

ABSTRACT

Brown planthopper (BPH) is one of the most serious rice pests in Sri Lanka. The most effective way of BPH management is considered as host plant resistance. Hence, continuous identification of genetic resources having broad based and durable resistance to BPH is important to face against resistance breakdown of existing BPH resistant rice varieties by incorporation of new BPH resistant genes into modern rice cultivars. The study aimed to find out the possibility of using genetic resources of wild rice, *Oryza nivara* in order to develop broad based and durable resistance for BPH in cultivated rice varieties in the future.

The present study evaluated the basis of BPH resistance in *O. nivara* (WRAC 01, 02, 04, 07, 11, 12, 14, 19, 21, 22, 24, 25, 35, 41, 46, 62 and 9864) with Ptb 33, Bg 380 and Bg 379/2 check varieties by screening for resistance and characterizing the genes by molecular techniques. In addition, morphological and molecular characterization was done to examine the diversity among accessions by descriptors for rice and through Simple Sequence Repeats (SSR) markers respectively. Two BPH populations collected from Bathalagoda, Bombuwala which were reared on Bg 380 and a virulent BPH population collected from rice fields in Kegalle area and reared on Bg 379/2 was used for screening tests. Response of test accessions to feeding by BPH was assessed by using Standard Seed Box Screening test (SSBS) and standard honeydew test. Meantime, antibiosis, antixenosis and oviposition responses of BPH on test accessions were investigated. Also, to inspect genetic variation among BPH populations by SSBS, a differential set of four resistant cultivars with known resistant genes for BPH (Ptb 33- *bph2*, *Bph3*; Rathu Hennati - *Bph 3*; Baba wee - *bph4* and Pokkali-*Bph9*) were used. Molecular screening for BPH resistance was carried out using specific molecular markers for *bph2*, *Bph10*, *Bph13*, *Bph 3* and *bph18(t)* genes and estimation of genetic distance among accessions was done by using RM 85, RM 11, RM 19, RM 190, AJ 096 and RM 589 primers.

Results of different bioassay tests confirmed resistant to moderate level of resistance in the majority of *O. nivara* accessions studied. Among all, WRAC 35, WRAC 21, WRAC 02 and WRAC 01 showed the best performances over Ptb 33, indicating their superior level of resistance to available BPH populations in Sri Lanka and the potential of using these accessions to upgrade cultivated rice varieties in future. Furthermore, considering the

reaction of three BPH populations to differential set of resistant cultivars, genetic variation of Kegalle population was detected, which support the emergence of virulent biotype in field and has the potential to overcome the BPH resistance in Bg 379/2.

Molecular screening for BPH resistance revealed positive results with WRAC 02, 04, 25, 07 and 21 accessions for *bph 2* gene and with WRAC 46 for *Bph10* gene. However, none of the *O. nivara* accessions was recorded as positive for *Bph3* and *bph18(t)* genes. Although, *O. nivara* accessions excluding 9864, showed positive results for *Bph13* gene, this work confirms the virulence of Sri Lankan BPH against *Bph13* gene as Bg 380 (Susceptible check) was positive for the marker (AJ 096). Therefore, high level of resistance observed in WRAC 35 and WRAC 01 could be due to the presence of other known or new genes. Hence, further investigations for other known genes and exploiting them to widen the genetic base of cultivated rice varieties needs to be continued.

Results of morphological characterization revealed vast morphological diversity among all test accessions and varieties. Four principle components were extracted, which accounted over 82% of total variance of the seventeen quantitative traits studied and they were grouped in to five clusters at a rescaled distance of 15. Although, morphological characterization of test accessions did not showed a clear separation of resistant and susceptible groups, accessions which are highly resistant to BPH (WRAC 35, WRAC 21, WRAC 02 and WRAC 01) were clustered more closely in the dendrogram based Nei's genetic distance.

To get more advanced picture on genetic diversity of test accessions, primers representing each and every chromosome should be used in future studies. Also, further studies on the relationship between resistance and the phloem chemistry of test plants should be continued for a better explanation of resistant mechanism among individuals.