Bacterial Blight: A Major Threat to Rice Ecosystems - Symptoms, Epidemiology, Pathogen Insights and Control Measures

Gaganashree K P[1] and Karthik R[2]

[1]PhD scholar, Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad - 580005. Email ID: karthikrj1611@gmail.com

[2]PhD scholar, Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad - 580005

Corresponding Author:

Introduction

Rice serves as the staple food for populations across rural and urban areas of humid and sub-humid Asia, contributing approximately 23% of global caloric intake (Panda *et al.*, 2017). However, rice productivity in India faces significant challenges from both biotic and abiotic stresses. Plant breeders aim to identify beneficial genes for traits like stress tolerance and incorporate them into elite cultivars to develop resilient rice varieties, addressing the global food demand. Key biotic stresses, including bacterial blight (BB), and abiotic constraints like nutrient deficiencies significantly impact rice yields.

Fig. 1. Rice leaves infected with Bacterial leaf blight (BLB)

Bacterial Blight: A Major Threat

Bacterial blight (BB), caused by *Xanthomonas oryzae* pv. *oryzae* (Xoo), is a devastating disease. It was first identified in Japan in the late 19th century and has since been a persistent threat. The bacterium is gram-negative, rod-shaped, and thrives in temperatures between 25-30 °C. It spreads through the xylem, producing extracellular polysaccharides that block xylem vessels, leading to disease symptoms and providing a source of secondary inoculum.

Symptoms and Damage

BB symptoms manifest in three phases:

1. **Leaf Blight Phase**: Characterized by yellow to brown linear stripes with wavy margins, extending from the leaf tip. This phase can lead to significant leaf death and reduced photosynthesis (Fig 1).

2. **Kresek Phase**: The most destructive phase involves systemic infection, causing leaves to droop, turn yellow or grey, and eventually wither.

3. **Pale Yellow Leaf Phase**: Seen predominantly in tropical regions, this phase causes youngest leaves to turn pale yellow before withering.

Epidemiology

BB spreads via wind, rain, irrigation water, and insects. The pathogen persists in rice stubbles, wild rice species, and weed rhizospheres. Environmental conditions like high temperatures, humidity, and the presence of susceptible cultivars exacerbate the disease. Severe outbreaks in India, such as those in the 1979-1980 northwest epidemics and the 2014 Thanjavur outbreak, highlight its impact. BB can cause yield losses exceeding 50% in susceptible regions (Yugander *et al.*, 2018).

Genetic Variation in the Pathogen

Xoo is highly variable, with new pathogenic variants continuously emerging. Studies in India and Asia have identified multiple pathotypes and races of *Xoo*, showcasing its diversity. Resistance gene studies reveal significant interactions between *Xoo* strains and resistance genes, emphasizing the importance of stacking multiple genes for broad-spectrum resistance. For instance, the combination of *xa5*, *xa13*, and *Xa21* has been effective against most Indian *Xoo* strains (Mishra *et al.*, 2013).

Control Measures for Bacterial Blight

BB management involves integrated approaches, including chemical, biological, and cultural methods, though their effectiveness varies:

1. **Chemical Control**: Antibiotics like streptomycin and chloramphenicol have been used to combat BB. However, over-reliance on these chemicals poses sustainability challenges.

2. **Biological Control**: Plant growth-promoting Bacillus species and rhizobial inoculants have shown promise in reducing BB impact by improving plant health.

3. **Cultural Practices**: Proper nutrient management and agrochemical applications at critical growth stages have been employed to mitigate BB damage.

Despite these measures, systemic solutions are needed. Host plant resistance offers the most sustainable strategy for long-term management.

Host Plant Resistance for Bacterial Blight: Conventional breeding programs have focused on developing BB-resistant varieties. Early successes include the Japanese varieties Shiga Sekitori 11 and Asakaze. At the International Rice Research Institute (IRRI), resistance genes from donors like TKM6 and Tadukan were incorporated into high-yielding varieties like IR20 and IR26. In India, over 100 BB-resistant varieties have been developed, including PR4141 and Ajaya (Sundaram *et al.*, 2008).

Limitations of Conventional Breeding: Conventional breeding is labour-intensive, time-consuming, and limited by issues like tight linkage between desirable and undesirable traits. Resistance based on single genes is prone to breakdown with the emergence of new *Xoo* pathotypes. To overcome these challenges, breeding efforts now emphasize using multiple resistance genes and quantitative trait loci (QTLs).

Marker-Assisted Breeding: Marker-assisted selection (MAS) enables the precise and efficient incorporation of resistance genes into elite rice varieties. Advances in genomics have identified 42 BB resistance genes, including 16 recessive ones. Combining these genes into pyramids has been effective in achieving durable resistance. Genes like *Xa21*, *xa13*, and *xa5* offer broad-spectrum resistance and are used in various combinations for enhanced efficacy.

Advances in Resistance Breeding: Recent studies have mapped BB resistance genes to six rice chromosomes. These genes provide both qualitative and quantitative resistance. While dominant genes confer strong, race-specific resistance, recessive genes like *xa13* offer broad-spectrum protection. Combining these genes in pyramids has proven effective in controlling diverse *Xoo* strains.

For instance, combinations like *Xa4* + *xa5* + *xa13* and *Xa21* + *xa5* + *xa13* have been widely effective across India. Resistance is bolstered by using wild rice species and mutant populations as sources of novel resistance genes. Deploying such gene combinations in breeding programs ensures stable and durable resistance over time and across diverse agro-climatic conditions.

Conclusion: Bacterial blight poses a significant challenge to rice cultivation, necessitating integrated management approaches. While cultural and chemical controls provide short-term relief, host plant resistance remains the most effective and sustainable strategy. Advances in molecular breeding, particularly marker-assisted selection, have revolutionized resistance breeding by enabling the rapid deployment of multiple resistance genes in elite cultivars. Ongoing efforts to identify and utilize novel resistance genes will be crucial in ensuring global rice productivity in the face of evolving *Xoo* pathotypes and changing environmental conditions.

References

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