

QUANTITATIVE RESISTANCE TO MAGNAPORTHE ORYZAE REVEALED BY SEQUENTIAL GWAS IN ADVANCED RICE BREEDING POPULATIONS

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Rice blast caused by *Magnaporthe oryzae* is a major rice disease worldwide. Despite the detailed knowledge on resistance genes available, little is known about how these genes interact with quantitative blast resistance loci and with the genetic background. Knowledge on these interactions is crucial for assessing the usefulness of introgressed resistance loci in breeding germplasm. In this work, resistance to blast was mapped using sequential GWAS in two breeding populations, one with 305 indica type, and the other with 245 tropical japonica inbred lines. Interactions and main effects of blast resistance loci were assessed in a multilocus model. Major effect blast resistance gene clusters were detected in both tropical japonica (Pii/Pi3/Pi5) and indica (Piz/Pi2/Pi9), and more complex genetic architectures were revealed with subsequent GWAS scans. In tropical japonica, SNP-QTL S9_9786203 colocalized with Pii/Pi3/Pi5 and had significant interaction with S1_1631976, S1_37612210, and S8_14597990. Together with S10_17378459, these SNP-QTL explained 64% of the phenotypic variance in the tropical japonica population. In the indica population, a blast resistance SNP-QTL S6_10469906 colocalized with Piz/Pi2/Pi9. Together with S1_3350405, S4_31419616, and S7_12704004, these QTL explained 35% of the phenotypic variance in the indica population. A significant interaction was found among S6_10469906, S4_31419616, and the genetic background. Our results suggest that epistatic interactions can play a major role modulating major effect blast resistance loci such as Pii/Pi3/Pi5. Furthermore, the additive and epistatic effects of multiple QTL bring additional layers of quantitative resistance with a magnitude comparable to that of major effect loci. These findings highlight the need of genetic background-specific validation of markers for molecular assisted blast resistance breeding and provide insights for developing quantitative resistance to blast disease in rice.