Rice Research: Open Access

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Rice Blast Resistance Genes in Rice Molecular Breeding: A Strategy

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Introduction

Rice blast is one of the most damaging diseases to rice cultivation around the world. The most successful and cost-effective way to manage blast has been the development and fair use of resistant varieties. We summarised the cloning and use of rice blast resistance genes such as Pi1, Pi2, Pi9, Pi54, Pigm, and Piz-t in this study. The presence of few R (resistance) genes that impart resistance to both seedling and panicle blast, the resistance effect of pyramided lines is not the result of a clear aggregation of resistance continuum, and only a few R genes have been successfully used for molecular breeding are the three major problems in current rice blast resistance breeding. As a result, novel rice blast R gene utilisation techniques in molecular breeding have been suggested, including correctly recognising R gene use in major modern rice varieties, developing a core resistant germplasm with excellent detailed traits, and screening and using broad-spectrum and robust resistance gene combinations. Finally, the current state of blast resistance enhancement was addressed, including new genes controlling resistance discovered through GWAS (genome-wide interaction study) and genetic editing to enhance rice blast resistance. PAMP-triggered immunity occurs when rice is targeted by M. oryzae and pattern recognition receptors (PRRs) on the cell surface identify pathogen-associated molecule patterns (PAMPs) and stimulate the defensive mechanism by cell wall modulation, callose deposition, and the expression of defense-related proteins in host cells (PTI) [1]. Chemicals and resistant varieties are now the most popular methods of rice blast control. Chemical regulation, in addition to increasing prices, pollutes the air and puts food welfare at risk [2]. The rapid detection and cloning of rice blast R and AVR genes has aided understanding of the molecular mechanisms of rice blast fungus interaction and co-evolution, thanks to the advancement of genome sequencing technologies. It not only provides new genetic tools for improving rice blast resistance, but also new technological ideas for regulating disease-resistance signalling pathways through genetic editing to improve resistance. To breed new resistant cultivars, a few molecular markers have been designed to quickly incorporate clustered and paired NLRs into the Tetep genome. The R genes conferring a resistant genotype on elite rice cultivars or key resistant germplasms may be detected as more donors of R genes are sequenced [3]. Understanding the partial resistance of non-race specificity, which is mediated by several quantitative trait loci (QTLs), has become a hot topic as genetic research into blast resistance has increased. Partially resistant plants are commonly thought to be a quantitative trait. However, since a single partial R gene has a limited resistant effect, it must be paired with several partial resistance genes to achieve successful resistance. The formation of core germplasms harbouring target partial resistance without linkage drag would become a significant step in rice blast resistance progress in the future, thanks to the development of high-throughput molecular breeding methods. These newly discovered genes not only provide new genetic tools for breeding broad-spectrum and long-lasting rice cultivars, but they also provide new methods for improving rice blast resistance.

References

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