24. Inheritance of bacterial blight resistance in the landrace Acc. 32753

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Rice is the most important food crop and a primary food source for more than two third of the world's population. In India, bacterial blight (BB) of rice caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) is considered as one of the most destructive diseases, especially in irrigated and rainfed lowland ecosystems (G. S. Laha et al., 2008). Yield loss ranges from 74-81% in susceptible cultivars (Gnanamanickam et al., 2005). Since chemical control is often ineffective, development of varieties carrying one or more resistance genes is considered an economically feasible and environmentally safe strategy for management of the disease (Khush, 1993). Over 30 BB resistance genes have been identified so far in rice (Khush and Angeles, 1999) from different cultivated rice and wild rice species. Large scale cultivation of high yielding varieties with single genes for resistance resulted in a significant shift in the pathogen race frequency and consequently resistance break down leading to epidemics. This necessitates identification of new genes for resistance from diverse sources and their pyramiding to impart durable resistance in the cultivated varieties. Landraces of rice constitute an important germplasm source for resistance breeding. One of the landrace accessions, Acc. 32753 has consistently displayed a very high level of BB resistance when screened with multiple pathotypes of the BB pathogen. The present study was designed to study the inheritance of BB resistance in the land race accession.

In order to study the gene(s) underlying resistance in Acc. 32753 a cross was made between Acc. 32753 and TN1, a BB susceptible cultivar. The F_1 plants were observed to be susceptible when screened with a hyper virulent isolate, DX133 collected from Raipur. This indicates the possible involvement of recessive gene(s) in governing BB resistance. The F_1 plants were selfed to develop a $F_{2:3}$ mapping population consisting of 389 individuals. Among these, 306 plants were susceptible and 83 were observed to be resistant (3S: 1R) ($\chi^2 = 2.77$, $P > 0.05$) indicating one locus-segregation. When the F_2 plants were selfed to generate F_3 families and analyzed, 83 F_3 lines were observed to be homozygous resistant, 198 were heterozygous and 108 were homozygous susceptible (1:2:1; $\chi^2 = 1.24$, $P > 0.05$).

In order to study whether the gene identified in Acc. 32753 is allelic to the known recessive resistance genes, Acc. 32753 was crossed with near isogenic lines (NILs) with the genetic background of IR24 harboring a single recessive resistance genes *xa5, xa8* or *xa13*. The F_1s derived from the crosses Acc. 32753/IRBB8 and Acc. 32753/IRBB13 were susceptible, while the F_1s derived from the cross Acc. 32753/IRBB5 was resistant, suggesting the possible involvement of *xa5* in controlling BB resistance in the landrace. In order to further confirm this, Acc. 32753 along with IRBB5 and TN1 were amplified with the PCR based RFLP marker RG556 (Yoshimura et al., 1995), which is closely linked to *xa5*. The landrace was observed to show amplification pattern similar to that of IRBB5 (Fig. 1), When the F_2 population derived from the cross Acc. 32753/IRBB5 was screened for BB resistance, all the plants were observed to be resistant confirming the presence of *xa5* in Acc. 32753.

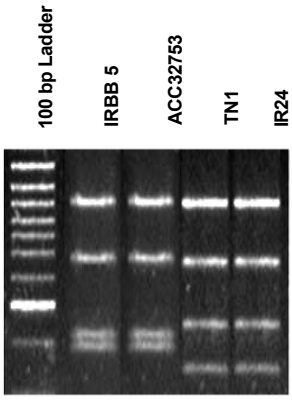

Fig 1: Amplification pattern of ACC32753 with RG556

In order to further confirm presence of *xa5* in the landrace, the candidate gene from *xa5*, viz. TFIIAγ (Iyer et al., 2005) was amplified from the genomic DNA of Acc. 32753, IRBB5, TN1 and IR24 (susceptible to BB), using primer pairs targeting exon 2, which is associated with *xa5* encoded function. The primers pairs amplified a 260 bp fragment in both resistant and susceptible genotypes, but resistant genotypes possesses a 2 bp substitution, GTC to GAG (415503-415554 bp of exon 2), resulting in an amino acid change, i.e. from valine in susceptible genotypes to glutamic acid in resistant genotypes (substitution at 39th amino acid position). Analysis of sequence of the four genotypes analyzed revealed presence of 2 bp functional polymorphism diagnostic of *xa5* in both IRBB5 and Acc. 32753, while TN1 and IR24 carried the non-functional allele (Fig. 2). This clearly indicates that *xa*5 is indeed the candidate gene governing resistance in Acc. 32753.

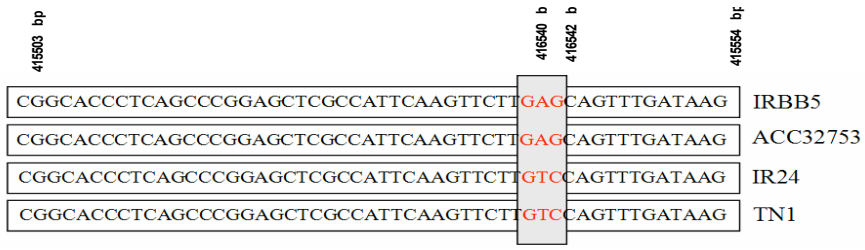

Fig. 2 Sequence comparison in the region of functional polymorphism between resistant and susceptible genotypes

Interestingly, when we compared the level of BB resistance of Acc. 32753 with that IRBB5, it was observed that the latter showed a higher degree of resistance (SES score 1) as compared to IRBB5, which showed a score of 3. This could be due to the effect of different genetic backgrounds of Acc. 32753 and IRBB5, which may be responsible for modulating the level of resistance of *xa5*. Sundaram et al. (2009) have also reported similar results wherein, *xa5* showed different levels of BB resistance between two varieties Samba Mahsuri and Triguna. We are presently investigating this aspect by analyzing NILs of *xa5* in different genetic backgrounds.

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