

Molecular progress on the mapping and cloning of functional genes for blast disease in rice (*Oryza sativa* L.): current status and future considerations

ABSTRACT

Rice blast disease, which is caused by the fungal pathogen *Magnaporthe oryzae*, is a recurring problem in all rice-growing regions of the world. The use of resistance (R) genes in rice improvement breeding programmes has been considered to be one of the best options for crop protection and blast management. Alternatively, quantitative resistance conferred by quantitative trait loci (QTLs) is also a valuable resource for the improvement of rice disease resistance. In the past, intensive efforts have been made to identify major R-genes as well as QTLs for blast disease using molecular techniques. A review of bibliographic references shows over 100 blast resistance genes and a larger number of QTLs (~500) that were mapped to the rice genome. Of the blast resistance genes, identified in different genotypes of rice, ~22 have been cloned and characterized at the molecular level. In this review, we have summarized the reported rice blast resistance genes and QTLs for utilization in future molecular breeding programmes to introgress high-degree resistance or to pyramid R-genes in commercial cultivars that are susceptible to *M. oryzae*. The goal of this review is to provide an overview of the significant studies in order to update our understanding of the molecular progress on rice and *M. oryzae*. This information will assist rice breeders to improve the resistance to rice blast using marker-assisted selection which continues to be a priority for rice-breeding programmes.

Keyword: Blast; *Magnaporthe oryzae*; gGene cloning; Marker-assisted selection; Quantitative trait loci mapping; Resistant gene; Rice; *Oryza sativa* L.