

ASSOCIATION OF CANDIDATE DEFENSE GENES WITH QUANTITATIVE RESISTANCE TO RICE BLAST USING MOLECULAR AND *IN SILICO* APPROACHES

We used candidate gene approach to integrate molecular analysis of host-pathogen interactions, gene mapping and development of disease resistance in rice cultivars. Candidate genes (CG) are DNA sequences with similarity to known genes or conserved motifs reported to infer their biological functions. Through associations with disease resistance, they become candidate defense (DR) genes for conferring particular phenotypes. Advanced backcross lines of Vandana x Moroberekan were used to demonstrate this approach to dissect the genetic and molecular basis of durable resistance to blast. Moroberekan, a japonica cultivar from Africa, is known to exhibit durable resistance to blast in Asia.

To accumulate different mechanisms involved in quantitative blast resistance, 15 BC3F5 lines of Vandana x Moroberekan showing partial resistance at IRRI and Cavinti, Philippines and carrying CG alleles were selected and crossed in all pairwise combinations. The top 84 F5 selections are currently being evaluated in multilocation environment to determine resistance to blast and agronomic performance. Eleven DR genes were analyzed based on analyses of several mapping populations and microarray data. These are oxalate oxidase, aldose reductase, 14-3-3 protein, thaumatin, oxalate oxidase-like proteins, eukaryotic aspartyl protease, HSP90, PR1-b, chitinase 2a, dihydrofolate reductase and adenosyl homocysteinase. Polymorphic SSR markers co-localizing with these genes as well as gene-specific PCR primers were used to analyze the top 84 selections. We have found polymorphism in the 1kb upstream region of two putative oxalate oxidases in chromosome 3. Resistant selections showed similar pattern as Moroberekan. In silico analysis of each gene for conserved motifs identified cis-elements at the 1kb upstream regions. There was variation in the number of copies of cis-elements related to biotic stress response such as W boxes, WNPR1 and WRKY for each gene indicating that they have potential associations with the response of rice to rice blast.

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