



RICE PANICLE DISEASE AND ITS MANAGEMENT STRATEGIES

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(Received, 28th November 2023, Revised 27th October 2024, Published 8th November 2024)

Abstract Rice cultivation in Pakistan is important for local food security and international trade, especially through export of popular brands like Kernel and Super Basmati. However, the industry faces significant challenges from various biotic and abiotic stresses, including leaf blight (BLB) caused by *Thomomonas oryzae* PV. which can cause decline. The prevalence of BLB is increasing in Pakistan, affecting weak Basmati varieties and causing up to 30% crop failure, especially when the disease occurs during the critical growth period. This disease and others like bacterial infection caused by *Burkholderia glumae*, demonstrate the interaction between bacteria, climate change (such as temperature and humidity) and genetics. MAS promote Plant Growth-Promoting Rhizobacteria (PGPR) which are medicinal and antibacterial. Extensive research has identified several genes (R genes) against BLB such as XA1, XA21 and XA7, which have been successfully incorporated into various rice varieties to enhance disease resistance. Genetic modification, although promising for rapid incorporation of protective genes, requires careful monitoring to ensure safety and efficacy across generations. Crop production, and entrance screening, including in wild rice, also play an important role in identifying emerging sources of disease resistance. Future research will focus on developing these technologies to improve crop production and disease resistance, thereby protecting food security in Pakistan and beyond.

Keywords: Bacterial Leaf Blight; Marker-Assisted Selection; Plant Growth-Promoting Rhizobacteria; Bacterial Blight Resistance Gene

Introduction

Rice (*Oryza sativa* L.) is projected to feed 9.3 billion people as a staple grain by the end of 2050; it is primarily grown in tropical and subtropical regions. After wheat, rice is the second most produced crop in Pakistan in terms of cultivated area. In addition to being an essential crop for Pakistan, rice makes up a sizable portion of the nation's exports. For their unique flavor and scent, the Kernel and Super Basmati cultivars are well-known throughout the world. But Pakistan's position as a rice exporter has deteriorated; in May, exports fell by 19% year over year to 1.6 million tonnes. (Afroz et al., 2012) reports that Pakistan exported an estimated 3.8 million tonnes in 2017, down from 3.9 million tonnes in 2016 (Luo et al., 2012). Numerous biotic and abiotic factors affect rice production worldwide; in certain regions, complex interactions between pathogens, host plants, and climate also have an impact (Mulaw et al., 2018). Temperature has been identified as one of the key factors, and the availability of long-term and spatio-temporally consistent data on rice productivity and climate variables allow for the quantification of the effect of climate on variations in rice yields (Junaid and Gokce, 2024; Rasheed and Malik, 2022). High temperatures are especially damaging to rice during

the reproductive stage, with spikelet sterility occurring when temperatures exceed 35°C during flowering. Additionally, high temperatures modulate their interactions with other factors, such as genotype, solar radiation, relative humidity, and management practices (e.g., N application). This interaction thus explains a potential reason for regional differences in yield reductions due to climate change, even for regions with similar temperature profiles (Abbas et al., 2024a; Zarbafi and Ham, 2019).

Burkholderia glumae infection is also associated with lower yields; under extreme disease pressure, yield losses can reach 75%. High temperatures and humidity are also linked to these yield reductions. With reports of grain and seedling rot in Asia in 1956 and 1976, respectively, the disease cycle of *B. glumae* is well known. Up until the booting stage, the bacteria lives in the subterranean plant tissue and spreads through contaminated seeds. Grain rot occurs in the affected panicles as a result of its migration to the aerial parts during heading and subsequent infection of the panicles upon emergence (Abbas et al., 2024b; Zhou-qi et al., 2016). During the flowering stage (stages 11 and 12), high relative humidity and rainfall promote the infection process. In contrast to Asia, where the infection mainly causes rot in grains and

seedlings, *B. glumae* in the Americas can, in extreme cases, cause spikelet sterility; this condition is known

as bacterial panicle blight (BPB) (Ortega and Rojas, 2021).

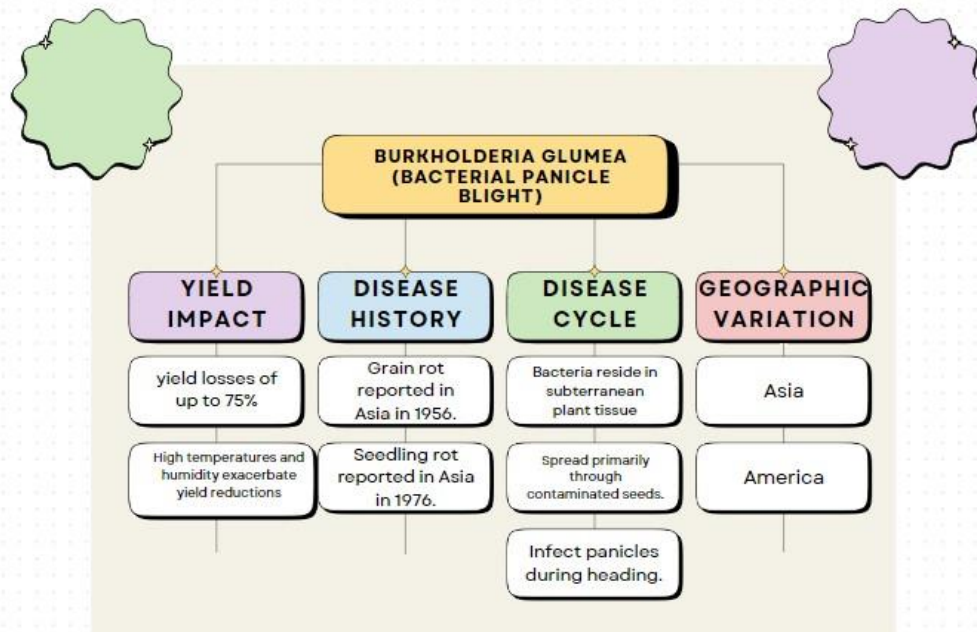


Figure 1. *Burkholderia glumae* (Bacterial Panicle Blight)

When *Burkholderia glumae* is stressed during the reproductive stage, it can result in grain sterility on genotypes that are sensitive to temperature (ALI, 2022; Luo et al., 2012). The ideal temperature range for *Burkholderia glumae* multiplication is between 30° and 35°C. However, controlled experiments have demonstrated that temperatures ranging from 20° to 32°C can lead to the development of bacterial panicle blight (BPB) and grain rot. These investigations also demonstrated the importance of relative humidity greater than 95%, especially during the early stages of infection. However, these findings do not clearly define the specific ranges of temperature and humidity necessary for BPB development under tropical field conditions. Additionally, it is uncertain whether the *B. glumae* infection pattern responsible for grain rot in Asia is identical to that operating in the tropical Americas where BPB occurs (Ortega and Rojas, 2021). Bacterial panicle blight (BPB) was first confirmed in rice fields in the districts of Montería and La Doctrina, located on the Caribbean coast of Colombia, in 2007. It was found that *B. glumae* associated with a yield decline for the first time in Colombia since its discovery in 1989. By 2011, rice yields in Colombia had plummeted, and in the years that followed BPB began to emerge as a major pest (Khan et al., 2012). Then, *B. glumae* were detected by several methods of detection in BPB samples from various rice-growing regions in the country to confirm the distribution of the pathogen. However, the estimates of disease incidence and severity along with the climate-disease relationships for each region need

to be carefully assessed with C 2011 Blackwell Publishing Ltd, 537(3), 309–319 accent on the uncertainty (Sharma et al., 2005).

Current Status of Panicle Blight Disease in Pakistan

Due to its suitability as an agrarian country with favorable temperatures and climates, rice cultivation is given the most importance in Pakistan. Rice is the third most important crop in Pakistan, and it uses more than 10% of the cultivated land area of the country, contributing 17% to total cereal grain production. In addition to all these advantages, there are problems in the agricultural sector such as the introduction of pests and pathogenic species due to international trade and travel. These introductions represent a serious risk to rice production, resulting in large-scale yearly losses from bacterial, viral, and fungal diseases (Bryan et al., 2000). Of these, *Xanthomonas oryzae* pv. *oryzae* (Xoo), the cause of bacterial leaf blight (BLB), is one of the most destructive diseases that affect rice crops in Asia, Australia, Latin America, and the United States. Since its discovery in Kyushu, Japan, between 1884 and 1885, BLB has spread throughout the world (Babujee and Gnanamanickam, 2000).

Early in the rice plant's growth cycle, during the tillering stage, the symptoms of bacterial leaf blight usually appear on leaf blades and move up the plant from lower to upper sections. Severe cases cause pale yellow discoloration of the affected leaf blades, and occasionally yellow to white stripes develop near the leaf margins, which can cause tissue death (Webster

and Gunnell, 1992). Significant yield losses have historically resulted from BLB infestations in several locations. In 1985, Japan, for example, reported losses of 25–35%, while the Philippines and India reported losses of 24–50% and 12–32%, respectively (Liu et al., 2005). Renowned Basmati rice varieties, which are particularly vulnerable to the disease, are being negatively impacted by BLB, which is still spreading throughout Pakistan. According to (Bhasin et al., 2012), BLB infections in Pakistan can cause yield losses of up to 30–50% or even complete crop failure if infections happen during the tillering stage (Fuji, 1999). Renowned Basmati rice varieties, which are particularly vulnerable to the disease, are being negatively impacted by BLB, which is still spreading throughout Pakistan. The famous basmati rice is particularly susceptible to the disease and is badly affected by BLB which is currently spreading in Pakistan. According to (Bhasin et al., 2012), BLB disease in Pakistan can cause crop loss of 30% to 50% and even complete crop loss if the disease occurs during tillering. BLB infections in Pakistan can cause yield losses of up to 30–50% or even complete crop failure if infections happen during the tillering stage (Hayashi et al., 2010). The prevalence of BLB is 11–26% in Khyber Pakhtunkhwa (KP), 16–22% in Punjab and 11–16% in Sindh. This study aims to provide new information on the prevalence and distribution of BLB in rice-growing areas of Pakistan. This information is important to inform future research and management in the face of climate change (Hua et al., 2012).

Bacterial leaf Blight

Biologic stresses, including pathogens, weeds, insects, and pests, cause 40% of the world's rice crop to fail annually (Zhou et al., 2006). A plethora of biotic stressors have been identified globally, including in Pakistan, that impact rice. Among them are rice yellow mottle disease, brown leaf spot, bacterial leaf blight, paddy blast, stem rot, foot rot/Bakanae, and brown leaf spot. Notably, *Xanthomonas oryzae* pv. *Oryza* (Xoo), the cause of bacterial leaf blight (BLB), is particularly prone to rice. It is regarded as one of the oldest rice diseases in Asia and causes large losses in several rice-growing regions worldwide (Hayashi et al., 2010). In Pakistan's rice-growing regions, the number of BLB attacks has increased recently. Studies have indicated that of the three types of rice, Super Basmati is most vulnerable to the Xoo pathogen, with a maximum incidence of 89.5% for PXO 340 symptoms. On the other hand, PXO 280, with a maximum disease incidence of 75.96%, and PXO 340, with a 71.53% incidence, showed susceptibility at the maximum tillering phase for the Basmati 2000 variety, despite

its high resistance at both growth phases (Sharma et al., 2012).

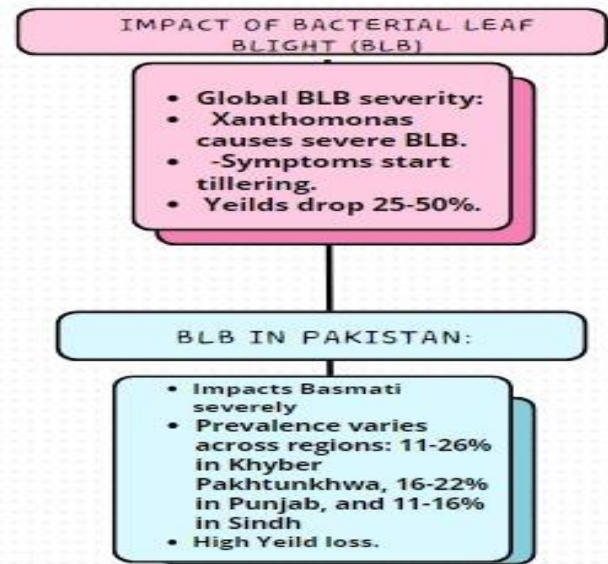


Figure 2. Impact of Bacterial Leaf Blight in Pakistan

Disease management

Various economic and management-friendly measures should be used to reduce the severity of BLB. These strategies include chemical resistance, biological control, and genetic resistance through plant breeding (Joshi et al., 2009).

Control by Biological Means

Beneficial root bacteria called plant-promoting rhizobacteria (PGPR) can improve crops by reducing disease severity and increasing yield. PGPR has shown commercial potential in reducing crop disease (BLB) (Miah et al., 2013). It is available in new suspension and powder formulations. According to (Gnanamanickam, 2009), these rhizobia inoculants can improve crop yield, plant growth, seed vigor, and nutritional quality. PGPR inhibits pathogens through social interaction, competition for resources and space, and enhanced immune response (Valent and Chumley, 1989).

Control by chemical means

Studies show that different treatments have different effects on bacterial blight (BLB). For example, a disinfecting rice seed with 30% chlorine bleach and chlorinated irrigation water has been shown to reduce BLB infestation. Additionally, foliar sprays containing 20 g/L of cow manure extract have been reported to inhibit the growth of BLB (Zhang and Xie, 2014). Six broad-spectrum antibiotics, including ampicillin, kanamycin, streptomycin, chloramphenicol, and Sinobionic, were tested against five isolates of Xoo. The results showed that the antibiotics were able to control BLB in vitro (Crist et al., 2017).

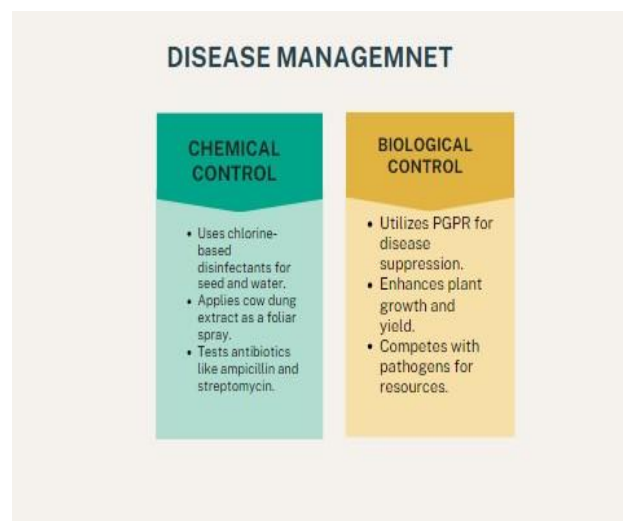


Figure 3. Disease Management

Genetic Resistance against Bacterial Leaf Blight

Due to the devastating effect of leaf blight (BLB) on rice, extensive research has been conducted on its diagnosis, treatment, and management (Crist et al., 2017). Genetic improvement has also proven to be the best strategy in many studies. How to increase the resistance to BLB in wheat through genetics has been investigated and clarified. To date, 38 resistance genes (R genes), both recessive and dominant, from Xa1 to Xa38 (before Xa for *Xanthomonas*) have been identified and assigned (Nandakumar et al., 2009). Six of these genes (Xa1, Xa5, Xa13, Xa21, Xa3/Xa26, and Xa27) have been successfully cloned and an additional gene (Xa2 disease prevention) has been successfully cloned as an effective way to control BLB in crops (Wu et al., 2012).

Rice's R Gene Classes

The two main types of R genes associated with rice disease resistance are nucleotide binding site leucine-rich repeat (NBS-LRR) and receptor kinases (RLK). The first R gene cloned in the cultivar belongs to the RLK class. Xa21 is frequently used in plant breeding programs because it is highly effective against many diseases (Xu et al., 2014).

Given that, it is the largest R genome. Xa1, a nucleotide-binding leucine-rich repeat protein, is an example of such a protein. Xa27 is unique in that it only expresses itself when rice is inoculated with the Xoo strain possessing the *avrXa27* gene (TAL effector) (Ham et al., 2011). *xa13* encodes a novel plasma membrane protein, while *xa5* encodes a small subunit of transcription factor IIA (TFIIA x) (Verdier et al., 2012). These genes represent multiple strategies for rice plants to resist diseases, contributing to the diversity of crop diseases (Chen et al., 2011).

Screening of germplasm against bacterial leaf blight

To find genotypes that require less stress, careful monitoring of crop diseases is necessary to control

bacterial blight (BLB). Several studies have investigated Pakistani and Basmati rice genotypes for resistance to *Xanthomonas oryzae* (Zhu et al., 2000). Only five out of fifteen Pakistani genotypes were found by Ali et al. Many varieties found to be under protection were found to be under protection and differences in protection were seen in different regions. Super Basmati is the most relevant among all the basmati varieties tested for many Xoo isolates. Also, a study comparing wild rice with various cultivars by the National Agricultural Research Centre, Islamabad revealed that *Oryza nivara*, *Oryza longistaminata*, and *Oryza grandiglumis* are resistant to different Xoo, indicating adaptation of resistance genes to resources in cultivation.

The analysis of medium and fine-grain rice has also contributed to our understanding of different rice species (Khan et al., 2012). They are resistant to many different agents, only a few varieties show resistance traits (Khush, 2005). A recent study found that 52 Basmati landraces and 5 cultivars carried multiple BLB resistance genes including Xa4, Xa5, Xa7 and Xa13. The potential for widespread use of Xa7 in breeding programs is indicated by its presence in plots and cultivars such as Basmati-385 and Basmati-2000 (Miyagawa, 2000). However, the low genetic diversity observed in cultivars from the Indian subcontinent highlights the importance of screening multiple sites for enhancing BLB resistance (Francis et al., 2013). These studies highlight the necessity of systematic screening techniques that are appropriate but still simple, with clearly defined selection parameters and in-depth germplasm analysis carried out in a controlled environment. For these screening programs to be implemented sustainably, labor and capital investments are two cost-related issues that must be addressed (Karki and Ham, 2014).

The function of marker-assisted selection (MAS) and conventional breeding in the production of BLB-resistant rice

Blending the genetic foundation of resistance with other rice plants' specific characteristics appears to be easy with the help of traditional breeding. For example, the Y73 near-isogenic line was created using asymmetric somatic hybridization with *Oryza meyeriana* wild rice (Gnanamanickam, 2009). In this study, Y73 showed much better BLB resistance than its recurrent parent Dalixiang (DLX) after Darshan Rice Dalixiang (DLX) was backcrossed with this cultivar: 'Y73'. Such abilities improve the accentuation of the variety development and especially the quality of BLB resistance traits (Maeda et al., 2006). Using BCs of the Chinese variety Minghui63-Zhou et al. (2011), were able to transfer allele Xa23 from *Oryza rufipogon* into several restorer lines together with the point marker-assisted

backcrossing. Every researcher tries to expand the resistant traits, e.g., (Bhasin et al., 2012) transferred the Xa30 (t) gene obtained from *Oryza nivara* into cultivated rice through backcrossing. (Nandakumar et al., 2009) worked on Xa21 and Xa7 resistant genes introducing them into a Minghui63 rice restorer line which resulted in higher BLB resistance in the synergistic breeding lines.

Several studies have successfully introduced BLB resistance genes into different rice cultivars using marker-assisted selection (MAS) and breeding methods. (Zhou-qi et al., 2016) used marker-assisted backcrossing to introduce a novel Xa23 gene from wild rice into backcross lines such as Minghui63, YR293, and Y1671. (Bhasin et al., 2012) identified and transferred the gene Xa30(t) from *Oryza nivara* to cultivated rice through backcrossing. By introducing two resistant genes, Xa21 and Xa7, into the rice restorer line Minghui63, (Zhu et al., 2000) produced pyramided lines with increased BLB resistance. Broad-spectrum BLB-resistant restorer lines (XH2431, 9311, and WH421) were constructed through line selection and MAS (Luo et al., 2012), while a restorer line with four target genes (Pi25, Xa21, xa13, and xa5) was constructed (Weerakoon et al., 2008) to produce hybrids with strong resistance to rice blast and BLB using MAS. The Xa5, Xa13, and Xa21 genes were successfully introduced into BLB-susceptible indica rice cultivars (Verdier et al., 2012), generating genotypes with enhanced resistance to most *Xanthomonas oryzae* isolates. These studies demonstrated that MAS can transform many BLB-resistant seeds and improve the agronomic traits of rice cultivars. These studies demonstrate how well MAS transfers several BLB resistance genes and enhances agronomic characteristics in rice cultivars.

Transgenesis

Genetic modification techniques involving the direct transfer of specific genes from wild or other sources into crops have been effective in disease prevention for improving rice production. This approach, bypassing conventional breeding methods, holds promise for introducing disease-resistance genes including bacterial leaf blight (BLB). For example, the Xa21 gene, known for its broad-spectrum resistance to BLB, was successfully transferred from perennial rice to the well-known rice IR24. Similarly, (Hemal Bhasin et al., 2012) introduced XA21 into rice through *Agrobacterium*-mediated transformation, which resulted in the stabilization of BLB resistance in several transgenic lines. These transgenic lines are promising for providing long-term protection against BLB without compromising yield (Bashar et al., 2010; Javed et al., 2024; Rasheed et al., 2024). Additionally, to enhance disease resistance in rice, researchers have explored the use of antimicrobial

peptides (AMPs) based on genetic modification. The study by Patkar and Chattoo in 2006 showed that transgenic indica rice expressing onion AMP was resistant to many diseases such as blight, blast, and sheath blight (Pinson et al., 2010). They extended this idea and combined AMP genes from Chinese shrimp to japonica rice to increase the resistance of rice to BLB (Luo et al., 2012). These developments demonstrate how advanced technology can be used to produce more disease-resistant rice varieties to combat challenging diseases in the agricultural sector (Compant et al., 2005).

However, issues such as genetic silencing, instability, and possible rearrangements in genetically modified plants are still a major concern. These issues need to be carefully considered and evaluated to ensure stable and effective delivery of vaccines to future generations. Despite these issues, genetic modification techniques are important for the development of long-term plans for rice seed diversification and agricultural disease prevention. Future research will focus on the outcome of technology adaptation and solving related problems to maximize the benefits of technology adaptation for global crop production and food security.

Conclusion

Leaf blight disease poses a serious threat to crop production, causing major crop losses. Although many control strategies have been investigated, the development of resistant rice varieties remains the best approach. Traditional breeders play a major role in this effort by using a variety of species, including wild rice, to screen for BLB resistance. However, breeding always takes a very long time. Incorporation of modern technology such as genetic modification shortens the cycle, allowing for greater growth. However, rigorous testing is essential to assess the effectiveness of the introduced genes. Selective marker services have yielded positive results and deserve further investigation in breeding programs to increase disease resistance. We are working to adapt this technology for practical use by breeders. Finally, cooperative breeding is important to control the threat posed by BLB.

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Declaration

Author contribution statement

All authors contributed equally.

Acknowledgement

Not applicable

Conflict of interest

There is no conflict of interest among the authors.

Data Availability statement

All authenticated data have been included in the manuscript.

Ethics approval and consent to participate

These aspects are not applicable in this paper.

Consent for publication

Not applicable

Funding

There were no sources providing support, for this paper.



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