

Entry No. IRRC-0393

Category	:	International Rice Research Conference
Select Theme	:	Genetics of Biotic tolerance: Breeding application
Endorsement email	:	
Genetics of Biotic interactions Stress tolerance Mitigation and Microbiome Keyword 1	:	Brown planthopper
Genetics of Biotic interactions Stress tolerance Mitigation and Microbiome Keyword 2	:	
Genetics of Biotic interactions Stress tolerance Mitigation and Microbiome Keyword 3	:	
Title of Entry	:	New Sources of resistance against rice brown planthopper, <i>Nilaparvata lugens</i> (Stal.) identified through phenotyping and genotypic analysis
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Select only one type of presentation	:	15 minute oral presentation
Abstract	:	Rice brown planthopper, <i>Nilaparvata lugens</i> (Stal.) is one of the most important rice pest widely distributed in almost all rice growing regions of Asia including India leading to yield losses ranging from 10-70%. Recently, BPH incidence has increased not only in Telangana but also in Northern India. Though several resistant varieties have been identified and cultivated, break down of resistance was observed either due to presence of only one or two resistance genes or only one resistance mechanism operating. Even the popularly cultivated resistant rice variety in Telangana and Andhra Pradesh i.e. MTU 1010 (Cotton Dora Sannalu) succumbed to BPH, warranting the need to intensify research efforts to identify new resistant sources for use in breeding programmes. Through field screening of 286 rice genotypes at Rice Research Centre, ARI, Rajendranagar during rainy season (kharif) 2015, identified 53 rice cultures with high (damage score – 3.0) and moderate (damage score 5.0) field tolerance, which were retested for confirmation of phenotypic reaction under poly house during rabi 2015-16 and kharif

	<p>2016, using the standard seed box screening technique. The cultures were scored based on standard evaluation system (IRRI, 2014). Of the twelve promising cultures identified, six rice cultures possessing acceptable yield and quality traits were further studied for mechanisms contributing to resistance. Among these, IET 23993 exhibited all the three mechanisms of resistance, while in GSR 234 antixenosis and tolerance mechanisms were operating. But in RNR 23079 and BobhuKongbu only antixenosis and HHZ 5 DT-1 DT-1 and HHZ 25 SAL DT-1 only antibiosis were found to offer resistance. Molecular characterization studies carried out at IBT, Rajendranagar using 23 molecular markers identified for BPH resistance revealed that IET 23993 possessed eight genes for BPH resistance, 6 genes in Bhobhu Kongbu and HHZ 25 SAL DT-1 DT-1, 4 genes in HHZ 5 DT-1 DT-1, 3 genes in RNR 23079 and two genes in GSR 234 and PTB 33, which needs further confirmation. Identification of new resistant sources having all the three mechanisms operating or having multiple genes offering resistance will pave way for development of varieties with durable resistance to BPH.</p>
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