

## Virulence profiling of *Xanthomonas oryzae* pv. *oryzae* isolates, causing bacterial blight of rice in India

A. Yugander · R. M. Sundaram · D. Ladhakshmi ·  
 S. K. Hajira · V. Prakasam · M. S. Prasad ·  
 M. Sheshu Madhav · V. Ravindra Babu · G. S. Laha

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**Abstract** Bacterial blight (BB) of rice caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*), remains a major production constraint in rice cultivation especially in irrigated and rainfed lowland ecosystems in India. The pathogen is highly dynamic in nature and knowledge on pathotype composition among the *Xoo* population is imperative for designing a scientific resistance breeding program. In this study, four hundred isolates of *Xoo* collected from diverse rice growing regions of India were analyzed for their virulence and genetic composition. Virulence profiling was carried out on a set of differentials consisting of 22 near isogenic lines (NILs) of IR24 possessing different BB resistance genes and their combinations along with the checks. It was observed that different NILs possessing single BB resistance gene were susceptible to about 59–94% of the *Xoo* isolates except IRBB 13 (containing BB resistance gene *xa13*), which showed susceptibility to about 35% of the isolates. Based on the reaction of the *Xoo* isolates on the differentials, they were categorized into 22 pathotypes. Among the 22 pathotypes, IXoPt-1 and IXoPt-2 were least virulent and IXoPt # 18–22 were highly virulent. Pathotype IXoPt-19 which was virulent on all single BB resistance genes except *xa13* constituted the major

pathotype (22.5% isolates) and was widely distributed throughout India (16 states). This was followed by pathotype IXoPt-22 (17.25%) which was virulent on all the NILs possessing single BB resistance genes. Molecular analysis was carried out using two outwardly directed primers complementary to sequence of *IS1112*, a repetitive element of *Xoo*. A high level of genetic polymorphism was detected among these isolates and the isolates were grouped into 12 major clusters. The data indicated complex nature of evolution of the *Xoo* pathotypes and there was no strong correlation between pathotypes and genetic clusters as each genetic cluster was composed of *Xoo* isolates belonging to different pathotypes. The study indicated that none of the single BB resistance genes can provide broad spectrum resistance in India. However, two-gene combinations like *xa5 + xa13* and different 3 or 4 genes combination like *Xa4 + xa5 + xa13*, *Xa4 + xa13 + Xa21*, *xa5 + xa13 + Xa21* and *Xa4 + xa5 + xa13 + Xa21* are broadly effective throughout India.

**Keywords** Rice · Bacterial blight · *Xanthomonas oryzae* pv. *oryzae* · Variability

A. Yugander and G. S. Laha contributed equally to this paper.

A. Yugander · R. M. Sundaram · D. Ladhakshmi ·  
 S. K. Hajira · V. Prakasam · M. S. Prasad ·  
 M. Sheshu Madhav · V. Ravindra Babu · G. S. Laha (✉)  
 ICAR-Indian Institute of Rice Research (ICAR-IIRR),  
 Rajendranagar, Hyderabad, Telangana State 500030, India  
 e-mail: lahags@yahoo.co.in

### Introduction

Bacterial blight (BB), caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) has become a major production constraint in rice cultivation in India and most of the east and south east Asian countries and in West Africa (Devadath 1992; Win et al. 2013). Primarily BB is a