A COMPREHENSIVE OVERVIEW ON SHEATH BLIGHT DISEASE OF RICE AND ITS MANAGEMENT

CHAUDHARY[1)*] Sorabh, Sushma SAGAR[2)] and Mehi LAL[1)]

[1)]ICAR-Central Potato Research Institute, Regional Station, Modipuram, Meerut-250 110, UP, India

[2)]Department of Agricultural Biotechnology, SVP University of Agriculture & Technology, Modipuram, Meerut-250 110, UP, India

**Corresponding author e-mail: sorabh.gene@gmail.com*

Abstract: Rice sheath blight disease, caused by *Rhizoctonia solani* Kühn (teleomorph *Thanatephorus cucumeris* [Frank] Donk), is a serious threat in rice growing countries. *R. solani* is a soil borne necrotic fungus that survives in plant debris as sclerotia, and is able to infect plants belonging to more than 27 plant families including economic important monocots and dicots. Management of sheath blight requires an integrated strategy based on the population structure, correct identification of pathogen at early stage and molecular aspects of rice defence responses against *R. solani.* This review summarizes elaborative and updated knowledge on taxonomic classification of the pathogen, disease etiology and economics, molecular aspects of *R. solani* pathogenicity and strategies for detection and diagnosis of the disease. Up to date information for management of sheath blight using various strategies are discussed Specifically, the effects of popular cultural practices influencing sheath blight incidence, various chemical fungicides, biological control individually and their combined effect on sheath blight are presented. Summarized and updated information of various biotechnological approaches *viz.,* genetic transformation, host-delivered RNAi technology, genome-editing tools and nanotechnological approaches to enhance resistance in rice against sheath blight is mentioned in this review.

Keywords: Sheath blight, *R. solani*, chemical control, Biocontrol, Rice transgenic, RNAi

INTRODUCTION

Rice (*Oryza sativa* L.) belongs to the family Poaceae, is one of the three major food crops of the world and form the staple diet of about half of the world's population. The world production of rice has been estimated to be at the extent of 769.6 million tons and the area underneath rice cultivation is estimated to be around 167.2 million hectare (FAOSTAT, 2018). Asia is the leader in rice production, accounting for about 90% of the world's production. Globally, India ranks first in rice acreage and second in rice production after China and it contributes 21.5% of global rice production. India is one of the leading exporters of rice, particularly basmati rice. The world population is increasing exponentially, simultaneously leading to reduction in cultivable lands, decreasing water levels and climatic change becoming major issues that must be addressed by researchers. To fulfil the rice requirement globally, it is estimated that about 114 million tons of extra milled rice desires to be produced by 2035, which is equal to an overall increase of 26% in the next 25 years (Kumar et al., 2013). At present, rice productivity has been increased four times from the past five decades that made possible by the adoption of semi-dwarf high-yielding varieties

(HYV) with applying modern agricultural practices. Rice cultivation is often subjected to various biotic stresses of which diseases like blast, sheath blight, stem rot, and bacterial blight are the importance ones, of these, rice sheath blight is an important fungal disease of rice (Zheng et al., 2013). Sheath blight occurs throughout temperate and tropical production areas and is most prominent where rice is grown under intense production system. The disease was first reported from Japan in 1910 and is referred as "oriental leaf and sheath blight" (Miyake, 1910). In India, this disease was initially recorded from Gurudashpur, Punjab (Parace and Chahal, 1963) and later it was reported from Uttar Pradesh (Kohli, 1966). Sheath blight is a crucial soil-borne fungal disease causing considerable yield loss 25-50% from Philippines, 20-50% from Japan and 5.2-50% from India (Naidu, 1992). Cultivar "Mahsuri" suffered as much as 69% reduction in grain yield due to sheath blight (Sinha and Prasad, 2008). Every year, the blight causes up to a 50% decrease in the rice yield if the disease reaches the flag leaves under favourable conditions around the world in susceptible cultivars when all the leaf sheaths and leaf blades are infected (Zheng et al., 2013; Shu et al., 2015).

The Pathogen & Taxonomy: The causal agent of sheath blight has been reported for the first time by Vano (1915) as *Pellicularia sasakii* (Shirai) S. Ito (Hashiba et al., 1972). It has also been reported in the literature as *Corticium sasakii* (Shirai) Matsumoto, *C. vagum* Berk. & Curt., and *Hypochnus sasakii* shirai (Lee and Rush, 1983; Ogoshi, 1987). Researchers now generally accept *Rhizoctonia solani* (Kühn) AG1 IA, perfect stage *Thanatephorus cucuneris* (Frank) Donk as the infectious agent of sheath blight.

The genus concept in *Rhizoctonia* was initially described by De Candolle in 1815 (Sneh et al., 1991). The foremost vital species of *Rhizoctonia*, *R. solani* was described by Julius Kühn on potato in 1858 and is the most extensively distributed and destructive species of *Rhizoctonia* (Ogoshi, 1996). The telomorph of *R. solani, Thanatephorus cucumeris* is classified in kingdom Fungi; subkingdom Eumycota; phylum Basidiomycota; class Heterobasidio-mycetes; order Ceratobasidiales; and family Ceratobasidiaceae (Webster and Weber, 2007). *R. solani* is a complex of genetically distinct groups of fungi with more than 100 species; having very diverse life histories (Anderson, 1982; Adams, 1988; Binder et al., 2005) that attack all known crops and horticulture species. *R. solani* AG1 isolates containing three subgroups including IA, IB, IC based on the size and shape of sclerotia and DNA base sequence homology (Sneh et al., 1991). Among *R. solani* AG1, the subgroup AG1 IA is one of the predominant causal agent of sheath blight from rice growing regions worldwide (Taheri et al., 2007; Bernardes-De-Assis et al., 2009; Gonzalez-Vera et al., 2010).

Taxonomic Grouping: The classification of genus *Rhizoctonia* founds complicated due to unavailability of specific characteristics, the classical intraspecies grouping of *R. solani* and other *Rhizoctonia* species was performed on the basis of affinity for hyphal fusion, *i.e.* anastomosis (Parmeter et al., 1969; Parmeter and Whitney, 1970; Ogoshi et al.,1984). Based on their hyphal anastomosis, the species complex has been divided in to various homogeneous groups. *R. solani* isolates have been divided into 14 AGs designated as AG1 to AG13 and a bridging isolate (BI) group (Carling et al., 2002). AGs are further subdivided into intraspecific groups

(ISGs) based on cultural morphology, nutritional requirements, temperature effect on growth, host specificity, frequency of hyphal anastomosis, and pathogenicity (Sneh et al., 1991). The interaction scale, such as perfect fusion, imperfect fusion, contact fusion and no fusion (Yang and Li, 2012), led anastomosis to categorize in four group's *viz.* C0- C3, as follows (Carling, 1996).

C0: No reaction. This reaction occurs between different AGs.

C1: Wall contact between hyphae is apparent, but both wall penetration and membrane contact do not occur; occasionally one or both anastomosing cells and adjacent cells die. This reaction occurs between different AGs or in the same AGs.

C2: Wall connection is obvious, but membrane contact is uncertain; anastomosing and adjacent cells always die. This reaction occurs in same AGs, but not between different VCPs.

C3: Walls fuse; membranes fuse, accompanied with protoplasm connection; anastomosis point frequently is not obvious; diameter of anastomosis point is equal or nearly equal hyphal diameter; anastomosing cells and adjacent cells may die, but generally do not. This reaction occurs in the same AGs, same vegetative compatibility populations (VCPs) and the same isolate.

The members of the same AG group represent ≥50 % frequency for hyphal fusion (*i.e.* from C3 to C1 reaction), except non-self-anastomosing isolates (Hyakumachi and Ui, 1988), while there occurs low frequency ≤30 % or no fusion among members of different AG (*i.e.* C0 reaction). On the other hand, the most reliable and widely accepted molecular biology has observed to be crucial and undetectable module towards determining the appropriate classification and grouping of organisms on the basis of genetic information and evolutionary base (Hebert and Gregory, 2005). Though molecular biology involves advanced tools to determine taxonomical relatedness, it concurrently supports classical groupings of organisms and was observed in the case of *R. solani,* as molecular markers based clustering as well as percent sequence similarity found supportive of the AGs and subgroups based on hyphal fusion anastomosis (Sharon et al., 2006).

Phenotypic Characteristics of *R. solani:* The young colonies may be nearly white but older colonies have some shades of brown on the media. However, any mycelia remaining permanently white or showing pigmentation other than any shade of brown are not considered as *R. solani* (Palo, 1926). Hyphae diameter varies widely both within and among the isolates. The diameter of hyphae within a colony varies widely according to age and composition of media and temperature (Palo, 1926; Dahl, 1953). Parmeter and Whitney (1970) described that isolates of *R. solani* possess the characteristics as listed in **Table 1**. Hyphal width ranged from 4.75 to 7.43 µm of *R. solani* isolates from rice (Lal and Kandhari, 2009). Thind et al., (2008) reported that growth of *R. solani* isolates from rice was faster (~66.6%) than potato isolates. Hyphal width of isolates from both hosts varied from 7.2 to 12.1 µm and rice isolates formed larger sclerotia (approx. 1.5-2.0 mm in diameter) and of potato isolates produced smaller (approx. 0.5-1.0 mm diameter) sclerotia. Chaudhary et al., (2018) found that optimum temperature for sclerotia germination for *R. solani* AG1 IA isolates was between 20 to 30°C.

Table 1.
Cultural and morphological characteristics of *R. solani* (Source: Parmeter and Whitney 1970)

S. N.	Morphological Characteristics
1.	Pale to dark brown mycelium, fast growing of relatively large diameter with branching near the distal septum of the hyphal cells, nearly at right angles in older hyphae.
2.	Branch hyphae constriction at the point of origin.
3.	Formation of a septum in the branch near the point of origin.
4.	Production of monilioid cells, often called barrel-shaped cells or chlamydospores in chain or aggregate.
5.	Production of sclerotia of nearly uniform texture and varying in size and shape from small, round sclerotia often less than 1 mm in diameter, to thin crusts several centimeters across.
6.	Pathogenicity to a wide range of hosts, resulting in a variety of symptoms including damping-off, rotting of roots and other underground parts, and blighting of stems and leaves.
7.	Possession of a basidiomycetous perfect stage variously referred to as *Thanatephorus* spp.
8.	Possession of a prominent septal pore apparatus.
9.	Possession of multinucleate cells in actively growing hyphae.

Symptoms, disease development and epidemiology: The main symptoms are lesions on the sheaths, at the base of plants, or close to the water line. The size, shape and colour of the lesion may vary in different environmental conditions (Lee and Rush, 1983). Initially, the symptoms appears in the form of circular, oblong, green-gray, water- soaked spots about 1 cm long on the sheath of lower leaves, when plants are the late tillering or early inter node elongation stage. These lesions can expanded to approx. 1 cm in width and 2-3 cm in length and spreads rapidly to upper leaf sheath and leaf blades of the same or adjacent tillers, ultimately causing death of whole leaf, tiller and the plant. The centre of the lesions might become pale green to white that are surrounded by purple-brown margin (Webster and Gunnel, 1992). Reduction in chlorophyll content and loss of photosynthetically active leaf area due to the appearance of lesions are the some damage mechanisms triggers by sheath blight (Damodaram Nadu et al., 1981). Disease development is most rapid in the early healing and grain filling growth stage produce poorly filled grain, particularly in the lower portion of the panicle. Addition losses may result from increased lodging or reduced tillering due to death of the culm (Lee and Rush, 1983). Therefore, an accelerated senescence of tillers at these growth stages may lead to the destruction of potentially growing tillers (Savary and Mew, 1996). Under favourable climatic conditions of low sunlight, application of high humidity (> 95%) and warm temperature (28-32^{0}C) infection spread rapidly by means of runner hyphae to upper parts of the plant and to adjacent plants causing the corresponding leaf blade to wilt and die within a few days (Rush and Lee, 1992). The vertical development of disease is primarily dependent on the average day light time within the first 5 days followed by average RH and temperature (Gao, 1997). The difference in virulence pattern of *R. solani* isolates was observed under phytotron and glass house condition (Lal et al.,

2013). *R. solani* also produces toxin that induce characteristic symptoms on rice leaves, wilting of seedlings, and inhibited rice radicle growth. Incidence of sheath blight disease in rice fields is dependent on the method of planting and plant population density. Planting of rice seedlings far from the bund resulted in reduced sheath blight incidence since bunds have weed hosts of *R. solani*. Wu et al., (2014) reported that high nitrogen (N) rate and dense planting were conducive to sheath blight development. Application of silicon fertilizer under high N rate failed to suppress the disease epidemic, especially when silicon concentration of the soil is high or there is enough plant-available silicon.

Infection Process: The events occurring during the infection process of *R. solani* include adhesion, penetration, colonization and host reaction. In favourable conditions, the sclerotia are capable of germination and formation of mycelia. When the mycelia became contact with rice plant surface, they can grow and produce infection structure such as infection cushions and/or lobate appressoria which directly penetrate into the plant tissues by penetration pegs. After a peg has penetrated, it continues to grow between the cuticle and the epidermal wall. Finally the cuticle and epidermal wall are penetrated, and the infectious organs may extend growth into the cell lumen (Demirci and Döken, 1998). Penetration is established by using hydrostatic pressure, even though degrading enzymes such as cutinases (Baker and Bateman, 1978), pectinases (Bertagnolli et al.,1996; Jayasinghe et al., 2004) and xylanases (Peltonen, 1995), are most probably also involved in infection and penetration. The production of endopectinlyase has been reported to be associated with the tissue degradation in later stage of infection (Gonzãlez-Garcia et al., 2006).

The fungus may also utilize natural openings *viz.,* stomata on stems, cotyledons and leaves or lenticels as entry portals to plant tissues. Wounds can also be used as entry portals, but penetration usually does not occur solely via wounds. The growing hypha first spread and fill out the wound with densely packed hyphae before penetrating into healthy tissues without the formation of infection structure (Parmeter, 1970; Back et al., 2002). The penetration activities and lesion formation by *R. solani* are controlled by several factors. The growth of *R. solani* on the rice sheath surface and formation of infection structures were not controlled by a contact stimulus (Marshall and Rush, 1980). They made surface replicas of outer sheath surface of rice cultivars which were resistant or susceptible to the sheath blight pathogen. On resistant rice cultivars, only formation of lobate appressoria was observed; whereas on susceptible and intermediate cultivars, both infection cushions and lobate appressoria are formed (Marshall and Rush, 1980). Once infection occurs, secondary spread takes place through direct contact (role of basidiospores uncertain). Sclerotia may move from one field to another through irrigation water, and during movement, they may produce mycelia and secondary or tertiary sclerotia (IRRI, 1996).

Molecular aspect of pathogenicity: The molecular mechanism of disease resistance to *R. solani* and its pathogenicity are not fully understood (Chaudhary et al., 2016; Parween et al., 2019). However, isolates within same anastomosis group showed distinct pathological behaviour on the same host (Ghosh et al., 2019). To date, only a few studies have been conducted to investigate the genome-wide expression profile of

rice after *R. solani* infection and the molecular mechanism of pathogenicity. Venu et al., (2007) observed numerous up- and down-regulated rice genes after infection with *R. solani* using Serial Analysis of Gene Expression (SAGE) and microarray analysis. Zhao et al., (2008) originated fifty unique cDNA clones and assigned them to five functional categories that had not previously been identified as induced in response to pathogens. Silva et al., (2012) used whole-genome sequencing to identify a total of 333 nsSNPs in resistant lines that were absent in the susceptible group. More than 200 genes with selected nsSNPs were assigned to 42 categories based on gene family/gene ontology. Zheng et al., (2013) identified 25 candidate pathogen effectors based on their functionality and evolution, and three were validated to trigger crop defense responses with the draft genome sequence of *R. solani* AG1 IA that was assembled. Zhang et al., (2017) compared RNA-seq data from resistant and susceptible genotypes and suggested that pathogen response was regulated by multi-gene networks. *R. solani* activated multiple resistance pathways, and differentially expressed genes (DEGs) were involved in the defense response, signal transduction and other processes. A series of genes involved in disease-related metabolic pathways were significantly regulated and demonstrated that *R. solani* AG1 IA infection negatively affects the growth of rice. Zhang et al., (2018) focused on an analysis of gene co-expression in response to *R. solani* AG1 IA and identified gene modules within the networks through weighted gene co-expression network analysis (WGCNA). The results showed that different changes occurred in resistance and susceptible rice genotypes and that the modules in the two groups contain a number of candidate genes possibly involved in pathogenesis, such as the VQ protein. Recently, Ghosh et al., (2019) found that several gene families (orthogroups) have expanded or emerged in the Indian strains of *R. solani,* which were associated with their pathogenecity and aggressiveness. Among them, the presence of adenosine triphosphate (ATP) citrate lyase, MAPKKK encoding gene ZnF_C2HC type transcription factors genes encoding cell wall degradeing enzymes (CAZymes) along with peptidases and proteases under expanded category while mating locus protein, MADS-box transcription factor (rlmA), MDR transporter, ABC transporter gene family as well as fatty acid synthetase encoding genes under emerged categories was noteworthy. Furthermore, for better understanding of Rice- *R. solani* interaction, it is necessary to isolate and characterize the genes involved in pathogenicity as well as from the infected plants. However, inconvenience of robust genetic transformation protocols in *R. solani* remains a challenge for functional characterization of pathogenicity genes. Further, the cloning of resistance determinants from rice opens up the possibility to being resistance against *R. solani.*

Biochemical responses in *R. solani*- rice interaction: At the biotic stress response, plant defence mechanisms display a coordinated and integrated set of metabolic alterations in an attempt to adapt to stress. During interaction between rice and *R. solani* at the molecular level have shown that the glycolytic pathway is activated accompanied by the activation of the phenylpropanoid pathway (Danson et al., 2000; Nose et al., 2002). Specific glycolytic enzymes include phosphofructokinase (PFK), triosephosphate isomerase (TPI), phosphoglycerate kinase (PGK), enolase and

pyruvate kinase (PK) were found to be highly expressed in leaf sheaths of *R. solani*-infected rice plants (Mutuku and Nose, 2010; 2012). The systemic resistance induction process increases enzymatic activity of peroxidase (POX) and polyphenol oxidase (PPO) responsible for catalyzing lignin formation, and phenylalanine ammonia lyase (PAL) involved in the biosynthesis of phytoalexins and phenols. The levels of ROS (Reactive Oxygen Species) and the extent of oxidative damage depend largely upon the level of coordination among ROS-scavenging enzymes (Liang et al., 2003; Chaudhary et al., 2017). The pathogenesis-related proteins (PRPs) β-1, 3-glucanase and chitinase, enzymes that belong to PR-2 and PR-3 families, respectively (van Loon et al., 2006) have been related more often to Systemic acquired resistance (SAR) and sometimes to Induced systemic resistance (ISR). In transgenic rice plant, phenolic compounds and activity profile of some enzymes such as SOD, POX, APX and hydrolytic enzyme such as chitinase, *β*-glucosidase have shown to play active role in resistant mechanism of plant disease (Anushree et al., 2016). Sareena et al., (2006) studied defense response in transgenic Pusa Basmati1 (PB1) rice lines engineered with rice chitinase gene (*chi11*) against the *R. solani*. After inoculation, with *R. solani* enhanced production of phenylalanine ammonia lyase, peroxidase, and polyphenol-oxidase enzyme activities in resulted followed by reduced symptom development in transgenic rice lines in comparison to non-transgenic control plants. Sayari et al., (2014) investigated the role of NH-1, several PR genes, phenylalanine ammonia-lyase, and lipoxygenase in the defense responses of rice against *R. solani*.

Detection and diagnosis of sheath blight disease: Sheath blight diseases caused by *R. solani* are relatively difficult to diagnose by visual examination alone in the early stages of infection due to similarity of the symptoms with those caused by other disorders. Moreover, various *Rhizoctonia* species have been isolated from rice sheaths showing similar symptoms. *R. oryzae*, the causal agent of "bordered sheath spot" and *R. oryzae-sativae*, the causal agent of "aggregate sheath spot" have been reported on rice (Inagaki et al., 2004; Inagaki, 1996). These pathogens produce symptoms very similar to sheath blight in the field. However, knowledge of the populations of pathogenic *Rhizoctonia* species and accurate identification of AGs is essential for integrated management strategies of the disease. Matsumoto and Matsuyama (1998), designed specific primers from unique regions within ITS regions of rDNA to detect and identify *R. solani* AG1 IA causing rice sheath blight. The pathogen could be identified from paddy field soils and rice plant tissues using this PCR assay. Lees et al., (2002) used a conventional primer set (Rs1F2 and Rs2R1) was designed from the nuclear ribosomal internal transcribed spacer (ITS1 and ITS2) regions of *R. solani*. Following PCR amplification, a 0.5-kb product was amplified from DNA of all isolates of AG-3 using primers Rs1F2 and Rs2R1. No product was amplified when DNA from isolates belonging to a range of other *R. solani* AGs or from a selection of other potato pathogens was tested, confirming the specificity of the primers for AG-3 only. A quantitative real-time polymerase chain reaction (qPCR) format was developed to detect and quantify *R. solani* AG-1 IA DNA from infected rice plants. A specific primer pair was designed based on the internal transcribed spacer (ITS) region of the fungal ribosomal DNA (rDNA). The specific detection of *R.*

solani DNA was used with quantities as low as 1 pg (Sayler and Yang, 2007). The qPCR assay could be used for detecting the sheath blight pathogen, quantifying fungal aggressiveness, and evaluating the resistance level of rice cultivars. Grosch et al., (2007) reported that RAPD-PCR was used for identifying a specific fragment from which SCAR primers were developed and used for PCR detection of the subgroup AG 1-IB. The designed SCAR primer N18-rev/N18-for allowed the unequivocal detection of the specific DNA fragment of 324 bp from field-grown lettuce plants with bottom rot symptoms or artificially inoculated plant species and from different types of inoculated field soils. A specific diagnosis PCR assay for *R. solani* subgroup AG 1-IB was established, which can be used as a highly specific, reproducible, and applicable test system in plant disease diagnosis. Okubara et al., (2008) developed SYBR Green I-based real-time qPCR assays specific to internal transcribed spacers ITS1 and ITS2 of the nuclear ribosomal DNA of *R. solani* and *R. oryzae*. The assays were diagnostic for *R. solani* AG-2-1, AG-8, and AG-10, three genotypes of *R. oryzae*, and an AG-I-like binucleate *Rhizoctonia* species. Quantification was reproducible at or below a cycle threshold (*C*t) of 33, or 2–10 fg of mycelial DNA from cultured fungi, 200–500 fg of pathogen DNA from root extracts, and 20–50 fg of pathogen DNA from soil extracts. However, pathogen DNA could be specifically detected in all types of extracts at about 100-fold below the quantification levels.

A one-step, immuno-chromatogarphic lateral flow device (LFD) was developed for detection of *Rhizoctonia solani* and certain related species. Antigens from representative isolates of *R. solani* AGs 1, 2-1, 2-3, 3, 4, 5, 6, 7, 8, 9, 10, 11, and BI gave a positive response in LFD tests (Thornton et al., 2004). The Loop Mediated Isothermal Amplification (LAMP) method was integrated with lateral flow devices (LFDs) to improve the efficiency for in-field detection of *Rhizoctonia solani* in plant tissues, seeds, and propagules. LAMP primers based on the internal transcribed spacer (ITS) DNA sequences were used for the detection of anastomosis groups of *R. solani*. The LAMP-LFD procedure was effective for the detection of *R. solani* in several infected plant species belonging to diverse families and has the potential for onsite diagnosis of *R. solani* in plants, seeds, propagules, and soils. The detection limit of LAMP-LFD protocol (10 fg) was comparable to that of qRT-PCR format (Patel et al., 2015). LAMP assay was utilized by Lu et al., (2015) for diagnosis and detection of *R. solani* (ITS-Rs-LAMP) and *Macrophomina phaseolina* (ITS-Mp-LAMP) in diseased soybean tissues in the field. The detection limit of the ITS-Rs-LAMP assay was 10 pg/µl of genomic DNA; and that of the ITS-Mp-LAMP assay was 100 pg/µl of genomic DNA.

Disease Management: In the old era of agriculture, the *Rhizoctonia* diseases was controlled by using general or non-specific approaches such as soil fumigation, soil amendments, planting practices, maintaining soil moisture, etc., either single or in combination. Where soil fumigation was carried out using methyl bromide (bromomethol), metam sodium in combination with seed coating using some fungicidal or pesticidal compounds such as pencycuron, thiram, imidacloprid, captafol, etc., of which, pesticidal activity has the ability to restrict few other pathogens also. However the high costs and harmful effects of these compounds on the environment

made them out of competition in the growing years. The agronomical practices such as irrigation intervals and planting practices, either alone or in combination found more effective than earlier mentioned approaches (Narayanasamy, 2011). A range of sheath blight disease control measures have been reported in the literature.

Agronomic practices: Rice sheath blight incidence is depends on the methods of planting and plant population density. Square method of rice transplantation contributed to increased sheath blight resistance, optimum high-yield density, higher leaf area index and dry matter production (Yang et al., 2008). Transplanting rice seedling far from the bund resulted in reduction of sheath blight incidence since buds have weed hosts of *R. solani.* Crop submergence had a negative effect on disease progress and resulted in reduced sheath blight disease development (Das and Dath, 1997). Soil amendment with organic fertilizers plays an important role in managing rice disease. Among the various soil organic amendments (*Azadirachta indica, Pongamia pinnata, Gliricidia maculata, Chromolaena odorata, Prosopis juliflora,* and *Terminalia bellirica*), *A. indica* @ 150 kg/ha as oil cake was most effective in reducing the sheath blight incidence (Kumar et al., 2006). The application of inorganic fertilizers can also influence saprophytic survival of the pathogen. The plant variety and nitrogen fertilizers are the major factors influencing the disease, both during wet and dry seasons. Varieties with taller stature, fewer tillers, and lower leaf N concentration, generally had lower lesion height, disease index, and consequently lower yield loss from the disease. Disease intensity and yield loss increased with increasing N rates, but the magnitude of yield loss varied among varieties (Tang et al., 2007). However, potassium and phosphorus reduced the sheath blight incidence. Among different plant nutrients, silicon (Si) based fertilizers plays an important role in imparting resistance against rice blast, brown spot, sheath blight and bacterial blight (Rodrigues and Datnoff, 2005; Song et al., 2016). Field studies indicated that application of silicon fertilizer and organic fertilizers increased early rice yields by 12 and 21%, late rice yields by 8 and 29% respectively (Wang, 2005).

Crop rotation: Crop rotation is considered as an agricultural management tool with ancient origins (Howard, 1996). Besides the advantages like maintenance of soil health, soil organic matter, reduction in soil erosion, etc., crop rotation specifically decrease the incidence of plant diseases caused by soil-borne pathogens (Pedersen and Hughes, 1992). Monocropping systems generally led to the made up of soil density of specific phytopathogens resulting in the decline of crop yield and quality (Honeycutt et al., 1996). However, it is least successful in case of pathogens with a wide host range or that produce long-lived survival structure such as sclerotia or oospores (Umaerus et al., 1989). The probability of sheath blight is less in fields planted to rice for the first time, unless water drains from other fields that have been planted to rice or if rice is flooded from a surface water source. If sheath blight has been a problem in a field in the past and is again planted to rice, you can expect sheath blight to recur even if the field has been planted to soybeans for 2 years. A rotation of 2 years in soybeans and 1 year in rice helps control sheath blight. However, since the fungus can survive in the soil or in plant debris for years and can reproduce on soybeans, rotation will not assure you that sheath blight will not be a problem.

Varietal resistance: Breeding disease-resistant rice cultivars are believed to be one of the most promising approaches to manage the disease. However, no rice cultivar has been found immune or possess completely resistant to sheath blight disease so far, mainly due to a lack of source for resistance in cultivated rice or in wild related species. However, traditional rice cultivars like Swarnadhan, Radha, Pankaj, Vikramarya, Tetep, Jasmine 85, Tequing, Bhasamanik, Lalsatkara and selected rice lines, *viz.* ARC 15762, ARC 18119, ARC 18275, ARC 18545, HKR 99-103, HKRH 1059 and IR 64683-87–2-2-3-3, have moderate level of resistance (Laha et al., 2017). Whereas, highest susceptibility index (6.76) on cv. Annapurna and lowest were on Manasarovar (4.80) & Swarnadhan (4.72) reported against sheath blight of rice (Lal et al., 2012). Using molecular plant breeding programs, researchers manipulate the identified pathogen resistant genes to develop commercially resistant cultivar. So far, these attempts were ineffective and this may be attributed to the resistance being controlled by quantitative trait loci (QTLs) or multiple genes (Li et al., 1995; Eizenga et al., 2015; Chen et al., 2017; Jiang et al., 2018). More than 50 QTLs for sheath blight resistance distributed on 12 rice chromosomes have been detected using various mapping populations, such as F_2 populations (Rush, 1999; Che et al., 2003; Arun et al., 2009), recombinant inbred lines (RILs) (Han et al., 2002; Liu et al., 2009; Channamallikarjuna et al., 2010), chromosomal segment substitution lines (CSSLs) (Zuo et al., 2013; Zuo et al., 2014), near-isogenic interogression lines (NILs) (Loan et al., 2004), double-haploid populations (DHs) (Kunihiro et al., 2002) and backcross populations (Sato et al., 2004; Tan et al., 2005; Eizenga et al., 2015). Singh et al., (2012) developed multiple disease resistance basmati rice by transferring the blast resistance gene Pi54 and sheath blight resistance quantitative trait loci (QTL) from Tetep, qSBR11-1 to 'Improved Pusa Basmati'. However, neither the identified QTLs have been utilized in development of sheath blight resistant cultivars nor their breeding value has been assessed so far (Badri et al., 2017).

Chemical control: Systemic or contact and certain non-systemic fungicides are widely used for combating rice sheath blight infection. Presently, systemic fungicides belonging to the strobilurin group are used extensively to combat sheath blight pathogen. Within the strobilurins group, azoxystrobin fungicide is widely used as it works effectively against pathogen infestation. The disease can also be effectively managed by applying various chemicals like validamycin 3L @ 2.5 ml/l or propiconazole 25 EC @ 1 ml/l or hexaconazole 5 EC @ 2 ml/l or carbendazim 50 WP @ 1 g/l or thifluzamide 24 SC @ 30 g a.i./ha (Laha et al., 2017). Many a times, the disease appears in patches near the bunds and progresses inside the main fields. In such cases, spraying can be restricted to those patches to reduce the amount of fungicide application and to check further spread of the disease inside the field. Singh et al., (2010) reported that hexaconazole and diniconazole reduced the disease severity by 72 and 69 %, respectively, along with an enhanced grain yield. Many combination products like Filia 52.5 SE (tricyclazole+propiconazole), Nativo 75 WG (trifloxystrobin+tebuconazole) and Lusture 37.5 SE (flusilazole+carbendazim) have also been found very effective against sheath blight disease. Bhuvaneswari and Raju (2012) tested combination of azoxystrobin 18.2% +difenoconazole 11.4% SC under

field condition and was found effective @ 1.25 ml/l and 1.0 ml/l, respectively. Tebuconazole @ 0.2% can be recommended as an alternate molecule to existing fungicides for effective management of blast and sheath blight diseases of paddy (Hegde, 2015). Tebuconazole + Ttrifloxystrobin 75 WG, Tebuconazole 250 EC, Iprodine + Carbendazim 50WP and Fluzilazole 40 EC were statistically at par with each other and with standard check fungicide Hexaconazole 5 EC in inhibiting *R. solani* (Raji et al., 2016). Pramesh et al., (2017) reported that the combination fungicide Azoxystrobin 11% + Tebuconazole 18.3% w/w SC @ 1000 ml ha^{-1} was found effective against sheath blight disease recording least percent disease index (PDI).

Plant extract/Botanicals: Various plant extracts are being used all over the world and among them, neem formulations are very effective in controlling sheath blight incidence as well as in increasing grain yields. Kandhari and Devakumar (2003) reported that neem oil, its saturated fraction and its stabilized formulations were effective in containing the disease incidence as well as in reduction of percent infected tillers. Biswas (2007) reported that field application of neem formulations, 0.03% (300 ppm azadirachtin) and 0.15% EC (1500 ppm azadirachtin) @ 4.5 ml/L was very effective in reducing disease incidence as well as in increasing grain yields. Besides, certain plant extracts such as *Odiyana wodier, Lawsonia alba, Ocimum sanctum*, and *Pongamia glabra* were found to be effective both in reducing the mycelial growth and sporulation of *R. solani in-vitro* conditions. Further, field studies with *O. wodier* and *O. sanctum* were very effective over control against *R. solani* (Karthikeyan and Chandrasekaran, 2007). The plant extract of *Gaultheria* spp. formulated as Biotos was found to be highly effective @ 0.25% concentration in controlling sheath blight severity and in increasing grain yields (Biswas, 2006). The leaf extract of *Pithecellobium dulce* and *Prosopis juliflora* were found highly effective in inhibiting mycelial growth of test pathogen *in vitro* and also in controlling sheath blight with a disease incidence of 32.3 and 33.3%, respectively, over 76.2% in control (Meena et al., 2002). The bulb extract of *Allium sativum* and rhizome extract of *Zingiber officinales* were found effective in suppressing the mycelial growth of sheath blight pathogen *in-vitro* (Kumar et al., 2017). The antifungal effects of 30 plant essential oil were tested *in-vitro* and found that *Mentha arvensis* and *Withania somnifera* were effective against *R. solani* (Ali et al., 2014).

Biological control: Biological control has emerged as an alternative and most promising means of the management of plant pathogens. Rice crop is grown under inundated conditions, therefore, the survival, growth and establishment of biocontrol agents is questionable. However, effective management strategy of sheath blight disease is feasible only when the biocontrol agents those are in vogue in rice based cropping systems survive, establish, proliferate and control sheath blight pathogen and also have a synergistic growth promoting effect on the crop. Besides, the biocontrol agent should be able to induce systemic resistance thereby contributing to the disease control. For organic cultivation of rice, bio-based products are important constituents.

Fungal bioagents: The possible uses of fungal bicontrol agents of rice pathogen have been viewed as an alternative disease management strategy. Among the several antagonists, species of *Trichoderma, Gliocladium, Aspergillus,* etc. have been found effective in reducing the sheath blight (Khan and Sinha, 2005). These fungal antagonists are either applied to rice seed, soil, root dip and foliar spray for managing the disease. Various fungi such as *Aspergillus niger*, *A. terreus*, *Gliocladium virens*, and *Trichoderma* spp. inhibited *in vitro* mycelial growth of *R. solani* (Khan and Sinha, 2007a; Vaish and Sinha, 2004; 2006). Nagaraju et al., (2002) reported that application of *T. viride* as root dip + spray was effective in reducing sheath blight severity under field conditions. Mathivanan et al., (2005) reported that combined applications of *T. viride* and *Pseudomonas fluorescens* was effective without any negative effects in reducing rice sheath blight besides increasing number of productive tillers, higher grain and straw yields. Tang et al., (2001) examined cellulase activity of *Trichoderma* spp and proved that *T. hamatum, T. aureoviride* and *G. virens* were effective. Field studies indicated that the fungal bioagents exhibited good antagonism, and a disease control effect of 32% was obtained with fungal antagonist mixture besides positive effects on seed setting rate and 1000-grain weight of rice plants. Bhagawati (2005) proved that soil application of *T. harzianum* and *T. viride* at a pH range of 5.1 to 6.0 disease suppression under field condition can be obtained. Besides, a concomitant increase in plant growth and yield was obtained. *T. harzianum* isolated from rice leaf sheath was found effective, in reducing disease severity and incidence of sheath blight and increasing grain yield (Khan and Sinha, 2007b). Naeimi et al., (2011) reported that *T. harzianum* strain AS12-2, was the most promising antagonist for control of sheath blight under field condition. de Franca et al., (2015) showed that isolates of *T. asperellum* was efficient in reducing disease severity and increasing yield and grain weight. Kumari et al., (2016) reported that among the 26 isolates of *Trichoderma* spp., seven isolates showed strong antagonistic potential against *R. solani.* Among the twelve bio- agents, *Aspergillus niger* was highly effective against *R. solani in-vitro* (Ali et al., 2014). It is noticed that most of the researcher used *Trichoderma, Gliocladium* and *Aspergillus* species against *R. solani.*

Bacterial bioagents/ PGPR: Among the bacterial antagonists, plant growth-promoting rhizobacteria (PGPR) offer a promising means of controlling plant diseases besides contributing to the plant resistance, growth and yield in rice (Mew and Rosales, 1992). Rhizosphere-isolated, free living soil bacteria with proven plant beneficial properties are known as PGPR (Kloepper and Schroth, 1978). Besides, PGPR role in increasing plant or root growth, they directly influence increased N uptake, phosphate solubilization, phytohormone synthesis, and production of iron chelating siderophores (Lalande et al., 1989; Bowen and Rovira, 1999). Among the PGPR, *Pseudomonas fluorescens* and *Bacillus* spp. offer an effective biocontrol of sheath blight besides inducing growth promoting effects and systemic resistance. Biocontrol potentials of *Bacillus subtilis, B. cereus, Enterobacter* sp., *Pseudomonas fluorescens, P. putida,* and *P. aureofaciens* on the growth of *R. solani in vitro* have been demonstrated (Gnanamanickam and Mew, 1990; Lee et al., 1990; Singh and Sinha, 2004). The application of talc-based formulation of two *Pseudomonas fluorescens* strains (PF1 and

FP7) through seed, root, soiland foliar spray significantly reduced the sheath blight incidence both under greenhouse and field conditions (Commare et al., 2002). A significant relationship between the antagonistic activity of *P. fluorescens* (PfMDU2 strain) against *R. solani* and its level of β 1, 3-glucanase, salicylic acid and HCN production was observed (Nagarajkumar et al., 2004).

Since the fungus *R. solani* survives in soil as sclerotia and produces Oxalic Acid (OA), therefore, it would be ideal to identify an antagonistic strain of *P. fluorescens* having a potential to detoxify the Oxalic Acid. Nagarajkumar et al., (2005) demonstrated the potential and feasibility of controlling rice sheath blight by OA-detoxifying *P. fluorescens* strain, PfMDU2. Seed treatment followed by soil application with talc-based powder formulation of *P. fluorescens* PfMDU2 significantly reduced the severity of sheath blight by 75% as compared to untreated control plant. Ren et al., (2006) worked on crude extracts of antagonistic bacterium, *P. aeruginosa,* against *R. solani* and reported that the biocontrol effect was dependent on the concentration of extracts and the treatment time. Li et al., (2007) reported that *Pseudomonas* strains, Pf7-14 (natural resistant to nalidixic acid) and P13-R (spontaneous rifampicin resistant mutants of P13) were highly antagonistic to *R. solani* and compatible with each other under *in vitro* conditions. Jayaprakashval et al., (2014) reported that reported that 5 strains of marine bacteria associated with *Fluorescent pseudomonad* were isolated from rhizosphere soil from coastal have good sheath blight controlling efficacy. Moreover, some rhizosphere isolates of *P. fluorescens* (4aYN11strain) also produce extracellular enzymes. A significant relationship between the antagonistic activity of the bacterium against *R. solani* and its level of extracellular enzymes and siderophores production was noticed (Yu et al., 2017).

Bacillus spp. are important gram positive PGPR in the biocontrol of plant pathogenic diseases. The bacterium produces endospores and microscopic studies revealed that isolates of *B. subtilis* and *B. megaterium* exhibited effective inhibition against the sheath blight and bakane diseases of rice (Luo et al., 2005). *B. subtilis* strain AUBS1 produces phenylalanine ammonia-lyase (PAL), peroxidase (PO) and certain pathogenesis-related proteins (PR) in rice leaves when applied against sheath blight disease. Application of bioagent also resulted in accumulation of thaumatin-like proteins, glucanases and chitinases (Jayaraj et al., 2004). *B. subtilis* strain H158 has been reported as an efficient antagonistic agent of different plant disease, especially sheath blight, through *in vitro* and in field conditions (Zhou et al., 2015). *Bacillus* spp. exhibited synergistic effect when applied in conjunction with other bio-pesticides. When used along with fungal bioagents such as *T. viride, B. subtilis* resulted in sheath blight disease reduction effectively in pot culture studies (Das et al., 1998). Chen and Kang (2006) reported that the fermented product of *Bacillus* strain Drt-11 when used in combination with commercial biofungicide Jinggangmeisu WP (20%) yielded significantly higher efficacies in sheath blight control than their individual applications. *B. subtilis* strain H158 was compatible with strobilurins and their combined application effectively controlled sheath blight and showed strong synergistic effects (Liu et al., 2017). Other bacteria showing biocontrol potentials against *R. solani* include *Streptomyces* spp. and *Serratia marcescens.* Antifungal

metabolites of *Streptomyces* spp. (PM5, SPM5C-1 and SPM5C-2) showed inhibitory action against the mycelial growth of rice sheath blight and blast pathogens *in vitro* conditions (Prabavathy et al., 2006). The culture filtrate or the autoclaved culture filtrate of *Streptomyces philanthi* strain RM-1-138 effectively suppressed sheath blight disease by up to 65.6 and 60.8%, respectively under greenhouse condition (Boukaew and Prasertsan, 2014). The Culture filtrates of the bioagent *Serratia marcescens* showed enhanced biocontrol activity when combined with low concentrations of fungicides like flutolanil, pencycuron and validamycin in terms of reducing sclerotial viability of *R. solani* (Someya et al., 2005).

Transgenic approach: As a promising technology for crop improvement, genetic engineering has been sought as the method of choice for achieving sheath blight resistance in rice. Constitutive over-expression of pathogenesis-related (PR) protein genes either singly or in combination has been widely used for developing transgenic plants resistance against plant pathogens (Punja, 2006; Becker-Ritt and Carlini, 2012). These strategies include over-expression of genes for chitinase, β-1, 3-glucanase, thaumatin-like proteins (*tlp*), ribosome-inactivating protein (RIP), defensin, thionin, polygalacturonase-inhibiting proteins (PGIPs), and antimicrobial peptides. Introgression of combinations of PR protein genes has yielded higher levels of resistance than the use of individual genes. There is several transgenic rice lines with different defense related gene/s with increased resistance to sheath blight listed in **Table 2.** First attempt to engineer rice plant to enhance resistance was done by Lin et al., (1995) by overexpressing rice chitinase gene (*chi11*), using constitutive maize ubiquitin promoter. Subsequently, rice *chi11* gene was used to transform different genotypes of rice (Nishizawa et al., 1999; Datta et al., 2000; 2001; Kumar et al., 2003; Sridevi et al., 2003; Kalpana et al., 2006; Maruthasalam et al., 2007). Recently, a high expressing novel chitinase gene was isolated from the sheath blight-resistant QTL region (qSBR11-1 on chromosome 11) of resistant Indica rice variety Tetep (Richa et al., 2016). Transformation of susceptible japonica rice line Taipei 309 (TP309) with the novel rice chitinase gene provided enhanced resistance against sheath blight pathogen, *R. solani* (Richa et al., 2017). Li et al., (2009) transformed rice overexpressing *Momordica charantia* class I chitinase gene (*McCHIT1*) and showed an enhanced resistance to *R. solani* and *M. oryzae*. Antifungal protein genes of a plant origin have been successfully used for production of partially resistant rice lines against the sheath blight fungus. For instance, transgenic rice plants expressing genes encoding PR proteins, such as chitinases (Li et al., 2009; Lin et al., 1995; Shah et al., 2009; Sridevi et al., 2003), β-1, 3-glucanase (Sridevi et al., 2008), Defensin (Shah et al., 2009), and thaumatin-like protein (Datta et al., 1999) show a high level of resistance to sheath blight.

Studies on co-expression of rice chitinase along with other PR protein showed synergistic effect for disease control in rice. Transgenic rice plants transformed with *Chi11, tlp,* and *Xa21* and showed resistance to both sheath blight and bacterial leaf blight (Maruthasalam et al., 2007). Transgenic rice constitutively co-expressing *tlp-D34* (thaumatin-like protein) gene and *chi11* showed enhancement of sheath blight resistance (Shah et al., 2013). Co-expression of a rice basic chitinase gene and a

ribosome-inactivating protein in rice caused a significant reduction in sheath blight development (Kim et al., 2003). Co-expression of *OsChi11* and *Osoxo4* genes in a green tissue-specific manner provided 63% resistance against sheath blight without affecting agronomical important traits (Karmakar et al., 2016).

Table 2.

Genetic engineered rice lines with enhanced resistance to sheath blight
(adopted and modified from Srinivasachary *et al.,*2010)

Rice cultivars	Transformed gene/s	Gene origin and other additional features	Reference
Yamahoushi, Nipponbare	Bar	Herbicide tolerance gene, reduced sheath blight infection when plants spayed with bialaphos or phosphinothricin	Uchimiay et al., (1993)
Chinsurah Boro II	Chi 11	Chitinase	Lin et al., (1995)
Chinsurah Boro II, IR72, IR1500	TLP-D34	Rice thamatin-like protein, a member of PR-5 group	Datta et al., (1999)
IR64, IR72, IR688998, MH63, Chinsurah Boro II	RC 7	Rice chitinase	Datta et al., (2000; 2001)
M202	pinA, pinB	Structural protein from *Triticum aestivum*	Krishnamurthy et al., (2001)
Swarna	Chi 11	Rice chitinase	Baisakh et al., (2001)
IR72	Chi, Xa21, Bt	Chitinase, receptor-like kinase, and *Bt* toxin	Datta et al., (2002)
Kenfong	MODI, RCH0	Modified maize ribosome-inactivating protein gene and basic chitinase	Kim et al., (2003)
Pusa Basmati 1	Chi 11	Rice chitinase	Sridevi et al., (2003)
ADT38, ASD16, IR50, Pusa Basmati 1	Chi 11, tip	Enhanced resistance to both ShB and ShR	Kalpana et al., (2006)
Pusa Basmati 1	Ace-AMP1	A non-lipid transfer protein with antimicrobial property isolated from *Allium cepa* showed enhanced resistance against sheath blight, Blast and BLB	Patkar and Chattoo (2006)
Pusa Basmati 1, White Ponni, ADT38, Co43	RC 7	Rice chitinase	Nandakumar et al., (2007)
ASD16, ADT38, IR72, IR64, White pooni	Chi 11, tlp, Xa21	Rice chitinase, thaumatin-like protein and serine- threonine kinase enhanced resistance to both sheath blight and BLB	Maruthasalam et al., (2007)
Pusa Basmati 1	Chi 11, β-1,3-glucanase	Rice chitinase and tobacco β-1,3-glucanase	Sridevi et al., (2008)
Pusa Basmati 1	Chi 11	Rice chitinase	Sripriya et al., (2008)
Pusa Basmati 1	Rs-AFP2	A defensin gene from *Raphanus sativus*	Jha and Chattoo (2009a)
Pusa Basmati 2	Dm-AMP1	A defense gene from *Dalia merkii*	Jha et al., (2009)
Pusa Basmati 1	Dm-AMP1, Rs-AFP2	Defensin genes from *D. merkii* and *R. sativus*	Jha and Chattoo (2009b)
JinHui35	McCHIT	A class I chitinase gene of bitter melon	Li et al., (2009)

Pusa Basmati 1	Chit 42	A chitinase gene from *Trichoderma* spp.	Shah et al., (2009)
White Ponni	*tlpD*34, PR5, *chi*11, PR3	Thaumatin like protein gene (*tlpD*34, PR5) combination with the chitinase gene (*chi*11, PR3)	Shah et al., (2013)
Kitaake	ACS2 (1 aminocyclo-propane- 1-carboxylic acid synthase	Rice ACS2 (1-aminocyclopropane-1-carboxylic acid synthase, a key enzyme of ET biosynthesis)	Helliwell et al., (2013)
Taipei 309	chitinase gene (RCH10) β 1,3-glucanase gene	Rice basic chitinase gene (RCH10) and the alfalfa β1,3-glucanase gene (*AGLU1*)	Mao et al. (2014)
Zhonghua 11	OsPGIP1	Over expressed OsPGIP1	Wang et al., (2015)
YSBR1	OsOSM1	Over expressed OsOSM1	Xue et al., (2016)
BR29	OsOXO4, OsCHI11	Co-expression of chitinase and oxalate oxidase 4 genes	Karmakar et al., (2016)
Taipei 309 (TP 309)	LOC_Os11g47510	Rice chitinase gene from Tetep	Richa et al., (2017)
Nipponbare	OsSWEER11	Inhibition of OsSWEER11 function in mesophyll cells	Gao et al., (2018)

RNAi- mediated gene silencing: RNA-mediated gene silencing (RNA interference, RNAi), is an evolutionarily conserved process for gene targeting in a wide variety of eukaryotic organisms (Baulcombe, 2004). For gene targeting, dsRNA homologous to the target gene is introduced into the organism either directly or indirectly as a construct, leading to its endogenous expression. Host- Delivered RNAi (HD-RNAi) or Host-induced gene silencing (HIGS) involves the production of double stranded RNA molecules targeting pathogen genes in the host where they are processed into short interfering RNA molecules (siRNAs). The siRNAs are taken by the pathogen upon infection inducing the RNA interference process and silence the targeted gene in the pathogen (Fairbairn et al., 2007). The role of *GF14e* gene in rice disease resistance was studied by suppressing its expression using RNA interference (RNAi) approach. *GF14e*-silenced transgenic plants showed enhanced resistance to the necrotrophic sheath blight pathogen *R. solani* and a virulent strain of *Xathomonas oryzae* pv. *oryzae* (Manosalva et al., 2011). Tiwari et al., (2017) used host- delivered RNAi method to transformed rice with the hairpin RNAi construct containing fusion of two pathogenicity Map Kinase 1 (PKM1) genes, RPMK1-1 and RPKM1-2 of *R. solani.* Due to host-delivered siRNA-mediated silencing of the target genes, the expression level of RPMK1-1 and RPMK1-2 was significantly lower in *R. solani* infecting transgenic rice, thereby enhancing sheath blight resistance in rice. Recently, Rao et al., (2019) analyzed pectin metabolism associated genes of *R. solani* through transcriptome sequencing of infected rice tissues. One candidate gene AG1IA_04727 encoding polygalacturonase (PG) was targeted through RNAi to develop disease resistance. Stable expression of PG-RNAi construct in rice showed silencing of AG1IA_04727 and suppression of sheath blight disease.

Genome- editing approach: Genome-editing technologies offer possibility of genome modification in a site-directed manner. This relies on the creation of targeted

DNA double strand breaks (DSBs) by sequence-specific nucleases (SSNs) at specified genomic locations, which will stimulate the cell's DNA repair machinery. SSNs are also considered as "molecular scissors" which belong to four categories, *i.e.,* MegaN (mega nuclease), ZFNs (Zinc finger nucleases), TALENs (transcriptionactivator-like effector nucleases) and CRISPR/Cas9 (clustered regularly interspaced short palindromic repeat/CRISPRs-associated protein 9) (Zhang et al., 2013; Cermak et al., 2015). Among the four methods, CRISPER/Cas9 system is considered as one of the most important and simple genome editing tool for understanding various biosynthetic pathways and resistance response mechanisms in crop plants (Jiang et al., 2013). Rice as a diploid and a monocot plant is considered one of the best choices for the CRISPR/Cas9 system for engineering disease resistance. Recently, Wang et al., (2016) mutated the *OsERF922* gene using CRISPR/Cas9 method. Mutated rice lines thus created showed enhanced rice blast resistance without affecting the main agronomic traits. A natural allele of a C2H2-domain transcription factor gene, bsr-d1, confers broad-spectrum resistance to rice blast in Digu rice variety. CRISPR/Cas9-mediated knockout of Bsr-d1 enhanced blast resistance without alteration in agronomic character (Li et al., 2017). Recently, Ma et al., (2018) generated rice plant resistant to blast disease through CRISPR/Cas9 by disrupting the *OsSEC3A* gene. The Ossec3a mutant rice plants disrupted in a putative subunit of a complex involved in exocytosis exhibited enhance defence reponses by up-regulation of pathogenesis, higher levels of salicylic acid (SA) content and SA-related genes and improved resistance against *Magnaporte oryzae.* In general, these findings revealed the powerful and advantageous use of the CRISPR/Cas9 system in crop improvement as regards fungal disease resistance.

Nanotechnological approach: Nanotechnology is an emerging field in the area of interdisciplinary research especially in biological sciences. Nanotechnology has led to the new ways to control diseases using nano-scale materials (Afreen et al., 2011; Chaudhary et al., 2012; Nejad et al., 2015). Nanoparticles have emerged as modern agents owing to their large surface to volume ratio which provides a large contact surface with pathogen sources. Silver nanoparticles have antimicrobial property and can attack microorganisms, including the cell membrane structure in large scale biological processes (Dibrov et al., 2002; Pal et al., 2007; Chaudhary and Paul, 2012). Silver nanoparticles with fungistatic, bacteriostatic and plasmonic properties are among the eco-friendly inhibitors against plant-pathogens compared with synthetic fungicides (Lamsal et al., 2011). The effect of colloidal silver nanoparticles on sclerotium-forming fungi, *R. solani, S. sclerotium* and *S. minor* was studied by Min et al., (2009) and demonstrated that nanoparticles strongly inhibited the mycelial growth and sclerotial germination. Silver nanoparticles were synthesized using *Acalypha indica* leaf extract and their antifungal activity was tested against fungal phytopathogen namely *Alternaria alternata, Sclerotinia sclerotium, Macrophomina phaseolina, Rhizoctonia solani, Botrytis cinerea* and *Curvularia lunata* at different concentration. Silver nanoparticles exhibited tremendous antifungl activity against all the tested pathogens @ 15 mg concentration (Krishnaraj et al., 2012). Moreover, the antifungal ability of silver nanoparticles has been evaluated against phyto-pathogenic fungi such as

Alternaria alternata, Botrytis cinerea (Ouda, 2014) and *Colletotrichum gloeosporioides* (Aguilar-Méndez et al., 2011). A nanoformulation of carbendazim has been developed using poly (ethylene glycol) (PEGs)-based functionalized amphiphilic polymers by Koli et al., (2015). The release kinetics and their bioefficacy were evaluated against *R. solani* using poison food technique and reported that single application of the formulation can control disease for the whole lifespan of crop. Nejad et al., (2016) conducted an *in vitro* and *in-vivo* study to evaluate the antifungal activity of silver nanoparticles against *R. solani* to reduce and prevent the sheath blight in rice seedlings. The highest inhibition level against sclerotia formation and mycelium growth was recorded at the concentration of 50 ppm. *In vivo* glasshouse experiments showed that SNPs at the same concentration favourably affects both the fresh and dry weight of rice plants with a remarkable suppressive effect on the lesion development in leaves. Recently, Chiranjeevi et al., (2018) demonstrated the bioefficacy of biogenic synthesized silver nanoparticles against sheath blight pathogen and found better in decreasing the sheath blight incidence *in vitro* at 170 ppm concentration. Moreover, several toxic nanoparticles from novel nanoagrochemical formulation may flow into the environment and food chains threaten human health and ecosystem. Hence, the complete understanding about the structural properties of newly synthesized nanoparticles, such as their morphology, size, functional groups, and active adsorption/loading capacity, may provide a useful guide as a starting point for the selection of suitable nanoparticles.

CONCLUSIONS

The *R. solani* pathogen has wide range of host plant. Therefore, it is being survived in various cropping system. Hence, accurate detection and identification of *R. solani* causing sheath blight is essential for timely and proper management of the disease. Although, varietal resistance is the best and cheapest method to control sheath blight disease. But full proof resistant variety is not available.

However, manipulating the pathogenicity-related genes in rice plant using RNA interference techniques or genome editing approaches may be helpful for developing disease resistance against *R. solani.* Generally, the bio-agents are very effective *in vitro*; however, their efficacy is reduced under field condition.

The chemical, particularly, systemic in nature has ability to developed resistance against the pathogen, whenever, it applied indiscriminate way. Therefore, it will be better to adopt integrated strategies to mange sheath blight of rice**.** Nanomaterial based agrochemicals delivery in the form of nanoparticles, nanocomosites, nanocapsule nanosphere etc. have several advantages over the conventional methods of rice crop protection.

However, at a definite concentration, application of nanomaterial based formulation can be toxic for rice plant and environment, which should be assessed prior to their field application.

REFERENCES

1. Adam, G. C. (1988). *Thanatephorus cucumeris* (*Rhizoctonia solani*) a species complex of wide host ranges. In G. S. Sidhu (ed) Advances in Plant Pathology (pp. 535-552) Academic Press.
2. Afreen, Rathod, V., Ranganath, E. (2011). Synthesis of monodispersed silver nanoparticles by *Rhizopus stolonifer* and its antibacterial activity against MDR strains of *Pseudomonas aeruginosa* from burnt patients. Int J Environ Sci.. 1: 1583–1592.
3. Aguilar-Méndez, M. A., Martín-Martínez, E. S., Ortega-Arroyo, L., Cobian-Portillo, G. (2011). Synthesis and characterization of silver nanoparticles: effect on phytopathogen *Colletotrichum gloesporioides*. J Nanopart Res., 13(6): 2525–2532.
4. Ali, M., Singh, R., Lal, M., Ali, I., Zuhaib, M., Kumar, S. (2015). Evaluation of different plant based essential oils against *Rhizoctonia solani* causing sheath blight of rice. Agriways, 3(1): 10-13.
5. Ali, M., Singh, R., Sengar, R.S., Lal, M., Singh, G., Mishra, P., Sachan, S. K. (2014). Evaluation of different fungal and bacterial Bioagents against *Rhizoctonia solani* causing sheath blight of rice. Biotech Today**,** 4(35): 34-37.
6. Anderson, N. A. (1982). The genetics and pathology of *Rhizoctonia solani*. Annu Rev Phytopathol., 20: 329-344.
7. Anushree, P. U., Naik, R. M., Satbhai, R. D., Gaikwad, A. P., Nimbalkar, C. A. (2016). Differential biochemical response of rice (*Oryza sativa* L.) genotypes against rice blast (*Magnaporthe oryzae*). Cogent Biology, 2: 1264162.
8. Arun, S., Annam, M. C., Shannonrm, P., Josephl, K., Arobert, S., Rodantee, T., Robert, F. (2009). Genetic mapping of sheath blight resistance QTLs within tropical japonica rice cultivars. Crop Sci., 49(1): 256–264.
9. Back, M. A., Haydock, P. P. J., Jenkinson, P. (2002). Disease complexes involving plant parasitic nematodes and soilborne pathogens. Plant Pathol., 51: 683-697.
10. Badri, J., Dey, S., Prakasam, V., Nymagoud, S., Priyanka, C., Shaik, H., Sundaram, R. M., Sheshu, M. M., Eswari, K. B., Bhadana, V. P., Ram, T., SubbaRao, L.V. (2017). Allelic variation of sheath blight QTLs among genotypes promising for sheath blight tolerance. J Rice Res., 10(1): 36-39.
11. Baisakh, N., Datta, K., Oliva, N., Ona, I., Rao, G. J. N., Mew, T. W., Datta, S. K. (2001). Rapid development of homozygous transgenic rice using anther culture harboring rice chitinase gene for enhanced sheath blight resistance. Plant Biotech., 18: 101–108.
12. Baker, C. J., Bateman, D. F. (1978). Cutin degradation by the plant pathogenic fungi. Phytopathol., 68: 1577-1584.
13. Baulcombe, D. (2004). RNA silencing in plants. Nature. 431: 356–363.
14. Becker-Ritt, A. B., Carlini, C. R. (2012). Fungitoxic and insecticidal plant polypeptides. Peptide Sci., 98(4): 367-384.
15. Bernardes-De-Assis, J., Storari, M., Zala, M., Wang, W. X., Jiang, D. H., Li, S. D. (2009). Genetic structure of population of the rice-infecting pathogen *Rhizoctonia solani* AG1-IA from China. Phytopathol., 99: 1090-1099.
16. Bertagnolli, B. L., Dal Soglio, F. H., Sinclair, J. B. (1996). Extracellular enzyme profiles of the fungal pathogen *Rhizoctonia solani* isolate 2B-12 and two antagonists, *Bacillus megaterium* strain B153-2-2 and *Trichoderma harzianum* isolate Th008. I. Possible correlations with inhibition of growth and biocontrol. Physiol Mol Plant Pathol., 48: 145-160.
17. Bhagawati, R. (2005). Effects of pH on antagonistic activity of *Trichoderma harzianum* and *Trichoderma viride* on sheath blight development and their survival. Oryza, 42(4): 290-293.
18. Bhuvaneswari, V., Raju, S. K. (2012). Efficacy of new combination fungicide against rice sheath blight caused by *Rhizoctonia solani* (Kuhn). J Rice Res., 5(1): 57-61.

19. Binder, M., Hibbett, D., Larsson, K., Larsson, E., Langer, E., Langer, G. (2005). The phylogenetic distribution of resupinate forms across the major clades of mushroom-forming fungi (Homobasidiomycetes). Syst Biodivers., 3(2): 1-45.

20. Biswas, A. (2006). Activity of strobilurins fungicides against sheath blight disease of rice: an overview. Environ Ecol., 3: 518- 520.

21. Biswas, A. (2007). Evaluation of neem formulations against sheath blight disease of rice. Ind J Plant Protec., 35(2): 296-298.

22. Boukaew, S., Prasertsan, P. (2014). Supression of rice sheath blight disease using a heath stable culture filtrate from *Streptomyces philanthi* RM-1-138. Crop Protec**.,** 61:1-10.

23. Bowen, G. D., Rovira, A. D. (1999). The rhizosphere and its management to improve plant growth. Adv Agron., 66:1-102.

24. Carling, D. E.,, Baird, R. E., Gitaitis, R. D., Brainard, K., Kuninaga, S. (2002). Characterization of AG-13, a newly reported anastomosis group of *Rhizoctonia solani.* Phytopathol.. 92: 893-899.

25. Carling, D.E. (1996). Grouping in *Rhizoctonia solani* by hyphal anastomosis. In B. Sneh, S. Jabaji-Hare, S. Neate & G. Dijst (Eds), *Rhizoctonia* species: Taxonomy, molecular biology, ecology, pathology and disease control (pp 1-9). Dordrecht: Kluwer.

26. Cermak, T., Baltes, N. J., Cegan, R., Zhang, Y., Voytas, D. F. (2015). High-frequency, precise modification of the tomato genome. Genome Biol., 16: 232.

27. Channamallikarjuna, V., Sonah, H., Prasad, M., Rao, G. J. N., Chand, S., Upreti, H. C., Singh, N. K., Sharma, T. R. (2010). Identification of major quantitative trait loci qSBR11-1 for sheath blight resistance in rice. Mol Breed., 25(1): 155–166.

28. Chaudhary, S., Paul, S. (2012). Antimicrobial studies of silver nanoparticles synthesized from *Vitis vinifera* extract. J Bionanosci., 6: 104-108.

29. Chaudhary, S., Kumar, M., Sengar, R. S., Chand, P., Mishra, P., Tomar, A. (2018). Effect of nutrient status, temperature and pH on mycelial growth, clerotial production and germination of Rhizoctonia *solani* isolated from paddy fields. Progres Agri., 18(1): 82-91.

30. Chaudhary, S., Kumar, M., Sengar, R. S., Chand, P., Mishra, P., Tomar, A. (2017). Anti-oxidative response in susceptible and resistant cultivars of *Oryza sativa* L. in response to infection by *Rhizoctonia solani.* South Asian J Food Technol Environ., 3(1): 507-515.

31. Chaudhary, S., Paul, S., Sagar, S. (2012). Biosynthesis of silver nanoparticles using *Vitis vinifera* extract and evaluation of their antimicrobial activity. Int J Bio-technol Res., 2**:** 1-12.

32. Chaudhary, S., Sagar, S., Tomar, A., Sengar, R. S., Kumar, M. (2016). Banded leaf and sheath blight: A menacing disease of maize (*Zea mays* L.) and its management. J Appl Nat Sci., 8(3): 1720-1730.

33. Che, K. P., Zhan, Q. C., Xing, Q. H., Wang, Z. P., Jin, D. M., He, D. J., Wang, B., 2003. Tagging and mapping of rice sheath blight resistant gene. Theor Appl Genet., 106(2): 293–297.

34. Chen, M., Kang, X. H. (2006). The research exploration to the effect of controlling rice sheath blight with *Bacillus* spp. Drt-11. Southwest China J Agri Sci., 19(1): 53-57.

35. Chen, Z. X., Feng, Z. M., Wang, L. P., Feng, F., Zhang, Y. F., Ma, Y. Y., Pan, X. B., Zuo, S. M. (2017). Breeding potential of rice TAC1 gene for tiller angle. Chinese J Rice Sci., 31(6): 590–598. (Chinese with English abstract).

36. Chiranjeevi, N., Kumar, P. A., Jayalakshmi, R. S., Prasad, K. V. H., Prasad, T. N. V. K. V. (2018). Bio efficacy of biogenic silver nanoparticles against rice sheath blight causing pathogen *Rhizoctonia solani* Kuhn. Int J Curr Microbiol Appl Sci., 7(7): 4148-4160.

37. Commare, R. R., Nandaumar, R., Kandan, A., Suresh, S., Bharathi, M., Raguchander, T., Samiyappan, R. (2002). *Pseudomonas fluorescens* based bio-formulation for the management of sheath blight disease and leaffolder insect in rice. Crop Protect., 21(8): 671-677.

38. Dahl, A. S. (1953). Effect of temperature on brown patch of turf (Abstr.). Phytopathol., 23:8.

39. Damodaram Nadu, V., Srinivasa Rao, B., Murty, P. S. S. (1981). Influence of sheath blight infection on the levels of chlorophyll & CO_2 uptake in rice. Indian Phytopathol., 34: 30-33.

40. Damson, J., Wasano, K., Nose, A. (2000). Infection of rice plants with the sheath blight fumgus causes an activation of pentose phosphate and glycolytic pathways. Euro J Plant Pathol., 106: 555-561.

41. Das, B., Dath, A. P. (1997). Effect of submergence of rice plants on the development of sheath blight. Int Rice Res Notes., 22(2): 39-40.

42. Das, B. C., Khairuzzaman, A. S. M., Bora, L. C. (1998). Biological seed treatment for management of sheath blight of rice. J Mycol Plant Pathol**.,** 28(1): 45-47.

43. Datta, K., Baisakh, N., Thet, K. M., Tu, J., Datta, S. K. (2002.) Pyramiding transgenes for multiple resistance in rice against bacterial blight, yellow stem borer and sheath blight. Theor Appl Genet. 106: 1–8.

44. Datta, K., Koukolikova, N. Z., Baisakh, N., Oliva, N., Datta, S. K. (2000). Agrobacterium-mediated engineering for sheath blight resistance of indica rice cultivars from different ecosystems. Theor Appl Genet. 100: 832–839.

45. Datta, K., Tu, J., Oliva, N., Ona, I., Velazhahan, R., Mew, T. W., Muthukrishnan, S., Datta, S. K. (2001). Enhanced resistance to sheath blight by constitutive expression of infection-related rice chitinase in transgenic elite indica rice cultivars. Plant Sci. 60: 405–414.

46. Datta, K., Velazhahan, R., Oliva, N., Ona, I., Mew, T., Khush, G. S. (1999). Over-expression of the cloned rice thaumatin-like protein (PR-5) gene in transgenic rice plants enhances environmental friendly resistance to *Rhizoctonia solani* causing sheath blight disease. Theor Appl Genet. 98: 1138–1145.

47. de Franca, S. K. S., Cardoso, A. F., Lustosa, D. C., Ramos, E. M. L. S., Filippi, M. C., da Silva, G, B. (2015). Biocontrol of sheath blight by *Trichoderma asperellum* in tropical lowland rice. Agron Sustain Dev. 35: 317-324.

48. Demirci, E., Döken, M. T. (1998). Host penetration and infection by the Anastomosis groups *Rhizoctonia solani* Kühn isolated from potatoes. Turk J Agri Forest. 22: 609-613.

49. Dibrov, P., Dzioba, J., Gosink, K. (2002). Chemiosmotic mechanism of antimicrobial activity of Ag (+) in *Vibrio cholera*. Antimicrob Agents Chemother., 46: 2668–2670.

50. Eizenga, G. C., Jia, M. H., Pinson, S. R., Gasore, E. R., Prasad, B. (2015). Exploring sheath blight quantitative trait loci in a Lemont/O. meridionalis advanced backcross population. Mol Breed., 35(6): 1–19.

51. Fairbairn, D. J., Cavallaro, A. S., Bernard, M., Mahalinga-lyer, J., Graham, M. W., Botella, J. R. (2007). Host-delivered RNAi: an effective strategy to silence genes in plant parasitic nematodes. Planta, 226: 1525–1533.

52. FAOSTAT.(2018). FAO Statistical data, http://faostat.fao.orii/

53. Gao, Y., Zhang, C., Han, X., Wang, Z.Y., Ma, L., Yuan, D. P., Wu, J. N., Zhu, X. F., Li, J. M., Li, D. P., Hu, Y. B., Xuan, Y. H. (2018). Inhibition of OsSWEER11 function in mesophyll cells improves resistance of rice to sheath blight disease. Mol Plant Pathol., 19(9): 2149-2161.

54. Gao, Y. (1997). Preliminary report on vertical development of rice sheath blight by grey system theory. J Jilin Agric Uni. 19(4): 109-112.

55. Ghosh, S., Mirza, N., Kanwar, P., Tyagi, K. and Jha, G. (2019). Genome analysis provides insight about pathogenesis of Indian strains of *Rhizoctonia solani* in rice. Funct Integr Genomic, https://doi.org/10.1007/s10142-019-00687-y

56. Gnanamanickam, S. S., Mew, T. W. (1990). Biological control of rice diseases (blast and sheath blight) with bacterial antagonists: An alternate strategy for disease management. In B. T. Grayson, M. B. Green & L.G. Copping (Eds) Pest management in rice (pp. 87–110), Elsevier Applied Science Pub. Ltd, New York.

57. Gonzãlez-Garcia, V., Portal Onco, M. A., Rubio Susan, V. (2006). Review: biology and systematics of the genus *Rhizoctonia*. Spanish J Agri Res., 4(1): 55-79.

58. Gonzaliz-Vera, A. D., Bernardes-De-Assis, J., Zala, M., McDonald, B. A., Correa-Victoria, F., Graterol-Matute, E. J. (2010). Divergence between sympatric rice and maize-infecting populations of *Rhizoctonia solani* AG1-IA from Latin America. Phytopathol. 100:172-182.

59. Grosch, R., Schneider, J. H., Peth, A., Waschke, A., Franken, P., Kofoet, A., Jabaji-Hare, S. H. (2007). Development of a specific PCR assay for the detection of *Rhizoctonia solani* AG 1-IB using SCAR primers. J Appl Microbiol. 102(3): 806–819.

60. Han, Y. P., Xing, Y. Z., Chen, Z. X., Gu, S. L., Pan, X. B., Chen, X. L., Zhang, Q. F. (2002). Mapping QTLs for horizontal resistance to sheath blight in an elite rice restorer line, Minghui 63. Acta Genetica Sinica. 29(7): 622–626. (Chinese with English abstract).

61. Hashiba, T., Yamaguchi, T., Mogi, S. (1972). Biological and ecological studies on the sclerotium of *Pellicula*riasasakii (Shirai) S. Ito. Ann Phytopatol Soc Japan., 38: 414-425.

62. Hebert, P. D., Gregory, T. R. (2005). The promise of DNA barcoding for taxonomy. Syst Biol. 54(5): 852–859.

63. Hegde, G. M. (2015). Efficacy of Tebuconazole 25%Wg against Blast and Sheath Blight diseases of Rice in Central Western Ghats of Uttar Canada District. The Bioscan. 52(3): 222-226.

64. Helliwell, E. E., Wang, Q., Yang, Y. (2013). Transgenic rice with inducible ethylene production exhibits broad-spectrum disease resistance to the fungal pathogens *Magnaporthe oryzae* and *Rhizoctonia solani.* Plant Biotech J. 11: 33–42.

65. Honeycutt, C. W., Clapham, W. M., Leach, S. S. (1996). Crop rotation and N fertilization effects on growth, yield, and disease incidence in potato. Am Potato J. 73: 45-61.

66. Howard, R. J. (1996). Cultural control of plant diseases: a historical perspective. Can J Plant Pathol. 18: 145–150.

67. Hyakumachi, M., Ui, T. (1988). Development of the teleomorph of non-self-anastomosing isolates of *Rhizoctonia solani* by a buried-slide method. Plant Pathol. 37: 438–440.

68. Inagaki, K., Qingyuan, G., Masao, A. (2004). Overwintering of rice sclerotial disease fungi, *Rhizoctonia* and *Sclerotium* spp. in paddy fields in Japan. Plant Pathol J. 3: 81–87.

69. Inagaki, K. (1996). Distribution of strains of rice bordered sheath spot fungus, *Rhizoctonia oryzae,* in paddy fields and their pathogenicity to rice plants. Ann Phytopatol Soc Japan., 62: 386–392.

70. IRRI. (1996). Standard Evaluation System for Rice. pp. 52. INGER Genetic Resources Centre, International Rice Research Institute: Manila.

71. Jayaprakashvel, M., Sharmika, N., Vinothini, S., Venkatramani, M., Muthezhilan, R., Hussain, A. J. (2014). Biological control of sheath blight of rice using marine associated *Fluorescent pseudomonads*. Biosci Biotechnol Res Asia. 11(1): 115-121.

72. Jayaraj, J., Yi, H., Liang, G. H., Muthukrishnan, S., Velazhahan, R. (2004). Foliar application of *Bacillus subtilis* AUBS1 reduces sheath blight and triggers defense mechanisms in rice. Zeitschrift fur Pflanzenkrankheiten and Pflanzenschutz. 111(2): 115-125.

73. Jayasinghe, C.K., Wijayaratne, S.C.P., Fernando, T.H.P.S. (2004). Characterization of cell wall degrading enzymes of *Thanatephorus cucumeris*. Mycopathol. 157: 73-79.

74. Jha, S., Chattoo, B. B. (2009a). Expression of a plant defensin in rice confers resistance to fungal phytopathogens. Trans Res. 19: 373–384.

75. Jha, S., Chattoo, B. B. (2009b). Transgene stacking and coordinated expression of plant defensins confers fungal resistance in rice. Rice, 2: 143–154.

76. Jha, S., Tank, H.G., Prasad, B.D., Chattoo, B.B. (2009). Expression of Dm-AMP1 in rice confers resistance to *Magnaporthe oryzae* and *Rhizoctonia solani.* Trans Res. 18: 59- 69.

77. Jiang, S.F., Wang, C.J.Z., Shu, C.W., Zhou, E.X. (2018). Cloning and expression analysis of *RsPhm* gene in *Rhizoctonia solani* AG-1IA of rice sheath blight pathogen. Chinese J Rice Sci. 32(2): 111–118. (Chinese with English abstract).

78. Jiang, W., Zhou, H., Bi, H., Fromm, M., Yang, B., Weeks, D. P. (2013). Demonstration of CRISPR/Cas9/sgRNA-mediated targeted gene modification in Arabidopsis, tobacco, sorghum and rice. Nucleic Acids Res. 41: e188.

79. Kalpana, K., Maruthasalam, S., Rajesh, T., Poovannan, K., Kumar, K. K., Kokiladevi, E., Raja, J. A., Sudhakar, D., Velazhahan, R., Samiyappan, R. (2006_. Engineering sheath blight resistance in elite indica rice cultivars using genes encoding defense proteins. Plant Sci. 170: 203–215.

80. Kandhari, J., Devakumar, C. (2003). Effect of neem oil and its fractions against sheath blight (*Rhizoctonia solani* Kühn) of rice. J Mycopathol Res. 41(2): 185-187.

81. Karmakar, S., Molla, K. A., Chanda, P. K., Sarkar, S. N., Datta, S. K., Datta, K. (2016). Green tissue-specific co-expression of chitinase and oxalate oxidase 4 genes in rice for enhanced resistance against sheath blight. Planta. 243:115–130.

82. Karthikeyan, A., Chandrasekaran, B. (2007). Bioefficacy of plant extracts in the management of sheath blight disease of rice. J Ecobiol. 21(3): 279-282.

83. Khan, A. A., Sinha, A. P. (2007a). Factors effecting of *Trichoderma* spp. as biocontrol agents against sheath blight of rice. Indian Phytopath. Proceeding of the 19th training on "Plant Disease Management on Small Farms". (pp. 177–182). Center of Advanced Studies in Plant Pathology, G.B. Pant University and Technology, Pantnagar.

84. Khan, A. A., Sinha, A. P. (2007b). Biocontrol potential of *Trichoderma* species against sheath blight of rice. Indian Phytopathol. 60(2):208–213.

85. Kim, J. K., Jang, I. C., Wu, R., Zuo, W. N., Boston, R. S., Lee, Y. H., Ahn, I. P., Nahm, B. H. (2003). Co-expression of a modified maize ribosome-inactivating protein and a rice basic chitinase gene in transgenic rice plants confers enhanced resistance to sheath blight. Trans Res. 12: 475–484.

86. Kloepper, J. W., Schroth, M. N. (1978_. Plant growth promoting rhizobacteria on radish. Proceedings of the Fourth Conference Plant Pathogenic Bacteria. INRA, Angers, France.

87. Kohli, C. K. (1966). Pathogenicity and host range studies on paddy sheath blight pathogen *Rhizoctonia solani* Kühn. J Res Punjab Agri Uni., P.A.U. 3:7-40.

88. Koli, P., Singh, B.B., Shakil, N.A., Kumar, J., Kamil, D. (2015). Development of controlled release nanoformulations of carbendazim employing amphiphilic polymers and their bioefficacy evaluation against *Rhizoctonia solani*. J Environ Sci Health B. 50(9): 674–681.

89. Krishnamurthy, K., Balconi, C., Sherwood, J. E., Giroux, M. J. (2001). Wheat puroindolines enhance fungal disease resistance in transgenic rice. Mol Plant Microbe Interact. 14: 1255–1260.

90. Krishnaraj, C., Ramachandran, R., Mohan, K., Kalaichelvan, P. T. (2012). Optimization for rapid synthesis of silver nanoparticles and its effect on phytopathogenic fungi. Spectrochimica Acta Part A: Mol Biomol Spectro. 93: 95-99.

91. Kumar, K. K., Poovannan, K., Nandakumar, R., Thamilarasi, K., Geetha, C., Jayashree, N., Kokiladevi, E., Raja, J.A.J., Samiyappan, R., Sudhakar, D., Balasubramanian, P. (2003). A high throughput functional expression assay system for a defence gene conferring transgenic resistance on rice against the sheath blight pathogen, *Rhizoctonia solani.* Plant Sci. 165: 969-976.

92. Kumar, M. K. P., Gowda, D. K. S., Moudgal, R., Kumar, N. K., Gowda, K. T. P., Vishwanath, K. (2013). Impact of fungicides on rice production in India. In M. Nita (ed). Fungicides- Showcases of integrated plant disease management from around the world (pp. 1), Intech Open Ltd., London, UK.

93. Kumar, M. P., Ramaswamy, G. R., Basavarajappa, M. P. (2006). Efficacy of soil amendment against sheath blight of rice caused by *Rhizoctonia solani* Kühn. Kar J Agri Sci., 19(2): 422-423.

94. Kumar, V., Chaudhary, V. P., Kumar, D., Kumar, A., Sagar, S., Chaudhary, S. (2017). Efficacy of botanicals and fungicides against *Rhizoctonia solani* inciting sheath blight disease on Rice (*Oryza sativa* L.). J Appl Nat Sci. 9(4): 1916-1920.

95. Kumari, A., Kumar, R., Maurya, S., Panday, P. K. (2016). Antagonistic potential of different isolates of *Trichoderma* against *Rhizoctonia solani.* Euro J Exp Biol. 6: 2.

96. Kunihiro, Y., Qian, Q., Sato, H., Teng, S., Zeng, D. L., Fujimoto, K., Zhu, L. H. (2002). QTL analysis of sheath blight resistance in rice (*Oryza sativa* L.). Acta Genetica Sinica. 29(1): 50–55. (Chinese with English abstract).

97. Laha, G.S., Singh, R., Ladhalakshmi, D., Sunder, S., Prasad, M.S., Dagar, C.S., Babu, V.R. (2017). Importance and management of rice diseases: A global perspective. In B. S. Chauhan, K. Jabran & G. Mahajan (eds). Rice Production Worldwide (pp. 306-360), Springer International Publishing AG, Switzerland.

98. Lal, M., Kandhari, J. (2009). Cultural and morphological variability in *Rhizoctonia solani* isolates causing sheath blight of rice. J Mycol Plant Pathol. 39(1):77-81.

99. Lal, M., Kandhari, J., Singh, V. (2012). Characterization of virulence pattern in *Rhizoctonia solani* Khun causing sheath blight of rice. Indian Phytopathol. 65(1) 60-63.

100. Lal, M., Vivek, S., Kandhari, J., Kumar, S. (2013). Characterization of virulence pattern in *Rhizoctonia solani* Kühn causing sheath blight of rice under different environmental condition. Biochem Cell Arch. 13(2) 355-358.

101. Lalande, R., Bissonnette, N., Coutlee, D., Autoun, H. (1989). Identification of rhizobacteria from maize and determination of their plant-growth promoting potential. Plant and Soil. 115: 7-11.

102. Lamsal, K., Kim, S.W., Jung, J.H., Kim, Y.S., Kim, K.S., Lee, Y.S. (2011). Application of silver nanoparticles for the control of *Colletotrichum* species *in vitro* and pepper anthracnose disease in field. Mycobiol. 39(3): 194–199.

103. Lee, F. N., Rush, M. C. (1983). Rice sheath blight: a major rice disease. Plant Dis. 67: 829–832.

104. Lee, Y. H., Shim, G. Y., Lee, E. J., Mew, T. W. (1990). Evaluation of biological activity of *fluorescent pseudomonads* against some rice fungal diseases *in vitro* and glasshouse. Koreian J Plant Pathol. 6:73–78.

105. Lees, A. K., Cullen, D. W., Sullivan, L., Nicolson, M. J. (2002). Development of conventional and quantitative real-time PCR assays for the detection and identification of *Rhizoctonia solani* AG-3 in potato and soil. Plant Pathol. 51: 293-302.

106. Li, P., Pei, Y., Sang, X. C., Ling, Y. H., Yang, Z. L., He, G.H. (2009). Transgenic indica rice expressing a bitter melon (*Momordica charantia*) class I chitinase gene (*McCHIT1*) confers enhanced resistance to *Magnaporthe grisea* and *Rhizoctonia solani.* Euro J Plant Pathol. 125: 533–543.

107. Li, W., Zhu, Z., Chern, M., Yin, J., Yang, C., Ran, L. (2017). A natural allele of a transcription factor in rice confers broad-Spectrum blast resistance. Cell. 170: 114–126.e15.

108. Li, X.M., Lan, B., Huang, R.K., Tu, Y.Q., Xu, Z.G., Mew, T.W. (2007). Population dynamics of antagonistic bacterial strains Pf7-14 and P13, a compatible combination, in rice plants. Acta Agri Uni Jiangx. 29(6): 917- 921.

109. Li, Z. K., Pinson, S. R. M., Marchetti, M. A., Stansel, J. W., Park, W. D. (1995). Characterization of quantitative trait loci (QTLs) in cultivated rice contributing to field resistance to sheath blight (*Rhizoctonia solani*). Theor Appl Genet. 91: 382–388.

110. Liang, Y. C., Chen, Q., Liu, Q., Zhang, W. H., Ding, R. X. (2003). Exogenous silicon (Si) increases antioxidant enzyme activity and reduces lipid peroxidation in roots of salt stressed barley (*Hordeum vulgare* L.). J Plant Physiol. 160: 1157–1164.

111. Lin, W., Anuratha, C. S., Datta, K., Potrykus, I., Muthukrishnan, S., Datta, S. K. (1995). Genetic engineering of rice for resistance to sheath blight. Nature Biotechnol. 13: 686–691.

112. Liu, G., Jia, Y., Correa-Victoria, F. J., Prado, G. A., Yeater, K. M., Mcclung, A., Correll, J. C. (2009). Mapping quantitative trait loci responsible for resistance to sheath blight in rice. Phytopathol. 99(9): 1078–1084.

113. Liu, L., Liang, M., Li, L., Sun, L., Xu, Y., Gao, J., Wang, L., Hou, Y., Huang, S. (2017). Synergistic Effects of the combined application of *Bacillus subtilis* H158 and Strobilurins for rice sheath blight control. Biol Control. 117: 182-187.

114. Loan, L. C., Du, P. V., Li, Z. K. (2004). Molecular dissection of quantitative resistance of sheath blight in rice (*Oryza sativa* L.). Omonrice. 12: 1–12.

115. Lu, C., Song, B., Zhang, H., Wang, Y., Zheng, X. (2015). Rapid diagnosis of soybean seedling blight caused by *Rhizoctonia solani* and soybean charcoal rot by *Macrophomina phaseolina* using LAMP assay. Phytopathol. 105: 1612-1617.

116. Luo, J. Y., Xie, G. L., Li, B., Luo, Y. C., Zhao, L. H., Wang, X., Liu, B., Li, W. (2005) Gram-positive bacteria associated with rice in China and their antagonists against the pathogens of sheath blight and bakanae disease in rice. Rice Sci. 12(3): 213-218.

117. Ma, J., Chen, J., Wang, M., Ren, Y., Wang, S., Lei, C., Chen, Z., Sodmergen,(2018). Disruption of OsSEC3A increases the content of salicylic acid and induced plant defence responses in rice. J Exp Bot. 69(5): 1051-1064.

118. Manosalva, P. M., Bruce, M., Leach, J. E. (2011_. Rice 14-3-3 protein (GF14e) negatively affects cell death and disease resistance. Plant J., 68: 777–787.

119. Mao, B., Liu, X., Hu, D., Li, D. (2014). Coexpression of *RCH10* and *AGLU1* confers rice resistance to fungal sheath blight *Rhizoctonia solani* and blast *Magnorpathe oryzae* and reveals impact on seed germination. World J Microbiol Biotechol. 30: 1229–1238.

120. Marshall, D. S., Rush, M. C. (1980). Infection cushion formation on rice sheaths by *Rhizoctonia solani*. Phytopathol. 70: 947-950.

121. Maruthasalam, S., Kalpana, K., Kumar, K. K., Loganathan, M., Poovannan, K., Raja, J.A.J. (2007). Pyramiding transgenic resistance in elite indica rice cultivars against the sheath blight and bacterial blight. Plant Cell Rep. 26: 791–804.

122. Mathivanan, N., Prabavathy, V. R., Vijayanandraj, V. R. (2005). Application of talc formulations of *P. fluorescens* Migula and *Trichoderma viride* Pers. ex S.F. Gray decrease the sheath blight disease and enhance the plant growth and yield in rice. J Phytopathol. 153(11/12): 697- 701.

123. Matsumoto, M., Matsuyama, N. (1998). Trials for identification of *Rhizoctonia solani* AG 1-IA, the causal agent of rice sheath rot disease using specifically primed PCR analysis in diseased plant tissues. Bull Inst Trop Agri, Kyushu University. 21: 27–32.

124. Meena, B., Ramamoorthy, V., Muthusamy, M. (2002). Effect of some plant extracts on sheath blight of rice. Curr Res. 31(3/4): 49-50.

125. Mew, T. W., Rosales, A. M. (1992). Control of *Rhizoctonia* sheath blight and other diseases by rice seed bacterization. In E. S. Tjamos, G. C. Papavizas & R. J. Cook (eds). Biological Control of Plant Diseases (pp. 113-123), Plenum Press, New York.

126. Min, J.S., Kim, S.K., Kim, S.W., Jung, J.H., Lamsal, K., Kim, S.B., Jung, M., Lee, Y.S. (2009). Effect of colloidal silver nanoparticles on sclerotium-forming phytopathogenic fungi. The Plant Pathol J. 25(4): 376-380.

127. Miyake, I. (1910). Studies uber die pilze der Reispflanze in Japan. J Coll Agri, Tokyo. 2:237-276.

128. Mohammadi, M., Banihashemi, M., Hedjaroude, G. A., Rahimian, H. (2003). Genetic diversity among Iranian isolates of *Rhizoctonia solani* Kühn anastomosis group1 subgroups based on isozyme analysis and total soluble protein pattern. J Phytopathol. 151(3): 162–170.

129. Mutuko, J. M., Nose, A. (2012). Activities in rice plants responding to *Rhizoctonia solani* Kuhn infection: Activation of Gycolysis and connection to Phenylpropanoid pathway. Plant Cell Physiol. 53(6): 1017-1032.

130. Mutuko, J.M., Nose, A. (2010). *Rhizoctonia solani* infection in two rice lines increases mRNA expression of metabolic enzymes genes in glycolytic, oxidative pentose phosphate pathways and secondary metabolism. Trop Agri Dev. 54: 119-131.

131. Naeimi, S., Khosravi, V., Hoda, H., Shokri, Marzangoo, R., Oskou, T., Omrani, M., Bagheri, F. (2011). Biological control of rice sheath blight with promising *Trichoderma* strains in paddy fields. AGRIS. 21(2): 34.

132. Nagarajkumar, M., Bhaskaran, R., Velazhahan, R. (2004). Involvement of secondary metabolites and extracellular lytic enzymes produced by *Pseudomonas fluorescens* in inhibition of *Rhizoctonia solani,* the rice sheath blight pathogen. Microbiol Res. 159(1): 73-81.

133. Nagarajkumar, M., Jayaraj, J., Muthukrishnan, S., Bhaskaran, R., Velazhahan, R. (2005). Detoxification of oxalic acid by *Pseudomonas fluorescens* strain PfMDU2: Implications for the biological control of rice sheath blight caused by *Rhizoctonia solani.* Microbiol Res. 160: 291-298.

134. Nagaraju, P., Naresh Dronavalli, Biradar, D.P. (2002). Biological control of sheath blight (*Rhizoctonia solani*) in transplanted rice (*Oryza sativa*). Indian J Agri Sci. 72(5): 306-307.

135. Naidu, V. D. (1992). Influence of sheath blight of rice on grain and straw yield in some popular local varieties. J Res Assam Agri Uni. 10: 78-80.

136. Nandakumar, R., Babu, S., Kalpana, K., Raguchander, T., Balasubramanian, P., Samiyappan, R. (2007). Agrobacterium-mediated transformation of indica rice with chitinase gene for enhanced sheath blight resistance. Biologia Plantarum. 51: 142–148.

137. Narayanasamy, P. (2011). Detection of fungal pathogens in plants. In Microbial plant pathogens–detection and disease diagnosis (pp 5–199). Springer, Netherlands.

138. Neeraja, C.N., Shenoy, V.V., Reddy, C.S., Sarma, N.P. (2003). Isozyme polymorphism and virulence of Indian isolates of the rice sheath blight fungus. Mycopathol. 156(2): 101-108.

139. Nejad, M.S., Bonjar, G.H.S., Khatami, M., Amini, A., Aghighi, S. (2017). *In vitro* and *in vivo* antifungal properties of silver nanoparticles against *Rhizoctonia solani,* a common agent of rice sheath blight disease. IET Nanobiotechnol. 11(3): 236–240.

140. Nejad, S.M., Khatami, M., Bonjar, G.H.S. (2015). *Streptomyces somaliensis* mediated green synthesis of silver nanoparticles. Nanomedicine J. 2(3): 233–238.

141. Nishizawa, Y., Nishio, Z., Nakazono, K., Soma, M., Nakajima, E., Ugaki, M. (1999). Enhanced resistance to blast (*Magnaporthe grisea*) in transgenic japonica rice by constitutive expression of rice chitinase. Theor Appl Genet. 99: 383–390.

142. Nose, A., Wasano, K., Damson, J. (2000). Possibilities for developing sustainable rice cultivars; a case study on resistant rice lines to sheath blight. Japnese J Crop Sci. 71: 298-299.

143. Ogoshi, A. (1984). Studies on the taxonomy of the genus *Rhizoctonia.* Ann Phytopathol Soc Japan. 50: 307-309.

144. Ogoshi, A. (1987). Ecology and pathogenecity of anastomosis and intraspecific groups of *Rhizoctonia solani* Kuhn. Ann Rev Phytopathol. 25(1): 125-143.

145. Ogoshi, A. (1996). The genus *Rhizoctonia*. In B. Sneh, S. Jabaji-Hare, S. Neate & G. Dijst (eds), Rhizoctonia species: Taxonomy, molecular biology, ecology, pathology and disease control (pp 1-9), Dordrecht: Kluwer.

146. Okubara, P. A., Schroeder, K. L., Paulitz, T. C. (2008). Identification and quantification of *Rhizoctonia solani* and *R. oryzae* using real-time polymerase chain reaction. Phytopathol. 98: 837-847.

147. Ouda, S. M. (2014). Antifungal activity of silver and copper nanoparticles on two plant pathogens, *Alternaria alternata* and *Botrytis cinerea.* Res J Microbiol. 9: 34–42.

148. Pal, S., Tak, Y., Song, J. (2007). Does the antibacterial activity of silver nanoparticles depend on the shape of the nanoparticle: a study of the gramnegative bacterium *Escherichia coli*. Appl Environ Microbiol. 73: 1712–1720.

149. Palo, M. A. (1926). *Rhizoctonia* diseases of rice. A study of the disease and of the influence of certain conditions upon viability of the sclerotial bodies of the causal fungus. Philippine Agriculture 15: 361-376.

150. Paracer, C. S., Chahal, D. S. (1963). Sheath blight of rice caused by *Rhizoctonia solani* Kühn – A new record in India. Curr Sci., 32: 328-329.

151. Parmeter, J. R. Whitney, H. S. (1970). Taxonomy and nomenclature of the imperfect state. In J. R. Parmeter (ed) Rhizoctonia solani, Biology and Pathology (pp 7-19) University of California Press, Berkeley, Los Angeles and London.

152. Parmeter, J.R., Sherwood, R. T. Platt, W. D. (1969). Anastomosis grouping among isolates of *Thanatephorus cucumeris.* Phytopathol., 59: 1270-1278.

153. Parmeter, J. R. (1970). *Rhizoctonia solani*: Biology and Pathology (pp 255). University of California Press, Berkeley, Los Angeles and London.

154. Parween, D., Sultan, E., Dalei, K., Sahu, B. B. (2019). Arabidopsis PEN2, a promising gene in upraising penetration resistance against rice necrotrophic fungus *Rhizoctonia solani.* Peer J Preprint., **7**: e27611v1.

155. Patel, J. S., Brennan, M. S., Khan, A., Ali, G. S. (2014). Implementation of loop-mediated isothermal amplification methods in lateral flow devices for the detection of *Rhizoctonia solani.* Can J Plant Pathol., 37: 118-129.

156. Patkar, R. N., Chattoo, B. B. (2006). Transgenic indica rice expressing ns-LTP-like protein shows enhanced resistance to both fungal and bacterial pathogens. Mol Breed., 17: 159-171.

157. Pedersen, E. A., Hughes, G. R. (1992). The effect of crop rotation on development of the septoria disease complex on spring wheat in Saskatchewan. Can J Plant Pathol., 14: 152–158.

158. Peltonen, S. (1995). Comparison of xylanases production by fungal pathogens of barley with special preference to *Bipolaris sorokiniana.* Mycol Res., 99: 717-723.

159. Pramesh, D. M., Saddamhusen, A., Muniraju, K. M., Guruprasad, G. S. (2017). A new combination fungicide active ingredients for management of sheath blight disease of paddy. Adv Res., 8(5): 1-7.

160. Punja, Z. K. (2006). Recent developments towards achieving fungal disease resistance in transgenic plants. Can J Plant Pathol., 28: S298-308.

161. Raji, P., Sumiya, K.V., Dhany, S., Sheela, M.S., Narayanankutty, M.C. (2016). Promising fungicides for the management of sheath blight of rice. Int J Agri Sci Res., 6(1): 273-278.

162. Rao, T. B., Chopperla, R., Methre, R., Punniakotti, E., Venkatesh, V., Sailaja, B., Reddy, M. R., Yugander, A., Laha, G. S., Madhav, M. S., Sundaram, R., Ladhalakshmi, D., Balachandran, S. M., Mangrauthia, S. K. (2019). Pectin induced transcriptome of a *Rhizoctonia solani* strain causing sheath blight disease in rice reveals insights on key genes and RNAi machinery for development of pathogen derived resistance. Plant Mol Biol., 100: 59-71.

163. Ren, X. P., Xie, G. L., Wang, X. (2006). Application and colonization of *Pseudomonas aeruginosa* ZJ1999 for biocontrol of *Rhizoctonia solani,* pathogen of rice sheath blight. Chinese J Biol Cont., 22(1): 54-57.

164. Richa, K., Tiwari, I. M., Devanna, B. N., Botella, J. R., Sharma, V., Sharma, T. R. (2017). Novel Chitinase gene LOC_Os11g47510 from Indica Rice Tetep provides enhanced resistance against sheath blight pathogen *Rhizoctonia solani* in Rice. Front Plant Sci., 8:596.

165. Richa, K., Tiwari, I.M., Kumari, M., Devanna, B.N., Sonah, H., Kumari, A. (2016). Functional characterization of novel chitinase genes present in the sheath blight resistance QTL: qSBR11-1 in rice line tetep. Front Plant Sci., 7: 244.

166. Rodrigues, F. A., Datnoff, L. E. (2005). Silicon and rice disease management. Fitopatologia Brasileira 30(5): 457-469.

167. Rush, M, C., Lee, F. N. (1992). Sheath blight. In R. K. Webster & P. S. Gunnel (eds). Compendium of rice diseases (pp 22-23), American Phytopathological Society, St. Paul, M. N.

168. Rush, M. C. (1999.) Tagging major quantitative trait loci for sheath blight resistance in a rice variety Jasmine 85. Chinese Sci Bullet 44: 1783–1789.

169. Sareena, S., Poovannan, K., Kumar, K. K., Raja, J. A. J., Samiyappan, R, Sudhakar, D., Balasubramania, P. (2006)**.** Biochemical responses in transgenic rice plants expressing a defence gene deployed against the sheath blight pathogen, *Rhizoctonia solani.* Curr Sci.**,** 91: 1529–1532.

170. Sato, H., Ideta, O., Ando, I., Kunihiro, Y., Hirabayashi, H., Iwano, M., Miyasaka, A., Nemoto, H., Imbe, T. (2004). Mapping QTLs for sheath blight resistance in the rice line WSS2. Breed Sci. 54(3): 265–271.

171. Savary, S., Mew, T. W. (1996). Analyzing crop losses due to *Rhizoctonia solani*: rice sheath blight, a case study. In B. Sneh, S. Jabaji-Hare, S. Neate & G. Dijst (eds). Rhizoctonia species: Taxonomy, molecular biology, ecology, pathology and disease control (pp 1-9), Dordrecht: Kluwer.

172. Sayari, M., Babaeizad, V., Ghanbari, M.A.T., Rahimian, H. (2014). Expression of the pathogenesis related proteins, NH-1, PAL, and Lipoxygenase in the Iranian Tarom and Khazar rice cultivars, in reaction to *Rhizoctonia solani*- The causal agent of rice sheath blight. J Plant Protect Res. 54: 36–43.

173. Sayler, R. J., Yang, Y. (2007). Detection and quantification of *Rhizoctonia solani* AG-1 IA, the rice sheath blight pathogen, in rice using real-time PCR. Plant Dis. 91: 1663-1668.

174. Shah, J.M., Raghupathy, V., Veluthambi, K. (2009). Enhanced sheath blight resistance in transgenic rice expressing an endochitinase gene from *Trichoderma virens*. Biotechnol Lett. 31: 239–244.

175. Shah, J.M., Singh, R., Veluthambi, K. (2013). Transgenic rice lines constitutively co-expressing *tlp-D34* and *chi11* display enhancement of sheath blight resistance. Biologia Plantarum. 57: 351–358.

176. Sharon, M., Kuninaga, S., Hyakumachi, M., Sneh, B. (2006). The advancing identification and classification of *Rhizoctonia* spp. using molecular and biotechnological methods compared with the classical anastomosis grouping. Mycosci. 47: 299–316.

177. Shu, C., Chen, J., Sun, S., Zhang, M., Wang, C., Zhou, E. (2015). Two distinct classes of protein related to GTB and RRM are critical in the sclerotial metamorphosis process of *Rhizoctonia solani* AG-1 IA. Funct Integra Genomic. 15(4):449-59.

178. Silva, J., Scheffler, B., Sanabria, Y., De Guzman, C., Galam, D., Farmer, A., Woodward, J., May, G., Oard, J. (2012). Identification of candidate genes in rice for resistance to sheath blight disease by whole genome sequencing. Theor Appl Genet. 124(1):63-74.

179. Singh, A., Singh, V. K., Singh, S. P., Pandian, R. T. P., Ellur, R. K., Singh, D., Bhowmick, P. K., Gopala Krishnan, S., Nagarajan, M., Vinod, K. K., Singh, U. D., Prabhu, K. V., Sharma, T. R., Mohapatra, T., Singh, A. K. (2012). Molecular breeding for the development of multiple disease resistance in Basmati rice. AoB Plants. pls029.

180. Singh, R. V., Sinha, A. P. (2004). Management of rice sheath blight by *Pseudomonas fluorescens* and grain yield. Ann Plant Protect Sci. 13: 410–414.

181. Singh, R., Sunder, S., Dodan, D. S. (2010). Standardization of inoculation method in nursery beds and management of sheath blight of rice through host resistance, chemicals and botanicals. Indian Phytopathol. 63:286–291.

182. Singh, V., Lal, M.**,** Singh, G. (2013). Effect of application method of biocontrol agents on management of sheath blight and plant growth promotion of Rice. Ann Plant Protect Sci. 21(1): 215-216**.**

183. Sinha, A.P. and Prasad, G., 2008. Integrated management of sheath blight disease of rice. *Proceeding of the 19th training on "Plant Disease Management on Small Farms",* pp. 177–182. Center of Advanced Studies in Plant Pathology, G.B. Pant University and Technology, Pantnagar.

184. Sneh, B., Burpee, L., Ogoshi, A. (1991). Identification of *Rhizoctonia* species. St. Paul: The American Phytopathological Society.

185. Someya, N., Nakajima, M., Watanabe, K., Akutsu, K. (2005). Synergistic antifungal activity of the culture filtrates of *Serratia marcescens* strain B2 and chemical fungicides against the sclerotial viability of the rice sheath blight pathogen, *Rhizoctonia solani.* Biocontrol Sci. 10(3): 97-100.

186. Song, A., Xue, G., Cui, P., Fan, F., Liu, H., Yin, C., Sun, W., Liang, Y. (2017). The role of silicon in enhancing resistance to bacterial blight of hydroponic and soil cultured rice. Sci Report 6: 24640.

187. Sridevi, G., Parameswari, C., Sabapathi, N., Raghupathy, V. Veluthambi, K. (2008). Combined expression of chitinase and ß-1, 3-glucanase genes in indica rice (*Oryza sativa* L.) enhances resistance against *Rhizoctonia solani.* Plant Sci. 175: 283–290.

188. Sridevi, G., Sabapathi, N., Meena, P., Nandakumar, R., Samiyappan, R. (2003). Transgenic indica rice variety Pusa Basmati1 constitutively expressing a rice chitinase gene exhibits enhanced resistance to *Rhizoctonia solani.* J Plant Biochem Biotechnol. 12: 93–101.

189. Srinivasachary, Willocquet, L., Savary, S. (2010) Resistance to Sheath Blight (*Rhizoctonia solani* Kühn) [(Teleomorph *Thanatephorus cucumeris* (A. B. Frank) Donk.] Disease: Current Status and Perspectives. Euphytica. 178: 1–22.

190. Taheri, P., Hofte, M. (2007). Riboflavin-induced resistance against sheath blight of rice functions through the potentiation of lignin formation & Jasmonic acid signalling pathway. Commun Agri Appl Biol Sci, 72: 309-313.

191. Tan, C. X., Ji, X. M., Yang, Y., Pan, X. Y., Zuo, S. M., Zhang, Y. F., Zou, J. H., Chen, Z. X., Zhu, L. H., Pan, X. B. (2005). Identification and marker assisted selection of two major quantitative genes controlling rice sheath blight resistance in backcross generations. Acta Genetica Sinica. 32(4): 399–405.

192. Tang, J. B., Ma, B. T., Wang, L. X., Li, P., Chen, H. (2001). Biocontrol of *Rhizoctonia solani* with *Trichoderma* spp. Chinese Rice Res Newslet. 9(4): 8.

193. Tang, Q. Y., Peng, S. B., Buresh, R. J., Zou, Y. B., Castilla, N. P., Mew, T. W., Zhong, X. H. (2007). Rice varietal difference in sheath blight development and its association with yield loss at different levels of N fertilization. Field Crops Res. 102(3): 219-227.

194. Thind, T.S., Aggarwal, R. (2008). Characterization and pathogenic relationships of *Rhizoctonia solani* isolates in a potato-rice system and their sensitivity to fungicides. J Phytopathol. 156(10): 615-621.

195. Thornton, C. R., Andrew, C. G., Forrest, R., Lamotte, R. (2004). A one-step, immuno-chromatogarphic lateral flow device specific to *Rhizoctonia solani* and certain related species, and its use to detect and quantify *R. solani* in soil. Phytopathol. 94: 280-288.

196. Tiwari, I. M., Jesuraj, A., Kamboj, R., Devanna, B. N., Botella, J. R., Sharma, T. R. (2017). Host delivered RNAi, an efficient approach to increase rice resistance to sheath blight pathogen (*Rhizoctonia solani*). Sci Report **7**: 7521.

197. Uchimiay, H., Iwata, M., Nojiri, C., Samarajeewa, P. K., Takasatsu, S., Ooba, S., Anzai, H., Christensen, A. H., Quail, P. H., Toki, S. (1993). Bialaphos treatment of transgenic rice plants expressing a *Bar* gene prevents infection by the sheath blight pathogen (*Rhizoctonia solani*). Nature Biotechnol. 11: 835–836.

198. Umaerus, V. R., Scholte, K., Turkensteen, L. J. (1989). Crop rotation and the occurrence of fungal diseases in potatoes. In J. Vos, C.D. Van Loon & G.J. Bollen (eds). Effects of crop rotation on potato production in the temperate zones (pp 171–189), Kluwer Academic, Dordrecht.

199. Vaish, D. K., Sinha, A. P. (2004). Characterization of isolates of *Trichoderma spp.* for their biocontrol ability against *Rhizoctonia solani.* Indian J Plant Pathol. 22:123–127.

200. Vaish, D. K., Sinha, A. P. (2006). Evaluation of fungal antagonists against *Rhizoctonia solani* causing sheath blight of rice. Indian J Agri Res. 40: 79–85.

201. van Loon, L. C., Rep, M., Pieterse, C.M. (2006). Significance of inducible defense-related proteins in infected plants. Ann Rev Phytopathol. 44: 135–162.

202. Venu, R. C., Jia, Y., Gowda, M., Jia, M. H., Jantasuriyarat, C., Stahlberg, E., Li, H., Rhineheart, A., Boddhireddy, P., Singh, P., Rutger, N., Kudrna, D., Wing, R., Nelson, J. C., Wang, G. L. (2007). RL-SAGE and microarray analysis of the rice transcriptome after *Rhizoctonia solani* infection. Mol Geneti Genom. 278(4):421-31.

203. Wang, M. Q. (2005). Effect of complete silicon fertilizer on rice yield. Acta Agriculturae Shanghai. 21(1): 71-73.

204. Wang, R., Lu, L., Pan, X., Hu, Z., Ling, F., Yan, Y., Liu, Y., Lin, Y. (2015). Functional Analysis of OsPGIP1 in rice sheath blight resistance. Plant Mol Biol. 87: 181–191.

205. Wang, F., Wang, C., Liu, P., Lei, C., Hao, W., Gao, Y., Liu, Y.G., Zhao, K. (2016). Enhanced rice blast resistance by CRISPR/Cas9-targeted mutagenesis of the ERF transcription factor gene OsERF922. PLoS One. 11: e0154027.

206. Webster, J., Weber, R. W. S. (2007). Introduction to fungi. Cambridge University Press.

207. Webster, R. W., Gunnel, P. S. (1992). Compendium of Rice diseases, (pp: 22-23). American Phytopathological Society, Minnesota, U. S. A.

208. Wu, W., Shah, F., Shah, F., Huang, J. (2014). Rice sheath blight evaluation as affected by fertilization rate and planting density. Austral Plant Pathol. 44: 183–189.

209. Xue, X., Cao, Z. X., Zhang, X. T., Wang, Y., Zhang, Y. F., Chen, Z. X., Pan, X., Zuo, S. M. (2016). Overexpression of OsOSM1 enhances resistance to rice sheath blight. Plant Dis. 100: 1634-1642.

210. Yang, X. T., Lin, X. Q., Wang, X. H., Luo, S. Z. (2008). Effects of different transplanting patterns on grain yield and disease resistance of super hybrid rice. Acta Agriculturae Zhejiangensis, 20(1): 6-9.

211. Yang, G., Li, C. (2012). General description of *Rhizoctonia* species complex. In: C.J. Cumagun (ed) Plant Pathology (pp. 41–52).

212. Yu, Y. Y., Jiang, C. H., Wang, C., Chen, L. J., Li, H. Y., Xu, Q., Guo, J. H. (2017). An improved strategy for stable biocontrol agents selecting to control rice sheath blight caused by *Rhizoctonia solani.* Microbiol Res. 203: 1-9.

213. Zhang, J., Chen, L., Fu, C., Wang, L., Liu, H., Cheng, Y., Li, S., Deng, Q., Wang, S., Zhu, J., Liang, Y., Li, P., Zheng, A. (2017). Comparative transcriptome analyses of gene expression changes triggered by *Rhizoctonia solani* AG1 IA infection in resistant and susceptible rice varieties. Front Plant Sci. 8:1422.

214. Zhang, J., Zhao, W., Fu, R., Fu, C., Wang, L., Liu, H., Li, S., Deng, Q., Wang, S., Zhu, J., Liang, Y., Li, P., Zheng, A. (2018). Comparison of gene co-networks reveals the molecular mechanisms of the rice (*Oryza sativa L.*) response to *Rhizoctonia solani* AG1-IA infection. Funct Integra Genomic, 18(5): 545-557.

215. Zhang, Y., Zhang, F., Li, X., Baller, J. A., Qi, Y., Starker, C. G., Bogdanove, A. J., Voytas, D. F. (2013). Transcription activator-like effector nucleases enable efficient plant genome engineering. Plant Physiol. 161: 20–27.

216. Zhao, C. J., Wang, A. R., Shi, Y. J., Wang, L. Q., Liu, W. D., Wang, Z. H., Lu, G. D. (2008). Identification of defense-related genes in rice responding to challenge by *Rhizoctonia solani.* Theor Appl Genet. 116(4):501-16.

217. Zheng, A., Lin, R., Zhang, D., Qin, P., Xu, L., Ai, P., Ding, L., Wang, Y., Chen, Y., Liu, Y., Sun, Z., Feng, H., Liang, X., Fu, R., Tang, C., Li, Q., Zhang, J., Xie, Z., Deng, Q., Li, S., Wang, S., Zhu, J., Wang, L., Liu, H., Li, P. (2013). The evolution and pathogenic mechanisms of the rice sheath blight pathogen. Nature Commun. 4: 1424.

218. Zhou, M. Y., Wang, A. J., Liu, L. M., Huang, S. W. (2015). Synergistic effects of potential biocontrol bacterium H158 mixed with fungicides against the pathogen of rice sheath blight. China Rice. 21: 60-65.

219. Zuo, S. M., Yin, Y. J., Pan, C. H., Chen, Z. X., Zhang, Y. F., Gu, S. L., Zhu, L. H., Pan, X. B. (2013). Fine mapping of qSB-11LE, the QTL that confers partial resistance to rice sheath blight. Theor Appl Genet. 126(5): 1257–1272.

220. Zuo, S. M., Zhang, Y. F., Yin, Y. J., Li, G. Z., Zhang, G. W., Wang, H., Chen, Z. X., Pan, X. B. (2014). Fine-mapping of qSB-9TQ, a gene conferring major quantitative resistance to rice sheath blight. Mol Breed 34(4): 2191–2203.