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ORIGINAL ARTICLE

Biochemical and SSR marker-based insights into rice defense mechanisms against *Pyricularia oryzae*

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Abstract

Rice blast, caused by *Pyricularia oryzae*, significantly impacts worldwide rice production, resulting in yield losses of over 50%. Knowledge of the biochemical and genetic bases of host resistance is essential to develop sustainable strategies to control disease. In this study, completely randomized design (CRD) was used to determine the defense responses of eleven rice genotypes against a virulent monosporic isolate (RL-17) of *P. oryzae* at 72, 96 and 120 h after inoculation (HAI) combined with molecular techniques. Maximum induction of superoxide dismutase (11.39 $Umin^{-1}mg^{-1}$protein), peroxidase (251.23 Umg^{-1}protein), and β-1,3-glucanase (0.032 Umg^{-1}protein) was observed in BRRI dhan74 at 120 HAI. Concurrently, this genotype also maintained high cellular membrane stability by reducing electrolyte leakage (24%) and chlorophyll degradation resulting in the lowest disease score (2.9). BRRI dhan33 and BRRI dhan75 showed similar trends of strong enzyme defense activation and moderate levels of resistance. BRRI dhan63, however, showed the maximum disease severity (score 7.5) coupled with higher electrolyte leakage (38%) and a decline in defensive enzymes. Molecular characterization of blast resistance genes (*Pib*, *Pi5*, *Pik-h*, *Pik-p*, *Pi9*, *Piz-t*, *Piz*, *Pita-2*) using eight gene-based molecular markers, showed that BRRI dhan74 and BRRI dhan33 harbored the highest scores of resistance alleles (four genes each) and remained in distinct branch, indicating similar genetic introgression. This integrative biochemical and molecular approach identifies BRRI dhan33, BRRI dhan74, and BRRI dhan75 as promising donors for blast resistance breeding. Unlike prior studies, this work uniquely integrates temporal enzyme dynamics with resistance-gene profiling, offering the comprehensive insight into rice blast resistance mechanisms in Bangladeshi genotypes.

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