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Strategies towards Enhancement of Rice Disease Resistance

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Editorial

Emerging pests and phytopathogens have decreased crop yield and efficiency, putting global food security in jeopardy. Traditional breeding techniques, molecular marker-based breeding technologies, and the use of genetically engineered crops have all contributed to global food security. However, owing to a number of caveats, their use in crop enhancement has been severely restricted. Genome editing techniques such as transcriptional activator-like effector nucleases (TALENs) and the clustered frequently interspaced short palindromic repeats (CRISPR)-associated endonuclease Cas9 (CRISPR/Cas9) have successfully solved the shortcomings of traditional breeding methods and are now widely accepted for crop enhancement. Because of its performance, amicability, versatility, low cost and adaptability, the CRISPR/Cas9 technology has emerged as the most efficient genome editing method available. Data suggests that genome editing has a lot of promise for enhancing disease resistance in crop plants [1]. In this study, we provided a brief overview of the processes of various genome editing systems before discussing recent advances in CRISPR/Cas9 system-based genome editing for rice disease resistance enhancement using various strategies. The potential applications of recently established genome editing approaches including CRISPR/Cas12a (formerly known as Cpf1) and base editors for improving rice disease resistance were also addressed in this study. While genome editing relies on the targeted mutation of S genes to introduce disease resistance in plants, it can come at a cost in terms of fitness. S genes, which code for proteins involved in pre-penetration structures, defence suppression, and replication machinery, can cause phenotypic anomalies and nutritional deficiency, which can impact plant growth and development. Sweet rice mutants induce resistance to the BLB pathogen by restricting sugar supply, but this can also result in decreased plant stature and pollen abortion. Targeted editing of various promoter regions of the S genes has been shown for SWEET genes in rice, and this may be mitigated. Disease tolerance can also be established by adding synthetic versions of the S gene that are similar to the allele that actually appears in immune genotypes, rather than completely knocking out a S gene. With no developmental expense, this new allele will induce plant resistance while still demonstrating normal protein functions. Some S genes that differ only at the single nucleotide polymorphism stage may benefit from the newly established base editing techniques, which can be used to precisely introduce single base transformations. Furthermore, since plants have several pathogen inducible promoters and regulatory components, a pathogen induced CRISPR mechanism may be used to transiently turn off the S gene with no compromise [2]. A CRISPR vector system that can take advantage of the pathogen inducible promoter should be developed to show their efficacy in disease tolerance in field crops. When unique allelic variants are involved in resistance reaction, however, the insertion of a custom design sequence into the genome would be more suitable [3]. A CRISPR system combined with the HR mechanism will indefinitely increase the likelihood of introducing the R gene allele into the desired target site for disease resistance growth. CRISPR toolboxes must be developed and studied to extend their applications in resistance breeding for plants, despite the fact that HR is still technically difficult in plants due to low performance and a lack of multiplexing protocols.

References

1. Takatoshi T (2019) The Gametic Non-Lethal Gene Gal on Chromosome 5 Is Indispensable for the Transmission of the Co-Induced Semidwarfing Gene d60 in Rice. Biology 8: 17-26
2. Akama K (2020) An In Vivo Targeted Deletion of the Calmodulin-Binding Domain from Rice Glutamate Decarboxylase 3 (OsGAD3) Increases γ-Aminobutyric Acid Content in Grains. Rice: 13-20.
3. Subbalakshmi L (2020) The Performance of Kavuni Rice in the Western zone of Tamil Nadu. Journal of Rice Research 13: 1.

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