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Bulked Segregant Analysis to Detect Main Effect of QTL Associated with Sheath Blight Resistance in BPT-5204/ARC10531 Rice (Oryza sativa L)

Shailesh Yadav[1]*, Ghanta Anuradha[1], Ravi Ranjan Kumar[3], Vemireddy LR[1], Ravuru Sudhakar[2], Balram M[1] and Siddiq EA[1]

[1]Institute of Biotechnology, ANGRAU, Rajendranagar, Hyderabad-500030 India
[2]Seed Research and Technology Centre, Rajendranagar, Hyderabad-500030 India
[3]Department of Molecular Biology and Genetic Engineering, Bihar Agricultural University, Sabour-813210, India

Corresponding Author : Shailesh Yadav, Institute of Biotechnology, Acharya N G Ranga Agricultural University, Rajendranagar, Hyderabad, India Tel: +91-7893473471 E-mail: shaileshagri9@gmail.com

The population consisting of 210 F2:3 individuals from the cross between BPT-5204 (highly susceptible to sheath blight) and ARC-10531 a land race from Assam (moderately resistant to sheath blight) was analyzed to identify the markers associated with sheath blight resistance and to study any association of any morphological trait to disease incidence. The frequency distribution curve of F2:3 progenies for disease trait were continuous, indicating the polygenic control over the trait. The range of relative lesion height was 21-75% with a mean of 38.59% .No significant association between sheath blight disease and other morphological traits were detected in F2:3 populations. Parental polymorphisms were surveyed with 500 primer pairs of simple sequence repeats (SSR), revealed 70 polymorphic markers between the parents. In order to detect the major effect, QTL associated with sheath blight resistance, a strategy of combining the DNA pooling from selected segregants and genotyping was adopted. The association of putative markers identified based on DNA pooling from selected segregant was established by Single Marker Analysis (SMA).The results of SMA revealed that SSR markers, RM336 (chromosome#7) and RM205 (chromosome#9) showed significant association with sheath blight and accounted for 21.8% and 17.3% of total variation respectively. The results obtained from the DNA pooling of phenotypic extremes could be a useful strategy to detect the genetic loci with major effects of the complex trait such as disease resistance in rice.

In the present scenario of increasing global human population, decreasing arable land, predicted increases of water scarcity, soil salinity, severe diseases, emerging resistance of pests and pathogens to pesticides and climate change pose significant challenges to modern rice research. The biotic stresses viz. , blast, stem rot, sheath blight, and bacterial blight diseases causes severe economic losses to rice productivity. Among them Sheath blight (ShB) is an important fungal disease caused by Rhizoctonia solani Kuhn causing up to 25% of yield loss and degrades rice quality. In hot and very high humid condition, yield loss can even reach as high as 50%. With the increasing application of nitrogenous fertilizers and the popularization of semi dwarf cultivars with more tillers, ShB is becoming the most serious disease in many rice-producing areas in the world. The fungus R. solani Kuhn is soil borne pathogen which survives either as sclerotia or mycelia in plant debris. After the initial infection, the pathogen moves on the plant through surface hyphae and develops new infection structures over the entire plant, causing significant necrotic damage. The architecture of the canopy and the associated microclimate has strong effects on both the mobilization of primary inoculums and the further spread of the disease. Absolute resistance to R.solani is not available in any of the rice germplasm grown worldwide. However, it has been reported that resistance to R. solani is a typical quantitative trait controlled by polygenes in rice. In rice because of availability of high resolution molecular maps, complete sequence information and extensive germplasm collections, mapping of quantitative trait loci (QTLs) for disease resistance such as sheath blight is feasible in crop improvement programme. In this context has reported for the first time the identification of rice QTL resistant to ShB using RFLP markers. To date, around 50 ShB resistance QTLs (ShBR QTLs) have been detected over all 12 rice chromosomes in cultivated varieties, deep-water varieties and wild species. Some of them were identified in multiple mapping populations and/or environments and not associated with either heading date (HD) or morphological traits, and they are believed to be stable ShB QTLs. However QTL mapping is usually carried out by genotyping large number of progenies which is labor intensive, time consuming and cost-ineffective. Several strategies have been proposed to identify molecular markers near a gene/QTL of interest with reduced number of plants to be genotyped. The two main strategies are selective genotyping and bulk segregant analysis (BSA). Selective genotyping is relatively a low-cost approach to detect QTL with large effects by genotyping individuals from the two tails of the phenotypic distribution. Bulked Segregant Analysis (BSA) serves as an affordable strategy for mapping large effect QTLs by genotyping only the extreme phenotypes instead of the entire mapping population. BSA has been successfully used in rice for identifying markers linked to QTL associated with grain quality parameters blast resistance heat tolerance, drought tolerance gall midge resistance and sheath blight resistance. In the present study, bulked segregant analysis approach was used to identify large effect QTLs for sheath blight resistance and to observe the disease association with any of morphological traits

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