

23. Identification of a new gene introgressed from *Oryza brachyantha* with broad- spectrum resistance to bacterial blight of rice in India

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Bacterial blight, caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) is one of the major diseases of rice occurring in almost all the rice growing ecologies of the world causing significant yield losses annually (Mew, 1987). Chemical control measures are not quite effective for managing this disease and hence the importance of host plant resistance has been well recognized to combat this disease. So far 31 resistance genes for bacterial blight in rice have been identified from different cultivars and wild relatives of *Oryza* (Nino-Liu et al., 2006 Chu et al., 2006 Wang et al., 2007). Muralidharan et al. (2003) observed differential reaction of near isogenic lines (NILs) of single gene, pyramided lines with 2-4 gene combinations and donors in multi-environment tests indicating the variability in the virulence of the pathogen and suggested to develop high yielding varieties with durable and broad-spectrum resistance by pyramiding different resistance genes depending upon their effectiveness. Of the 31 genes so far identified, four dominant genes viz., *Xa21* (*O. longistaminata*), *Xa23* (*O. rufipogon*), *Xa27* (*O. minuta*) and *Xa29(t)* (*O. officinalis*) have been introgressed from wild species of *Oryza* which show broad-spectrum of resistance to several virulent races of bacterial blight (Khush et al., 1990 Zhang et al., 1998 Gu et al., 2004 and Tan et al., 2004).

Two introgression lines (IR 65483-118-25-31-7-1-5-B, IR 65483-141-2-4-4-2-5-B) derived from IR 56 x *O. brachyantha* (Acc. 101232) along with recurrent parent IR 56 and donor *O. brachyantha* were obtained from IRRI, Philippines. They were initially screened against a virulent isolate (DX-044) collected from the susceptible plant of wild rice *O. rufipogon* and two introgression lines and *O. brachyantha* were found to have immune reaction while recurrent parent IR56 was susceptible. Further, these two introgression lines, parental lines, the NILs carrying different resistant genes (IRBB lines) and susceptible (TN-1, BPT5204) and resistant (IET 8585) checks were screened during kharif 2006 against 21 different virulent isolates of bacterial blight collected from 11 states of India covering different rice growing ecologies which are being maintained at Directorate of Rice Research, Hyderabad (Table 1).

The wild species *O. brachyantha* showed resistance reaction to all the isolates except the one (DX-090) collected from Ludhiana in Punjab state. The two introgression lines showed similar pattern of resistance, namely, resistance reaction against 16 isolates, moderate resistance to one isolate and susceptible reaction to four isolates (Table 1). On other hand, IRBB lines showed differential reaction to different isolates (Table1). These results indicate that the gene introgressed from *O. brachyantha* is quite different from those in IRBB lines used in this experiment. To study the inheritance of the bacterial blight resistance gene introgressed from *O. brachyantha*, both the introgression lines were crossed with the recurrent parent IR 56 and susceptible check BPT 5204 carrying no resistant gene to bacterial blight. Their F₁ plants were found to be resistant against DX-044 isolate and F₂ populations segregated in a ratio of 3:1 (resistant: susceptible) (Table 2). In addition, the F₂ population of IR65483-118-25-21-7-5-B x IR65483-141-2-4-4-2-5-B did not show segregation for susceptibility and all the plants were resistant. These results suggest that the two introgression lines have the same single dominant gene for resistance to BB isolate DX-044.

Further, the introgression line IR 65483-141-2-4-4-2-5-B was crossed with IRBB21 line carrying *Xa21*, and the F₂ populations segregated in the ratio of 15:1 (resistant : susceptible) against the DX-020. This segregation pattern clearly indicated that the resistant genes from *O. brachyantha* and *Xa21* are non-allelic and inherited independently. The wild species *O. brachyantha* (FF genome) is distantly related to cultivated and other wild rices from where bacterial blight resistant genes are identified and several incompatibility barriers restrict the natural gene flow from one species to another. The broad - spectrum bacterial blight resistance gene introgressed from *O. brachyantha* is designated as *Xa34* (t). We are in the process of mapping this gene with molecular markers.

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