

Durable Resistance to Rice Blast Mediated by Race-nonspecific Genes in Rice: A Mini Review

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ABSTRACT

Rice blast is a major biotic constraint of rice worldwide, that causes a serious threat to rice production. Genetic improvement of blast resistance is one of important objectives in rice breeding programs. Race-specific resistance genes (R-genes) confer complete resistance to rice blast fungus, but a breakdown of resistance mediated by R-genes has been frequently caused by new races of blast pathogen. To avoid the risk of genetic vulnerability, the use of race-nonspecific resistance has been concentrated in Japanese upland rice varieties whose resistance has been maintained for a long time. However, linkage drag between genes underlying race-nonspecific resistance and undesired traits has hindered its use. Among QTLs detected, a single recessive resistance gene, pi21 was identified by map-based cloning and characterized. The use of pi21 has improved durable resistance in rice breeding programs in Japan. Three QTLs conferring race-nonspecific resistance to rice blast were detected on chromosomes 4 and 12. Among them, a single recessive gene, pi21 was isolated by positional cloning and characterized. This allele has been used for genetic improvement of durable blast resistance through DNA marker-assisted selection in rice breeding programs in Japan and Africa Rice Center.

KEY WORDS: RICE BLAST RESISTANCE, RACE-SPECIFIC, RACE-NONSPECIFIC, QTLs, POSITIONAL CLONING.

INTRODUCTION

Rice blast caused by the fungus *Magnaporthe oryzae* is a major destructive disease in rice cropping areas around the world. More than 100 resistance genes to rice blast have been identified and more than 30 of them have been cloned (Ashkani et al., 2016). Race-specific R genes encode nucleotide-binding site (NBS) leucine-rich repeat (LRR) proteins that interact with pathogen effectors and trigger defense reactions according to the gene-for-gene model of recognition. R-genes dramatically enhance blast resistance and result in stable rice production, but their extensive use poses a serious risk of emerging new races of the blast pathogen and the quick breakdown of resistance which is defined as genetic vulnerability. On the other hand, race-nonspecific resistance is quantitatively controlled by multiple quantitative trait loci (QTLs) or genes and is concentrated on the durability of resistance to rice blast, (Okuno and Fukuoka 2020, Maria et al 2021).

Mapping and map-based cloning of QTLs for race-nonspecific resistance: Two resistance QTLs on chromosome 4 and one on chromosome 12 were firstly identified using

Japanese resistant rice variety (Fukuoka & Okuno 2001; Fukuoka et al. 2012). Each QTL explained from 13.7% to 45.7% of the total phenotypic variation. One of QTLs on chromosome 4 was inherited as a single recessive gene and was designated pi21. This gene encodes a protein with a putative heavy-metal-binding domain and a proline-rich region (Fukuoka 2001). Comparison of sequences between resistant and susceptible varieties identified 21- and 48-bp deletions in the resistant variety. Transgenic complementation testing confirmed that a loss-of-function mutation in Pi21 improves resistance to rice blast.

Asian cultivated rice (*Oryza sativa* L.) has 12 haplotypes determined by insertion/deletion variations at three sites in the proline-rich region, which is presumed to be involved in protein-protein interactions in multicellular organisms. Inoculation testing using a series of backcrossed lines carrying each of the Pi21 haplotypes in the same genetic background indicated that only the line carrying the haplotype of a resistant variety showed improved the resistance to rice blast. The results suggest that the two deletions in the resistance pi21 allele are optimal to cause the loss of function, which increases the resistance to rice blast.

Durable resistance to rice blast mediated by pi21: Slow induction of defense by pi21 contributes to pathogen control

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without penalty on yield. The pi21 allele is effective against diverse fungus races, so the use of pi21 might not be a strong driving force for changes in the structure of pathogen populations. The durability of resistance mediated by pi21 may be confirmed by prolonged resistance of varieties under natural field conditions.

Monitoring of newly released varieties carrying pi21 will provide further evidence to confirm or disprove the durability of resistance mediated by pi21. Besides, this allele alone may not be sufficient to control blast disease under high disease pressure. Two breeding approaches are proposed to increase the durability of resistance to rice blast in rice, i) the use of multiline varieties carrying different resistance genes and ii) combining multiple resistance genes in the same genotype (Fukuoka & Okuno 2019).

Pyramiding race-nonspecific resistance genes for sustainable control of rice blast: Pyramiding multiple resistance QTL alleles is considered to additively enhance race-nonspecific resistance (Fukuoka et al., 2015). However, knowledge of the impact of QTL pyramiding on the robustness of plant defense in rice is limited. A more important observation is that a QTL pyramid improves the stability of resistance; the coefficient of variation of lesion area across field tests in the line carrying four resistance QTL alleles was smaller than those in lines with only one or two. The study demonstrated the importance of pyramiding of minor QTL alleles for strengthening the durability of resistance, even if the effect of each QTL allele is sensitive to the environment.

CONCLUSION

Three QTLs conferring race-nonspecific resistance to rice blast were detected on chromosomes 4 and 12. Among them, a single recessive gene, pi21 was isolated by positional cloning and characterized. This allele has been used for genetic improvement of durable blast resistance through DNA marker-assisted selection in rice breeding programs in Japan and Africa Rice Center.

Data Availability Statement: The database generated and /or analysed during the current study are not publicly

available due to privacy, but are available from the corresponding author on reasonable request.

Conflict of Interest: Author declare no conflicts of interests to disclose.

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