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Review Article

Sheath Blight and Bacterial Blight Resistance in Rice: Mechanisms, Progress and Future Perspectives for Sustainable Rice Production

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ABSTRACT

Rice (*Oryza sativa* L.) is a staple food for nearly half of the world's population, including Pakistan. But several diseases are always posing a threat to rice farming, with bacterial blight and sheath blight being the two most common causes. *R. solani* is the main source of rice sheath blight and stood crop’s most destructive diseases. Reviewing published data on pathogenicity and disease management is crucial to developing effective crop protection against sheath blight. It also helps identify research gaps that need more in-depth investigation. Although there has been progress in identifying rice and pathogen-related genes linked to pathogenesis, the underlying processes are still unknown. Research on the applications of; agronomic techniques, chemical control, biological control, and genetic improvement in disease management strategies has been conducted. Optimizing the application of nitrogen fertilizer in combination to plant-plant spacing can minimize the transmission of infection, whereas SMART agricultural technologies; like crop monitoring using Unmanned Aerial Systems help detect and treat sheath blight disease early on. Biological agents and natural fungicides can be used to effectively prevent sheath blight while reducing the negative effects on the environment. Genetic strategies that hold potential to control sheath blight include the use of exogenous dsRNA to suppress pathogen gene expression, genome editing to create rice lines less susceptible to sheath blight, and the development of transgenic rice lines that over express or silence genes related to pathogenesis. The pathogen’s flexibility, the absence of resistant rice types, the lack of single resistance genes for breeding, and farmers' restricted access to informative programs about optimum management methods all work against effective crop protection against sheath blight.

Keywords: Sheath blight, susceptible, disease, conventional approach, transgenic, molecular tools

INTRODUCTION

For Pakistan's economic and food security, rice is an essential crop. Rice farming is, however, severely hampered by the persistent threat of bacterial and sheath blight. While *Xanthomonas oryzae pv. oryzae*, a bacterial pathogen, is the source of bacterial blight, *R. solani* is the causal agent of fungal sheath blight.

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The rice crop is greatly impacted by rice diseases, especially sheath and bacterial leaf blight.

It is essential to comprehend the mechanisms and modes of action that underlie resistance in order to create solutions that effectively reduce these dangers. Japan published the first report of Sheath Blight (ShB) in rice in 1910. Afterwards, ShB in rice spread throughout [1] the area, especially in areas where rice was farmed under intensive cultivation [2]. The disease was known by a variety of names as it spread to other Asian nations, including "Banded blight of rice" and "Sclerotial blight" [3]. *R. solani Kühn*, the ShB pathogen, lives both in soil as well as in water as a sclerotia, that can be viable for up to 3-years. When it comes into contact with plants, it transforms into mycelia [4]. The disease first appears in rice during the late tillering to joint elongation stages, and it reaches its most virulent stage during panicle differentiation. Lesions on the sheath, which cause the sheath to become softer and lodge, as well as a blockages of grain filling, are the initial signs of the disease [5]. According to Tsiboe *et al*. (2017), the fungus spreads quickly through interaction with plant parts like tillers and leaves as well as through sclerotia, that are closely packed masses of hyphae, found in the surface of water [6]. According to Norman *et al.* (2003), the use of nitrogen fertilizers, rice variety susceptibility, growth phases of the plant at the time of infection, and cultivation practices all affect how severe the disease is [7, 8].

Because of the pathogen's broad host range and sclerotia's resilience to harsh environmental conditions, rice ShB is challenging to control. The sneakiest way is that as the pathogen changes over time, the sclerotia are able to get past the resistance that may have been a laborious effort on the part of farmers and breeders. To stop ShB from spreading, data collected through research on the pathogen's biology and the infection process must be utilized. Then, it must be decided how to use and support this information using ShB management techniques. Here, we offer an overview of the most recent findings regarding pathogenicity's molecular basis, host's range, identification criteria, and infection modalities.

There have been reports of severe cases and high incidence of bacterial leaf blight in rice in many places of the world [9, 10]. Consequently, in order to prevent potential epidemics, methods appropriate to specific ecosystems must be developed. Among these several control strategies, host-plant resistance is an essential control strategy. Understanding varietal resistance is necessary to choose cultivars that are resistant to the disease for an extended period of time [11, 13]. Breeders of rice encounter several environmental obstacles, such as disease-causing bacterial infections. Many crops, including rice and cassava, are susceptible to severe bacterial leaf blight, which is caused by a gram-negative bacterium from the *Xanthomonas* genus [14]. It results in annual yield reductions in rice that are roughly 50% [15].

Farmers in Japan's southern region first reported seeing BB in 1884. In India, bacterial leaf blight during the South-West monsoon season—also known as the kharif or wet season is a major concern. It is a vascular disease with distinct symptoms that begin at the tips of the leaves and move downward, causing the leaves to dry out and turn yellow. The ideal temperature range for disease development is 25 to 34 degrees Celsius, with a relative humidity of at least 70%. The bacterial blight (BB) pathogen enters the host by wounds and hydathodes, two naturally occurring openings in leaves, and then colonizes the xylem vessels. In the field, disease incidence rises with plant growth and rises at the flowering stage; symptoms begin during the tillering stage. This bacterium results in poor maturation, fractured grain during milling, and a decrease in weight of dry matter rice. The bacterial leaf blight, a vascular disease that lead to the rice crops to turn yellow, white, or tannish-grey along the veins, leaf margins, and leaf blades; lesions can even extend to the sheath [16]. Understanding the fundamentals of the pathogen-host interaction that results in a compatible or incompatible illness reaction is the focus of some study. When *Xoo* infects the rice plant, the disease could get worse as the plant grows even if symptoms may first appear at the tillering stage. It has been shown that the bacteria may thrive best in temperatures between 28 and 34°C, and that the rice plants that are < 21 days old are prone to the disease. The management of BB has involved the use of pharmaceutical and biological treatments in addition to strengthening host resistance [17]. Their functional life is limited to a few years, though, as many resistant cultivars have their resistance break down.

In order to evaluate the variety within the germplasm and offer information on resistance/susceptibility for use in breeding practice in the future, rice has to be screened for bacterial leaf blight resistance [18]. Moreover, artificial inoculation may always provide a definitive result when screening for varietal resistance because an adequate inoculation can start the disease [19]. Recently, a wide range of strategies have been developed to control rice fungal disease. Attempts to prevent the disease's chemical and biological spread have made extensive use of disease forecasting and culture techniques [20]. Unfortunately, these actions don't really do much. Using pesticides is not only costly but also unfavorable to the environment. Some methods, like multiline [21], mixes [22], and pyramid [23], depend on applying specific and complete resistance genes to develop blast resistance, whereas other methods concentrate on building up partial resistance [24]. The molecular function of various blast resistance genes has been reported, and numerous quantitative trait loci (QTL) for blast resistance have been mapped [25]. Partial resistance suggests more universal processes and is therefore regarded as more enduring, which explains why QTL research is so appealing. The most affordable and ecologically friendly method of disease prevention is host resistance [26].

One effective strategy for lowering the usage of pesticides that harm the environment is the use of resistant rice varieties. Plant breeders have created a variety of blast-resistant cultivars that are suited to various rice-growing regions across the world by employing traditional plant breeding procedures. Plant breeders now have more resources at their disposal to create ecologically friendly rice production systems due to recent developments in rice genomics [27]. It will surely be possible to generate new rice varieties with high blast disease resistance due to the new insights into the nature of rice disease resistance that come from molecular biology studies on disease resistance gene-mediated defense responses. Thus, expediting the development of blast resistance rice requires a grasp of and application for molecular biology. From the beginning to the introduction of a varietal, conventional rice breeding is a laborious process that usually takes ten to fifteen years [28]. Environmental factors have a major role in conventional breeding.

Furthermore, MAS provide more effective selection methods for rice breeding in a shorter amount of time. Compared to phenotypic selection, MAS are more dependable, efficient, and effective. Moreover, MAS has the potential to greatly reduce variety development times, making it more economical in some situations than phenotypic selection. Moreover, MAS makes it possible to develop complicated features that are impractical to achieve with traditional techniques. While MAS is undoubtedly not an ideal solution for all issues, it is a viable alternative to traditional breeding. In rice, significant strides have been achieved in the cloning and discovery of genes that resist disease, the characterization of defense mechanisms, and the understanding of signal transduction that triggers defense mechanisms. Partial resistance can be specific, according to a number of studies [29, 30]. Numerous rice cultivars that are totally resistant to *Magnaporthe grisea* have recently been created [31]. When MAS is used to more accurately enable the early-stage selection, it is difficult to identify blast resistance genes transferred to diverse genetic backgrounds using conventional methods [32]. This review centers on the advancements made in comprehending the molecular basis of rice resistance to blast disease and conventional breeding.

The principal objectives of this review are to: (i) highlight the current approaches to improving blast resistance in rice breeding, including tissue culture, conventional breeding, and various biotechnological tools; (ii) explore a novel and intriguing concept that develops rice for durable blast resistance using molecular data; and (iii) conduct a comprehensive review of the literature on blast resistance genes, QTL and gene mapping, MAS, and gene transformation.

The infection and disease cycle of rice sheath blight and bacterial leaf bight

Sclerotria from a previous cropping season are usually the cause of *R. solani* infections [33]. The roots of recently planted seedlings first pierce at or near the water level when hyphae from sclerotia in the soil establish a network [34]. Warm temperatures (between 28 and 32 °C), high humidity (around 95%), and high nitrogen fertilizer levels all promote infection [35]. As the disease advances through the typical stages of early to late necrosis, the cycle comes to an end when sclerotia from the afflicted rice plants infect the soil (Fig. 1). Pathogen effectors and RS toxin and mannose are produced when *R. solani* infiltrates plant tissues [36].

The fungus spreads by getting inside the damaged plant's stomata and producing lobate aspersoria, or infection cushions. According to Groth and Nowick (1992) the development of aspersoria sets off enzymatic breakdown that results in the necrosis of the host plant and makes it possible for the fungal infection to infiltrate the plant. Classical sheath blight is identified by an acropetal succession of 0.5–3 cm green or grey spheroid lesions on the leaf sheath [37, 38]. The pathogen creates necrotic lesions that are 2-3 cm long and 1 cm wide when it moves from the leaf sheath to the leaf blades, panicles, and tillers. The lesions' beached centers and borders take on a purple-brown hue [39].

When lesions on the upper part of the leaves eventually come together to cover the entire stem and sheath of the plant, this is known as stem lodging. Stem lodging disrupts the design of the canopy, impeding the flow of water. Because stem lodging obstructs water transmission, it reduces photosynthetic capability and upsets the architecture of the canopy. This leads to a decrease in grain filling, and ultimately the virus kills the plant [40]. The BB R genes, which provide resistance against several Xoo strains, were identified from wild relatives, landraces, mutants, and cultivated species. Sustainable rice cultivation requires rice types to be improved for resistance to common and damaging diseases. Previous attempts to generate BB resistant types have been unsuccessful due to significant levels of heterogeneity in the disease populations in growing locations. More resilient disease resistance may result by pyramiding major or minor resistance genes into a common genetic background. The primary BB resistance genes discovered by various research teams have been thoroughly examined and applied to the development of BB resistant cultivars.

Sheath Blight Resistance Mechanisms

The intricate interaction of genetic, molecular, and physiological variables in rice leads to sheath blight resistance.

The synthesis of compounds that are antifungal, the reinforcement of cell wall structures, and the activation of genes linked to defense are important elements [41].

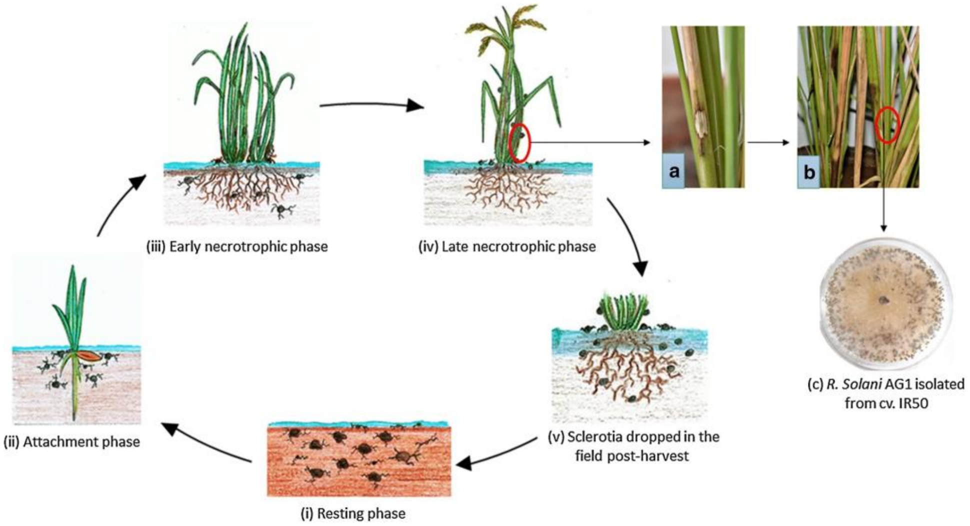

Figure 1. ***Rhizoctonia solani*** disease cycle illustrating various stages of sclerotia production and disease symptoms on rice [39].

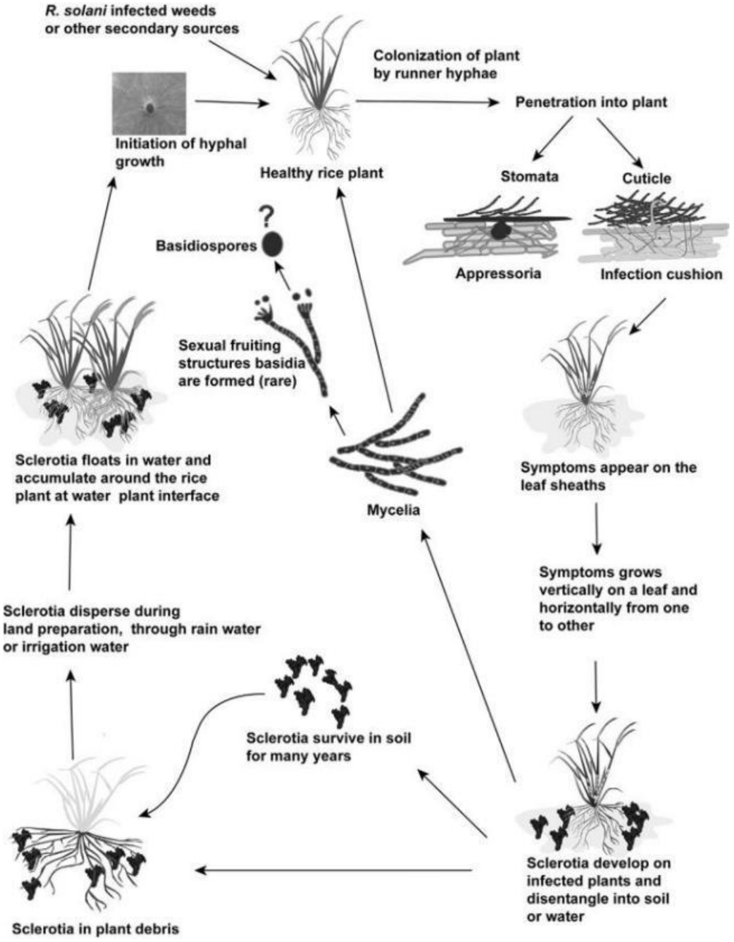

Figure 2. ***Rhizoctonia solani*** disease cycle illustrating various stages of sclerotia production and disease symptoms on rice [63].

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Numerous studies have been conducted on the function of quantitative trait loci (QTLs) in controlling resistance, which has resulted in the identification and distribution of resistant rice varieties in Pakistan.

Cultural Approach

Micro-climatic conditions can be altered by cultural management to lessen the severity of RSB. It is possible to achieve healthy seedlings for transplantation by reducing the soil-borne inoculum throughout May and June by solarizing the soil. Because disease spreads quickly, a high density of seed rates and seedlings cannot be encouraging. In the same way, sparse planting is advised over close planting as it results in a lower incidence of RSB illness [42]. In addition, sparse planting results in a delayed tillering and heading stage, ripening time, more stems per hill, less stems per meter square and fewer tillers per hill. In addition, crop submersion and periodic wetting and drying inhibit the spread of the disease and have a negative correlation with it. Similarly, bio agents can be used to boost rice cultivar growth and manage disease in submerged environments. According to earlier research, the square transplantation approach produces the highest dry matter production and leaf area index while producing the highest possible yield. But there was also a higher frequency of disease [43]. Remaining food is burned, stubbles are removed, and heavy summer ploughing reduces the weed hosts and the RSB disease. Additionally, reducing the inoculum density and controlling diseases can be achieved by cleaning the bunds and leaving the field fallow for a year. Furthermore, organic amendments can also be used to manage the condition [44]. For example, using green organic manures like *Sesbania aculeata* reduces the population of RSB illness.

The incidence of RSB disease was also decreased by using organic amendments using green organic manure plants, and the production of rice crops was greatly increased. The application of farmyard manure also significantly lessens the severity of the condition. The high rice production and the huge reduction in pests like hoppers, borers, and leaf folders, as well as diseases like blast and RSB disease, were the outcomes of using organic fertilizers, which include composts and animal manures. Beneficial microorganisms including *Trichoderma spp*. were found in greater quantities when plots treated with organic manures were compared to plots treated with inorganic fertilizers. The disintegration and multiplication of antagonists, together with volatile and non-volatile compounds, are the reasons behind the suppression of the disease by organic amendments. Furthermore, studies on site-specific nutrition management between plots have demonstrated that the RSB disease, a nitrogen-dependent variable that affects plant germplasm, is a major factor restricting rice crop output. It suggests that the severity of the disease can be increased using nitrogenous fertilizers.

Varieties that have more plant height, fewer tillers, and fewer leaves have higher nitrogenous contents and lower yield losses due to decreased lesions and disease index. Excessive nitrogen dosages may potentially accelerate the disease's onset. Applying silicon is an effective strategy to manage the disease, especially in soil with low or limited plant availability of silicon [45]. Its polymerization and the release of phytoalexin, phenolic, and pathogenesis-related proteins are what create that mechanical barrier [46].

Moreover, a lack of silicon increases the susceptibility of rice to red streak bacteria (RSB), and a high nitrogen treatment lowers the crops' availability of silicon [47]. Furthermore, when the conditions are right, the disease's incidence increases during the vulnerable periods of plant growth, thus the timing of sowing should be taken into account. The optimal viral activity is linked to favorable environmental factors, soil properties, and sensitive rice crop growth stages. Consequently, shifting the date of sowing aids in preventing RSB illness. Furthermore, adopting cultural practices and using fungicides sparingly can both greatly lessen the severity of the disease [48].

Breeding Approach

The most cost-efficient, environmentally friendly, and successful approach is to breed cultivars resistant to RSB disease. However, using traditional breeding techniques to create cultivars that are completely resistant to the RSB disease has not succeeded. On the other hand, certain germplasm has managed to develop a partial resistance to the illness; this resistance is regulated by a number of genes or specific chromosomal areas referred to as quantitative trait loci (QTLs) [49]. Thus, positional or map-based cloning of essential resistance genes should be sped up significantly to identify QTLs, map them, validate their validity, and ultimately characterize them. This could help in the development of rice cultivars resistant to sheath blight.

A statistically significant relationship between allelic variation at a specific locus and a phenotypic trait that exhibits continuous fluctuation in a genetically segregating or evolving population is known as a quantitative trait locus (QTL) [50]. Sharma *et al*. (2009) stated that RSB disease (RSB) is directly influenced by QTLs on chromosome 1 [50]. Consistent results throughout time suggest that identified QTLs are stable and have the potential to improve disease through marker-assisted selection [50]. Moreover, physiological resistance is associated with mechanisms that could reduce the efficacy of one or more stages of RSB infection. It is challenging to develop rice cultivars resistant to RSB using conventional breeding techniques as quantitative features govern RSB.

A few studies have discovered that rice cultivars can become more resistant to RSB by pyramiding QTLs using marker-assisted selection. But problems may arise when QTLs interact with distinct genetic backgrounds. It follows that not all QTLs are effective in all varieties of rice, which makes pyramiding and utilizing QTLs to treat RSB disease more challenging. Thus, pyramiding two or more QTLs encoding genes resistant to disease may improve disease management, according to a small body of studies [51]. Due to the lack of a resistant variety that can combat against RSB disease. The cultivated and wild rice species lack the appropriate amount of resistance, making disease management challenging. The resistance that is not race-specific, there are no known R genes that connect to the disease, and QTL factors solely confer resistance to the disease. Finding an alternate strategy for generating strong, broad-spectrum disease resistance is therefore crucial. Enhancing disease resistance through genetic engineering is a potentially useful tool [52, 53].

A possible method for increasing disease resistance is genetic engineering [54, 55]. In addition to not having the desired resistance level, fungicides have detrimental effects on human health, the environment, and soil microbes. Furthermore, rice is more susceptible to RSB because artificial selection during domestication reduced the genetic diversity of rice cultivars. In this sense, genetic engineering—also known as the transgenic approach—has potential because it can enhance genetic variation by incorporating distinct genes, or QTLs, from genetically diverse lines into rice lines that are more adapted for farming. Because RSB disease has complex features, reliable phenotyping is crucial for cloning and identifying QTLs that confer disease resistance. Plant height, heading date, plant density, and environmental variables like pH, temperature, humidity, and even soil fertility all have an impact on the phenotype of RSB disease. To assess the RSB greenhouse, research is conducted to mitigate the effects of the aforementioned problems and offer reliable data. However, the vast majority of QTL's were found in the field. Finding QTL's/Genes via the conventional genetic linkage method takes a lot of time and involves bi-parental population mapping and genotyping. In more recent times, broader genetic variations for more complicated diseases like RSB have been discovered through the use of the genome-wide association study (GWAS). However, no adequate QT-loci have been found for RSB resistance yet.

An Effective Use of Transgenic Approaches for Disease Resistance

The greatest choices for sustainable agriculture, aside from crop rotation and integrated pest control would be to develop resistant rice cultivars through conventional breeding or genetic engineering [56]. Transgenic plant technology is becoming more and more common as a means of expressing desired genes for certain traits. Traditional breeding efforts to produce this feature have been hampered by the unavailability of resistant rice germplasm against RSB. In rice and other plant species, several putative genes for resistance to fungus-related diseases have been found and identified recently. The development of highly effective genetic engineering methods for a variety of rice genotypes has opened up new research directions regarding the effects of defense genes, such as pathogenesis-related genes with anti-fungal activity, on rice expression.

To create rice lines with greater resistance to the sheath blight fungus, a variety of antifungal genes originating from plants, antimicrobial genes, master switch genes of defensive response, and genes able to inhibit the fungal enzyme and virulence factor were employed. Signal transduction pathways that coordinate several signal systems have an impact on *R. solani* resistance [57]. Hebiba, a rice mutant lacking JA, was more susceptible to RSB, confirming the significance of jasmonic acid (JA) in resistance. When *R. solani* infects the crop, the LOX-gene transcript is up regulated. Overexpression of WRKY-30 in transgenic rice plants activates genes associated with jasmonate and accumulates jasmonate endogenously, increasing RSB tolerance. WRKY80 activates WRKY4 and JA/ET to provide RSB tolerance. According to recent studies, RSB disease resistance is associated with JA and phenylpropanoid metabolism [58].

Therefore, it has been discovered that the WRKY genes are involved in defensive responses in plants and regulate a range of biological activities; including growth, development, stress, embryogenesis, and resistance to RSB disease.

There is evidence to show that ethylene plays a role in the signaling of the *R. solani* disease response. PR1b, PR5, and RSB resistance are increased in transgenic rice that overexpresses a gene involved in ethylene biosynthesis. Moreover, cyanide, a toxic by product of ethylene synthesis, might be more resistant. Conversely, elevated expression of the RSB disease indicator gene PBZ1 and the SAR marker gene PR1b indicated that the rice disease was caused by the salicylic acid (SA) driven pathway. It is well acknowledged that activating the PR genes results from stimulating the SAR pathway. During RSB infection, rice showed distinct activation of the PAL gene and six PR genes (PR-3, PR-5, PR9-10 and PR12-13), suggesting the involvement of SAR activation. Resistance to RSB disease has been demonstrated [59]. Effective resistance against RSB disease is not provided by a single PR gene. Therefore, a higher level of resistance to RSB can be conferred by combining two PR genes. The following genes have been identified: maize ribosome-inactivating gene MOD-1, barley chitinase and barley-1, 3-glucanases, tobacco-1, 3-glucanases (GLUC), rice chitinases gene (OsCHI11), thaumatin-like protein, rice chitinases (CHI11), and Arabidopsis. A notable degree of disease resistance was shown by this combination [60]. Furthermore, rice harvests become more resistant to the effects of nicotinic acid, zinc sulphate and DL-norvaline [61]. These substances worked better together than they did separately. For instance, gamma amino butyric acid and salicylic acid together reduced lesion length more effectively than control plants. Chitinase enzymes, which are produced by some rice cultivars, are important components of resistance to Rice Sheatg Blight (RSB) disease. After inoculation in cultivars with moderate resistance, chitinase activity can be found in 24 hours and 36 hours after inoculation in cultivars with sensitive resistance. Furthermore, the level of chitinases in the moderately resistant cultivars was found to be higher than that in the susceptible cultivars, as verified by western blot analysis. In one study, 41 homozygous rice lines with chitinases and -1, 3-glucanases genes mutated genetically; 92% of these lines were classified as moderately resistant or moderately vulnerable. The transformants were identified by the application of both molecular and functional methods. Genes and micro-RNAs implicated in rice resistance to RSB from 1995 to 2019 have been studied before [62].

Bacterial Blight Resistance Mechanisms

There are several different mechanisms of resistance to bacterial blight, including both basal and race-specific ones. The hypersensitive response and systemic acquired resistance are two of the innate immune responses that plants mount in response to the identification of pathogen-associated molecular patterns (PAMPs) [63]. Furthermore, the implementation of prominent resistance genes, such *Xa21* and *Xa4*, has demonstrated efficacy in bestowing long-lasting resistance against several strains of *Xanthomonas oryzae* pv. *oryzae*.

Mode of Action at Molecular Levels

Detailed insights into the molecular interactions between the rice plant and the pathogens reveal a sophisticated defense network. Signaling pathways involving phyto-hormones, reactive oxygen species, and secondary metabolites play pivotal roles in orchestrating the defense responses [64]. Recent studies have elucidated the molecular events associated with effector-triggered immunity and the deployment of resistance genes, providing a foundation for advanced molecular breeding strategies.

Current Strategies for Resistance Breeding

In Pakistan, the development of resistant rice varieties is crucial for sustainable agriculture. Traditional breeding methods, coupled with marker-assisted selection, have been employed to introduce resistance genes into popular rice varieties. The identification of quantitative trait loci (QTLs) associated with resistance has facilitated the development of resistant cultivars. Collaborative efforts between research institutions and agricultural agencies have led to the release of several resistant rice varieties in Pakistan.

Molecular Mechanisms of Resistance

Understanding the molecular basis of resistance is essential for developing effective strategies against sheath blight and bacterial blight. For sheath blight, resistance mechanisms involve the activation of defence-related genes, production of anti-fungal compounds, and the regulation of cell wall integrity. In bacterial blight, the recognition of pathogen-associated molecular patterns (PAMPs) triggers a cascade of defence responses, including the hypersensitive response and systemic acquired resistance.

Future Directions

The future of rice cultivation in Pakistan depends on innovative approaches to enhance resistance against sheath blight and bacterial blight. Advances in genome editing technologies, such as CRISPR-Cas9, offer the potential to precisely modify specific genes associated with resistance. Additionally, exploring the untapped genetic diversity of wild rice relatives can broaden the genetic pool for resistance breeding programs.

Challenges and Opportunities

Despite significant progress, challenges persist in achieving durable resistance against sheath blight and bacterial blight. Rapid evolution of pathogens and changing environmental conditions necessitate continuous research efforts. Collaborative initiatives involving farmers, researchers, and policy makers are crucial for the successful implementation of resistance strategies.

Conclusion

There is an urgent need for increased rice production worldwide due to the world's growing population. One effective strategy for lowering the usage of pesticides that harm the environment is the use of resistant rice varieties. Plant breeders have created a variety of blast-resistant cultivars that are suited to various rice-growing regions across the world by employing traditional plant breeding procedures. However, because the rice blast fungus is unstable, blast disease still poses a threat to the rice crop. Plant breeders now have more resources at their disposal to create ecologically friendly and sustainable rice production systems due to recent developments in rice genomics. The affordability and ease of use of molecular techniques in integrating them with traditional breeding methods is of utmost importance to rice breeders. This article, in my opinion, will provide an overview of the main applications of conventional breeding to various molecular techniques that can be used to speed up the development of blast-resistant rice cultivars by maintaining rice yields to meet demand and ensure global food security in the upcoming years and decades. In conclusion, continuous attempts to strengthen resistance against bacterial and sheath blight are necessary for Pakistan's rice production to be sustainable. The combination of state-of-the-art molecular techniques with conventional breeding methods offers a viable path toward the development of robust rice cultivars. Pakistan can guarantee the safety and prosperity of its rice farming industry by tackling the obstacles and grasping the new chances that present themselves.

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