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Review Article

Rice Sheath Blight: A Comprehensive Review on the Disease and Recent Management Strategies

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Abstract | Rice sheath blight (RSB) disease became one of the major threats to rice crops worldwide. The causal agent of RSB is the necrotrophic fungus *Rhizoctonia solani*. Finding appropriate management strategies to combat the disease to minimize rice yield losses and reduce global food security threats is challenging. However, scientists are still figuring out the best way to safeguard rice crops from RSB. Recently various pathogenesis-related (*PR*) *viz.* PR-3, PR-5, PR-9, PR-10, PR-12, and PR-13 and *WRKY* genes have been discovered in rice crops which are engaged in plant defensive responses and responsible for various biological processes, including growth, development, stress, embryogenesis, and resistance to RSB disease. Conventional fungicides are now being replaced with eco-friendly fungicides and biological agents, including mycoviruses that can effectively control RSB disease and minimize the hazardous effects of chemicals. Here, we summarize the disease cycle, symptoms, and effects of environmental variables on RSB disease development. Furthermore, recent advances in studies on the management of disease using cultural, chemical, and biological approaches including mycoviruses, transgenic approaches, gene loci/markers, gene silencing, and genome editing are also summarized. Finally, the expression of resistant-related genes in rice crops and biological agent mechanisms of action are discussed.

Introduction

Rice (*Oryza sativa*) is an essential food for half of the world's population, providing 23% of their daily calorie consumption (Abbas *et al.*, 2021). It is mainly consumed in Asian countries. Globally, three billion people consume rice as a staple food. China and India are currently major producers of rice. China ranked first and India second, and together, they produce 51.4% of world-milled rice production (Seck

et al., 2012). About 480 million tons of milled rice are produced annually. According to the United Nations (UN), about 8.6 billion in population is expected by 2030 (Tiwari *et al.*, 2020). Therefore, fulfilling the demand for rice for the increasing population is very important. The major hindrance in obtaining optimum yield is rice sheath blight (RSB) disease. RSB causes 20-70% yield loss (Qi *et al.*, 2017). *Rhizoctonia solani* Kühn [teleomorph- *Thanatephorus cucumeris* Frank (Donk)], a necrotrophic soil-borne fungus that was first discovered as a potato parasite in 1898 by Kuhn, causes RSB (Almasia *et al.*, 2008). There are 14 different anastomosis groups (AGs) in *R. solani*, making the pathogen genetically diverse. AG1 to AG13 comprised 13 groups, whereas AGB1 serves as a bridging isolation. Based on DNA sequence homology and sclerotia shape, *R. solani* AG1 isolates have been divided into three subgroups: IA, IB, and IC. Based on studies of isozyme comparison and rDNA-ITS sequence RFLP, as well as the analysis of fats, the presence of further subgroups/interspecific groupings like ID, IE, and IF was hypothesized and discussed. According to the general consensus, RSB disease is caused by *R. solani* AG1-IA. RSB was initially reported from Japan in 1910 from rice crops. This disease has affected 15-20 million hectares of rice fields in China and contributes to 6 million tons of yield losses yearly (Hossain *et al.*, 2016). In Pakistan, RSB is one of the most devastating diseases of rice. In Pakistan, the losses due to this infection vary from 30 to 50 % (Abbas *et al.*, 2019). The disease can only be controlled with chemical fungicides and cultural techniques, as no resistance has been discovered in available rice germplasm (Qi *et al.*, 2017). Likewise, the fungus's high genetic variability, broad host compatibility, and ability to survive from one crop season to the next by developing dormant sclerotia made control even more challenging (Singh *et al.*, 2019). Besides, the lack of recognized germplasm with an appropriate resistance level for use in the resistance breeding program is the principal impediment to treating sheath blight disease. Plants have developed various defense mechanisms to protect themselves from pathogens. Sophisticated molecular mechanisms aid the implementation of these tactics. Many prior studies have shed light on the plant's molecular defense mechanisms against various pathogens. Despite its economic importance, the molecular basis of *R. solani* and rice-*R. solani* interaction has not been thoroughly explored (Molla *et al.*, 2020). As a result, researchers are now focusing on the molecular decoding characteristics and genetics of RSB tolerance and examining the pathogenic processes of the disease. Reviews on management strategies and crop improvement for sheath blight resistance have recently been published. Singh *et al.* (2019) have discussed the genetics and molecular biology of the disease, but no comprehensive reviews have been published.

Symptoms and disease cycle

The sclerotia are the primary inoculum of the rice sheath blight (RSB) disease. The sclerotia reach the tillers near the water surface during the irrigation of rice crops. If the environmental conditions are favorable, the sclerotia germinate, form hyphae, enter into rice sheaths, and continuously grow inside and on the surface of the rice crop. As a result, longitudinal and water-soaked lesions appear on the leaf sheath, and later, these lesions progress from leaf sheaths to leaves. Finally, whole plants become infected; however, primary tillers remain green. At the later stages of infection, the hyphae of the fungus aggregate into clusters of mycelia, and eventually, mature sclerotia are formed. The sclerotia finally fall into the soil. If the conditions are favorable, the fallen sclerotia germinate and cause secondary infections (Taheri and Tarighi, 2011). Hence, the survival of the sclerotia is critical in the disease cycle of rice crops, as shown in Figure 1 (Reconstructed from Molla *et al.*, 2020). Sclerotia can survive in the soil and stubble for years before infecting healthy rice plants the following crop season. Sclerotia can float great distances in irrigation water in the field due to their buoyancy, promoting disease propagation. The pathogen penetrates the plant through lobate appressoria, infection cushions, or both (Marshall and Rush, 1980). The sclerotia can remain viable for several years under harsh environmental conditions such as temperature, starvation, desiccation, chemicals, and severe radiation. The viability potential for a long time is due to sclerotia's particular structure and functions, which facilitated these specialized resistant bodies to tolerate such hostile environmental conditions. According to prior studies, *R. solani* sclerotia may survive in the soil for 8-10 years without a host and can be used as the principal inoculum for RSB (Feng *et al.*, 2017).

Impact of environmental influences on disease development

Among the environmental factors, temperature and humidity are critical for causing infection and developing RSB. The required humidity for disease
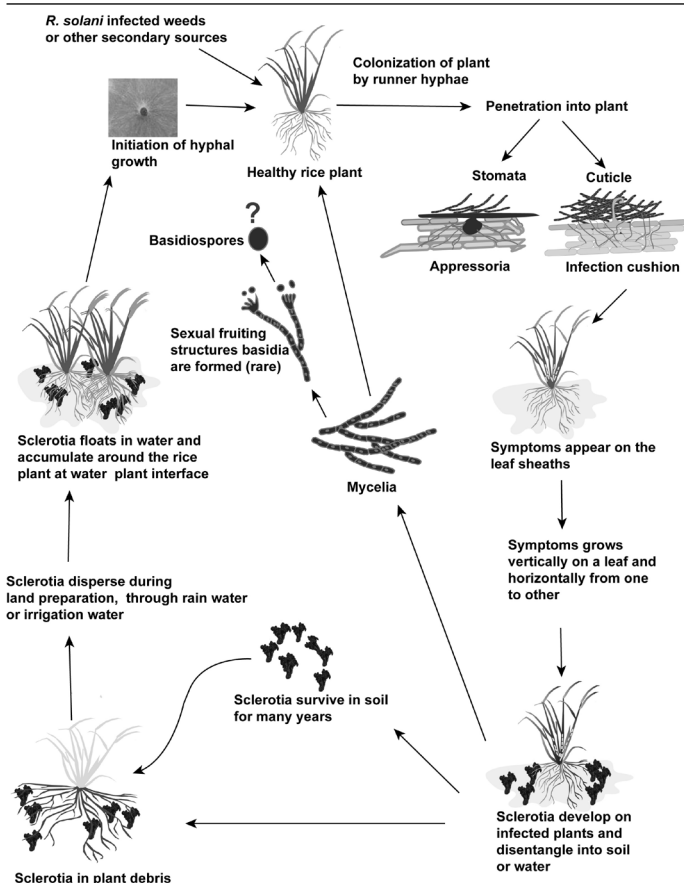
Figure 1: *Disease cycle of rice sheath blight.*

development is 96-100%, and the temperature is 28-32°C (Su *et al.*, 2012). Previous studies revealed that maximum and minimum temperature and evaporation rate influence the severity and incidence of the disease. Relative humidity and temperature are considered the most critical factors for disease development. The wet season is more suitable for disease development than the dry season (Pasalu *et al.*, 2004). Tiwari and Chaure (1997) reported that mycelial growth and sclerotial formation are the highest at 25-30°C, and 80-95% relative humidity is ideal for disease development (Tiwari and Chaure, 1997). Lesion development was also favored by a temperature of 28°C with 100% relative humidity and continuous but low precipitation during disease development (Hashiba and Kobayashi, 1996). The disease is more severe in sandy than in clayey soil. The disease incidence was higher in humid soil with a water-holding capacity (WHC) of 50-60%. However, infection becomes slow when applied 20 days after sowing. Low moisture level enhances seedlings' infections, whereas water logging reduces the infection in rice seedlings. Soil pH also plays a vital role in the severity of the diseases. The optimum pH recorded for the mycelia perpetuation and sclerotial formation is 6.0-7.0. Furthermore, the

disease becomes more severe in shady than in open fields (Singh and Srivastava, 2015).

RSB is more severe in the carbon dioxide elevated atmosphere. Under pot experiments, disease development and intensity were more severe in twenty to thirty days old seedlings under artificial inoculation conditions (Feng *et al.*, 2017). Secondary hosts such as weeds, self-perpetuated rice, and rice from rice stubbles of the previous crop play a significant role in initiating disease epidemics, particularly in tropical environments. However, the relative relevance of primary inoculum from these secondary hosts has not been quantified. Furthermore, the architecture of the crop canopy and the related microclimate influence the mobility of primary inoculum and disease dissemination. Crop canopy architecture depends on several factors such as crop growing method, amounts of fertilizers applied, and type of germplasm grown in that area (Singh and Srivastava, 2015).

The secondary spread of the disease depends mostly on running hyphae that develop from the initial lesions on the leaf's sheaths of the rice crop towards the upper parts, i.e., along with the tillers and leaves and across the adjacent plant units, i.e., the vertical and horizontal spread of the disease (Abbas *et al.*, 2019). The spread of mycelial strands and disease progress is speedy vertically in the greenhouse experiments, i.e., the hypha moves downward and upward from the inoculation place. However, in field conditions, the spread of mycelia strands and disease progress occurs horizontally. The lesion spreads and covers the entire leaf sheath and tillers (Abbas *et al.*, 2021). Finally, the tillers become soft, rupture, and lodging takes place. The lodging alters the canopy structure of rice crops, reduces the photosynthetic capability, and severely affects the total biomass of the rice crop and other vegetative and yield parameters. Also, lower percentages of filled spikelets are noted, which reduces the total seed weight. In addition, lodging prevents the transport of water and nutrients through the xylem and phloem; consequently, the grain filling is affected (Abbas *et al.*, 2021). In the tropic, secondary hosts such as weeds or rice regrowth from stubbles are responsible for initiating a disease epidemic.

As rice needs more water to grow, sclerotia can move from one field to another through irrigation (Qi *et*

al., 2017). Besides irrigation, rain and floods are also responsible for dispersing sclerotia to other fields and becoming a source of infection in rice fields. RSB is an aggregated disease compared to other plant diseases, and this aggregation phenomenon can be used to assess the disease resistance in rice cultivars. Besides, the severity and incidence of the disease are different in different environmental settings, regions, locations, and geographical regions. These variations in severity and incidence of this disease depend on host genotype, the virulence of the pathogen, the emergence of novel strains of the pathogen, soil features, plant environment, usage of fungicides, time, dose, and methods of fungicide application, cultural practices, and farmer preferences, for example, growing the same crop again and again (monocropping). The primary spread mechanism of sheath blight disease explains that the disease is highly aggregated compared to other plant diseases (Pin *et al.*, 2012). This aggregation of the disease is a central feature of RSB epidemics and a critical element in assessing resistance in rice crops. Recently pathogenic variability of *R. solani* has played a significant role in varying degrees of disease severity and incidence. Furthermore, plot-to-plot interaction is not a significant issue in RSB disease. Even under favorable conditions, the disease rarely exceeds one meter from the initial source (Abbas *et al.*, 2021). Furthermore, the onset of sclerotial formation depends on environmental signals such as nutrient deficiency, light intensity and quality, pH, temperature, antioxidant contents, and changes in aeration (Singh and Srivastava, 2015).

Materials and Methods

Cultural approach

Cultural management involves deviations in microclimatic conditions to reduce RSB severity. Soil solarization during May and June can reduce the soil-borne inoculum, and healthy seedlings can be achieved for transplantation. A high density of seed rates and seedlings cannot be encouraging because disease spreads rapidly. Likewise, close planting should be avoided, and sparse planting is recommended because sparse planting causes lower RSB disease occurrence. Besides, sparse planting produces fewer stems per meter square, more stems per hill, less no of tillers per hill, delayed tillering and heading stage, and ripening time. Besides, the submergence of crop and alternate wetting and drying is negatively correlated with the

disease and reduces the disease's progress. Likewise, an increase in the growth of rice cultivars by bioagents and control of the disease can be achieved under submerged conditions. Previous studies have shown that the square method of transplantation increases the leaf area index and dry matter production and results in optimum yield. However, disease incidence was also higher (Yang *et al.*, 2008). Burning of leftovers, stubbles, and deep summer plowing eliminates the weed hosts, thus reducing the disease of the RSB. Furthermore, bunds cleanings and keeping the field fallow for one year can reduce the inoculum density and control diseases. Besides, the disease can also be managed by organic amendments. For example, the RSB disease population is minimized by applying green organic manures such as *Sesbania aculeata*. Organic amendments with the green organic manure plants also reduced the incidence of RSB disease and significantly enhanced rice crop yield. Farmyard manure application also causes a significant reduction in disease severity. Organic fertilizers, including composts and animal manures, resulted in the high yield of rice and diseases like RSB disease, blast, and pests like hoppers, borers, and leaf folders reduced significantly. When comparing plots with organic manures to plots that received inorganic fertilizers, beneficial bioagents such as *Trichoderma* spp. were discovered in larger numbers. The suppression of the disease by organic amendments is due to volatile and non-volatile substances, decomposition, and multiplication of antagonists. Furthermore, inquiry on site-specific nutrient management between plots revealed that the RSB disease is a plant germplasm and nitrogen-dependent variable and a major yield-reducing factor in rice crops. It means that the disease severity intensifies with nitrogenous fertilizers application.

Varieties with taller stature, fewer tillers, and fewer leaves have nitrogenous contents and low yield losses due to lower lesions and disease index. Additionally, high doses of nitrogen can accelerate the disease incidence. Applying silicon to manage the disease is an effective strategy, especially in soil with low or limiting plant available silicon (Rodrigues *et al.*, 2003). That mechanical barrier is due to its polymerization and the release of phenolics, phytoalexins, and pathogenesis related proteins (Datnoff and Rodrigues, 2005). Furthermore, silicon deficiency makes the rice susceptible to RSB, and heavy nitrogen application reduces the silicon availability to the

crops (Rodrigues *et al.*, 2003). Moreover, the time of sowing should be considered because the incidence of the disease becomes more severe at the susceptible stages of plant growth when the conditions become favorable. Favourable environmental factors, soil conditions, and susceptible growth stages of the rice crops are accountable for the maximum activity of the pathogen. Therefore, changing sowing dates help in the avoidance of RSB disease. Besides, the judicious application of fungicides and the adoption of cultural practices can significantly reduce the disease severity (Srinivasachary *et al.*, 2011).

Breeding approach
Breeding cultivars resistant to RSB disease is the most eco-friendly, economical, and effective method. However, completely resistant cultivars against RSB disease have failed through conventional breeding methods. However, partial resistance to the disease has been achieved in some germplasms, and the resistance is controlled by multiple genes or certain chromosomal regions known as quantitative trait loci (QTLs) (Zuo *et al.*, 2014). As a result, identifying QTLs, mapping them, validating them, and then describing them could significantly accelerate the map-based or positional cloning of essential resistance genes, potentially assisting in developing sheath-blight-resistant rice cultivars. A quantitative trait locus (QTL) is a statistically significant relationship between allelic variation at a particular locus and a phenotypic attribute that shows continuous variation in a genetically segregating or changing population (St Clair, 2010). According to Sharma *et al.* (2009), QTLs on chromosome 1 directly impact RSB disease (RSB). The stability of identified QTLs and their potential for disease improvement through marker-assisted selection is indicated by the consistent results across the years (Sharma *et al.*, 2009). Moreover, physiological resistance is related to functions that can decrease the efficiency of one or more infection stages of the RSB. Quantitative traits govern RSB; therefore, the development of RSB resistant rice cultivars is complicated through traditional breeding strategies. A few studies have found that pyramiding QTLs by marker-assisted selection can help rice cultivars become more resistant to RSB. However, when QTLs interact with other genetic backgrounds, difficulties develop. As a result, not all QTLs work correctly in different rice varieties, making pyramiding and using QTLs to combat RSB disease more difficult. Hence, few shreds of evidence show better disease

management by pyramiding two or more QTLs disease-resistant genes. As there is no resistant variety available that exhibit resistance against RSB disease. There is an absence of the desired resistance level in the cultivated and wild rice species; therefore, managing the disease has become difficult. The non-race-specific resistance QTL factors only provide resistance to the disease, and no R genes corresponding to the disease have been discovered to date. Therefore, it is essential to identify alternative methods for developing broad-spectrum and robust resistance to the disease. Genetic engineering is a promising tool that augments disease resistance (Chen *et al.*, 2019; Karmakar *et al.*, 2017). Besides, the desired resistance level is absent, and fungicides have considerable noxious effects on the soil microbes, the environment, and human health. Besides, reducing the genetic diversity of rice cultivars due to artificial selection during rice domestication further makes rice vulnerable to RSB. In this context, Genetic engineering, i.e., The transgenic technique, which broadens genetic variety by introducing novel genes QTLs from genetically diverse lines into agronomically better rice lines, is promising. RSB disease has complex traits, and phenotyping should be done accurately, which is very important for cloning and mapping QTLs for resistance to the disease. Moreover, the phenotype of RSB disease is predisposed by plant height, heading date, plant density, and environmental factors such as temperature, humidity, pH, and even soil fertility. Therefore, for evaluating the RSB greenhouse, experiments are conducted to reduce the effects of the factors mentioned above and obtain reliable data. On the other hand, the majority of the QTLs were discovered in the field. The traditional genetic linkage approach for identifying QTLs/Genes takes a long time and requires biparental population mapping and genotyping. The genome-wide association study (GWAS) has recently been utilized to identify broader genetic differences for complex diseases such as RSB. However, no QTL for RSB resistance has been defined adequately to date.

Transgenic approach
Aside from crop rotation and integrated pest control, developing resistant rice cultivars, either through genetic engineering or conventional breeding, would be one of the best alternatives for sustainable agriculture (Willocquet *et al.*, 2004). Transgenic plants are becoming more and more popular as a means of expressing a gene of interest for a certain

characteristic. Due to a shortage of resistant rice germplasm against RSB, traditional breeding for this characteristic has yet to be successful. Recently, many putative fungal disease resistance genes have been found and characterized in rice and other plant species. The advent of excellent genetic engineering methods for various rice genotypes opens up new possibilities for studying the effects of essential defense genes on their expression, such as pathogenesis-related (PR) genes with antifungal activity.

Several antifungal genes of plant origin, antimicrobial genes, master switch genes of defensive response, and genes capable of blocking the fungal enzyme and virulence factor were used to create rice lines with increased resistance to the sheath blight fungus. Multi-signal system coordination signal transduction pathways affect *R. solani* resistance (Willocquet *et al.*, 2004). Hebiba, a Jasmonic acid (JA) deficient rice mutant, was more susceptible to RSB, confirming JA's role in resistance. On *R. solani*-infected rice plants, the LOX gene transcript is enhanced. *WRKY30* overexpression in transgenic rice plants increases RSB tolerance through activating jasmonate related genes and endogenous JA accumulation. *WRKY80* confers RSB tolerance via activating *WRKY4* and *JA/ET*. Recent investigations link JA and phenylpropanoid metabolism to RSB disease resistance (Abbas *et al.*, 2021). Hence, the *WRKY* genes, are engaged in plant defensive responses and responsible for various biological processes, including growth, development, stress, embryogenesis, and resistance to RSB disease, have been found. Evidence suggests ethylene may have a function in *R. solani* disease response signaling. Transgenic rice overexpressing an ethylene biosynthetic gene increases *PR1b* and *PR5* expression and RSB resistance. Cyanide, a harmful byproduct of ethylene production, may also have improved resistance. On the other hand, increased expression of the systemic acquired resistance (SAR) marker gene *PR1b* and the RSB disease indicator gene *PBZ1* suggested that the salicyclic acid (SA) mediated pathway was involved in the development of the rice disease. It is well accepted that inducing the SAR pathway leads to the activation of the PR genes. At various periods during RSB infection, six *PR* genes (*PR3*, *PR5*, *PR9*, *PR10*, *PR12*, and *PR13*) and the PAL gene were activated in rice, suggesting the participation of SAR activation.

Datta *et al.* (2000; 2001; 2002) have shown resistance to RSB disease. Single *PR* gene is not providing efficient resistance against RSB disease. Therefore, combining two *PR* genes can confer a higher level of RSB resistance. For example, the genes for barley chitinase and barley-1, 3-glucanases, maize ribosome-inactivating gene *MOD1* and rice basic chitinases gene *RCH10*, *CHI11* and thaumatin-like protein, rice chitinases (*CHI11*) and tobacco-1, 3-glucanases (*GLUC*), rice chitinases gene (*OsCHI11*), and Arabidopsis This combination demonstrated a significant level of disease resistance (Karmakar *et al.*, 2017). Salicylic acid, benzothiadiazole, acetylsalicylic acid, DL-gamma amino n butyric acid, gamma amino butyric acid, amino-iso-butyric acid, indole-3-pyruvic acid, indole-3-acetic acid (IAA), indole-3-butyric acid, indole-3-butyric acid, indole-3-butyric acid (IBA) Resistance is also induced in rice crops by nicotinic acid, isonicotinic acid, DL norvaline, propionic acid, benzoic acid, para-aminobenzoic acid, and zinc sulfate (Sood *et al.*, 2013). The combination of these chemicals was more effective than they applied singly. For example, salicylic acid coupled with gamma amino butyric acid was more effective than control plants in reducing lesion length. Some rice cultivars produce chitinase enzymes, which are major factors contributing to resistance against RSB disease. In the moderate resistance cultivars, chitinase activity can be detected 24 hours post-inoculation, whereas in the susceptible cultivars, chitinase activities can be detected 36 hours post-inoculation. Moreover, it was confirmed by western blot that the chitinases amount in the moderately resistant cultivars was greater than chitinases in the susceptible cultivars. In a study, chitinases and -1, 3-glucanases genes were genetically changed into 41 homozygous rice lines, and 92% of them were either moderately resistant or moderately vulnerable. The transformants were characterized by using molecular and functional approaches. Studies from 1995-2019 regarding genes and microRNAs involved in rice resistance against RSB have been reviewed previously (Singh *et al.*, 2019). Recent studies on the genes/microRNAs involved in rice resistance against RSB are shown in Table 1.

Host-induced gene silencing and gene editing approach
Currently, host-induced gene silencing (HIGS) is used whereby the host produces dsRNA that targets pathogen genes and is processed into siRNAs. Upon infection, the pathogen procured these siRNAs. As a result, its target genes are silenced. HD-RNAi has been successfully applied again to viral, parasitic

Table 1: *Recent reports of resistant rice cultivars generated using defense-related genes and/or microRNAs.*

Genes/ Others	Type	Function	Method	Transformation system	References
OsACBP5	Acyl-CoA-binding proteins	Enhanced resistance	Overexpression	*Agrobacterium*-mediated	(Panthapulakkal Narayanan *et al.*, 2020)
SiR109944	Small interfering RNA	Suppresses plant immunity	Overexpression	Biolistic method	(Qiao *et al.*, 2020)
Snakin-1	Snakin-1 peptide	Antifungal activity	Overexpression	*Agrobacterium*-mediated	(Das *et al.*, 2021)
Pi54	Resistance gene	Enhanced resistance	Overexpression	Gene gun mediated	(Singh *et al.*, 2020)
WRKY TFs	Transcription factors	Enhanced resistance	Overexpression	Agrobacterium-mediated	(Kouzai *et al.*, 2020)
OsMESL	Methyl esterase-like	Enhanced resistance	Repressed expression	Protoplast transformation	(Lin, 2021)
P2K1/DORN1	Purinoceptor	Enhanced resistance	Overexpression	Protoplast transformation	(Kumar *et al.*, 2020)
OsGSTU5	Glutathione-*S* transferase (*GST*)	Enhanced resistance	Overexpression	Agrobacterium-mediated	(Tiwari *et al.*, 2020)

plants, pests, and fungi. The benefit of this technique is that it allows pathogen genes to be silenced without introducing new proteins into food and food products. HD-RNAi has been utilized to treat mildew, rust, and wilting diseases in crops so far. The fungal infection level of RSB was significantly lower in transgenic rice lines. The development of transgenic lines is essential to prevent the rice from RSB disease (Tiwari *et al.*, 2017). Thanks to recent advances in gene editing technology, pathogenesis-related genes can now be targeted. CRISPR/Cas9 gene editing has recently been utilized to prevent RSB disease infestation (Gao *et al.*, 2018). To obtain sugar molecules for nourishment, the pathogen *R. solani* activates the *OsSWEET11* sugar transporter in infected rice tissues. However, it was discovered that when the sugar transporter *OsSWEET11* was knocked out using CRISPR-Cas9, rice crops became less sensitive than *OsSWEET11* overexpressing wild-type plants (Gao *et al.*, 2018).

Host resistance

Host plant resistance plays a substantial role in disease management for sustainable rice production. It is eco-friendly, and no extra charges are needed to introduce disease-resistant cultivars. In the breeding programs, the hunt for disease-resistant cultivars is an essential requirement. Previous studies have found that rice germplasm had a high degree of resistance or lack of immunity against RSB. Breeders are continuously trying to develop resistant or tolerant cultivars against RSB. Still, no success has been achieved due to the lack of resistant varieties that could be donors for the cultivated varieties. Though several cultivars have been found with diversified resistance levels, no variety has shown immunity to RSB (Zou *et al.*, 2000). Screening of resistant varieties against RSB is still ongoing. Landraces, cultivars, advanced breeding lines, and local accessions were also used to find sources of resistance to the RSB disease and/ or multiple illnesses. Even the resistance to the RSB disease in the cultivable varieties (cultivars) varies from susceptible to moderate resistance, and the yield losses were found to be 30% in the susceptible cultivars. In contrast, in the moderate resistance, the losses were 8% (Groth, 2008). Furthermore, resistance among cultivars also depends on the criteria applied for disease assessment.

Overexpression of chitinase and 1, 3-glucanase in rice can protect *R. solani* anastomosis groups from damage (Sripriya *et al.*, 2017). Similarly, the gene *OsACS2*, which codes for an enzyme involved in ethylene biosynthesis, boosts endogenous ethylene production and enhances RSB resistance (Helliwell *et al.*, 2013). Overexpression of the gene *OsOSM1*, which encodes a protein from the pathogenesis-related protein five families, improved rice crop resistance to RSB (Xue *et al.*, 2016). When genes *OsCHI11* and *AtNPR* were pyramided in the rice lines, they improved the resistance against RSB more than in single-gene transformants lines. However, the gene that confers substantial resistance in rice varieties has been found (Karmakar *et al.*, 2017). The rice sugar transporter gene, *OsSWEET11*, is involved in the pathophysiology of RSB. Upon infection by RSB, the gene expression in the leaves increased. When this gene was mutated, and transgenic rice plants were less susceptible to RSB, it was found that transgenic lines had become more susceptible than wild-type controls when the gene was overexpressed. However, the rice yield was reduced in mutant and overexpressed transgenic lines.

In conclusion, the transgenic lines resistant to RSB can be obtained by manipulating the expression of genes involved in the pathogenesis of the RSB so that disease incidence reduces and a high yield is obtained (Gao *et al.*, 2018).

Chemical control

Chemicals have controlled RSB disease at the field level, as reported by various researchers (Peng *et al.*, 2014). Foliar application of multiple fungicides has successfully managed the RSB disease or its pathogen under field and greenhouse conditions, but their efficacy against sclerotial germination was very low (Uppala and Zhou, 2018). Ideal fungicides need to be multisided, inhibiting sclerotial germination and hyphal growth and reducing disease spread. At present, systemic fungicides are widely used to manage sheath blight disease and with certain non-systemic fungicides. Notwithstanding, the pathogen gains resistance to these fungicides and demands the development of novel fungicides and screening of certain common fungicides before employing integrated disease management (IDM). Fungicides such as carbendazim, hexaconazole, propiconazole, thifluzamide and difenoconazole have been applied to control the RSB in different world regions. These earlier fungicides against RSB were copper, organic mercury, and organo-arsenic based. Fungicides such as carbendazim, fenpropimorph, fludoxaniiil, iprodione, pencycuron, propiconazole, and tolclofos methyl were also found to be effective against the RSB under the greenhouse and field conditions (Groth, 2008). Fungicides should not be applied in the same field or plot repeatedly; otherwise, their efficacy against the RSB is reduced due to the re-emergence of a novel pathogen strain. Besides, repeated usage of fungicides makes sclerotia resistant. Consequently, the germination rate of sclerotia will be increased; as a result, causing severe infection. The fungicides such as carbendazim and mancozeb are applied at

different plant developmental stages and found to be effective against disease development. The most popular strobilurin fungicides are azoxystrobin, trifloxystrobin, and pyraclostrobin. These fungicides move systemically through the vascular bundles of the plants. Furthermore, the overuse of fungicides with a single mode of action has resulted in the generation of strobilurin-resistant *R. solani* AG-1 IA isolates. The first strobilurin-resistant isolates of *R. solani* were reported in the United States in 2011, and fungicidal resistance quickly spread, depriving rice producers of a vital tool for controlling RSB disease. As a result, finding effective fungicides with a different mode of action is critical (Uppala and Zhou, 2018). Recent reports about the usage of fungicides against the RSB are shown in Table 2.

Phytochemicals

Numerous phytochemicals, such as steroids, tannins, flavonoids and alkaloids, have demonstrated antimicrobial activity against plant diseases (Persaud *et al.*, 2019). This phytochemical's range of fungicidal activity was from 33-100% and was varied with tested pathogens (Lee *et al.*, 2001). Neem formulations have been broadly used to manage RSB disease and improve grain yield. Field application of neem formulation at the rate of 4.5 mL/L effectively reduced RSB and increased yield (Kandhari and Devkumar, 2003). Greenhouse studies include applying stabilized and saturated fractions of neem oil, reducing the disease incidence and the number of infected tillers. Similarly, phytochemicals from the plants such as *O. wodier, P. glabra, L. alba,* and *O. sanctum* inhibited 70-80% of mycelial growth and sporulation of RSB disease pathogen under in vitro conditions. The extracts from plants (*O. wodier* and *O. sanctum*) were more effective in diminishing the severity of RSB than control plants (Karthikeyan and Chandrasekaran, 2007). Similarly, a product Biotos from *Gaultheria* spp. effectively prevented the disease severity and

Table 2: *Recent reports regarding the usage of fungicides against RSB disease.*

Fungicides	Experiment	Spray in fields	Best conc. *in-vitro*	Reference
β-Carboline Alkaloids	*In-vitro*	none	25.56 µg/mL	(Zeng *et al.,* 2020)
75% tebuconazole. azoxystrobin WG, 75% Trifloxystrobin. tebuconazole WG and 24% thiluzamide SC	*In-vivo*	20 g/667 m²	none	(Huang *et al.,* 2020)
BT emulsifiable concentrate	*In-vitro/ In-vivo*	1,000 to 2,000 mg/liter	6 mg/liter	(Maliang *et al.,*)
Polydispersed Ag NP	*In-vitro*	none	2.5–10 µg/mL	(Kora *et al.,* 2020)
Azomethines	*In-vitro*	none	11.9 to 22.4 µg/ml	(Siddhartha *et al.,* 2020)
Phenazine	*In-vitro*	none	100 µg/ml	(Karmegham *et al.,* 2020)

increased grain yield. Biotos was more effective against RSB than Achook and Tricure. Plant extracts such as *A. sativum*, *P. juliflora*, *G. pentaphylla*, *L. aspera*, and *V. negundo* were also effective against the disease. Similarly, palmarosa oil at the rate of 0.1% concentration effectively suppressed the mycelia growth and inhibited the sclerotial germinations of the pathogen. Recently extracts of lemongrass, thick leaf thyme, marigold, and clove were applied at the rate of 15% reduced mycelial growth of RSB pathogen. Rice seeds were treated with extracts of either fresh or dried leaves of *C. odorata*, and rice crops were sprayed in another trial. Under controlled and semi-field circumstances, seed treatment and spraying significantly reduced the sheath blight disease by 68 percent (Persaud *et al.*, 2019).

Biological control

Nowadays, due to public concerns about the chemicals and their environmental issues, researchers are focusing on biocontrol agents and, to date, fruitful stories concerning the use of biological agents against plant pathogens. The utilization of biocontrol agents though gaining popularity; however, in the rice scenario, its usage is still limited. This is due to some ground realities. The rice is hydrophytes and needs saturated conditions. Therefore, the biocontrol agents' survival, growth, and establishment are challenging. However, disease control can be feasible only when the biological agents adapt to the rice ecosystem, survive, establish, increase, manage the disease, and promote plant growth. Aside from these characteristics, biocontrol agents should induce disease resistance to the RSB. Many bacterial and fungal antagonists have been isolated from the rice fields and successfully managed the disease. Mew and Rosales (1986) provided the first report on isolating bacterial strains from the rhizosphere of IRRI rice fields in the Philippines to treat RSB disease. Bacterial biocontrol agents colonized plant sections, protecting them against pathogenic agents and preventing the spread of disease (Van Loon *et al.*, 1998). Plant growth-promoting rhizobacteria (PGPR) are BCAs that enhance plant development while suppressing pathogens (PGPR). Various PGPR has also been reported from the rice, which managed plant diseases and enhanced rice crops' growth and yield. In addition, microorganisms isolated from rice seeds and the rice environment successfully controlled plant diseases while boosting development and productivity. *Pseudomonas* spp., *Actinomycetes,* and

Bacillus spp. are widely used to control RSB (Van *et al,.* 2001; Nandakumar *et al.*, 2001).

Fungal biocontrol agents have been investigated intensively to manage RSB disease. These BCAs were screened and isolated from the locations or agroclimatic zones where the pathogen was active and found to be more effective than BCAs isolated from other sites or agroclimatic zones. Many BCAs have been isolated from the rice fields and found to suppress the RSB disease. Those fungal biocontrol agents belonged to genera, i.e., *Trichoderma* (*Tr.*) (*T. viride*, *T. harzianum*, and *T. koningii*), *Aspergillus*, *Gliocladium*, *Chaetomium,* and *Streptoverticillium* were found to suppress the RSB disease in previous studies. However, among these fungal BCAs, genera *Trichoderma* and *Gliocladium* are widely used to manage RSB. *Trichoderma* spp. is effective against RSB disease and effective against several plant diseases. Foliar application of these BCAs was more effective in suppressing the RSB. Among these BCAs, with the usage of *T. harzianum* high yield and grain weight were achieved with the recommended dose for the BCAs 4 or 8g/L. The overall combination of foliar spray, root dipping, and soil treatment effectively suppresses the RSB (Naeimi *et al.*, 2010; Jayaprakashvel *et al.*, 2010).

Mycoviruses

Most mycoviruses are found to be associated with latent infection in their host fungi. They are transmitted naturally by hyphal anastomosis and heterokaryosis, and that transmission is called lateral transmission. Some of them are transmitted through spores called serial transmission. Fungi typically exchange cytoplasm during their long-life cycles, and most fungi produce sexual and asexual spores. Mycoviruses, efficiently use these ways and transmit to another host. Though they donot have a cellular phase, they seem to be successfully present in almost all the fungal taxa, especially in the filamentous group of fungi. Though these viruses have been discovered recently, phylogenetic analysis revealed that the mycoviruses are of ancient origin (Ghabrial and Suzuki, 2009). Many dsRNA of mycoviral origin was recovered from the cultural filtrates of *Penicillium* spp. Hence, there was a motivation for further search for fungal viruses worldwide. The myco-virology, as compared to other virology disciplines, was novel. Mycoviruses cause little or no obvious symptoms in their fungal hosts, so many mycologists discard those

malformed fungal colonies showing abnormalities. Therefore, we can see a delay in mycoviruses research compared to research on other viruses (Pearson *et al.*, 2009). The double-stranded RNA (dsRNA) viruses have the majority in the mycoviruses category. Recently ssRNA and spherical-shaped ssDNA viruses were discovered (Liu *et al.*, 2014). Some of the mycoviruses are covered in rigid particles, and some do not have typical virus morphology. As animal and plant viruses are deleterious to animals' and plants' health, mycoviruses do not show symptoms on fungi, and most have beneficial effects. However, some of them are deleterious and change the phenotype of fungi and morphology; as a result, those altered shape fungi cannot infect plants because their virulence has decreased. Technically the decrease in virulence is called hypovirulence. Some of the mycoviruses become very severe on their host and increase hypervirulence (Lin *et al.*, 2012). The first successful biological control was the usage of Cryphonectria hypovirus 1 (ssRNA mycovirus) to manage chestnut blight caused by *Cryphonectria parasitica* (Nuss, 2005). The research on mycoviruses has revealed that these mycoviruses, upon infecting plant pathogens, make the plant pathogen beneficial to plants. The novel discoveries of mycoviruses derive us from thinking that these mycoviruses can change the trophic mode of several fungal plant pathogens and make them beneficial for crops. Therefore, there is a need to discover mycoviruses of RSB disease that can change the trophic mode of *R. solani,* and might be few strains of *R. solani* would be beneficial to rice. In conclusion, with the judicious use of these mycoviruses, crop health can be improved. In conclusion, the study on mycoviruses associated with RSB disease and its pathogen, *R. solani* is in the preliminary stage. More research is required to apply these mycoviruses against rice diseases under greenhouse and field conditions.

Mechanism of action of biological control agents
Researchers have proposed several biocontrol strategies for the successful management of RSB. Competition for nutrition and space, antibiosis, parasitism, and the generation of systemic resistance in the host tissue are only a few examples (Nandakumar *et al.*, 2001) and the release of volatile compounds. A good biocontrol agent (BCA) contains attributes that often work collectively for controlling the disease (Figure 2). For example, the ability of BCAs to colonize and compete is related to BCAs how to penetrate hosts and pathogens, the exudation of specific enzymes, the

capability to induce resistance and population density maintenance, volatile compound secretions, and upon interaction, active metabolites production with plants. Competition is also called niche overlap when two microbial populations simultaneously demand the same resource. Competition between the pathogen and BCAs can be for space or nutrients such as carbohydrates, nitrogen, or oxygen. The BCAs should be sufficient at the correct time and location near the pathogen to suppress its pathogenic activities. Space competition means some bacterial BCAs produce an extracellular polysaccharide capsule that promotes adhesion to the plants (Compant *et al.*, 2005).
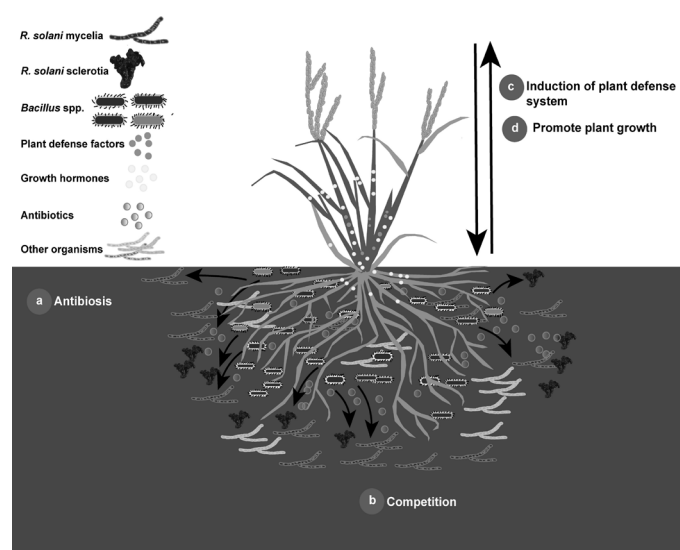
Figure 2: *Mode of action of BCAs against RSB pathogen (R. solani): For example, Bacillus spp. are applied to rice for biological control of RSB where they act via a range of modes of action, but four modes of action are essential* **(a),** *Antibiosis by producing secondary metabolites such as antibiotics* **(b),** *Competition, i.e., competition for space and nutrients* **(c),** *Induce resistance in rice plants* **(d),** *They promote rice growth by secreting growth hormones.*

The other mechanism of action of BCAs is antibiosis. BCAs produce specific or non-specific metabolites, lytic agents, or enzymes. Using these substances, the BCAs inhibit or destroy the pathogen. In antibiosis, the BCAs produce antibiotics, which may be volatile or non-volatile substances that generally operate at a concentration of less than ten ppm. Most of the BCAs, when finding carbon (substrate), begin to produce antibiotics. This strategy prevents other microbes and uses the remaining amount of carbon. Antibiotics must be created in sufficient amounts in situ at the precise interaction time with the pathogen to be effective. For example, bacteriocin is an antibiotic that creates pores in the pathogen's membrane and causes cellular contents leakage, and finally, the pathogen dies. Likewise, another antibiotic called pyrrolnitrin

produced by *P. cepacia* can reduce the growth of the pathogen. Besides, plants protect themselves against pathogens by releasing phytoalexins, lignifying plant cell walls, creating lytic enzymes, and expressing various pathogenesis-related proteins. BCAs can be used to demonstrate induced resistance in a region apart from plant components, and locally induced resistance is simply the suppression of disease by dead cells. For example, *Tr. erinaceum* and *B. subtilis* induced resistance against sheath blight disease (Swain *et al.*, 2019). Also, antagonists suppress pathogens by releasing VOC. These molecules are characterized by low molecular weight, high vapour pressure, and low water solubility. Therefore, they become volatile as a gas. Many antagonists release obnoxious odors that inhibit the growth of the pathogen in close storage conditions. For example, in many cases, Ethylene is produced by the antagonist's metabolic actions. For instance, *bacillomyxin* L and *fengycin* A compounds are emitted by *B. velezensis* Strain G34 inhibited mycelial growth of many fungal pathogens, including R. solani, the pathogen of RSB disease (Lim *et al.*, 2017). Parasitism is a frequent mechanism in which antagonists lyse or destroy the pathogen's structure or propagules. This mechanism works mainly against soil-borne and foliar pathogens.

Conclusions and Recommendations

In conclusion, RSB has a broad host range; the absence of resistance genes in rice crops and lack of appropriate management practices can cause outbreaks. So far, the most common management strategy is the extensive application of fungicides, which negatively impact the environment, humans, and other organisms. Moreover, their continuous usage has caused soil, water, and food resources to be contaminated. Furthermore, resistance to pathogens has also emerged due to the prolonged use of fungicides. Hence, the more appropriate RSB management method is to apply eco-friendly natural fungicides and biological agents. Besides, cultural practices, including an excellent plant to plant and row to row distance, removing infected plant debris, and non-host crop rotation, will aid in restricting the development of RSB. Moreover, using tolerant cultivars and transgenic lines is another sustainable approach. To uncover resistance genes and elucidate pathogenicity mechanisms, more QTL analysis, and transcriptome investigations are needed. Biotechnological approaches, including developing lines through gene editing and gene silencing, are promising methods to inhibit the RSB. Studying these lines' productivity and disease response under field conditions will be fascinating, especially in RSB-affected locations. Furthermore, there is a need to explore the pathogenicity-related genes to understand the mechanism of infection by RSB disease. Furthermore, CRISPR-mediated gene-editing technologies can effectively manage RSB. Likewise, early RSB detection using Unmanned Aerial Systems and forecasting models can minimize the disease spread and management costs.

Novelty Statement

The current paper summarizes updated knowledge regarding rice sheath blight with special focus on management plans.

Author's Contribution

Aqleem Abbas: Prepared the outline and wrote introduction

Mustansar Mubeen: Finalize the figures and mycoviruses part of the manuscript.

Yasir Iftikhar: Finalize the tables and biological control part of the manuscript.

Qaiser Shakeel: Plagiarism check, corrections, language editing and wrote culture management methods

Hafiz M. Imran Irshad: Wrote breeding and transgenic approaches

Maria del Carmen Zuñiga Romano: Gene silencing and gene editing and host resistance approaches.

Sarfaraz Hussain: Chemicals and phytochemical approaches.

Conflicts of interest
The authors have declared no conflict of interest.

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