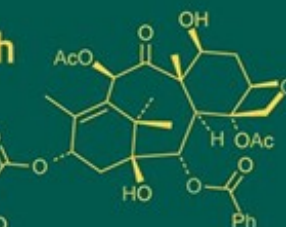
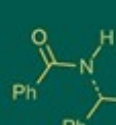


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Reecha Sharma

PAU Regional Regional
 Research Station, Faridkot,
 Punjab, India

Jagjeet Singh Lore

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

Genetic improvement of rice for bacterial leaf blight resistance: Advances in resistance genes, breeding strategies and genomic approaches

Reecha Sharma¹, Jagjeet Singh Lore²

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ABSTRACT

Rice (*Oryza sativa* L.) is a major staple crop that contributes substantially to global food and nutritional security. However, rice production is severely constrained by bacterial leaf blight (BLB), a destructive disease caused by *Xanthomonas oryzae* pv. *oryzae* (Xoo). The disease can cause substantial yield losses, particularly under warm and humid conditions favorable for pathogen development and spread. Genetic improvement of rice for durable disease resistance is considered one of the most effective, economical, and environmentally sustainable approaches for managing BLB. Numerous resistance genes, commonly designated as Xa genes, have been identified from cultivated rice and wild relatives. Conventional breeding, marker-assisted selection, molecular breeding, gene pyramiding, quantitative trait locus mapping, genome-wide association studies, genomic selection, and genome-editing technologies have accelerated the development of BLB-resistant rice cultivars. The deployment of multiple resistance genes in a single genetic background has received particular attention because it can broaden the resistance spectrum and potentially delay the emergence of pathogen populations capable of overcoming individual resistance genes. Recent advances in CRISPR/Cas-based genome editing have additionally enabled targeted modification of susceptibility-associated genes and regulatory regions involved in bacterial infection. This review discusses the genetic basis of BLB resistance in rice, major resistance genes, conventional and molecular breeding strategies, gene pyramiding, genomic approaches, and emerging genome-editing technologies. Integrating these approaches with high-yielding and climate-resilient rice breeding could facilitate the development of durable BLB-resistant cultivars and contribute to sustainable rice production.

Keywords: *Oryza sativa*, Bacterial leaf blight, *Xanthomonas oryzae* pv. *oryzae*, Xa genes, Disease resistance, Molecular breeding, Marker-assisted selection, Gene pyramiding

1. Introduction

Rice (*Oryza sativa* L.) is among the world's most important cereal crops and serves as a primary source of dietary energy for a large proportion of the global population. Increasing population, changing climatic conditions, declining availability of agricultural resources, and the emergence of pests and diseases continuously threaten stable rice production. Among the major biotic stresses affecting rice, bacterial leaf blight (BLB) is particularly important because of its destructive nature and its ability to spread rapidly under favorable environmental conditions (Chukwu *et al.*, 2019) [1]. Bacterial leaf blight is caused by the Gram-negative bacterium *Xanthomonas oryzae* pv. *oryzae*. The pathogen primarily colonizes the vascular tissues of rice leaves and produces characteristic water-soaked lesions that progressively develop into yellowish to whitish lesions. Severe infections can result in extensive leaf drying, reduced photosynthetic activity, poor grain filling, and considerable yield reduction. The disease is especially problematic in intensively cultivated rice-growing regions where susceptible cultivars are grown continuously (Chukwu *et al.*, 2019) [1]. Management of BLB through cultural practices and chemical treatments can provide some degree of disease suppression, but these approaches may have limitations in terms of effectiveness, cost, environmental impact, and long-term sustainability. Consequently, host-plant resistance has become a central component of integrated BLB management (Chukwu *et al.*, 2019) [2]. Genetic improvement provides an opportunity to develop rice cultivars that possess inherent resistance while maintaining desirable agronomic characteristics. More than several resistance loci associated with BLB resistance have been identified, including major resistance genes and quantitative resistance loci. These discoveries have provided valuable genetic resources for breeding programs (Hu *et al.*, 2008) [3]. The transition from conventional selection to marker-assisted and genomics-assisted breeding has considerably increased the efficiency of resistance breeding. Molecular markers linked to resistance genes allow breeders to identify desirable plants at early developmental stages without relying exclusively on disease-screening experiments. Furthermore, gene pyramiding facilitates the combination of

Corresponding Author:**Reecha Sharma**

PAU Regional Regional
 Research Station, Faridkot,
 Punjab, India

multiple resistance genes in a single cultivar (Ji *et al.*, 2018) [4]. Recent developments in genome editing, particularly CRISPR/Cas systems, have introduced new possibilities for precise genetic improvement. Instead of introducing resistance genes through several generations of crossing, genome editing can modify specific host genes involved in susceptibility or pathogen recognition. Therefore, combining traditional genetic resources with modern genomic technologies represents a promising strategy for developing durable BLB-resistant rice.

2. Bacterial leaf blight of rice

Bacterial leaf blight is one of the most economically important bacterial diseases of rice. The causal organism, *X. oryzae* pv. *oryzae*, survives and spreads through infected plant material, water, crop residues, and other pathways. Disease development is strongly influenced by environmental conditions, particularly high temperature, humidity, rainfall, and excessive nitrogen fertilization (Jiang *et al.*, 2008) [5]. The pathogen generally enters rice plants through natural openings such as hydathodes or wounds. After entering the plant, it multiplies within the vascular system and spreads through the xylem. Bacterial colonization interferes with water movement and induces characteristic symptoms (Khush *et al.*, 1990) [6]. Typical symptoms include water-soaked lesions along leaf margins and tips, which subsequently become yellow or straw colored. Under severe disease pressure, lesions can expand along the leaf blade and eventually cause extensive leaf necrosis. Young seedlings may also develop a severe systemic form known as kresk, which can result in rapid wilting and plant death (Kottapalli *et al.*, 2007) [7]. The severity of BLB depends on several interacting factors, including pathogen population, rice genotype, environmental conditions, crop management, and the genetic diversity of pathogen strains. This variability creates a major challenge for breeding programs because resistance effective against one pathogen population may not necessarily provide adequate protection against another.

3. Genetic basis of bacterial leaf blight resistance

Resistance to BLB in rice is genetically complex. Some resistance is controlled by major genes that provide strong and relatively specific protection against particular pathogen races or strains, whereas other forms of resistance are controlled by multiple genes with smaller individual effects (Lee *et al.*, 2003) [8]. The major BLB resistance genes are commonly designated *Xa* genes. These genes may encode proteins involved in pathogen recognition, signal transduction, transcriptional regulation, or other defense-related processes. Recognition of pathogen-derived molecules can activate downstream defense responses, including production of reactive oxygen species, strengthen-

ing of cell walls, activation of defense-related genes, and restriction of bacterial multiplication (Liu *et al.*, 2011) [9]. In addition to major resistance genes, quantitative resistance loci contribute to partial resistance. Quantitative resistance is particularly important because it may remain effective against genetically diverse pathogen populations and may impose less selective pressure for the rapid evolution of virulent pathogen races (Mew *et al.*, 1993) [10]. Therefore, modern rice breeding increasingly aims to combine major resistance genes with quantitative resistance loci to achieve both high levels and greater durability of resistance.

4. Major resistance genes used in rice improvement

Several bacterial leaf blight resistance genes, commonly designated as *Xa* genes, have been identified in cultivated rice and its wild relatives and subsequently utilized in rice improvement programs. These genes differ in their mechanisms of resistance, spectrum of effectiveness, and interaction with diverse populations of *Xanthomonas oryzae* pv. *oryzae* (Xoo). Among the extensively studied resistance genes, *Xa4*, *xa5*, *xa13*, and *Xa21* have received considerable attention because of their potential to provide effective resistance and their usefulness in breeding programs. The *Xa4* gene is one of the widely utilized dominant resistance genes and has been incorporated into several rice breeding programs. Its contribution to resistance against different Xoo Populations and its compatibility with agronomically desirable backgrounds have made it an important genetic resource for improving BLB resistance. In contrast, *xa5* is a recessive resistance gene that encodes a variant of a transcription factor involved in host–pathogen interactions (Nino-Liu *et al.*, 2006) [11]. The altered function of this gene can interfere with bacterial infection and multiplication, thereby contributing to resistance against several Xoo strains. Another important recessive gene, *xa13*, is associated with a host susceptibility mechanism required for successful bacterial infection. Reduced expression or altered function of the corresponding host factor can restrict bacterial growth within rice tissues. The *Xa21* gene is particularly important in rice disease-resistance research because it was originally identified from the wild rice species *Oryza longistaminata* and subsequently transferred into cultivated rice. It encodes a receptor-like protein involved in pathogen recognition and activation of plant defense responses. The utilization of *Xa21* has demonstrated the importance of wild rice relatives as reservoirs of novel resistance genes. Collectively, these genes provide valuable genetic resources for developing rice cultivars with improved resistance to bacterial leaf blight. However, because pathogen populations are genetically diverse and capable of evolving virulence, the effectiveness of individual resistance genes may decline over time, emphasizing the importance of combining multiple resistance sources in breeding programs.

Table 1. Major bacterial leaf blight resistance genes used in rice improvement

Resistance gene	Type	Genetic source/association	Major significance
<i>Xa4</i>	Dominant	Rice germplasm	Widely used for BLB resistance breeding
<i>xa5</i>	Recessive	Cultivated rice	Provides resistance through alteration of host transcriptional processes
<i>xa13</i>	Recessive	Rice germplasm	Interferes with host susceptibility mechanisms required for bacterial infection
<i>Xa21</i>	Dominant	<i>Oryza longistaminata</i>	Important source of broad-spectrum resistance
<i>Xa23</i>	Dominant	Wild rice germplasm	Strong resistance against several Xoo populations
<i>Xa26</i>	Dominant	Rice germplasm	Associated with quantitative and race-dependent resistance
<i>Xa27</i>	Dominant	Rice germplasm	Involved in pathogen recognition and defense responses
<i>Xa33</i>	Dominant	Rice genetic resources	Useful source for improving resistance against diverse pathogen populations

BLB: Bacterial leaf blight; **Xoo:** *Xanthomonas oryzae* pv. *oryzae*.

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Table 2. Comparison of major breeding approaches for bacterial leaf blight resistance

Breeding approach	Basic principle	Major advantage	Major limitation
Conventional breeding	Crossing resistant and elite parents followed by phenotypic selection	Simple and widely applicable	Time-consuming and strongly dependent on phenotyping
Backcross breeding	Transfer of resistance into an elite cultivar	Maintains desirable characteristics of recurrent parent	Requires several generations
Marker-assisted selection	Selection using DNA markers linked to resistance genes	Early and precise selection	Requires reliable molecular markers
Gene pyramiding	Combining multiple resistance genes	Can provide broader and more durable resistance	Requires accurate detection of multiple genes
QTL mapping	Identification of genomic regions controlling quantitative resistance	Useful for partial resistance	Requires suitable mapping populations
GWAS	Association of genome-wide markers with resistance phenotypes	Can identify novel resistance loci	Requires diverse populations and accurate phenotyping
Genomic selection	Prediction of breeding value using genome-wide markers	Accelerates selection for complex traits	Requires a well-trained prediction model
Genome editing	Targeted modification of resistance or susceptibility genes	High precision and rapid genetic improvement	Regulatory and technical challenges

Table 3. Potential advantages of pyramiding BLB resistance genes in rice

Gene combination	Expected breeding value	Potential benefit
<i>Xa4</i> + <i>xa5</i>	Combination of dominant and recessive resistance	Broader genetic resistance
<i>Xa4</i> + <i>xa13</i>	Complementary resistance mechanisms	Improved resistance stability
<i>xa5</i> + <i>xa13</i>	Multiple recessive resistance components	Potentially enhanced resistance
<i>Xa21</i> + <i>xa13</i>	Different mechanisms of host defense	Broader protection against Xoo
<i>Xa4</i> + <i>xa5</i> + <i>xa13</i>	Multiple resistance genes	Increased resistance spectrum
<i>Xa4</i> + <i>xa5</i> + <i>xa13</i> + <i>Xa21</i>	Multi-gene pyramid	Potential for durable and broad-spectrum resistance

Note: The effectiveness of a particular gene combination depends on the rice genetic background and the Xoo population against which it is evaluated.

Table 4. Modern genomic technologies for improving BLB resistance in rice

Technology	Application in BLB breeding	Expected outcome
QTL mapping	Identification of genomic regions associated with resistance	Discovery of quantitative resistance loci
GWAS	Detection of resistance-associated genomic variants	Identification of novel resistance alleles
Transcriptomics	Analysis of genes activated during pathogen infection	Identification of defense-related genes and pathways
Genomic selection	Prediction of breeding value using genome-wide markers	Faster selection of superior breeding lines
Marker-assisted selection	Tracking specific resistance genes	Accurate introgression of resistance
CRISPR/Cas genome editing	Modification of susceptibility or defense-related genes	Targeted improvement of resistance
High-throughput phenotyping	Rapid assessment of disease symptoms	Improved selection efficiency
Pangenomics	Comparison of genomic diversity among rice varieties	Discovery of rare and novel resistance alleles

Table 5. Important traits to combine with bacterial leaf blight resistance

Trait	Importance in rice improvement
High grain yield	Improves farmer productivity and economic returns
Grain quality	Determines consumer and market acceptance
Drought tolerance	Maintains productivity under water limitation
Heat tolerance	Reduces yield losses under high temperatures
Salinity tolerance	Supports rice production in salt-affected areas
Nitrogen-use efficiency	Reduces fertilizer requirements
Short/appropriate maturity duration	Facilitates crop intensification and adaptation
Resistance to other diseases	Provides protection against multiple biotic stresses
Pest resistance	Reduces dependence on chemical pesticides
Suitable plant architecture	Supports improved yield and harvesting efficiency

(continued on next page)

Table 6. Major challenges and future strategies for durable BLB resistance

Challenge	Consequence	Possible strategy
Pathogen evolution	Breakdown of resistance	Gene pyramiding and continuous pathogen surveillance
Xoo genetic diversity	Variable effectiveness of resistance genes	Multi-isolate and multi-location screening
Narrow genetic diversity	Limited availability of novel resistance	Utilization of landraces and wild relatives
Linkage drag	Undesirable traits introduced with resistance	Marker-assisted backcrossing
Environmental variation	Unstable resistance expression	Multi-environment testing
Complex quantitative resistance	Difficult phenotypic selection	GWAS and genomic selection
Long breeding cycles	Delayed cultivar development	MAS and genome editing
Regulatory challenges	Delayed adoption of genome-edited varieties	Appropriate biosafety and regulatory assessment
Resistance breakdown	Reduced long-term effectiveness	Combining major genes with quantitative resistance

5. Conventional breeding for BLB resistance

Conventional breeding remains an important and widely used approach for developing bacterial leaf blight-resistant rice cultivars. The process generally involves crossing a resistant donor possessing one or more desirable resistance genes with an elite but susceptible or moderately resistant cultivar that has superior agronomic characteristics. The resulting progenies are subsequently evaluated and selected over several generations for disease resistance and desirable traits such as grain yield, maturity duration, plant architecture, grain quality, and adaptability. Resistant donor lines may originate from cultivated varieties, traditional landraces, or wild relatives of rice, thereby providing breeders with diverse sources of resistance. Disease screening under controlled and field conditions is an essential component of conventional breeding because it enables the identification of plants expressing appropriate levels of resistance against specific pathogen populations (Pradhan *et al.*, 2015) [12]. Backcross breeding can be employed when the objective is to transfer a resistance gene into an established high-yielding variety while retaining most of the recipient parent's desirable characteristics. Although conventional breeding has contributed significantly to the development of disease-resistant rice varieties, it can be time-consuming because several generations may be required to achieve genetic fixation and recover desirable agronomic traits. In addition, phenotypic selection for disease resistance can be influenced by environmental conditions, pathogen diversity, disease pressure, and the developmental stage of the plant. These limitations have encouraged the integration of conventional breeding with molecular tools. Nevertheless, conventional hybridization and phenotypic selection remain fundamental because they provide the genetic framework within which molecular and genomic approaches can be applied. Combining traditional breeding knowledge with modern molecular techniques can substantially increase the efficiency of developing rice cultivars possessing stable BLB resistance together with high yield and desirable grain characteristics.

6. Marker-assisted selection

Marker-assisted selection (MAS) has significantly improved the efficiency and precision of rice breeding for bacterial leaf blight resistance. Unlike conventional phenotypic selection, which depends largely on the visible expression of disease symptoms, MAS uses DNA markers associated with specific resistance genes or genomic regions to identify desirable plants at an early stage of development. This approach enables breeders to select plants carrying target resistance alleles before exposure to the pathogen and reduces the influence of environmental factors on selection decisions. Molecular markers linked to important BLB resistance genes such as *Xa4*, *xa5*, *xa13*, and *Xa21* can be used to track these genes during breeding populations and backcross generations. MAS is particularly valuable for recessive resistance genes because plants carrying the desired allele may not always be reliably distinguished through conventional phenotypic screening alone. Another major advantage of MAS is its abil-

ity to facilitate the simultaneous selection of several resistance genes, thereby supporting gene-pyramiding strategies. Through marker-based screening, breeders can identify progeny carrying combinations of resistance genes without depending exclusively on disease-screening experiments. MAS can also accelerate backcross breeding by allowing breeders to select plants carrying the target resistance gene while simultaneously recovering the genetic background of the elite parent. Furthermore, the integration of MAS with high-throughput genotyping and genomic approaches has increased the potential for rapid development of improved rice cultivars (Pradhan *et al.*, 2015) [12]. However, the effectiveness of MAS depends on the availability of reliable, closely linked or functional markers and accurate information about the resistance phenotype. Therefore, combining marker-assisted selection with rigorous phenotypic evaluation remains essential for confirming the stability and effectiveness of BLB resistance under diverse environmental and pathogen conditions.

7. Gene pyramiding for durable resistance

Gene pyramiding is an important molecular breeding strategy in which two or more resistance genes are combined within a single rice genotype to achieve broader and potentially more durable resistance against bacterial leaf blight. The strategy is particularly valuable because individual resistance genes may provide effective protection against only specific pathogen populations, and the widespread cultivation of varieties carrying a single resistance gene can increase selection pressure on pathogen populations. By combining genes with different resistance mechanisms or recognition specificities, the probability that a pathogen population will simultaneously overcome all resistance components may be reduced. Important BLB resistance genes such as *Xa4*, *xa5*, *xa13*, and *Xa21* have been combined in different breeding programs to develop rice lines with enhanced resistance. Marker-assisted selection has greatly facilitated gene pyramiding by allowing breeders to identify progenies carrying multiple target genes even when their individual phenotypic effects cannot be easily distinguished. Pyramiding can also be combined with quantitative resistance loci to improve the stability of resistance across different environments and pathogen populations (Ronald *et al.*, 1992) [13]. However, the successful deployment of pyramided genes requires careful evaluation because interactions among resistance genes and the genetic background of the recipient variety can influence the final resistance phenotype. Furthermore, the effectiveness of a pyramided genotype should be assessed against diverse and evolving Xoo populations rather than against a single pathogen isolate. Consequently, gene pyramiding, when supported by molecular markers, diverse pathogen screening, and multi-location field evaluation, represents a promising strategy for developing rice cultivars with broad-spectrum and durable bacterial leaf blight resistance. 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).

8. Genomic approaches in BLB resistance breeding

Recent advances in genomics have considerably expanded the ability of researchers to identify and utilize genetic factors associated with bacterial leaf blight resistance in rice. Quantitative trait locus (QTL) mapping, genome-wide association studies (GWAS), genomic selection, and high-throughput genotyping have become valuable components of modern rice breeding programs. QTL mapping enables researchers to identify genomic regions contributing to quantitative or partial resistance by analyzing segregating populations derived from genetically contrasting parents. Such QTLs can subsequently be incorporated into elite breeding materials using molecular markers. In contrast, GWAS exploits naturally occurring genetic variation within diverse rice populations to identify associations between molecular markers and disease-resistance phenotypes. This approach has the potential to identify novel resistance loci and allelic variants that may not be detected through conventional biparental mapping populations. Genomic selection represents another promising approach in which genome-wide molecular marker information is used to predict the breeding value of individuals before extensive phenotypic evaluation (Sundaram *et al.*, 2008) [14]. This can reduce breeding cycles and facilitate simultaneous improvement of disease resistance and complex quantitative traits such as grain yield and quality. The integration of genomic information with high-throughput phenotyping and pathogen characterization can further improve the accuracy of resistance selection. In the future, combining genomic selection with information on pathogen diversity and environmental conditions may allow breeders to develop rice cultivars with more stable resistance across different production environments. Thus, genomic approaches are transforming BLB resistance breeding from a largely phenotype-dependent process into a more precise, data-driven strategy for the discovery and deployment of useful resistance alleles.

9. CRISPR/Cas-mediated improvement of BLB resistance

CRISPR/Cas-based genome editing has emerged as a powerful technology for the precise genetic improvement of rice for bacterial leaf blight resistance. Unlike conventional breeding, which requires repeated crossing and selection to transfer desirable genes, genome editing enables targeted modification of specific genomic sequences associated with disease susceptibility or defense responses. One important strategy involves editing host susceptibility genes that are exploited by Xoo during infection. Certain bacterial effectors manipulate host transcriptional processes and activate plant genes that facilitate bacterial colonization and multiplication. Modification of the corresponding host susceptibility factors can therefore reduce pathogen development while retaining essential plant functions. Genome editing has also created opportunities to modify regulatory regions controlling the expression of defense-related genes, potentially enhancing the plant's ability to respond to pathogen attack. The ability to introduce precise mutations in multiple target genes makes CRISPR/Cas technology particularly attractive for developing broad-spectrum resistance. In addition, genome editing can potentially be combined with conventional resistance genes and genomic breeding approaches to create cultivars possessing multiple layers of protection (Tian *et al.*, 2014; Wang *et al.*, 2015) [15, 16]. However, edited plants require comprehensive evaluation for off-target effects, agronomic performance, resistance stability, and possible effects on yield and grain quality. Regulatory requirements and public acceptance also need to be considered before large-scale deployment. Despite these challenges, CRISPR/Cas technology represents an important next-generation tool for rice improvement and has the potential to complement conventional breeding, marker-assisted selection, and gene pyramiding in the development of durable bacterial leaf blight-resistant rice cultivars.

10. Combining disease resistance with yield and grain

quality

The development of bacterial leaf blight-resistant rice cultivars should not be limited to disease resistance alone, because farmers require varieties that combine resistance with high yield, desirable grain quality, appropriate maturity, and adaptability to diverse agroecological conditions. Incorporating resistance genes into elite high-yielding backgrounds can sometimes be challenging because undesirable traits may be introduced along with the resistance source, particularly when resistance genes are obtained from landraces or wild relatives. Therefore, breeding programs need to carefully select progenies that maintain both effective disease resistance and superior agronomic performance. Modern breeding strategies allow resistance genes and quantitative resistance loci to be combined with traits such as drought tolerance, salinity tolerance, heat tolerance, improved nitrogen-use efficiency, suitable plant architecture, and enhanced grain quality. Marker-assisted selection and genomic selection can facilitate simultaneous improvement of several traits by enabling breeders to track favorable alleles across generations (Wang *et al.*, 2022; Yoshimura *et al.*, 1998) [17, 18]. Multi-parent populations and genomic breeding populations may also provide greater opportunities to combine resistance with complex quantitative traits. Furthermore, evaluating advanced breeding lines under different environmental conditions is essential because the expression of both disease resistance and yield-related traits can vary considerably with temperature, rainfall, soil conditions, and pathogen pressure. Integrating disease-resistance breeding with climate-resilience and quality improvement can therefore contribute to the development of rice cultivars that are not only resistant to bacterial leaf blight but also productive, stable, and acceptable to farmers, processors, and consumers. Such multi-trait improvement is particularly important for sustainable rice production under changing climatic conditions and increasing pressure on agricultural resources.

11. Challenges in developing durable BLB resistance

Despite considerable progress in the genetic improvement of rice for bacterial leaf blight resistance, the development of durable and broadly effective resistance remains a major challenge. One of the principal limitations is the genetic diversity and continuous evolution of *Xanthomonas oryzae* pv. *oryzae* populations. Pathogen strains may vary in their ability to overcome specific resistance genes, and the extensive cultivation of rice varieties carrying the same resistance source can create strong selection pressure for the emergence and spread of virulent pathogen populations. Consequently, resistance conferred by an individual gene may become less effective over time. Another important challenge is the limited utilization of genetic diversity available in traditional rice varieties and wild relatives, despite their potential to provide novel resistance alleles. Introgression of such genes can also be accompanied by undesirable traits, resulting in linkage drag that may negatively affect yield, maturity, plant architecture, or grain quality. Environmental variation further complicates resistance breeding because disease development and resistance expression can be influenced by temperature, humidity, rainfall, nutrient availability, and crop-management practices. In addition, resistance identified under artificial inoculation or controlled experimental conditions may not always provide equivalent protection under diverse field environments. Although molecular breeding, genomic selection, and genome-editing technologies have improved the precision of resistance improvement, their successful application requires reliable molecular markers, well-characterized genetic resources, accurate phenotyping, and extensive validation (Yoshimura *et al.*, 1998; Yuan *et al.*, 2010; Zhou *et al.*, 2015; Zhang, 2009; Zeng *et al.*, 2004; Zhou *et al.*, 2011; Asma *et al.*, 2022; Ranjithkumar *et al.*, 2022) [19, 20, 21, 22, 23, 24, 25, 26]. Regulatory considerations and the acceptance of genome-edited crops may also influence the adoption of advanced breeding technologies. Addressing these challenges will require continuous surveillance of pathogen populations, conservation and char

acterization of rice genetic diversity, integration of multiple resistance mechanisms, and systematic evaluation of improved breeding materials across environments. A coordinated combination of conventional breeding, molecular genetics, genomics, and precision genome editing will therefore be essential for achieving stable and durable BLB resistance in future rice cultivars.

12. Future prospects

Future BLB resistance breeding will increasingly depend on the integration of multiple technologies rather than reliance on a single breeding method. The combination of traditional genetic resources with high-throughput phenotyping, molecular markers, GWAS, genomic selection, transcriptomics, and genome editing can accelerate the identification and deployment of useful resistance alleles. Particular attention should be given to combining major *Xa* genes with quantitative resistance loci. Such combinations may provide stronger and more durable protection than individual resistance genes. Artificial intelligence and machine-learning approaches may further assist breeders by integrating genomic, phenotypic, environmental, and pathogen datasets. These approaches could improve prediction of genotype-by-environment interactions and help identify optimal parental combinations (Zhou *et al.*, 2015; Zhang, 2009) [21, 22]. The conservation and characterization of rice landraces and wild relatives should also remain a priority because they represent important reservoirs of genetic diversity.

13. Conclusion

Bacterial leaf blight remains a major constraint to sustainable rice production, particularly in regions where favorable environmental conditions and intensive cultivation promote disease development. Genetic resistance provides an economical and environmentally sustainable approach to BLB management. The identification of major *Xa* genes and quantitative resistance loci has provided a strong foundation for genetic improvement. Conventional breeding has successfully introduced resistance into elite rice backgrounds, while marker-assisted selection and gene pyramiding have increased the precision and efficiency of resistance breeding. Genomic approaches, including QTL mapping, GWAS, and genomic selection, are facilitating the discovery and utilization of additional resistance resources. More recently, CRISPR/Cas-based genome editing has provided opportunities for targeted modification of susceptibility mechanisms and development of improved resistance. The future of BLB-resistant rice breeding lies in integrating diverse genetic resources with molecular and genomic technologies. Combining broad-spectrum and quantitative resistance with high yield, grain quality, and climate resilience will be essential for developing next-generation rice cultivars capable of supporting global food security under increasingly challenging agricultural conditions.

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