

## 黑龙江省稻瘟病菌生理小种毒力基因分析与抗病育种策略

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Pathogenic Races and Virulence Gene Structure of *Magnaporthe oryzae* Population and Rice Breeding Strategy for Blast Resistance in Heilongjiang ProvinceLEI Cai-Lin<sup>1</sup>, ZHANG Guo-Min<sup>2,\*</sup>, CHENG Zhi-Jun<sup>1</sup>, MA Jun-Tao<sup>2</sup>, WANG Jiu-Lin<sup>1</sup>, XIN Ai-Hua<sup>2</sup>, CHEN Ping<sup>1</sup>, XIAO Jia-Lei<sup>2</sup>, ZHANG Xin<sup>1</sup>, LIU Ying-Xue<sup>2</sup>, GUO Xiu-Ping<sup>1</sup>, WANG Jie<sup>1</sup>, ZHAI Hu-Qu<sup>1</sup>, WAN Jian-Min<sup>1,\*</sup>

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摘要

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**摘要** 近年来黑龙江省稻瘟病危害程度加重, 给水稻生产造成巨大损失。为了解当地稻瘟病菌生理小种及其毒性基因的组成与分布, 有针对性地利用抗性基因, 选育抗病品种和使之合理布局, 本文利用9个日本鉴别品种、7个中国鉴别品种、31个抗稻瘟病单基因系及12个当地主栽品种, 对2006年采自该省主要积温区不同水稻品种的173个稻瘟病菌株进行致病性测定。结果鉴定出55个日本小种, 优势小种为O17、O77、O37、377和O47, 总频率为42.29%。鉴别力比较结果证实日本鉴别品种比中国鉴别品种更适合于当地稻瘟病菌致病性变异与小种分化研究。在12个主栽品种中, 除龙粳14、龙盾104外, 其他品种已经或正在丧失对稻瘟病的抗性。*Pi9*基因在所有积温区对稻瘟病菌株的抗谱最广(平均94.80%), 是当前黑龙江省水稻育种上极有价值的抗性基因; 基因*Piz-5(CA)*、*Piz-5(R)*、*Pita-2(R)*、*Pita-2(P)*、*Pi12(t)*和*Pi20(t)*对供试菌株有高于70%的抗谱, 也具有较高的利用价值。黑龙江省当前抗稻瘟病育种的策略应该是, 在利用抗源龙粳14、龙盾104和*Pi9*的基础上, 通过分子标记辅助选择方法聚合一至多个广谱抗性基因; 同时加强对稻瘟病菌种群的监测和新抗源的发掘, 有针对性地向主栽品种导入新的抗性基因。

**关键词:** 稻瘟病菌 生理小种 毒力基因 水稻 抗性基因

**Abstract:** The rice blast became more severe in Heilongjiang province during the past few years, causing a large loss of rice yield. A total of 173 *Magnaporthe oryzae* (*M. oryzae*) isolates, collected from different rice-cropping districts of the province in 2006, were tested for their pathogenicity against 9 Japanese and 7 Chinese differential varieties (DVs) together with 31 rice monogenic lines (MLs) with different blast resistance genes and 12 local leading cultivars. Out of these 173 isolates, 55 Japanese races (pathotypes) were identified by using the Japanese DVs, and the predominant races were O17, O77, O37, 377, and O47, accounting for 42.29% of all the tested isolates. The comparison of differential ability between Japanese and Chinese DVs testified that the former one was much more suitable for *M. oryzae* pathotyping in Heilongjiang province. Among 12 leading cultivars tested, only Longjing 14 and Longdun 104 still kept good resistance to blast disease. The resistance gene *Pi9* showed broadest resistance spectrum (on average 94.80%) to all the blast isolates tested, and was of the highest utilization value in rice blast resistance breeding. The resistance genes *Pi-z5(CA)* *Pi-z5(R)*, *Pi-ta2(R)*, *Pi-ta2(P)*, *Pi-12(t)*, and *Pi20(t)* also showed high utilization values due to their resistance spectra of around 70%. The most effective breeding strategy for blast resistance should be as follows: 1) to utilize rationally Longjing 14, Longdun 104 and *Pi9* as resistance donors, and pyramid one to several more broad-spectrum resistance genes into elite leading cultivars by means of marker-assisted selection; 2) to strengthen the monitoring of predominant virulent races and their temporal and spatial variation; and 3) to explore new resistance resources extensively and transfer the new broad-spectrum resistance genes into leading cultivars purposefully.

**Keywords:** *Magnaporthe oryzae* Pathotype Virulence gene Rice Resistance gene

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