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**Review Article**

# Rice Sheath Blight: Major Disease in Rice

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**A B S T R A C T**

Rice production worldwide is affected by various biotic and abiotic stresses. Among biotic stresses, diseases are considered as major constraints for rice production, in which rice sheath blight caused by *Rhizoctonia solani* [Teleomorph: *Thanatephorus cucumeris* (Frank) Donk] is one of the most important diseases with ability to cause major damage to crop, where intensive agriculture is carried out. *Rhizoctonia solani* have wide host range and still now there is no complete resistance source has been identified for this disease, so management of sheath blight primarily relies on chemical control. However, recently Many QTLs governing resistance to sheath blight were identified worldwide. In this article, the information available on various aspects of Rice and Rice Sheath Blight disease has been presented and discussed along with future strategies for disease management.

## Introduction

Rice is one of the important food crops and provides an essential part of the daily dietary intake for nearly half of the world's population (Maclean *et al.,* 2002). However, rice production worldwide is affected by various biotic and abiotic stresses (Richa *et al.,* 2016). Among biotic stresses, diseases are considered as major constraints for rice production as 10 to 30 per cent of the annual rice harvest is lost due to infection by many diseases. (Skamnioti and Gurr, 2009). Of different diseases, the most common and severe diseases in rice are blast and sheath blight (Wopereis *et al.,* 2009). Rice sheath blight disease caused by *Rhizoctonia solani* has led to large scale yield losses, especially in U.S.A, Japan, China, and India, where intensive agricultural practices are being followed (Gautam *et al.,* 2003). While, under favourable environmental conditions, sheath blight fungus can reduce yield by up to 50 % (Richa *et al.,* 2016).

### Rice and its importance

Rice (*Oryza sativa*) belongs to the genus *Oryza* (Family: Poaceae) which includes two cultivated and more than 25 wild species that are either perennial or annual, and diploid or tetraploid. The cultivated species are *Oryza sativa* L. and *Oryza glaberrima* L. The species *Oryza sativa* is composed of three sub species, *indica*, *japonica* and *javanica* (Gowda *et al.,* 2003).

The *inidica* is predominately tropical subspecies, while *japonica* is of temperate type and *javanica* is grown in equatorial region. The genetic diversity of *indica* sub species is thought to be more than japonica varieties (Zhang *et al.,* 1992).

Rice was domesticated probably in north-eastern India and southern China about 8000 years ago and is the staple food for more than 50 % of the world's population (Gowda *et al.,* 2003). It accounts for over 20 % of global calorie intake. Over 90 % of the world's rice is produced and consumed in the Asian region with 6 countries (China, India, Indonesia, Bangladesh, Vietnam and Japan) accounting for about 80 % of the world's production and consumption (Abdullah *et al.,* 2015).

Even though the world's rice production increased from 257 million tons in 1966 to 600 million tons in 2000, the increase has not matched the demand for rice because of the corresponding increase in the human population. It is estimated that rice production must increase by at least 40 % by 2030 to meet ever-increasing demands (Ashkani *et al.,* 2015). Rice yield growth has reached a plateau and no significant increase is being realized in productivity levels. In addition to this, continuous rise in population has resulted in decreased in per capita consumption of rice in the world from 68.6 Kg 64.2 Kg and in India from 86.8 Kg to 64.2 Kg in 1990 and 2002, respectively (Abdullah *et al.,* 2015).

India is one of the largest producers of cereal as well as the largest exporter of cereal products worldwide. India's export of cereals during 2013–14 stood at Rs. 63,452.09 cores. Rice (including basmati and non-basmati) occupies the most sizable share in India's total cereals export with 64.40 % during this period. Countries such as Iran, Saudi Arabia, Indonesia, UAE, and Bangladesh mainly imported cereals from India during 2013–14 (Khatkar *et al.,* 2016).

## Major constraints of rice production

The major rice production constraints in India are drought and submergence, bacterial blight, leaf blast, sheath blight, weeds, brown plant hopper and poor soil fertility. Besides these biotic and abiotic stresses poor management practices such as low input use, inappropriate plant spacing, late sowing and selection of wrong cultivars are some of the other technical constraints (Jha *et al.,* 2012). The projected losses due to biotic stresses range from 15 to 85 per cent (Rola and Widawsky, 1998).

Insect-pests are serious yield reducing constraints for rainfed rice production in the eastern India. Damage caused by the insect-pests is one of the major components of yield gap accounting nearly 30 per cent of the difference between potential and actual farm yield (Jha *et al.,* 2012).Weeds are other important constraint as they compete with the rice crop and lead to 10 to 65 % loss in rice production (Rola and Widawsky, 1998).

Diseases are very important constraints for rice production. Occurrence of various diseases in rice varieties grown in India is very common. As a result an average yield loss of 25-30 per cent per annum due to diseases is a regular feature in India (Jha *et al.,* 2012). Among all the diseases of rice, the most common and severe diseases are blast and sheath blight.

## Rice genome

Rice *(Oryza sativa* L.) is a true diploid (2n=24) with twelve chromosome pairs and 12 linkage groups. Because of having smallest genome size (430 Mb), availability of high density genetic map, relative ease of transformation, cultivar development through pollen and anther culture and synteny with other major cereals, rice is considered as a model crop (Jena and Mackill, 2008). The draft sequences of rice genome for *indica* (LYP9) and *japonica* (Nipponbare) have been made available to public (Yu *et al.*, 2002).

With the genome sequence of rice now readily available (Goff *et al.*, 2002, Takashi *et al.*, 2005), the breeding and biotechnological methods can be efficiently utilized to achieve the objective of producing more rice per unit area. Further, with the advent of genomics and biotechnological methods new gene of interest for biotic or abiotic stress can be identified which can be further utilized for crop improvement. The sequence of rice enabled to development of high density genetic SSR maps which could be effectively utilized for rice breeding programmes.

## Rice Sheath blight

### History and Geological Distribution

Sheath blight, also known as 'oriental sheath and leaf blight' of rice caused by *Rhizoctonia solani* Kuhn [Teleomorph: *Thanatephorus cucumeris* (Frank) Donk] was first reported in Japan by Miyake (1910) as *Sclerotium irregulare* was the causal organism of the disease. Subsequently, its occurrence was recorded throughout the temperate and tropical rice growing areas including Africa, Bangladesh, Brazil, Burma, Colombia, China, Cuba, Germany, Fiji, Formosa, India, Indonesia, Iran, Korea, Liberia, Madagascar, Malaya, Malaysia, Netherland, Nigeria, Papua New Guinea, Philippines, Russia, Senegal, Sri Lanka, Surinam, Taiwan, Thailand, Trinidad, Tobago, UK, USA, Venezuela and Vietnam (Sing *et al.*, 2016). Later it was found that the sheath blight fungus to be identical with *Hypochnus sasakii*. Similar disease was found on rice in the Philippines which was caused by *Rhizoctonia solani* group. Some scientist reported that sheath blight disease of rice from Ceylon and referred the causal organism as *Rhizoctonia solani* Kuhn. Again similar disease was reported from USA as 'banded sheath spot of rice'. Since the disease was first identified in oriental countries, it was also named as 'Oriental sheath blight of rice' (Ou *et al.*, 1973).

In India, Butler (1918) first noticed the sheath blight disease, with symptoms similar to those of banded sclerotial disease of sugarcane. Later, Paracer and Chahal (1963) reported the presence of this disease from Gurdaspur district in Punjab. They described the disease as sheath blight of rice caused by *Rhizoctonia solani.* This disease has become a major production constraint in Punjab, Haryana, eastern Uttar Pradesh, Uttarakhand, Bihar, West Bengal, Odisha, Chhattisgarh, Andhra Pradesh, Tamil Nadu, Karnataka, Kerala, Jammu and Kashmir, Madhya Pradesh, Assam, Manipur and Tripura (DRR, 2006-2010) due to wide spread cultivation of high yielding rice varieties with a narrow genetic base, heavy dependency on chemical fertilizers and apparent change in climate.

### Economic importance

Sheath blight disease of rice (*Oryza sativa* L.), caused by *Rhizoctonia solani* Kuhn has assumed economic importance in the last two decades with the introduction of modern semi dwarf nitrogen responsive cultivars. It is one of the most destructive rice diseases worldwide and can lead to severe losses in rice productivity and grain quality by infecting and destroying rice sheath and leaves (Marchetti and Bollich, 1991). It occurs in all rice production areas worldwide. The disease is particularly important in intensive rice production systems. Yield losses of 5–10 % have been estimated for tropical lowland rice in Asia (Savary *et al.,* 2000). The pathogen has a wide host range and can infect plants belonging to more than 32 families and 188 genera (Srinivasachary *et al.,* 2011).

The sheath blight was in epidemic form in the districts of Srikakulm and Vijayangaram of Andhra Pradesh during 1993 and 1994 (Mathur *et al.,* 1999). Chahal in 2005 reported that sheath blight of rice caused severe loss in Punjab in the years 1978, 2003 and 2004. The yield loss due to sheath blight ranges between 20-50 per cent depending on the severity of infection (Rao, 1995). The estimation of losses due to sheath blight of rice in India has been reported to be up to 54.3 per cent (Chahal, 2003). It has been reported that in China 15 to 20 million hectares of rice field affected by sheath blight lead to yield losses of 6 million tonnes every year (Chen *et al.,* 2012). In 2012, sheath blight affected about 491,932 ha of rice in Japan (JPPA 2013). In the USA, crop losses due to rice sheath blight have been recorded up to 50 % in susceptible cultivars (Prasad and Eizenga 2008). A crop loss of up to 40 % has been recorded in Bangladesh (Shahjahan *et al.,* 1986).

In Karnataka the disease was recorded in low to moderate form with disease severity ranging from 6-15%. In poorly managed fields high intensity (>50 %) of the disease was recorded in some private varieties and hybrids. During 2015, disease severity of > 60 % was recorded in hybrid PAC 837 and Tata akshay in Mandya and Mysuru district (Chetana *et al.,* 2016)

Several researchers have screened thousands of germplasm and no absolute resistance to sheath blight disease in rice germplasm has been reported so far.

The reason being resistance to sheath blight is governed by several minor genes or QTL each with small effect. Only moderate resistance to sheath blight has been reported in rice germplasm like Jasmine 85 (Zou *et al.,* 2000), Tetep (Channamallikarjuna *et al.,* 2010), Teqing (Zuo *et al.,* 2014), ARC l053l (Yadav *et al.,* 2015) *etc*. and about 50 QTLs have been identified (Zou *et al.,* 2000; Channamallikarjuna *et al.,* 2010; Zuo *et al.,* 2014).

## Rice Sheath blight fungus: *Rhizoctonia solani* Kuhn

Sheath blight is a fungal disease of rice caused by a necrotrophic soil-borne fungus *Rhizoctonia solani* with telomorpic stage *Thanatephorus cucumeris* (Frank) Donk, and comes under AG-1 as anastomosis group. It was first identified as a parasite of potato in 1898 by Kuhn (Hossain *et al.,* 2016). Miyake (1910) first described this disease in Japan and named the causal fungus as *Sclerotium irregulare*. Later found the fungus to be identical to *Hypochnus sasakii*, a fungus first reported by Sasakii on leaves of camphor trees (Shirai, 1906). Various workers in different places reported very similar disease *viz*. Reinking (1918) and Palo (1926) in Philippines and Park and Bertus (1932) in Sri Lanka.

*Rhizoctonia solani* is a soil borne necrotrophic pathogen and it survives either as sclerotia or mycelia in the debris of host plants. The sclerotia float to the surface of flooding water in the rice fields and germinate on rice sheaths forming infection cushions or appressoria during the infection process (Richa *et al.,* 2016).

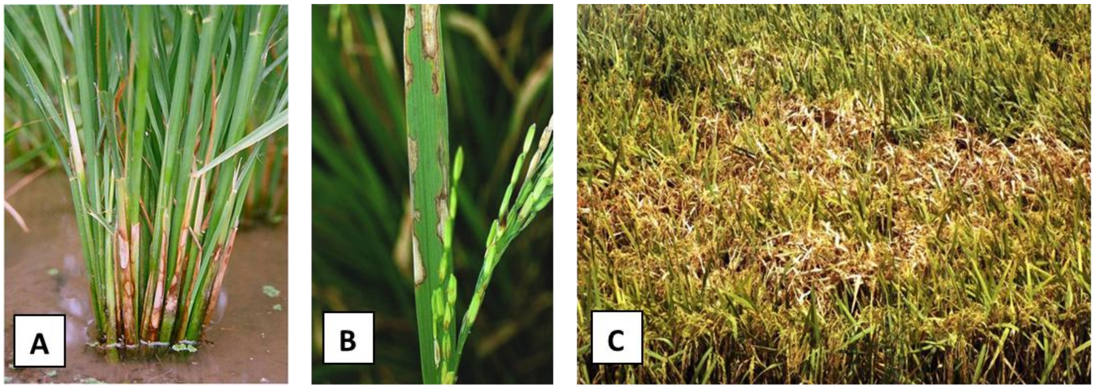


**Fig.1** Characteristic symptoms of Rice Sheath Blight Disease caused by *Rhizoctonia solani*
A: Irregular lesions on the rice sheaths during tillering; B: Many lesions on the leafs gives the appearance of snake skin; C: Field view of sheath blight affected field.

Initially the young hyphae are colourless but become yellow and ultimately brown with age, 8-12 µm in diameter with a septum near each hyphal branch and a slight constriction at the branch which tend to branch at right angles. The straight running and lobate hyphae are the two types of mycelia produced by the fungus. Lesions are produced by the straight running mycelium, which creep on the surface of plant tissue. Lobated mycelium determines the size and shape of lesions which are produced in patches of varying size (Ou, 1973).

According to Hashiba and Mogi (1975), *R. solani* sclerotia is composed of cluster of melanin encrusted thick walled hyphae rich in nutrients formed by increased branching from short, thick, lateral hyphae. It is difficult to separate the sclerotia from surrounding embedding mycelia, when produced on living leaf sheath. Individual sclerotia may be up to 5 mm in diameter. The shape of the sclerotia is roughly spherical or somewhat flattened and irregular. Young sclerotia are composed of compact masses of hyphal cells about 5 µm wide, the cell wall 0.9 µm thick.

## Symptoms

The disease was named as 'Sheath blight' because of its primary infection on leaf sheath. The most critical stage for the infection to occur was at maximum tillering stage, while leaf sheath becomes discoloured at or above water level. Initially the disease appears on leaf sheath as elliptical or oval to irregular, 1-3 cm long, greenish gray spots with brown margin at or above the water line. Presence of many such spots on the leaf sheath gives the appearance of snake skin (Fig 1). Under favourable conditions, the infection spreads rapidly to the upper plant parts and also to the neighbouring plants by means of normal emergence and expansion of the ears and results in poor filling of the grains. The pathogen is also known to cause panicle infection resulting in production of unfilled or partially filled discoloured seed bearing brownish black spots or black to ashy gray patches (Singh *et al.*, 2016). Sometimes the disease produce large lesions which are irregularly elongated and appear on any part of the leaf sheath and sometimes, extending on to the leaf blade. The disease attacks the leaf sheath, leaf blades and in severe cases symptoms also observed on emerging panicles (Rangaswamy and Mahadevan, 1998). However, at maximum tillering and ear head phase, the rice crop is most vulnerable to sheath blight pathogen (Singh *et al.,* 1988). Sheath blight pathogen in advanced stage of infection and disease development forms brown sclerotia, which are easily detached from the affected plant parts.

## Disease cycle

Although basidiospores produced by *Thanatephorus cucumeris* on host plant can initiate infection, it is generally considered unimportant in the epidemiology of rice sheath blight. The pathogen survives through sclerotia and mycelia in infected plant debris/straw and also through weed hosts in tropical environments while in temperate regions, primary source of inoculum is sclerotia. In double cropped areas, the fungus perpetuated through ratoons acting as a source of primary inoculum. Agricultural operations such as ploughing, leveling, transplanting and weeding help the surviving sclerotia to come at water surface and make the initial contacts with the host. Rain water runoff and flood irrigation permit good dispersal of floating sclerotiaand consequently provide the primary foci of infection (Singh *et al.,* 2016).

The pathogen has a very wide host range of 250 plant species, including commercially grown crops (Chahal *et al.,* 2003). It has been reported to infect 188 species in 32 families in Japan, 20 species belonging to 11 families in Taiwan and 10 grasses and a *Cyperus sp*. in Thailand (Dath, 1990). In India, Roy (1993) reported 62 economic plants and weeds belonging to 20 families including maize, sorghum, fingermillet, pearlmillet, sugarcane, spinach, lettuce, greengram, blackgram, soybean, pigeonpea, *Brassica spp*., turmeric and common or golden polypody (*Polypodium sp*.) as alternate hosts of the pathogen. Beside these, several other cultivated and weed plants viz. *Pennisetumm americanum, Solanum tuberosum, Cynodon dactylon, Digitaria adscendus, Echinochloa crusgalli* and *Cyperus rotundus* (Chahal *et al.,* 2003); *E. colona, Euphorbia microphylla, Leptochloa chinensis, Dactyloctenium aegypticum, Dicanthium annulatum and Paspalum distichum* (Singh *et al.,* 2012); wheat, jowar, ragi, sugarcane, *Digitaria ciliaris, Euphorbia hirta, Paspalum scrobiculatum* and *Commelina benghalensis* (Lenka *et al.,* 2014) were also found to be infected by the pathogen.

In addition, the seed-borne nature of the pathogen has also been established. The seed infection and transmission of the pathogen from seed to seedlings in the form of brownish black to blackish discoloured lesions on coleoptile, radical, leaf and sheath varied from 9.9- 39.1 % and 4.6-14.0 % under field conditions (Sivalingam *et al.,* 2006).

## Epidemiology

*R. solani* can attack rice plants at any growth stage (Dath, 1990) but disease incidence and severity increase with increase in plant age (Singh *et al.,* 2004) and the resistance and susceptibility in rice genotypes were better differentiated on mature plants than on seedlings (Dath, 1990).

In China, development of Sheath blight was observed to be slow at early growth stages but it was rapid at tillering and later growth stages (Thind *et al.,* 2008). In nursery beds, the maximum disease intensity was recorded in 30-40 days old seedlings (Singh *et al.,* 2010).

Maximum air temperature, morning relative humidity and leaf wetness have been reported to be the key factors for disease development in the field (Biswas *et al.*, 2011). The maximum disease development was recorded at a temperature range of 25-30°C and 80-100 % RH (Bhunkal *et al.*, 2015a).

Sheath blight occurred more severely in crop canopy with high contact frequency between tissues (Huang *et al.*, 2007), in early maturing and short, high tillering and compact cultivars (Bhunkal*et al.*, 2015b). However, in southern United State, short and medium grain *japonica* type rice possessed higher level of resistance than long grain *indica* type cultivars (Lee and Rush, 1983).

Disease severity and yield loss from sheath blight increased with increasing N levels (Tang *et al.*, 2007). The disease severity was observed to be less with the slow release nitrogen fertilizer crotonilidine diurea, guanyl urea phosphate, silica, phosphorus alone and in combination with potash (Dath, 1990). Enhancement in the dose of N and P application decreased incubation period and phenolic contents and increased the disease severity while the trend was reverse with the application of K, Zn, S and Fe (Prasad *et al.*, 2010). Soil amendment with neem cake, FYM, vermi-compost and rice husk (Senapoty, 2010) and spray of the Ganoderma diethyl ester formulation (Sajeena *et al.*, 2008) reduced the disease considerably.

## Sources of resistance

Although extensive efforts have been made to identify resistant sources against sheath blight in different parts of the world, yet high level of disease resistance (qualitative resistance) has rarely been found among the cultivars, breeding lines or related wild species of *Oryza* (Nadarajah *et al.*, 2014; Lore *et al.*, 2015).

However, varieties like Swarnadhan, Radha, Pankaj, Vikramarya and few others have been reported to have moderate level of field resistance. Only few accessions of traditional rice cultivars like Tetep, Jasmine 85, Tequing, Bhasamanik, Lalsatkara, ARC 15762, ARC 18119, ARC 18275, ARC 18545, D-256, MTU 1010, YSBR 1 (Wang *et al.*, 2009; Srinivasachary *et al.*, 2011; Lore *et al.*, 2015) and selected rice lines like IR 40 and KK 2 (Singh and Dodan, 1995), HKR 99-103, HKRH 1059 and IR 64683-87-2-2-3-3 (Singh *et al.*, 2010), CN 1272-55-105, CR 2612-1-2-2-1, CR 2649-7, HKR 05-476, HKR 07-191, KJT 3-2-7-72, OR 2315-6, OR 2329-22, OR 2407-KK-19, R 1570-2144-2-1547, RP 2151-173-1, RP Bio Path 3, TRC 05-2-6-4-39-3-6, UPR 2327-23 (Agarwal and Sunder, 2013b) and N-22 (Acc. 4819), N-22 (Acc. 6264), N-22 (Acc. 19379), HKR 05-476, Tetep (Bhunkal *et al.*, 2015b) have been found to possess moderate level of resistance.

High level of resistance has been reported in rice lines LSBR 5 and LSBR 33 (Xie *et al.*, 1992) and YSBR 1 in China (Zuo *et al.*, 2009), BPL 7-12 and BML 27-1 in India (Dubey *et al.*, 2014a,b) and Pecos in Malaysia and USA (Sharma *et al.*, 2009; Willocquet *et al.*, 2011). Moderate to good level of resistance has been reported from different wild rice accessions like *O. nivara*, *O. rufipogon*, *O. meridionalis*, *O. officinalis*, *O. barthi* and *O. latifolia* (Ram *et al.*, 2008; Prasad and Eizanga, 2008).

## Quantitative trait loci (QTL) for sheath blight Resistance

The inheritance of resistance to sheath blight is not thoroughly understood. Majority of the researchers are of the view that it is a typical quantitative trait controlled by polygenes/multiple loci. However, in some rice cultivars such as Jasmine 85 and Teqing, sheath blight resistance is controlled by few major genes (Pan *et al.,* 1999). So far 60 QTLs scattered across 12 chromosomes have been identified for resistance to sheath blight (Sato *et al.,* 2004; Liu *et al.,* 2009; Sharma *et al.,* 2009; Channamallikarjuna *et al.,* 2010; Srinivasachary *et al.,* 2011; Zeng *et al.,* 2011; Zuo *et al.,* 2011; Pandian *et al.,* 2012; Dubey *et al.,* 2014a) in Tadukan, Lemont, ZYQ 8, LSBR-2, LSBR-33, Tetep, Teqing, Jasmine 85, Minghui 63 and WSS 2.

However, many of them are reported to be associated with plant morphological traits especially plant height and days to heading (Groth and Nowick, 1992). Singh *et al.,* (2012) developed improved Basmati rice lines by combining *Xa13, Xa21, Pi54* and a major QTL *qSBR 11-1* for bacterial blight, blast and sheath blight resistance through marker assisted back cross breeding. Pyramiding sheath blight resistance QTLs viz. qSB-9TQ and qSB-3TQ (Pinson *et al.,* 2005); qSB-7TQ And qSB-9TQ (Chen *et al.,* 2014) and TACTQ and morphological trait QTL qSB-9TQ (Zuo *et al.,* 2010) has been observed to be a potential approach in improving sheath blight resistance and minimizing yield loss caused by the disease.

Rice is staple food of India, to feed on growing population with continuously declining land, we need to increase the productivity by decreasing the disease incidence. Management of this disease is completely dependent on cultural practices and application of chemicals because of non-availability complete resistant donor. Still now 60 QTLs has been identified for sheath blight resistance in various varieties and some of the varieties/lines shown moderate level of resistance. A significant progress in research has been made on various aspects of the disease world-wide. However, further study is required on pathogenic variability particularly mapping of gene(s) for virulence in pathogen and resistant genes/QTLs governing disease resistance in the host. So integrated approach, host plant resistance along with cultural practices and chemical application will give better result in future for rice sheath blight.

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