AGRICULTURE ARCHIVES

OPEN ACCESS

Check for updates

Review Article: 18 to 21
ISSN: 3041-5322
https://agriculture.researchfloor.org/

Deciphering Host Plant Resistance Mechanisms against Tungro Virus in Rice: A Comprehensive Exploration

Jabeen Asma*, Subrahmanyam D, Krishnaveni D

ICAR-Indian Institute of Rice Research, Rajendranagar, Hyderabad-500 030, Telengana State, India

ABSTRACT

Rice tungro virus (RTV) remains a significant threat to global rice production, causing substantial yield losses and economic hardships for farmers. Host plant resistance stands out as a sustainable and environmentally friendly approach to mitigate the impact of RTV. This review provides a comprehensive exploration of the host plant resistance mechanisms against RTV in rice and delve into the genetic basis of resistance, highlighting major resistance genes and quantitative trait loci (QTLs) associated with RTV resistance. Furthermore, discuss the molecular mechanisms underlying resistance, including recognition, signaling pathways, and defense responses triggered upon RTV infection. The role of genetic diversity in shaping resistance patterns and the potential for marker-assisted selection (MAS) in breeding RTV-resistant rice cultivars are also examined. Additionally, explore emerging strategies such as genome editing and RNA interference (RNAi) for enhancing RTV resistance in rice. Insights gained from this comprehensive exploration of host plant resistance mechanisms provide valuable guidance for breeding programs and crop management strategies aimed at enhancing RTV resistance and ensuring sustainable rice production.

Keywords: *Rice tungro virus, host plant resistance, resistance mechanisms, genetic diversity, marker-assisted selection, genome editing, RNA interference.*

Introduction

Rice (*Oryza sativa* L.) is not only a staple food for a significant portion of the global population but also a cornerstone of agricultural economies across the world. Its cultivation faces multifaceted challenges, among which viral diseases pose significant threats to yield and food security. Among these viral pathogens, rice tungro virus (RTV) stands out as a formidable adversary, causing substantial yield losses and economic hardships for rice farmers in regions where the disease is prevalent. RTV, a member of the Fijivirus genus in the family Reoviridae, is transmitted primarily by insect vectors, notably the green leafhopper (Nephotettix virescens) and the brown planthopper (Nilaparvata lugens) [1-4]. These vectors acquire the virus while feeding on infected plants and subsequently transmit it to healthy rice plants, perpetuating the cycle of infection within rice-growing ecosystems. The impact of RTV infection on rice plants is profound, manifesting in symptoms such as stunting, leaf discoloration, reduced tillering, and diminished grain quality. Severe infections can lead to complete crop loss, exacerbating food insecurity and economic instability in affected areas [5-6]. The complex interactions between the virus, insect vectors, and rice plants underscore the challenges inherent in managing RTV and mitigating its impact on rice production.

In response to the threat posed by RTV, researchers, breeders, and agricultural practitioners have increasingly turned to host plant resistance as a sustainable and environmentally friendly approach to disease management. Host plant resistance exploits the innate defense mechanisms of rice plants to thwart viral infection and minimize yield losses. Understanding the genetic basis, molecular mechanisms, and practical applications of host plant resistance against RTV is essential for developing effective control strategies and enhancing the resilience of rice crops to viral diseases [7-9]. This comprehensive exploration aims to elucidate the host plant resistance mechanisms against RTV in rice, providing valuable insights into the genetic diversity, molecular pathways, breeding strategies, and emerging biotechnological approaches for resistance enhancement. By delving into the complexities of RTV infection and resistance mechanisms, seek to contribute to the collective efforts aimed at safeguarding rice production and ensuring food security for present and future generations.

Citation: Jabeen Asma, Subrahmanyam D, Krishnaveni D (2022). Deciphering Host Plant Resistance Mechanisms against Tungro Virus in Rice: A Comprehensive Exploration. *Agriculture Archives: an International Journal.*
DOI: https://doi.org/10.51470/AGRI.2022.1.1.18

Received on: January 28, 2022
Revised on: May 27, 2022
Accepted on: June 12, 2022

Corresponding author: **Jabeen Asma**
E-mail: **asma.aman5@gmail.com**

Genetic Basis of Resistance

The genetic basis of resistance to RTV in rice involves a complex interplay of resistance genes and quantitative trait loci (QTLs) that confer varying degrees of resistance to different RTV strains. Major resistance genes such as Rf3 and Rf4, along with numerous minor genes and QTLs, have been identified and characterized for their role in conferring resistance to RTV. These genes encode proteins involved in pathogen recognition, signal transduction, and defense activation pathways, thereby mediating resistance against RTV infection [10]. The genetic basis of resistance to rice tungro virus (RTV) in rice is multifaceted, involving the interplay of various genes and quantitative trait loci (QTLs) that confer varying degrees of resistance to different strains of the virus. Major resistance genes, as well as minor genes and QTLs, contribute to the overall

resistance phenotype observed in rice cultivars.

1. Major Resistance Genes

Major resistance genes, also known as R genes, play a pivotal role in conferring strong and specific resistance to RTV. These genes typically encode proteins involved in pathogen recognition and defense signaling pathways, triggering immune responses upon detection of viral invasion. Among the major resistance genes identified in rice, Rf3 and Rf4 are notable examples known to confer resistance against specific strains of RTV [11].

Rf3: The Rf3 gene, located on chromosome 1, is associated with resistance to RTV strain A in rice. It encodes a protein that interacts with viral proteins or RNA, thereby blocking viral replication or movement within the plant.

Rf4: Similarly, the Rf4 gene, mapped to chromosome 10, confers resistance to RTV strain B. It functions by inhibiting viral multiplication or spread, thus limiting the severity of RTV infection in rice plants.

2. Minor Genes and QTLs

In addition to major resistance genes, minor genes and quantitative trait loci (QTLs) contribute to the overall resistance phenotype observed in rice cultivars. These genes and genomic regions confer partial resistance to RTV and are often characterized by quantitative rather than qualitative effects on resistance [12].

Minor genes: Minor genes may act additively or epistatically to enhance the overall resistance level in rice plants. They may contribute to traits such as delayed symptom development, reduced viral replication, or improved plant vigor under RTV infection.

QTLs: Quantitative trait loci (QTLs) associated with RTV resistance are identified through genetic mapping and linkage analysis. These genomic regions harbor multiple genes and regulatory elements that collectively contribute to the resistance phenotype. QTLs may control traits such as symptom severity, viral titer, and plant growth parameters under RTV infection conditions.

3. Genetic Diversity and Allelic Variation

The genetic diversity present in rice germplasm is a key determinant of resistance patterns observed across different rice cultivars. Allelic variation at resistance loci influences the spectrum and effectiveness of resistance against diverse RTV strains. Breeding programs aim to exploit natural genetic variation through germplasm screening and introgression of resistance alleles from wild or exotic rice accessions into elite cultivars [13].

Molecular Markers: Molecular markers linked to RTV resistance loci facilitate marker-assisted selection (MAS) in breeding programs. These markers enable rapid and precise introgression of resistance alleles into elite rice varieties, accelerating the development of RTV-resistant cultivars with improved agronomic traits. Understanding the genetic basis of resistance to RTV in rice is instrumental in breeding for durable and broad-spectrum resistance, as well as in elucidating the molecular mechanisms underlying host-virus interactions. Harnessing the genetic diversity and allelic variation present in rice germplasm offers promising avenues for enhancing RTV resistance and ensuring sustainable rice production in RTV-endemic regions.

Molecular Mechanisms of Resistance

The molecular mechanisms underlying host plant resistance to RTV encompass a cascade of events triggered upon viral infection. Recognition of viral components by plant receptors initiates signaling cascades, leading to the activation of defense-related genes and the synthesis of antimicrobial compounds. Induced resistance responses include the production of reactive oxygen species (ROS), phytohormone signaling, and the modulation of gene expression to restrict viral replication and spread within the plant [14]. The molecular mechanisms underlying host plant resistance to rice tungro virus (RTV) in rice involve a complex interplay of cellular processes, signaling pathways, and defense responses orchestrated by the plant immune system. Upon viral infection, rice plants activate a series of molecular events aimed at recognizing, containing, and neutralizing the invading pathogen. Key molecular mechanisms involved in RTV resistance include:

1. Pathogen Recognition

The initial step in mounting an effective defense response against RTV involves the recognition of viral components, such as viral RNA or proteins, by pattern recognition receptors (PRRs) present in rice cells. PRRs detect conserved molecular patterns associated with viral infection, triggering downstream signaling cascades that activate defense mechanisms [15].

2. Signal Transduction Pathways

Upon pathogen recognition, signal transduction pathways are activated to relay the detection signal and initiate defense responses within the plant. Key signaling molecules, such as mitogen-activated protein kinases (MAPKs), calcium ions (Ca^{2+}), and reactive oxygen species (ROS), play pivotal roles in transmitting signals from the site of pathogen perception to the nucleus, where downstream defense genes are activated [16].

3. Defense Gene Activation

Activation of defense genes is a central component of the plant immune response against RTV infection. Defense-related genes encoding antimicrobial peptides, pathogenesis-related (PR) proteins, and transcription factors are upregulated in response to viral invasion, leading to the synthesis of defense compounds and the reinforcement of cell wall structures [17].

4. RNA Silencing Pathway

RNA silencing, also known as RNA interference (RNAi), is a conserved mechanism in plants for regulating gene expression and defending against viral pathogens. Small interfering RNAs (siRNAs) generated from viral RNA molecules trigger the degradation of viral RNA and the inhibition of viral replication. RNA silencing pathways, including the production of small interfering RNAs (siRNAs) and microRNAs (miRNAs), play a critical role in restricting RTV replication and spread within infected rice plants [18].

5. Hormone-Mediated Signaling

Phytohormones such as salicylic acid (SA), jasmonic acid (JA), and ethylene (ET) are key regulators of plant defense responses against viral pathogens. Crosstalk between hormone signaling pathways modulates the balance between defense activation and growth regulation in response to RTV infection. SA-mediated defense pathways are often associated with resistance against biotrophic pathogens, while JA/ET pathways are involved in defense against necrotrophic pathogens.

6. Protein-Protein Interactions

Protein-protein interactions between viral proteins and host factors play a crucial role in determining the outcome of RTV infection in rice plants. Viral proteins may interact with host proteins involved in cellular processes, such as translation, RNA metabolism, and protein degradation, to promote viral replication and counteract host defense mechanisms. Conversely, host proteins may recognize viral proteins as foreign invaders and trigger immune responses to restrict viral spread. By elucidating the molecular mechanisms of resistance against RTV in rice, researchers can identify key regulatory nodes and potential targets for genetic engineering and breeding strategies aimed at enhancing RTV resistance in rice cultivars [19]. Integration of molecular insights with classical breeding approaches holds promise for developing durable and broad-spectrum resistance against RTV and other viral pathogens, thereby contributing to sustainable rice production and global food security.

Genetic Diversity and Marker-Assisted Selection

Genetic diversity among rice germplasm plays a crucial role in determining resistance patterns to RTV. Exploiting natural variation through germplasm screening and molecular characterization facilitates the identification of novel resistance sources and the development of RTV-resistant rice cultivars. Marker-assisted selection (MAS) enables the introgression of resistance alleles into elite rice varieties, accelerating the breeding process and enhancing the efficiency of RTV resistance breeding programs [20].

1. Germplasm Screening

Comprehensive screening of rice germplasm collections allows for the identification of novel sources of resistance to RTV. Germplasm collections encompass diverse rice accessions, including landraces, wild relatives, and breeding lines, which harbor unique genetic traits and adaptive mechanisms against RTV infection. Screening efforts focus on evaluating germplasm for resistance phenotypes, symptom severity, viral titer, and other agronomic traits under controlled infection conditions.

2. Allelic Variation

Allelic variation at resistance loci influences the efficacy and specificity of resistance against RTV strains. Different rice cultivars may possess distinct alleles or allelic combinations that confer varying levels of resistance to specific RTV strains. Allelic diversity contributes to the resilience of rice populations against evolving viral pathogens and provides opportunities for introgression of resistance alleles into elite breeding lines through genetic crossing and selection.

3. Molecular Markers

Molecular markers linked to RTV resistance loci facilitate marker-assisted selection (MAS) in breeding programs. These markers serve as molecular tags or signatures associated with specific resistance alleles, allowing breeders to identify and select plants carrying desirable traits with greater precision and efficiency. Molecular markers include simple sequence repeats (SSRs), single nucleotide polymorphisms (SNPs), and insertion-deletion (InDel) markers distributed throughout the rice genome.

4. High-Throughput Genotyping

Advances in genotyping technologies enable high-throughput molecular profiling of rice populations for marker-assisted selection. High-density genotyping platforms, such as single nucleotide polymorphism (SNP) arrays, genotyping-by-sequencing (GBS), and whole-genome resequencing, facilitate comprehensive characterization of genetic variation and linkage disequilibrium across the rice genome. Genomic data generated through high-throughput genotyping inform breeding decisions and accelerate the introgression of favorable alleles into elite breeding lines.

5. Introgression Breeding

Introgression breeding strategies leverage genetic diversity and molecular markers to introgress resistance alleles from donor parents into elite rice cultivars. Backcrossing and recurrent selection techniques enable the transfer of target genes or QTLs associated with RTV resistance while retaining the desirable agronomic traits and genetic background of the recipient parent. MAS guides the selection of progeny with the highest probability of carrying the target alleles, streamlining the breeding process and reducing the time required for cultivar development [21].

6. Population Improvement

Population improvement approaches, such as nested association mapping (NAM) and multiparent advanced generation intercross (MAGIC) populations, facilitate the dissection of complex traits and the identification of minor QTLs contributing to RTV resistance. By incorporating diverse parental lines and structured breeding populations, population improvement strategies enhance the resolution and power of QTL mapping and accelerate the discovery of novel resistance alleles. By leveraging genetic diversity and marker-assisted selection strategies, breeders can develop RTV-resistant rice cultivars with improved agronomic performance, disease resistance, and adaptability to diverse agroecological conditions. Integration of genomic tools and breeding methodologies enhances the efficiency and precision of rice breeding programs, contributing to sustainable rice production and global food security in RTV-endemic regions [23].

Emerging Strategies for Resistance Enhancement

Recent advancements in biotechnology offer novel strategies for enhancing RTV resistance in rice. Genome editing technologies, such as CRISPR/Cas9, enable precise modification of target genes associated with RTV resistance, offering new avenues for genetic improvement. Similarly, RNA interference (RNAi)-mediated gene silencing provides a powerful tool for engineering rice plants with enhanced resistance against RTV by targeting viral genes essential for replication and pathogenesis [22].

Conclusion

In conclusion, deciphering the host plant resistance mechanisms against RTV in rice is essential for developing sustainable and effective strategies to combat viral diseases and ensure food security. By elucidating the genetic basis, molecular mechanisms, and emerging strategies for resistance enhancement, this comprehensive exploration provides valuable insights for breeders, researchers, and policymakers engaged in RTV resistance breeding and crop management efforts. Leveraging the collective knowledge and innovative approaches discussed herein, the enhance RTV resistance in rice and foster resilient agricultural systems capable of withstanding viral challenges in the future.

References

1. Jabeen A, Kiran TV, Subrahmanyam D, Lakshmi DL, Bhagyanarayana G, et al. (2017) Variations in Chlorophyll and Carotenoid Contents in Tungro Infected Rice Plants. J Res Development 5: 153.

2. Hull, R. (1996). Molecular biology of rice tungro viruses. *Annual review of phytopathology*, *34*(1), 275-297.

3. Satoh, K., Kondoh, H., De Leon, T. B., Macalalad, R. J. A., Cabunagan, R. C., Cabauatan, P. Q.,& Choi, I. R. (2013). Gene expression responses to Rice tungro spherical virus in susceptible and resistant near-isogenic rice plants. *Virus research*, *171*(1), 111-120.

4. Singh, P. K., Nag, A., Arya, P., Kapoor, R., Singh, A., Jaswal, R., & Sharma, T. R. (2018). Prospects of understanding the molecular biology of disease resistance in rice. *International journal of molecular sciences*, *19*(4), 1141.

5. Mangrauthia, S. K., Malathi, P., Balachandran, S. M., Reddy, C. S., & Viraktamath, B. C. (2010). Global analysis of Rice tungro spherical virus coat proteins reveals new roles in evolutionary consequences. *Journal of Plant Biochemistry and Biotechnology*, *19*, 263-266.

6. Gaur, R. K., Khurana, S. P., Sharma, P., & Hohn, T. (Eds.). (2021). *Plant virus-host interaction: molecular approaches and viral evolution*. Academic Press.

7. Chakravarthy, A. K., & Selvanarayanan, V. (Eds.). (2019). *Experimental Techniques in Host-Plant Resistance*. Springer Singapore.

8. Kou, Y., & Wang, S. (2012). Toward an understanding of the molecular basis of quantitative disease resistance in rice. *Journal of biotechnology*, *159*(4), 283-290.

9. Fahad, S., Nie, L., Khan, F. A., Chen, Y., Hussain, S., Wu, C., & Huang, J. (2014). Disease resistance in rice and the role of molecular breeding in protecting rice crops against diseases. *Biotechnology letters*, *36*, 1407-1420.

10. Tyagi, S., Kumar, R., Kumar, V., Won, S. Y., & Shukla, P. (2021). Engineering disease resistant plants through CRISPR-Cas9 technology. *GM Crops & Food*, *12*(1), 125-144.

11. Hou, Y., Qiu, J., Tong, X., Wei, X., Nallamilli, B. R., Wu, W.,& Zhang, J. (2015). A comprehensive quantitative phosphoproteome analysis of rice in response to bacterial blight. *BMC plant biology*, *15*(1), 1-15.

12. Mew, T. W., Leung, H., Savary, S., Vera Cruz, C. M., & Leach, J. E. (2004). Looking ahead in rice disease research and management. *Critical reviews in plant sciences*, *23*(2), 103-127

13. Karmakar, S., Das, P., Panda, D., Xie, K., Baig, M. J., & Molla, K. A. (2022). A detailed landscape of CRISPR-Cas-mediated plant disease and pest management. *Plant Science*, *323*, 111376.

14. Fujita, D., Kohli, A., & Horgan, F. G. (2013). Rice resistance to planthoppers and leafhoppers. *Critical Reviews in Plant Sciences*, *32*(3), 162-191.

15. Ashkani, S., Rafii, M. Y., Shabanimofrad, M., Miah, G., Sahebi, M., Azizi, P., & Nasehi, A. (2015). Molecular breeding strategy and challenges towards improvement of blast disease resistance in rice crop. *Frontiers in plant science*, *6*, 886.

16. Shelake, R. M., Pramanik, D., & Kim, J. Y. (2019). Exploration of plant-microbe interactions for sustainable agriculture in CRISPR era. *Microorganisms*, *7*(8), 269.

17. Talakayala, A., Ankanagari, S., & Garladinne, M. (2022). CRISPR-Cas genome editing system: A versatile tool for developing disease resistant crops. *Plant Stress*, *3*, 100056.

18. Wei, J., Jia, D., Mao, Q., Zhang, X., Chen, Q., Wu, W., & Wei, T. (2018). Complex interactions between insect-borne rice viruses and their vectors. *Current opinion in virology*, *33*, 18-23.

19. Way, M. J., & Heong, K. L. (1994). The role of biodiversity in the dynamics and management of insect pests of tropical irrigated rice—a review. *Bulletin of Entomological Research*, *84*(4), 567-587.

20. Thomas, M., & Waage, J. (1996). *Integration of biological control and host plant resistance breeding: a scientific and literature review*. Technical Centre for Agricultural and Rural Cooperation.

21. Baldrich, P., & San Segundo, B. (2016). MicroRNAs in rice innate immunity. *Rice*, *9*(1), 6.

22. Val-Torregrosa, B., Bundó, M., & San Segundo, B. (2021). Crosstalk between nutrient signalling pathways and immune responses in rice. *Agriculture*, *11*(8), 747.

23. Rajesh, M. K., Rachana, K. E., Kulkarni, K., Sahu, B. B., Thomas, R. J., & Karun, A. (2018). Comparative transcriptome profiling of healthy and diseased Chowghat Green Dwarf coconut palms from root (wilt) disease hot spots. *European Journal of Plant Pathology*, *151*, 173-193.