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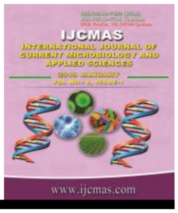

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Current Status of Rice Breeding for Sheath Blight Resistance

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ABSTRACT

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Rice is one of the three major food crops in the world. It is the staple food for most of the people of South-East Asia. Rice productivity fluctuates significantly from region to region; season to season due to biotic and abiotic stress. Sheath blight is one of the major biotic constraints in rice cultivation. It is caused by *Rhizoctonia solani Kuhn*. This disease can cause yield reduction between 20-50% depending on the severity of infection. Several genotypes reported for sheath blight resistance but none of the genotypes were found with absolute resistance. Sheath blight resistance is controlled by polygenes or quantitative trait loci (QTLs) each with small effect. Pyramiding of such QTLs is expected to increase resistance to sheath blight in the cultivars. Genetic engineering of crops with plant pathogenesis-related (PR) genes may give a promising and long-lasting solution for sheath blight disease management.

Introduction

Rice is one of the three major food crops in the world. It belongs to the genus *Oryza* and the tribe *Oryzae* of the family Gramineae (Poaceae). It is cultivating almost one fifth of the total land area covered under cereals. The United Nation declared ‘2004’ as International Year of Rice. The year's theme "Rice is life" - reflects the importance of rice as a primary food source. It is the staple food crop for more than 60% of the global population. Rice provides 21% of global human per capita energy and 15% of per capita protein (IRRI 2002). Calories from rice are particularly important in Asia, especially among the poor, where it accounts for 50-80% of daily caloric intake (IRRI, 2001). It is estimated that around 90 % and 91 % of world’s rice area and production respectively are present in Asia. But productivity of rice fluctuates significantly from region to region; season to season due to various biotic factors such as pest and diseases. The yield loss due to biotic stresses varies between 10-30% depending on severity. Rice is attacked by number of fungal, bacterial, viral and nematode diseases. Among all pathogenic organisms, fungal pathogens are limiting the rice productivity to a great extent. Blast, sheath blight and bacterial blight incidences have been reported from many rice growing areas of India. Sheath blight is one of the major biotic constraints occurring in most rice-producing areas. It is second in importance next to rice blast in reducing both grain yield and quality (Webster and Gunnell, 1992.

Sheath blight disease

Sheath blight disease caused by *Rhizoctonia solani Kuhn.* It survives either as sclerotia or mycelia in host plants' debris. Sclerotia can survive for 2 years in soil and spread during field preparation and flooding the field for irrigation (Webster and Gunnell, 1992; Brooks, 2007). During the infection process, the sclerotia germinate on rice sheaths forming infection cushions or appressoria. Then pathogen colonizes the entire plant through surface hyphae, developing new infection structures (Ou, 1985). According to Hashiba *et al.*, (1982) secondary spread of disease depends exclusively on running hyphae that progress out from the initial lesions, from the lower part of the crop canopy towards its upper part along tillers and leaves, and across adjacent plant units (individual plants or hills). This has been commonly referred to as the 'vertical' and 'horizontal' spread process. The Canopy architecture and the associated microclimate have strong effects on both the mobilization of primary inoculum and the further spread of the disease (Savary *et al*., 1995). Canopy architecture depends on a number of factors like the crop establishment method (Willocquet *et al*., 2000), fertilizer input (Cu *et al*., 1996; Slaton *et al*., 2002; Tang *et al*., 2007), and the morphology of the rice genotype itself. Microclimate with high temperature (28-32°C) and relative humidity (more than 90%) facilitates the spread of this disease (Kaur *et al*., 2015).

At early stage disease symptoms appears as circular, oblong or ellipsoid, greenish-grey water-soaked spots about 1cm long that occur on leaf sheath near the water level. Later these lesions enlarge and become oblong and irregular in outline, the center of which become grey white with brown margins. Due to the semi-saprophytic nature and uncharacterized pathogenicity mechanism of *R. solani*, it infects nearly 50 species besides rice. Earlier it was considering as minor disease of rice, but with the introduction of modern, semi dwarf nitrogen responsive cultivars it converted to major disease. Rice sheath blight can cause yield reduction between 20-50% depending on the severity of infection (Rao, 1995). In India, the estimation of losses due to this disease has been reported up to 54.3 % (Chahal *et al*., 2003).

Management of sheath blight

Sheath blight disease management is very difficult due to its wide host range. There are different control measures available for sheath blight like host resistance, cultural control, chemical control and biological control. Among all these host resistance is most valid and eco-friendly choice for almost all type of plant stress.

Host resistance

Several groups have attempted to identify sources of sheath blight resistance by screening local accessions, cultivars, landraces, and/or advanced breeding lines. Sources of sheath blight resistance have been sought for different rice-growing regions by different research groups. These studies resulted in the identification of genotypes with moderate to high levels of resistance. Summary of important Sheath Blight resistance sources reported so far in literature is presented in Table 1.

Although several genotypes reported for sheath blight resistance but none of the genotypes were found with absolute resistance (Lee and Rush, 1983; Chen *et al*., 2000; Eizenga *et al*., 2002; Jia *et al*., 2012; Dey *et al*., 2016) and their disease reaction is not consistent.

QTLs associated with sheath blight

Resistance to rice sheath blight is a complex, quantitative trait controlled by polygenes (Sha and Zhu., 1990; Li *et al* 1995; Pinson *et al*., 2005). First QTL linked to molecular marker RG118 identified by Li *et al* (1995) using F_{2-3} population of Lemont/Teqing. However, few researchers (Xie *et al*., 1992; Pan *et al*., 1999) proposed that sheath blight resistance in some rice varieties is controlled by only a few major genes. Over the past two decades, several sheath blight resistance quantitative trait loci (QTL) have been mapped and few of them are discussed here. Zou *et al* (2000) identified six QTLs *qSB-2*, *qSB-3*, *qSB-7*, *qSB-9-1*, *qSB-9-2* and *qSB-11*, contributing to sheath blight resistance, located on chromosomes 2, 3, 7, 9 and 11 respectively, using F_2 clonal population of Jasmine 85/Lemont. Sato *et al* (2004) also identified two QTLs for sheath blight resistance (*qSB-3* and *qSB-12*) on chromosomes 3 and 12 from the cross Hinohikari/WSS2//Hinohikari. $qSB\text{-}9^{Tq}$, a major QTL derived from Teqing was reported by Zuo *et al* (2008). The QTL *qSBR11-1* for sheath blight resistance was identified between the marker interval RM1233 (26.45 Mb) to sbq33 (28.35 Mb) on chromosome 11 from the population RILs of HP2216/Tetep (Channamallikarjuna *et al*., 2010)

Xu *et al* (2011) detected four QTL (*qShB1*, *qShB2*, *qShB3* and *qShB5*) using a double haploid (DH) population of 'Maybelle. Zhu *et al* (2014) identified two major rice sheath blight resistance QTLs, $qSB1\text{-}1^{HJX74}$ and $qSB11^{HJX74}$ using chromosome segment substitution lines. Two major QTLs, *qshb7.3* and *qshb9.2* positioned on the chromosome 7 and 9 also identified using BC_1F_2 mapping populations from the cross BPT-5204/ARC10531 (Yadav *et al*., 2015). But so far, identified QTLs have not been utilized in development of sheath blight resistant cultivars and their breeding value has not been assessed. The reported QTLs for sheath blight resistance in rice are depicted in Table 2.

Sheath blight breeding strategies

Hypothetically sheath blight resistance may have two main groups of mechanisms *viz*., disease escape and physiological resistance (Sattari *et al*., 2014). Disease escape is strongly determined by crop architecture. Morphological traits like plant height (Li *et al*., 1995; Peng *et al*., 2003 and Willocquet *et al*., 2010), heading date (Shiobara *et al*., 2013; Li *et al*., 1995 and Park *et al*., 2008) & stem thickness (Dey *et al*., 2016) positively correlated with sheath blight resistance. Sharma *et al* (2009) reported that the short stature at *sd-1* semi-dwarfing locus was strongly linked to higher sheath blight infection. Physiological resistance correlated with physiological process that is associated with a decrease in efficiency of one or several of the infection stages of the pathogen.

As we discussed earlier sheath blight resistance is governed by quantitative traits, development of sheath blight resistant rice varieties is very difficult through traditional breeding method. Pyramiding of QTLs through marker-assisted selection may results stable and potential cultivars. Chen *et al* (2014) improved *japonica* rice resistance to sheath blight by pyramiding $qSB\text{-}9^{TQ}$ and $qSB\text{-}7^{TQ}$ on chromosomes 9 and 7 respectively. Zuo *et al* (2014) reported that NILs carrying both $TAC1^{TQ}$ and $qSB\text{-}9^{TQ}$ showed more resistance than the NILs containing only one of them.

Further, there are evidences which show better disease management by pyramiding two or more disease resistance genes/QTLs. 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'.

Transgenic approach

Development of transgenic rice plants may provide a novel strategy to reduce yield losses caused by sheath blight disease. Plant pathogenesis-related (PR) genes like PR-3 chitinase (Datta *et al*., 2000) and PR-5(thaumatin-like protein) (Datta *et al*., 1999) provide resistance against sheath blight disease. Instead of single PR gene, combination of two PR genes shows more efficient for conferring a higher level of sheath blight resistance. Some example of PR combination are barley chitinase and barley b-1,3-glucanasegenes (Jach *et al*., 1995); maize ribosome inactivating gene MOD1 and rice basic chitinase gene RCH10 (Kim *et al*., 2003); CHI11and thaumatin-like protein (Kalpana *et al*., 2006); rice chitinase (CHI11) and tobacco b-1,3-glucanase(gluc) (Sridevi *et al*., 2008); rice chitinase gene (OsCHI11) and the Arabidopsis NPR1 (AtNPR1) gene (Karmakar *et al*., 2017). ASD16 has been reported as stable transgenic line against Sheath blight (Rajesh *et al*., 2016). Shah *et al* (2009) reported that transgenic rice expressing an endochitinase gene (cht42) from *Trichoderma virens* showed up to 62% reduction in the sheath blight disease index.

Durable and broad-spectrum resistance cultivars can be obtained by the pyramiding of transgenes. Datta *et al* (2002) utilized *Xa21* gene (resistance to bacterial blight), the *Bt* fusion gene (for insect resistance) and the chitinase gene (for tolerance of sheath blight) for gene pyramiding and identified stable elite rice lines resistant to disease and insect pests. Maruthasalam *et al* (2007) reported that a transgenic Pusa Basmati1 line pyramided with *chi11*, *tlp* and *Xa21* showed an enhanced resistance to both sheath blight and bacterial blight.

It is concluded that, rice sheath blight is second in importance next to rice blast in reducing both grain yield and quality. Germplasm with absolutely resistant to the pathogen have not been discovered till now. To reduce yield loss due to sheath blight, development of sheath blight resistant cultivars is important. However, only moderately resistant genotypes are reported.

These genotypes show variable disease reaction from one season to another season, which limit their use in breeding programme. Many QTLs for sheath blight resistance have been reported, but only few of them have been fine mapped. Validation of these QTLs is required before being used for marker-assisted breeding (MAB).

It has been observed in several cases, resistance to sheath blight is a cumulative effect of several minor QTLs. Earlier efforts were focused on improvement of sheath blight resistance in elite susceptible cultivars. Employing genotypes possessing moderate resistance to sheath blight governed by minor effect QTLs in breeding programmes will only result in distribution of such QTLs in the segregating populations. Further, this also poses difficulty in retrieving the same phenotype in mapping populations as that of resistant parent phenotype making it difficult to establish marker-trait associations. Hence, breeding strategies have to be modified in the development of sheath blight resistant cultivars. Here, we propose a two step breeding strategy to deal with difficult and complex traits like sheath blight.

Table.1 List of promising genotypes for sheath blight resistance

(Local accessions/varieties/ cultivars/land races)	**Reference**
NC 678, Dudsor, Bhasamanik	Das, 1970
Chin-kou-tsan, Zenith, CO.17, Dinominga, Puang Nahk 16, Baok, Toma-112, R.T.S.31, Kele Kala	Wu, 1971
Lalsatkara	Roy, 1977
ARC15762, ARC 18119, ARC 18275, ARC 18545	Bhaktavatsalam *et al.*, 1978.
IR24, IR26, IR29, Jaya, Jaganath, Mashoori, Pankaj, Rajeshwari, Supriya, Sabari, TKM6	Rajan and Nair, 1979
Nizersail, Rajasail, Tabend, Ta-poo-cho-z, Kattachambha, DA 29, ARC 5925, ARC 5943, ARC 14529, ARC 10572, ARC 10618, ARC10836	Manian and Rao, 1979
Tapoochoz, Bahagia, Laka	Crill *et al.*, 1982
Bharati, Rohini	Gokulapulan and Nair, 1983
Taraboli 1, Dholamula, Supkheru, Chidon	Borthakur and Addy,1988
BogII, Aduthurni, Chinese galendopuram, Arkavati, Saket-4, Neela, MTU-3, MTU-7, MTU-13, MTU-3642, BPT-6	Ansari *et al.*, 1989
Tetep, Tapoochoz, Guyanal	Sha and Zhu, 1990
LSBR-5, LSBR-33	Xie *et al.*, 1992
KK2, Dodan, IR40 and Camor	Singh and Dodan,1995
RU8703196, B82-761	Marchetti *et al.*, 1995 and Marchetti *et al.*, 1996
Chingdar, As 93-1, Panjasali, Up-52, Upland-2, Mairan, N-22 and 1/69-70	Singha and Borah, 2000
TIL 455, TIL 514, TIL 642	Pinson *et al.*, 2008
Jarjan, Nepal 555 and Nepal 8	Shiobara *et al.*, 2013
BPL 7-12, BML 27-1, BML 21-1 and Kajarahwa	Dubey *et al.*, 2014
Tetep and ARC10531	Yadav *et al.*, 2015
SM 801, 10–3, Ngnololasha, Wazuhophek, Gumdhan and Phougak and RP 2068-18-3-5	Dey *et al.*, 2016

Table.2 List of reported QTLs for sheath blight tolerance in rice

Table 2: List of reported QTLs for sheath blight tolerance in rice

Chr. no.	Locus	Marker interval or Nearest marker	Resistant parent	Susceptible parent	Mapping population	PV (%)	Reference
3	Qsbr3a	RG348–RG944	Teqing	Lemont	F_4 Bulk	27.7	Li *et al.*, 1995
9	Qsbr9a	RG910b–RZ777	Teqing	Lemont	F_4 Bulk	9.4	
2	qSB-2	G243-RM29 (RM29-RG171)	Jasmine 85	Lemont		14.4 (21.2)	Zou *et al.*, 2000
3	qSB-3	R250-C746	Jasmine 85	Lemont		26.5	
7	qSB-7	RG30-RG477	Jasmine 85	Lemont		22.2	
9	qSB-9-1	C397-G103	Jasmine 85	Lemont		9.8	
9	qSB-9-2	RG570-C356	Jasmine 85	Lemont		10.1	
11	qSB-11	G44–RG118	Jasmine 85	Lemont		20.5	
2	qSBR-2	RG171–G243A	Jingxi 17	Zhaiyeqing 8	DH	11.2	Kunihiro *et al.*, 2002
3	qSBR-3	G249-G164	Jingxi 17	Zhaiyeqing 8	DH	10.5	
7	qSBR-7	RG511-TCT122	Jingxi 17	Zhaiyeqing 8	DH	15.5	
11	qSBR-11	CT244-CT44	Jingxi 17	Zhaiyeqing 8	DH	9.5	
5	qSB-5	C624-C246 (C246-RM26)	Minghui 63	Zhenshan 97B	**RILs**	10.5 (9.5)	Han *et al.*, 2002
9	qSB-9	C472-R2638 (RM257- RM242)	Minghui 63	Zhenshan 97B	**RILs**	10.1 (6.9)	
5	Rsb1	RFLP+SSR	4011	XZX19	F_2	11.2	Che *et al.*, 2003
3	qSB-3	RM3856	WSS2	Hinohikari	BC_1F_1	19.4	Sato *et al.*, 2004
1	qSB-1	RG532x	Teqing	Lemont	RIL	8	Pinson *et al.*, 2005
2	qSB-2	C624x	Teqing	Lemont	RIL	7	
3	qSB-3-1	RG348x	Teqing	Lemont	RIL	18	
3	qSB-3-2	RZ474	Teqing	Lemont	RIL	10	
4	qSB-4-1	RG1094c	Teqing	Lemont	RIL	5.0	Pinson *et al.*, 2005
4	qSB-4-2	RZ590x	Teqing	Lemont	RIL	7.0	
5	qSB-5	Y1049	Teqing	Lemont	RIL	6.0	

6	qSB-6-1	C	Teqing	Lemont	RIL	5.0	
6	qSB-6-2	RZ508	Teqing	Lemont	RIL	7.0	
7	qSB-7	C285	Teqing	Lemont	RIL	5	
9	qSB-9	RZ404	Teqing	Lemont	RIL	6.0	
10	qSB-10	RG561	Teqing	Lemont	RIL	5.0	
12	qSB-12	G1106	Teqing	Lemont	RIL	9.0	
-	Rsb-2(t)	RM 218	A Mutant	Shuhui 881	-	-	Xiang *et al.*, 2007
9	$qSB\text{-}9^{Tq}$	Indel	Teqing	Lemont	BC_1F_1	-	Zuo *et al.*, 2008
9	qShB9-2	RM245	Jasmine 85	Lemont	RIL	24.3	Liu *et al.*, 2009
1	-	RM1339	Pecos	Rosemont	F_2	35	Sharma *et al.*, 2009
1	qSBR1-1	Hvssr68-RM306 (RM1232 -Hvssr68)	Tetep	HP2216	RIL	15.01 (8.13)	Channamallikarjuna *et al.*, 2010
3	qSBR3-1	RM251-RM338	Tetep	HP2216	RIL	9.96	
7	qSRB7-1	RM3691-RM336 (RM5481-RM3691)	Tetep	HP2216	RIL	10.02 (26.05)	Channamallikarjuna *et al.*, 2010
8	qSBR-8-1	RM210-Hvssr47	Tetep	HP2216	RIL	8.37	
	qSBR9-1	Hvssr9-27-RM257	Tetep	HP2216	RIL	9.19	
11	qSBR11-1	Sbq1–RM224 (Sbq11–RM224)	Tetep	HP2216	RIL	13.99 (11.99)	
11	qSBR11-2	RM3428–RM209	Tetep	HP2216	RIL	7.81	
11	qSBR11-3	RM536–RM20	Tetep	HP2216	RIL	21.59	
9	qShB9-2	RM 245	Jasmine 85	Lemont	RIL	27.2	Liu *et al.*, 2013
9	qSBR-9	Nag08KK18184-Nag08KK18871	Jarjan	Koshihikari	BC_2F_3	-	Shiobara *et al.*, 2013
1	$qSB1\text{-}1^{HJX74}$	ZY7.7-1-5	Amol3(sona)	HuaJingXian74	chromosome segment substitution lines	-	Zhu *et al.*, 2014
11	$qSB11^{HJX74}$	ZY27.92-11	Amol3(sona)	HuaJingXian74		-	
7	qshb7.3	RM 205	ARC10531	BPT-5204	BC_1F_2	21.76	Yadav *et al.*, 2015
9	qshb9.2	RM 336	ARC10531	BPT-5204	BC_1F_2	19.81	

Fig.1 Symptom of Rice Sheath blight

Firstly, genotypes with moderate resistance from the identified pool should be intermated for possible accumulation of several minor effect QTLs that would be evident from enhanced phenotypic effect in populations. Secondly, breeding line with increased resistance to sheath blight than either of it parents should be crossed to an elite susceptible cultivar. Further intermating in segregating populations would ensure retention of accumulated minor effect QTLs in elite background. Modified breeding strategy proposed here coupled with application of advanced genomic tools would widen the scope of development of high yielding elite cultivars with resistance to sheath blight.

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