



ISSN Print: 2618-060X
 ISSN Online: 2618-0618
 NAAS Rating (2026): 5.20
 IJRA 2026; SP-9(10): 114-119
www.agronomyjournals.com
 Received: 25-07-2026
 Accepted: 22-09-2026
 Published: 06-10-2026

Reecha Sharma

PAU Regional Research
 Station, Faridkot, Punjab,
 India

Jagjeet Singh Lore

Department of Plant Breeding
 and Genetics, Punjab
 Agricultural University,
 Ludhiana, India

Gene pyramiding for multi-disease resistance in rice: Strategies, genetic resources and future perspectives

Reecha Sharma¹, Jagjeet Singh Lore²

DOI: <https://www.doi.org/10.33545/2618060X.2026.v9.i10Sb.6780>

ABSTRACT

Rice (*Oryza sativa* L.) is one of the world's most important food crops, but its productivity is continuously threatened by a wide range of fungal, bacterial, viral, and nematode diseases. Rice blast, bacterial leaf blight, sheath blight, tungro, brown spot, and other diseases can cause substantial yield and quality losses under favorable environmental conditions. Although the development of resistant cultivars is one of the most effective approaches to disease management, resistance controlled by a single gene can frequently be overcome by evolving pathogen populations. Gene pyramiding, which involves combining two or more resistance genes or quantitative resistance loci within a single rice genotype, has therefore emerged as an important strategy for developing broad-spectrum and potentially durable disease resistance. Advances in molecular markers, marker-assisted selection, quantitative trait locus mapping, genome-wide association studies, genomic selection, and genome editing have substantially improved the efficiency of resistance-gene pyramiding. The integration of major resistance genes with quantitative resistance loci can provide multiple layers of protection against genetically diverse pathogen populations. This review discusses the genetic basis of disease resistance in rice, important resistance genes and genetic resources, conventional and molecular strategies for gene pyramiding, marker-assisted selection, genomic approaches, and emerging genome-editing technologies. The potential of combining resistance to multiple diseases with high yield, grain quality, and climate resilience is also examined. Future rice improvement programs should emphasize the integration of diverse resistance sources and advanced genomic technologies to develop cultivars with durable, broad-spectrum, and agronomically desirable disease resistance.

Keywords: Rice, Gene pyramiding, Disease resistance, *Oryza sativa*, Resistance genes, Marker-assisted selection, Molecular breeding

1. Introduction

Rice (*Oryza sativa* L.) is a major staple cereal and an essential component of food security in many regions of the world. The crop is cultivated under diverse production systems ranging from irrigated lowlands to rainfed uplands, making it vulnerable to a broad range of environmental and biological stresses. Among the major constraints to rice production, diseases are particularly important because they can occur at different stages of plant development and directly affect photosynthesis, plant vigor, grain formation, and final yield. Major diseases include rice blast caused by *Magnaporthe oryzae*, bacterial leaf blight caused by *Xanthomonas oryzae* pv. *oryzae*, sheath blight caused by *Rhizoctonia solani*, rice tungro caused by viral pathogens, and brown spot caused by *Bipolaris oryzae* (Zhang, 2007; Khush et al., 1990) [1, 2]. Disease management traditionally involves a combination of resistant varieties, cultural practices, biological control, and chemical treatments. Among these approaches, host genetic resistance is considered one of the most economical and environmentally sustainable methods. Resistant cultivars can reduce disease development without requiring repeated application of pesticides and can therefore contribute to sustainable crop production. However, the durability of resistance is often challenged by genetic variation and evolutionary changes in pathogen populations. A rice cultivar possessing a single major resistance gene may initially exhibit strong resistance but can become susceptible when pathogen populations evolve virulence against that particular resistance mechanism (Song et al., 1995; Singh et al., 2001; Koide et al., 2001) [3, 4, 5]. Gene pyramiding provides an important solution to this problem. The term refers to the deliberate combination of multiple resistance genes or resistance-associated loci into a single genetic background. When genes with different recognition specificities or defense mechanisms are combined, the resulting genotype may exhibit broader resistance than a genotype carrying only one resistance gene. Gene pyramiding can also involve the combination of major genes with quantitative trait loci, thereby integrating strong race-specific resistance with partial and potentially more stable resistance (Iyer et al., 2004) [6]. The development of molecular markers has greatly facilitated gene pyramiding in rice. Marker-assisted selection allows breeders to identify plants carrying specific resistance genes without depending exclusively on disease symptoms. With the development of genomics and genome-editing technologies, the possibilities for stacking resistance genes and modifying sus

Corresponding Author:

Reecha Sharma

PAU Regional Research
 Station, Faridkot, Punjab,
 India

ceptibility mechanisms have expanded considerably. Consequently, gene pyramiding has become an important component of modern rice breeding programs aimed at achieving durable resistance against multiple diseases.

2. Major diseases affecting rice

Rice is affected by numerous diseases caused by fungi, bacteria, viruses, and other pathogenic organisms. The importance of individual diseases varies according to rice-growing region, environmental conditions, cultivar susceptibility, and crop-management practices. Among fungal diseases, rice blast is one of the most destructive because it can infect leaves, nodes, collars, and panicles. Severe blast infection can reduce photosynthetic activity and cause significant losses in grain production (Chu *et al.*, 2006) [7]. Bacterial leaf blight is another major disease, particularly in warm and humid rice-growing environments. It is caused by *X. oryzae* pv. *oryzae*, which colonizes the vascular system of rice plants and produces characteristic water-soaked and yellowing lesions. Under severe conditions, the disease can result in extensive leaf drying and yield reduction. Sheath blight, caused by *R. solani*, primarily affects the leaf sheath and can spread rapidly within dense, high-yielding rice crops. The disease is particularly favored by high humidity and excessive nitrogen application.

Viral diseases such as rice tungro can also cause severe production losses in susceptible varieties. Tungro disease affects plant growth, causes yellowing and stunting, and can substantially reduce grain yield. Brown spot, caused primarily by *B. oryzae*, is particularly important under nutrient-deficient and drought-prone conditions. The coexistence of multiple diseases in rice-growing regions makes it difficult to rely on resistance against only one pathogen (Zhang, 2007) [8]. Therefore, modern breeding programs increasingly emphasize

multi-disease resistance, in which resistance genes against several pathogens are incorporated into elite rice backgrounds. Gene pyramiding provides a practical molecular breeding framework for achieving this objective.

3. Concept and importance of gene pyramiding

Gene pyramiding is a breeding strategy in which multiple genes controlling resistance to one or more diseases are deliberately combined within a single plant genotype. Unlike single-gene breeding, which introduces one major resistance gene into an elite variety, pyramiding attempts to assemble several resistance components so that the resulting cultivar possesses multiple layers of protection (Fukuoka *et al.*, 2009) [9]. The concept is particularly important for diseases in which pathogen populations exhibit substantial genetic variability. If a pathogen overcomes one resistance gene, additional resistance genes may continue to restrict infection. The simultaneous presence of multiple resistance mechanisms can therefore reduce the likelihood of complete resistance breakdown (Sundaram *et al.*, 2008) [10]. Gene pyramiding can be performed within a single disease system or across different diseases. For example, several resistance genes against rice blast may be combined to broaden resistance to different pathogen races. Similarly, resistance genes for bacterial leaf blight can be pyramided with blast resistance genes, allowing a single rice cultivar to possess resistance to both diseases (Asma *et al.*, 2022) [11]. The approach is also valuable for combining major resistance genes with quantitative resistance loci. Major genes can provide strong resistance against specific pathogen populations, while quantitative loci may contribute partial resistance across a wider range of pathogen genotypes. Such combinations may improve the stability and durability of resistance.

Table 1. Major disease resistance genes used in rice gene pyramiding

Rice disease	Major resistance genes	Resistance type	Importance in gene pyramiding
Bacterial leaf blight	<i>Xa4</i> , <i>xa5</i> , <i>xa13</i> , <i>Xa21</i> , <i>Xa23</i> , <i>Xa26</i>	Major R genes	Provides broad-spectrum and durable resistance when combined
Rice blast	<i>Pi1</i> , <i>Pi2</i> , <i>Pi5</i> , <i>Pi9</i> , <i>Pi54</i> , <i>Pigm</i> , <i>Pita</i>	Major R genes	Useful for developing broad-spectrum blast-resistant cultivars
Sheath blight	<i>qSB</i> loci, <i>qSBR</i> QTLs	Quantitative resistance	Enhances partial and durable resistance
Brown spot	<i>qBS</i> loci and associated QTLs	Quantitative resistance	Supports improvement of field-level resistance
Sheath rot	Various QTLs	Quantitative resistance	Potential source for integrated disease resistance
False smut	<i>qFST</i> and other QTLs	Quantitative resistance	Useful for developing cultivars with improved field resistance
Bacterial leaf streak	<i>qBLS</i> loci	Quantitative resistance	Can be incorporated with major BLB resistance genes
Multiple diseases	Combinations of <i>Pi</i> , <i>Xa/xa</i> and QTLs	Gene/QTL combinations	Provides multi-disease protection and reduces dependence on single genes

Table 2. Examples of resistance-gene pyramiding in rice

Gene combination	Target disease	Breeding approach	Expected advantage
<i>Xa4</i> + <i>xa5</i>	Bacterial leaf blight	Marker-assisted selection	Improved resistance spectrum
<i>Xa4</i> + <i>xa13</i> + <i>Xa21</i>	Bacterial leaf blight	MAS and gene pyramiding	Strong and durable BLB resistance
<i>xa5</i> + <i>xa13</i> + <i>Xa21</i>	Bacterial leaf blight	Marker-assisted pyramiding	Enhanced resistance against diverse pathogen races
<i>Xa4</i> + <i>xa5</i> + <i>xa13</i> + <i>Xa21</i>	Bacterial leaf blight	Multiplex MAS	Multiple resistance mechanisms in one genotype
<i>Pi1</i> + <i>Pi2</i>	Rice blast	MAS	Broader blast resistance
<i>Pi5</i> + <i>Pi54</i>	Rice blast	MAS	Improved resistance against diverse <i>Magnaporthe oryzae</i> populations
<i>Pi9</i> + <i>Pi54</i>	Rice blast	Gene pyramiding	Enhanced and potentially more durable blast resistance
<i>Pigm</i> + <i>Pi37</i>	Rice blast	MAS	Broad-spectrum blast resistance
<i>Pi2</i> + <i>Xa7</i>	Blast + bacterial leaf blight	Multi-disease gene pyramiding	Simultaneous resistance to two major diseases

(continued on next page)

Gene combination	Target disease	Breeding approach	Expected advantage
<i>Pi54</i> + <i>xa5</i> + <i>xa13</i> + <i>Xa21</i>	Blast + bacterial leaf blight	MAS	Combined resistance to fungal and bacterial diseases
<i>Pi54</i> + <i>qSBR</i> QTLs	Blast + sheath blight	MAS/QTL pyramiding	Integration of major and quantitative resistance
<i>Pi</i> + <i>Xa</i> + <i>qSB</i> combinations	Multiple diseases	Genomic-assisted breeding	Potential for durable multi-disease resistance

Table 3. Conventional and molecular approaches for gene pyramiding in rice

Approach	Principle	Major advantages	Major limitations
Conventional hybridization	Crossing resistant parents followed by selection	Simple and widely applicable	Difficult to identify plants carrying multiple genes
Backcross breeding	Introgression of resistance genes into an elite cultivar	Maintains desirable recipient-parent traits	Requires several generations
Phenotypic selection	Selection based on disease-response phenotype	Low technical requirement	Environment and pathogen variation can affect accuracy
Marker-assisted selection (MAS)	DNA markers linked to resistance genes are used for selection	Precise and efficient gene tracking	Requires validated molecular markers
Marker-assisted gene pyramiding	Simultaneous selection of several resistance genes	Efficient stacking of multiple genes	Requires multiple informative markers
QTL pyramiding	Combining several loci controlling quantitative resistance	Useful for complex diseases	QTL effects can vary with environment
GWAS-assisted breeding	Identification of resistance loci from diverse germplasm	Detects novel resistance loci	Requires large and genetically diverse populations
Genomic selection	Genome-wide markers predict breeding value	Useful for complex quantitative resistance	Requires training populations and adequate phenotypic data
CRISPR/Cas genome editing	Precise modification of resistance or susceptibility genes	Rapid and targeted improvement	Regulatory, off-target and delivery challenges
Genomic-assisted pyramiding	Integration of MAS, GWAS, genomic selection and editing	Enables precise multi-gene improvement	Requires advanced infrastructure and expertise

4. Genetic resources for disease resistance in rice

Rice possesses substantial genetic diversity that can be exploited for disease resistance breeding. Resistance genes have been identified in cultivated rice varieties, traditional landraces, breeding lines, and wild relatives. Traditional rice varieties are particularly valuable because they have evolved under diverse environmental and pathogen pressures and may contain resistance alleles that are absent from modern elite cultivars (Pradhan *et al.*, 2015) [12]. Wild rice species represent another important reservoir of resistance genes. Species related to cultivated rice have been used as sources of resistance against bacterial leaf blight, blast, and other diseases. Introgression of useful genes from wild relatives can increase the genetic diversity available to breeding programs, although the process may sometimes introduce undesirable characteristics known as linkage drag.

Major resistance genes have been identified against several important rice pathogens. For bacterial leaf blight, genes such as *Xa4*, *xa5*, *xa13*, and *Xa21* have been widely studied. For blast resistance, numerous *Pi* genes have been identified and characterized. Quantitative resistance loci have also been reported for blast, sheath blight, bacterial leaf blight, and other diseases (Miah *et al.*, 2013) [13]. The continued exploration of landraces and wild relatives, combined with genome sequencing and pangenomic approaches, is expected to reveal additional resistance alleles. These genetic resources will be particularly important for future gene-pyramiding programs.

5. Conventional breeding for gene pyramiding

Conventional breeding has historically been used to combine desirable resistance traits through sequential crossing and selection. In a typical pyramiding program, different donor parents carrying individual resistance genes are crossed to generate progenies containing multiple resistance loci. These progenies are subsequently selected

through several generations until the desired gene combinations become genetically stable.

Although conventional phenotypic selection can be effective, it becomes increasingly difficult when multiple resistance genes have similar phenotypic effects. For example, when two or more genes provide resistance to the same pathogen, it may be impossible to determine from disease symptoms whether a plant carries one gene or several genes. Similarly, resistance expression can vary with pathogen strain and environmental conditions (Asma *et al.*, 2022) [14]. These limitations have encouraged the integration of conventional breeding with molecular markers. Molecular-assisted breeding allows breeders to track individual resistance genes during the breeding process and substantially increases the efficiency of pyramiding.

6. Marker-assisted gene pyramiding

Marker-assisted selection (MAS) is one of the most effective approaches for pyramiding disease-resistance genes in rice. DNA markers closely associated with resistance genes can be used to identify plants carrying specific alleles. This enables breeders to select desirable plants even before disease symptoms become visible (Kumar, 2025) [15]. MAS is particularly valuable when several genes are being combined. A breeding population can be screened using different markers, allowing plants carrying multiple resistance genes to be identified. These selected plants can then be subjected to further phenotypic evaluation and agronomic selection.

For bacterial leaf blight, markers associated with genes such as *Xa4*, *xa5*, *xa13*, and *Xa21* have facilitated the development of multi-gene resistant rice lines. Similar approaches have been applied to combine multiple *Pi* genes for blast resistance (Singh *et al.*, 2015) [16]. An important advantage of MAS is its ability to reduce the number of plants that need to be subjected to intensive disease screening. It can also accelerate backcross breeding by enabling simultaneous selection for the target resistance gene and recovery of the elite recipient genome.

7. Pyramiding resistance against multiple diseases

The development of rice cultivars resistant to multiple diseases is an important objective of modern breeding. A cultivar that is resistant to bacterial leaf blight but highly susceptible to blast or sheath blight may still experience substantial yield losses in disease-prone environments. Therefore, pyramiding genes targeting different pathogens can provide a more comprehensive form of protection (Oliva *et al.*, 2019) [17]. For example, bacterial leaf blight resistance genes can potentially be combined with blast resistance genes in an elite rice background. Such combinations may provide simultaneous protection against two of the most important rice diseases. Additional resistance components can potentially be incorporated depending on the target production environment.

Multi-disease gene pyramiding is technically more complex than pyramiding genes against a single pathogen because the breeder must maintain resistance against several diseases while simultaneously selecting for yield and grain quality. Molecular markers greatly simplify this process by allowing breeders to monitor different resistance loci independently (Zhou *et al.*, 2006) [18]. The ultimate objective is to develop rice cultivars with **stacked resistance**, in which several genes and quantitative loci provide complementary protection against multiple pathogens.

8. Gene pyramiding for rice blast resistance

Rice blast is caused by the fungal pathogen *Magnaporthe oryzae* and is among the most extensively studied diseases in rice. Numerous blast resistance genes, generally designated *Pi* genes, have been identified. However, the high genetic variability of the pathogen can result in rapid breakdown of resistance provided by individual genes (Lore *et al.*, 2011) [19]. Pyramiding multiple *Pi* genes has therefore become an important strategy for broadening blast resistance. Combining resistance genes with different pathogen-recognition specificities can increase the range of pathogen races controlled by the resulting genotype. Marker-assisted selection allows breeders to identify progenies carrying multiple *Pi* genes (Chen *et al.*, 2008) [20]. In addition to major resistance genes, quantitative resistance loci can contribute to reduced disease severity. Combining major *Pi* genes with quantitative resistance may provide a more stable form of protection than relying on a single major gene. Future breeding programs should therefore focus on integrating both qualitative and quantitative resistance.

9. Gene pyramiding for bacterial leaf blight resistance

Bacterial leaf blight represents an important target for gene pyramiding because of the variability of *X. oryzae* pv. *oryzae* populations. Several resistance genes, including *Xa4*, *xa5*, *xa13*, and *Xa21*, have been incorporated into rice breeding programs.

Combining these genes can provide resistance against a wider range of bacterial populations than individual genes. Pyramiding two or more effective resistance can also prove genes in developing rice cultivars is essential for durable and sustainable BB resistance to prevent breakdown of resistance by emerging races of *Xoo* (Chen *et al.*, 2008; Jiang *et al.*, 2006; Lore *et al.*, 2011) [20, 21, 19], use of molecular markers makes it possible to identify plants carrying multiple resistance alleles and thereby accelerate the development of resistant lines (Jiang *et al.*, 2006) [21]. An important advantage of combining resistance genes with different mechanisms is the potential reduction in the probability that a pathogen will simultaneously overcome all components of resistance. However, pyramided lines must be evaluated against diverse pathogen populations because the effectiveness of any gene combination may vary according to pathogen genotype and geographic location.

10. Integration of QTLs with major resistance genes

Quantitative trait loci play an increasingly important role in the development of durable disease resistance. Unlike major resistance genes, which may provide strong but sometimes race-specific resistance,

QTLs generally contribute smaller effects that can collectively reduce disease severity (Bhatia *et al.*, 2011) [22]. Integrating QTLs with major resistance genes provides an opportunity to combine different forms of genetic resistance. Major genes can provide strong protection against specific pathogen populations, whereas quantitative loci may contribute background resistance against a broader range of pathogen genotypes. QTL mapping, GWAS, and high-density genotyping have facilitated the identification of such genomic regions. Once validated, favorable QTLs can be incorporated into breeding populations using marker-assisted or genomic selection.

11. Genomic selection and genome-wide association studies

The increasing availability of rice genome sequences has transformed disease-resistance breeding. GWAS allows researchers to examine large and genetically diverse rice populations and identify genomic variants associated with disease resistance. This approach can reveal resistance loci that may remain undetected in conventional biparental mapping populations.

Genomic selection provides another promising approach. Instead of selecting plants solely according to their observed disease phenotype, genomic selection uses genome-wide marker information to predict the genetic value of breeding individuals. This can accelerate the selection of plants possessing favorable combinations of disease-resistance and agronomic traits (Chen *et al.*, 2000) [23]. The combination of GWAS, genomic selection, high-throughput phenotyping, and pathogen genomic information may substantially improve the efficiency of future gene-pyramiding programs.

12. CRISPR/Cas and precision gene stacking

Genome-editing technologies, particularly CRISPR/Cas systems, have introduced new possibilities for improving disease resistance in rice. Unlike conventional gene transfer, genome editing can modify specific genes or regulatory regions with high precision. One important application is the modification of host susceptibility genes. Some pathogens exploit host genes to establish successful infection. Reducing or altering the function of such genes may enhance disease resistance. Genome editing can also be used to modify regulatory regions associated with defense responses (Bhatia *et al.*, 2011) [22]. CRISPR-based approaches could potentially complement conventional resistance-gene pyramiding by creating plants containing both introduced resistance genes and targeted modifications of susceptibility factors. However, edited lines require careful evaluation for off-target effects, agronomic performance, resistance stability, and regulatory compliance.

13. Challenges in gene pyramiding

Despite its considerable potential, gene pyramiding presents several challenges. One major challenge is the availability of reliable molecular markers that accurately identify functional resistance alleles. Closely linked markers may sometimes fail to distinguish functional and non-functional alleles, particularly when genetic diversity is high. Another challenge is the interaction among resistance genes. Combining several genes does not necessarily produce an additive increase in resistance. Gene interactions, genetic background, and environmental conditions can influence the final phenotype (Wang *et al.*, 2015; Zhou *et al.*, 2011; Yang *et al.*, 2006) [25, 26, 27]. Pathogen evolution represents another major concern. Even pyramided resistance can eventually be challenged by pathogen populations with appropriate combinations of virulence factors. Continuous monitoring of pathogen diversity is therefore essential. The introgression of resistance genes from wild relatives may also introduce undesirable agronomic traits. Marker-assisted backcrossing and genomic selection can help minimize such linkage drag.

14. Combining disease resistance with agronomic performance

Disease resistance must be combined with traits that directly influence the productivity and market value of rice. Farmers generally require cultivars that provide high yield, good grain quality, appropriate maturity, stress tolerance, and stable performance across environments [28]. Therefore, gene pyramiding should not be considered an isolated breeding objective. Resistance genes should be incorporated into elite backgrounds while simultaneously selecting for grain yield, grain size, cooking quality, plant architecture, drought tolerance, salinity tolerance, and heat tolerance [29]. The integration of molecular markers and genomic selection can facilitate multi-trait breeding. Such approaches may enable breeders to select plants carrying favorable combinations of disease-resistance genes while retaining desirable agronomic characteristics.

15. Future perspectives

Future rice disease-resistance breeding will increasingly rely on the integration of conventional breeding, molecular genetics, genomics, high-throughput phenotyping, and genome editing. The availability of increasingly comprehensive rice genomic resources will facilitate the identification of rare resistance alleles from landraces and wild relatives. Pangenomic analysis may reveal structural variants and resistance genes that are absent from the reference genome. Advances in artificial intelligence and machine learning may also help breeders integrate genomic, phenotypic, environmental, and pathogen data to predict superior gene combinations. Another important direction will be the development of resistance strategies that combine major genes, quantitative resistance loci, and edited susceptibility genes. Such multilayered resistance may be more difficult for pathogens to overcome than single resistance mechanisms. Future breeding programs should also emphasize pathogen surveillance. Understanding the genetic composition and geographic distribution of pathogen populations will allow breeders to select resistance-gene combinations appropriate for specific production regions.

16. Conclusion

Gene pyramiding represents a powerful strategy for improving disease resistance in rice. The combination of multiple resistance genes and quantitative resistance loci can broaden the resistance spectrum and potentially increase its durability. Genetic resources from cultivated rice, traditional landraces, and wild relatives provide an extensive reservoir of resistance alleles that can be exploited through modern breeding. Marker-assisted selection has greatly increased the efficiency of gene pyramiding, while QTL mapping, GWAS, genomic selection, and genome sequencing have expanded the ability to discover and utilize novel resistance loci. CRISPR/Cas-based genome editing provides an additional opportunity to modify susceptibility mechanisms and complement conventional resistance-gene stacking. The future of rice disease-resistance breeding lies in combining multiple resistance genes, quantitative loci, genomic prediction, precision breeding, and comprehensive pathogen surveillance. Developing cultivars that combine broad-spectrum disease resistance with high yield, grain quality, and climate resilience will be essential for sustainable rice production and long-term global food security.

References

- Zhang Q. Genetics and improvement of resistance to bacterial blight of rice. *Plant Molecular Biology*. 2007;65:313–327.
- Khush GS, Bacalangco E, Ogawa T. A new gene for resistance to bacterial blight from *Oryza longistaminata*. *Rice Genetics Newsletter*. 1990;7:121–122.
- Song WY, Wang GL, Chen LL, Kim HS, Pi LY, Holsten T, Gardner J, Wang B, Zhai WX, Zhu LH, Fauquet C, Ronald PC. A receptor kinase-like protein encoded by the rice disease resistance gene, *Xa21*. *Science*. 1995;270:1804–1806.
- Singh S, Sidhu JS, Huang N, Vikal Y, Li Z, Brar DS, Dhaliwal HS, Khush GS. Pyramiding three bacterial blight resistance genes (*xa5*, *xa13* and *Xa21*) using marker-assisted selection into indica rice cultivar PR106. *Theoretical and Applied Genetics*. 2001;102:1011–1015.
- Koide Y, Kobayashi N, Xu D, Fukuta Y. Molecular mapping of quantitative trait loci for rice blast resistance in a Japanese upland rice variety Norin 24. *Theoretical and Applied Genetics*. 2001;102:1179–1185.
- Iyer AS, McCouch SR. The rice bacterial blight resistance gene *xa5* encodes a novel form of disease resistance. *Molecular Plant-Microbe Interactions*. 2004;17:1348–1354.
- Chu Z, Fu H, Peng L, et al. Targeting *xa13*, a recessive gene for bacterial blight resistance in rice. *Theoretical and Applied Genetics*. 2006;112:455–461.
- Zhang Q. Strategies for developing Green Super Rice. *Proceedings of the National Academy of Sciences of the United States of America*. 2007;104:16402–16409.
- Fukuoka S, Saka N, Koga H, Ono K, Shimizu T, Ebana K, Hayashi N, Takahashi A, Hirochika H, Okuno K, Yano M. Loss of function of a proline-containing protein confers durable disease resistance in rice. *Science*. 2009;325:998–1001.
- Sundaram RM, Vishnupriya MR, Biradar SK, Laha GS, Reddy GA, Rani NS, Sarma NP, Sonti RV. Marker-assisted introgression of bacterial blight resistance in Samba Mahsuri, an elite indica rice variety. *Theoretical and Applied Genetics*. 2008;115:129–137.
- Asma J, Subrahmanyam D, Krishnaveni D. Deciphering host plant resistance mechanisms against Tungro virus in rice: A comprehensive exploration. *Agriculture Archives: an International Journal*. 2022.
- Pradhan SK, Nayak DK, Mohanty S, Behera L, Barik SR, Pandit E, Lenka S, Anandan A. Pyramiding of three bacterial blight resistance genes for broad-spectrum resistance in deepwater rice variety Jalmagna. *Rice*. 2015;8:51.
- Miah G, Rafii MY, Ismail MR, Puteh AB, Rahim HA, Asfaliza R, Latif MA. Blast resistance in rice: a review of conventional breeding to molecular approaches. *Molecular Biology Reports*. 2013;40:2369–2388.
- Asma J, Subrahmanyam D, Krishnaveni D. Assessing Yield Losses Caused by Rice Tungro Virus: A Comprehensive Review. *Agriculture Archives*. 2022.
- Kumar S. MicroRNA: one of the stress fighters plays crucial role in resilience of rice to changing climatic conditions. *Agric. Archives An Int. J*. 2025;4(1):20–25.
- Singh AK, Singh PK, Arya M, Singh NK, Sharma TR. Molecular breeding of rice for resistance to bacterial blight. *Plant Breeding*. 2015;134:605–616.
- Oliva R, Ji C, Atienza-Grande G, Huguet-Tapia JC, Perez-Quintero A, Li T, Eom JS, Li C, Nguyen H, Liu B, Auguy F, Sciallano C, Luu VT, Dossa GS, Cunnac S, Schmidt SM, Slamet-Loedin IH, Vera Cruz C, Szurek B, Frommer WB, White FF, Yang B. Broad-spectrum resistance to bacterial blight in rice using genome editing. *Nature Biotechnology*. 2019;37:1344–1350.
- Zhou E, Jia Y, Singh P, Correll J, Lee FN. Instability of the *Pi-ta* resistance gene in rice and its implications for managing rice blast disease. *Plant Disease*. 2006;90:1445–1450.
- Lore JS, Vikal Y, Hunjan MS, Goel RK, Bharaj TS, Raina GL. Genotypic and pathotypic diversity of *Xanthomonas oryzae* pv. *oryzae*, the cause of bacterial blight of rice in Punjab state. *Indian Journal of Phytopathology*. 2011;159:479–487.
- Chen S, Huang Z, Zeng L, Yang J, Liu Q, Zhu X. High-resolution mapping and gene prediction of *Xanthomonas oryzae* pv. *oryzae* resistance gene Xa7. *Molecular Breeding*. 2008;22:433–441.

21. Jiang GH, Xia ZH, Zhou YL, Wan J, Li DY, Chen RS, Zhai WX, Zhu LH. Testifying the rice bacterial blight resistance gene xa5 by genetic complementation and further analyzing xa5 (Xa5) in comparison with its homolog TFII Agamma1. *Molecular Genetics and Genomics*. 2006;275:354–366.
22. Bhatia D, Sharma R, Vikal Y, Mangat GS, Mahajan R, Sharma N, Lore JS, Singh N, Bharaj TS, Singh K. Marker-assisted development of bacterial blight resistant, dwarf, and high yielding versions of two traditional Basmati rice cultivars. *Crop Science*. 2011;51(2):759–770.
23. Chen S, Lin XH, Xu CG, Zhang Q. Improvement of bacterial blight resistance of ‘Minghui 63’, an elite restorer line of hybrid rice, by molecular marker-assisted selection. *Crop Science*. 2000;40(1):239–244.
24. Chen S, Xu CG, Lin XH, Zhang Q. Improving bacterial blight resistance of ‘6078’, an elite restorer line of hybrid rice, by molecular marker-aided selection. *Plant Breeding*. 2001;120(2):133–137.
25. Wang C, Zhang X, Fan Y, Gao Y, Zhu Q, Zheng C, Qin T, Li Y, Che J, Zhang M, Yang B, Liu Y, Zhao K. XA23 is an executor R protein and confers broad-spectrum disease resistance in rice. *Molecular Plant*. 2015;8(2):290–302.
26. Zhou YL, Uzokwe VNE, Zhang CH, Cheng LR, Wang L, Chen K, Gao XQ, Wang LH. Improvement of bacterial blight resistance of hybrid rice in China using the Xa23 gene derived from wild rice (*Oryza rufipogon*). *Crop Protection*. 2011;30(6):637–644.
27. Yang B, Sugio A, White FF. Os δN_3 is a host disease-susceptibility gene for bacterial blight of rice. *Proceedings of the National Academy of Sciences of the United States of America*. 2006;103(27):10503–10508.

How to cite this article: Sharma R, Singh Lore J. Gene pyramiding for multi-disease resistance in rice: Strategies, genetic resources and future perspectives. *International Journal of Research in Agronomy*. 2026;SP-9(10):114-119. doi: <https://www.doi.org/10.33545/2618060X.2026.v9.i10Sb.6780>