

## 实验简报

## 水稻条纹叶枯病抗性位点的检测和效应分析

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**摘要** 利用111个家系组成的热研2号(*Oryza sativa* subsp. *japonica* ‘Reyan2’) / Mi lyang23(*Oryza sativa* subsp. *indica* ‘Mi lyang23’)重组自交系(recombinant inbred lines, RIL)群体(F7), 采用重病区田间自然接种方法, 以病情指数作为条纹叶枯病的表型值, 鉴定了2个亲本及111个RIL家系对条纹叶枯病的抗性。使用QTL Cartographer软件复合区间作图法, 对水稻(*Oryza sativa*)条纹叶枯病抗性基因进行了QTL分析。结果检测到2个抗水稻条纹叶枯病的QTL, 分别位于第2和第11染色体上, 其中第11染色体上的QTL贡献率为19.58%, 表明这是一个主效的QTL, 该QTL及其附近的分子标记, 可以用于水稻条纹叶枯病抗性分子标记辅助育种。

**关键词** 水稻 QTL分析 重组自交系 水稻条纹叶枯病

## Analysis of Quantitative Trait Loci for Resistance to Stripe Disease in *Oryza sativa*

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**Abstract** In this research, we used a recombinant inbred line (RIL) population of 111 lines derived from a cross of Reyan2 (*Oryza sativa* subsp. *japonica* ‘Reyan2’) / Milyang23 (*Oryza sativa* subsp. *indica* ‘Milyang23’) by the single-seed descent method to detect quantitative trait loci (QTL) conferring resistance to rice stripe virus (RSV). Reactions of the two parents and the 111 RILs to RSV were investigated by natural methods of viral infection in the field and scored by disease index. QTL for resistance to RSV was analyzed by QTL Cartographer software. Chromosomes 2 and 11 each revealed one QTL controlling RSV resistance. The phenotypic variance explained by the QTL on chromosome 11 was 19.58%, so the locus is a major effective one controlling resistance to RSV and should be useful in breeding rice for resistance to RSV in a marker-assisted selection program.

**Keywords** *Oryza sativa* QTL analysis recombinant inbred line rice stripe disease

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