppers at laboratory, two QTL controlling RSV resistance were detected on chromosomes 7 and 11, respectively. Individual QTL accounted for 8.96~31.79% of the phenotypic variance in the BILs population. By natural inoculation, only one QTL was detected at the same location on chromosome 11, which accounted for 22.49% of the phenotypic variance. The results indicated that the QTL on chromosome 11 was important to control the resistance to RSV. This QTL should be useful in rice breeding for resistance to RSV in marker-assisted selection (MAS) program.

Key words [Rice](#) [Resistance to rice stripe virus](#) [BIL population](#) [QTL analysis](#)

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