

研究论文

### 水稻条纹病毒和介体灰飞虱抗性的QTL分析

孙黛珍<sup>1</sup>, 江玲<sup>1</sup>, 刘世家<sup>1</sup>, 张迎信<sup>1</sup>, 黄培鸿<sup>1</sup>, 程遐年<sup>1</sup>, 翟虎渠<sup>2</sup>, 万建民<sup>1, 2, \*</sup>

(<sup>1</sup>南京农业大学作物遗传与种质创新国家重点实验室, 江苏省植物基因工程技术研究中心, 江苏南京210095 <sup>2</sup>中国农业科学院作物科学研究所, 北京100081)

收稿日期 2005-7-5 修回日期 网络版发布日期 2006-5-18 接受日期 2005-11-8

**摘要** 水稻品种Kasalath高抗条纹病毒和介体灰飞虱。为剖析不同抗性类型基因之间的关系, 利用回交重组自交系群体Nipponbare/Kasalath/Nipponbare分析了条纹病毒和介体灰飞虱抗性的数量性状基因座。结果在第11染色体S2260 - G257标记区间检测到1个与条纹病毒抗性相关的QTL (qSTV11), LOD值为9.2, 贡献率为35.79%; 在第3染色体R1618 - C595 和R2170 - C1135标记区间各检测到1个与介体灰飞虱抗性相关的QTL (qSBPH3-a, qSBPH3-b), LOD值和贡献率分别为3.12和2.96, 11.69% 和11.36%, 表明条纹病毒和介体灰飞虱抗性由不同基因所控制, 而且两者之间不相关。此外, 还分别检测到两对与条纹病毒和介体灰飞虱抗性相关的上位性QTL, 暗示水稻对条纹病毒和介体灰飞虱的抗性受主效和上位性QTL的共同影响。进一步分析发现SSR标记BJ11-8与qSTV11紧密连锁, 为分子标记辅助选择高抗条纹叶枯病水稻品种提供了基础。

**关键词** [水稻条纹叶枯病](#) [介体灰飞虱](#) [回交重组自交系](#) [QTL分析](#) [上位性](#)

分类号 [S511](#)

### Detection of QTLs for Resistance to Rice Stripe Virus and Small Brown Planthopper in Rice (*Oryza sativa* L.)

SUN Dai-Zhen<sup>1</sup>, JIANG Ling<sup>1</sup>, LIU Shi-Jia<sup>1</sup>, ZHANG Ying-Xin<sup>1</sup>, HUANG Pei-Hong<sup>1</sup>, CHENG Xia-Nian<sup>1</sup>, ZHAI Hu-Qu<sup>2</sup>, WAN Jian-Min<sup>1 2 \*</sup>

(<sup>1</sup> State Key Laboratory for Crop Genetics and Germplasm Enhancement, Nanjing Agricultural University, Jiangsu Research Center of Plant Gene Engineering, Nanjing 210095, Jiangsu; <sup>2</sup> Crop Science Research Institute, Chinese Academy of Agricultural Sciences, Beijing 100081, China)

**Abstract** An indica variety, Kasalath, is highly resistant to rice stripe virus and small brown planthopper. In order to dissect the relationship between rice stripe virus and small brown planthopper resistance genes, the QTLs were detected using Nipponbare/Kasalath/Nipponbare backcross inbred lines. One putative QTL (qSTV11) for the ratio of disease rating index was mapped between the marker S2260 and G257 on chromosome 11, which explained 35.79% of the total phenotypic variation with LOD score of 9.2. The positive resistant effect came from Kasalath. The two QTLs (qSBPH3-a, qSBPH3-b) for non-preference index were detected on chromosome 3, and their contributions to the total variation were 11.69% and 11.36% with LOD scores of 3.12 and 2.96, respectively. This suggests that the rice stripe virus and small brown planthopper resistance are controlled by different genes and this view is testified by no significant correlation between RSV and SBPH resistance. Then, two pairs of epistatic QTLs for ratio of disease rating index and non-preference index were respectively detected, showing the rice stripe virus and small brown planthopper resistance were influenced by main-effect QTLs and epistatic QTLs. Additionally, further study found that SSR marker BJ11-8 was tightly linked to qSTV11. This facilitates the breeding process for resistance to rice stripe disease by marker-assisted selection.

**Key words** [Rice stripe virus](#) [Laodelphax striatellus](#) [Fallen](#) [Backcross inbred lines \(BILs\)](#) [QTL analysis](#) [Epistasis](#)

DOI:

通讯作者 万建民 [wanjm@njau.edu.cn](mailto:wanjm@njau.edu.cn)

#### 扩展功能

本文信息

▶ [Supporting info](#)

▶ [PDF\(416KB\)](#)

▶ [\[HTML全文\]\(0KB\)](#)

▶ [参考文献](#)

服务与反馈

▶ [把本文推荐给朋友](#)

▶ [加入我的书架](#)

▶ [加入引用管理器](#)

▶ [复制索引](#)

▶ [Email Alert](#)

▶ [文章反馈](#)

▶ [浏览反馈信息](#)

相关信息

▶ [本刊中 包含“水稻条纹叶枯病” 的相关文章](#)

▶ [本文作者相关文章](#)

- [孙黛珍](#)
- [江玲](#)
- [刘世家](#)
- [张迎信](#)
- [黄培鸿](#)
- [程遐年](#)
- [翟虎渠](#)
- [万建民](#)