

研究论文

# 云南抗白叶枯病稻种的RGA初析

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**摘要** 根据水稻抗白叶枯病Xa21基因的富含亮氨酸重复区域(LRR)和番茄抗细菌性斑点病(Pseudomonas syringae pv. tomato)的Pto基因编码蛋白质激酶的DNA序列, 设计2对引物用于扩增抗水稻白叶枯病品种中的抗病基因同源序列。经聚丙烯酰胺凝胶电泳和聚类分析, 结果表明供试抗病品种间具有丰富的RGA多态性, 用同一引物测定的属于同一簇的品种显示相似的抗性和抗谱。从XLRR for/XLRR rev引物的聚类图中可知, 在遗传距离为0.25时, 测试的47个抗白叶枯病水稻品种可分为9个簇。其中3、4、7组为主要组群, 第3组包括23个水稻品种, 在遗传距离为0.2时, 可进一步分为5个亚群。RGA分析结果为水稻抗病育种选择亲本和利用品种布局进行白叶枯病生态控制提供了依据。

**关键词** [水稻](#) [白叶枯病抗性](#) [抗病基因同源序列](#) [RGA指纹](#)

**分类号** [S511](#)

## Preliminary Analysis of Resistance Gene Analogs for Rice Cultivars to Bacterial Blight in Yunnan

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**Abstract** Polymerase chain reaction(PCR) primers corresponding to the conserved motifs of prototype resistance genes were used to characterize rice cultivars with resistance to bacterial blight in Yunnan Province. The RGA analysis was conducted by PCR amplification using two primers, i.e. XLRR for/XLRR rev for LRR of Xa21 resistance gene to Xanthomonas oryzae pv. oryzae and Pto-kin1/Pto kin2 for protein kinase of Pto resistance gene to Pseudomonas syringae pv. tomato, respectively. The results showed that abundant RGA polymorphism was observed among the resistance cultivars tested. The cultivars which were belonged to the same cluster showed similarly resistance or spectrum of resistance to Xanthomonas oryzae pv. oryzae isolates tested. Among the cultivars clusters which were formed by RGA profile of XLRR for/XLRR rev primer, forty-six varieties tested could be divided into 9 groups at genetic distance 0.25, group 3, 4, 7 were predominant, and the group 3 was divided into 5 subgroups including 23 cultivars at genetic distance 0.2. The RGA markers were useful in grouping genetically related varieties for rice breeding to bacterial blight control and to select parental germplasm with differential genetic background.

**Key words** [Rice](#) [Bacterial blight disease resistance](#) [Resistance gene analogs](#) [RGA profile](#)

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