

Inheritance of sheath blight disease resistance in submergence rice (*Oryza sativa* L.)

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Abstract

Sheath blight caused by *Rhizoctonia solani* Kuhn is one of the important diseases of rice, resulting in heavy yield loss in rice every year. Genetic nature of sheath blight has been found to be complex and controversial issue in the earlier studies. There were some reports about the major gene conferring resistance to sheath blight. Non allelic dominant major resistance gene was also reported in resistant cultivars. A total of 50 QTL associated with sheath blight resistance located on all 12 rice chromosomes have been reported, with 10 of these co-localizing with QTL for morphological attributes, especially plant height, or for heading date. The objective of this paper was to see inheritance pattern of sheath blight. All the plant in the F₁ shown resistant reaction with 22.25% disease severity, and in F₂ population the resistant or moderately resistant, and susceptible in the ratio of 3R / MR: 1S which is mainly due to presence of dominant effects of resistant QTL/genes *qSBR11-1*. The F₃ populations were classified into resistant, moderately resistant and susceptible in the ratio of 3:2:3. Further, the F₃ populations were classified in only two groups as resistant and susceptible then their ratio was 5Resistance/Moderately Resistance: 3Susceptible.

Highlights

- All the plant in the F₁ shown resistant reaction with 22.25% disease severity, and in F₂ population the resistant or moderately resistant, and susceptible in the ratio of 3R / MR : 1S.
- The backcross progenies (BC₂F₁) were found similar pattern of tolerant sheath blight as of tolerant parent Tetep.
- The chi-square value of F₂, F₃ and BC₂F₁ showed the non-significant at 5 per cent level of significance indicating that observed data are in accordance with expected ratio and follow mendelian pattern of inheritance to Sheath Blight

Keywords: Rice, sheath blight, genetic nature, per cent disease severity, QTLs

Rice is a basic food for millions of people and having considerable importance in food and nutritional security. It is the second most widely consumed food grain in the world next to wheat. In India, Rice is India's pre-eminent crop, and is the vital food for people in the eastern and southern parts of the country. India is the second largest producer of rice,

after China, accounting for twenty percent of world rice production. About 32.4% per cent of india's total rice area is under rainfed lowland condition, which are highly fraile ecosystem, always prone to flash floods (Singh *et al.* 2015). The variety with Sub1 gene showed yield advantage of 1 to 1.3 t/ha over the original varieties following the submergence



for up to 18 days (Mackill *et al.* 2012; Neeraja *et al.* 2007; Septiningsih *et al.* 2009; Singh *et al.* 2009; Singh *et al.* 2013). Sheath blight caused by *Rhizoctoniasolani* Kühn is one of the most important diseases of rice, causing in heavy yield loss in rice every year. None of the rice genotypes resistant to sheath blight has been identified till date. Nevertheless, in some rice genotypes a high degree of resistance to *R. solani* has been reported. An indica rice genotype, Tetep, is a well documented source of durable and broad spectrum resistance to rice blast as well as quantitative resistance to sheath blight (Channamallikarjuna *et al.* 2010).

Genetic nature of sheath blight has been found to be complex and contentious issue in the earlier studies. There were some reports about the major gene conferring resistance to sheath blight. Non allelic dominant major resistance gene was also reported in resistant cultivars, Jasmine and Teqing (Pan *et al.* 1999). On the contrary, genetics studies on the quantitative resistance to *R. solani* in rice have shown both multiple gene and major gene inheritance (Sha and Zhu 1989; Li *et al.* 1995; Zou *et al.* 2000). Because of the complexity of the resistance response and lack of detailed knowledge about the loci involved, breeding efforts to increase the resistance to *R. solani* have been largely unsuccessful (Li *et al.* 1995). The disease index of the populations was continuously distributed, hence controlled by quantitative trait loci. Several quantitative trait loci (QTL) for sheath blight resistance have been identified using mapping populations derived from *indica* or *japonica* rice. A total of 50 QTL associated with sheath blight resistance located on all 12 rice chromosomes have been reported, with 10 of these co-localizing with QTL for morphological attributes, especially plant height, or for heading date. Sixteen QTL, from the same or differing genetic backgrounds, have been mapped at least twice. Out of these, nine QTL were independent of morphological traits and heading

date. Therefore, the present study was undertaken to know the inheritance of sheath blight resistance in cross Swarna sub-1 × Tetep against *Rhizoctonia solani* khun.

Materials and Methods

Plant material and Experimental Design

Experimental materials comprise of two rice genotypes including one submergence tolerance cultivar Swarna sub-1 and one sheath blight resistant genotype Tetep (Table 1). Five generations viz; P₁, P₂, F₁, F₂ and F₃ from the cross (Swarna sub-1 × Tetep) were evaluated in this study. The F₁s were made at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi (UP) during Kharif, 2011. The subsequent generation - F₂ required for the study was developed in off season 2012 at NRRI, Cuttack, Odisha. The five generations P₁, P₂, F₁, F₂ and F₃ were evaluated in the main Kharif season, 2013 at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. The experiment was laid in a randomized complete block design with three replications. The parental lines and F₁s; F₂s and F₃s were planted in 1, 2 and 3 rows each of 5 m long at spacing of 30×15 cm, respectively. Data were recorded on 10 plants in case of parents and F₁s, 30 plants of F₂s and 75 plants in F₃s per replication.

Pathogenicity test and Observations Recorded

Disease screening was done by artificial disease inoculation of *Rhizoctoniasolani* (R.nagar strain) in the third leaf sheath from the top of the plant. Appearance of symptom was recorded 2 days after inoculation (DAI) and symptom lesion length and width were taken at 4th, 8th, 12th and 16th DAI intervals. The phenotypic traits were assessed on

Table 1: Parental description of *indica* rice cultivar, its duration and specific features

Genotype	Special features	Quality parameter	Duration (Days)	Recommendation for cultivation
Swarna Sub-1	Tolerance to Submergence	Amylase = 27%	140 - 145	Flash flood prone areas
Tetep	Tolerance to Sheath blight disease	Amylase = 32%	100 -105	Source of sheath blight resistance

randomly selected plants from each individual entry in the segregating generations for eleven quantitative traits *viz.*, number of productive tillers per plant (PTP), plant height (PH), days to 50 per cent flowering (DF), days to maturity (DM), length of panicle (LP), weight of panicle (WP), spikelet per panicle (SSP), test weight (TW), grain yield per plant (YPP), amylose content and gel consistency.

Statistical analysis

The mean value of each character was determined by summing up all the observations and dividing them by corresponding number of observations.

$$\bar{X} = \frac{\sum_{i=1}^N X_i}{N}$$

Where, numerator shows sum of all observations for the character and N = Number of observations.

The frequency of resistance and susceptible plants in segregating population for sheathblight resistance was grouped based on severity of the diseases. The frequencies were tested using χ^2 test with expected frequencies of resistant and susceptible plants. The formula for calculation of χ^2 test values is as follow:

$$\chi^2 = \sum (O - E)^2 / E$$

Where,

χ^2 = Chi square value

O = Observed frequency

E = Expected frequency

The value of χ^2 was taken at 5% and / or 1% level of significance for (n-1) degree of freedom (if n number of classes). The non-significant χ^2 value is the indication of goodness of fit of the observed

frequencies into expected frequencies. Now, as per goodness of fit to expected frequencies the number of genes could be estimated governing the resistance.

Results and Discussion

Phenotypic screening for Sheath Blight Resistance

In the present study the susceptible cultivar (Swarna sub-1) crossed with resistant cultivar (Tetep) and segregating pattern was studied in F_2 and F_3 population, by simultaneously inoculating parents, F_1 , F_2 , and F_3 plants. Reaction pattern was compared to that on differentials and isogenic lines. (Table 2). The average disease severity of resistant parent (Tetep) was 20.1% whereas susceptible parent Swarna sub-1 showed 64.07% disease severity due to absence of resistance QTL/genes under epiphytotic condition (Table 3). The area under the disease progress curve of resistance parent was 129.00 which are significantly less than the susceptible parent 415.86. Similarly, Singh *et al.* (2015) observed while analyzing lines for sheath blight resistance using highly virulent isolate Rs-K under field conditions, Tetep showed resistance with a score of 1 and the recurrent parent Pusa6B showed susceptible reaction with score of 7. Among the improved lines, only six lines showed resistance score of 1. The remaining three lines showed moderate resistance with a score of 3. The results showed that all the plant in the F_1 (96.50%) shown resistant reaction with 22.25% disease severity and AUDPC129.00. This indicates the possible involvement of dominance QTL/gene(s) in governing the resistance. The 200 F_2 plants derived from the cross Swarna sub-1 \times Tetep were individually scored and classified into three

Table 2: Scale for rice sheath blight diseases

Infection (%)	Score	Host response
No infection observed	0	Highly resistance (HR)
Lesions limited to below 20% of the plant height	1	Resistant (R)
21 – 30%	3	Moderately resistant (MR)
31 – 45%	5	Moderately susceptible (MS)
46 – 65%	7	Susceptible (S)
More than 65%	9	Highly susceptible (HS)

Table 3: Genetics of Sheath Blight disease resistance in the cross Swarna Sub-1 × Tetep.

Genotypes	% Disease incidence			AUDPC	Disease Score at 16 DAI	Host response at 16 DAI	Total no. of plants observed	Observed frequencies	Expected frequencies	Phenotypic ratio	χ^2
	4 DAI±SE	8 DAI±SE	12 DAI±SE								
Swarna Sub-1	8.80±0.75	26.35±1.26	41.18±2.93	64.07±1.67	415.86	S	200	200	200	-	-
Tetep	4.27±0.71	8.24±0.80	11.87±0.83	20.01±1.98	129.00	R	200	200	200	-	-
F _{1s}	5.17±0.73	10.95±1.20	14.41±1.00	22.25±0.92	156.28	R	200	193MR:7S	200	-	-
F _{2s}	5.23±0.39	11.46±0.38	16.84±1.26	24.36±2.71	172.38	R	200	42	50	3 R/MR	3.04
	6.89±0.57	16.44±1.14	27.96±1.87	37.31±2.59	266.00	MR	200	112	100	1 S	
	8.19±0.40	25.76±1.10	42.82±1.32	61.01±1.85	412.72	S		46	50		
	3.01±0.26	13.43±0.53	18.78±1.50	22.94±2.85	172.74	R		77	75		
F _{3s}	6.01±0.26	17.43±0.67	29.63±3.05	39.61±2.31	279.48	MR	200	57	50	5 R/MR	2.11
	8.41±0.26	23.64±0.67	44.62±3.05	58.43±2.31	406.60	S		66	75	3 S	

distinct classes as resistant, moderately resistant and susceptible. The average disease severity and AUDPC in resistant, moderately resistant, and susceptible plants of F_2 were 24.36% and 172.38, 37.31% and 266.00, 61.01% and 412.72. All the plants of F_3 populations obtained from the selfing of F_2 were also screened against *Rhizoctoniasolanis* strain *R.nagarwild* type, plants were individually scored and classified as resistant, moderately resistant, and susceptible. The average disease severity and AUDPC in resistant, moderately resistant, and susceptible plants of F_3 were 22.94% and 172.74, 39.61% and 279.48, 58.43% and 406.60, respectively.

Genetics for sheath blight Resistance

The 154 plants were resistant (resistant/ moderately resistant) and 46 susceptible in the ratio of 3R / MR: 1S which is mainly due to presence of dominant effects of major resistant QTL/genes *qSBR11-1*. The chi square value for F_2 generation was 3.04, which is non-significant at 5% level of significance indicating that observed data are in accordance with expected ratio but modification in the Mendelian ratio of inheritance in the F_2 populations showed masking gene action. Wang *et al.* (2012) studied the inheritance of sheath blight resistance in cross TeQing × Lemont using TIL:567 (TeQing into Lemont backcross introgression line) and reported digenic inheritance of resistance with one dominant gene and one recessive gene. They also suggested that chi-square analysis that the Resistant: Susceptible segregation ratios fitted a one-gene 3:1 model for TeQing into Lemont backcross introgression line (TIL: 567 population) and explained that *qSB9-2* and *qSB12-1* both act as dominant resistance genes. These findings were in agreement with earlier report by Xie *et al.*, (1990) Pan *et al.* (1999) Chen *et al.* (2002). Non allelic dominant major resistance gene was also reported in resistant cultivars, Jasmine and Teqing (Pan *et al.* 1999). Marshal and Rush, (1980) reported that evaluation of F_2 populations from crosses of the moderately resistance and susceptible cultivars suggests resistance may be dominance over susceptibility with 3:1 ratio. Pan *et al.* (1999) reported that the resistance cultivars, Jasmine 85, Teqing, each passes a non-allelic dominant major resistance genes. Wasanto (1988) reported that the resistance in Tetep was controlled by one or 2 dominant genes. However, the chromosomal location and tightly linked markers of the resistance genes have

yet to be identified. They also developed a short-culmnelite line, 2F15-92-9-22-20-11-19 (WSS2), from the progeny of Tetep. Although the tendency toward lodging in Tetep had been improved in WSS2, the other agronomic characteristic, especially fertility and yield, still remain extremely poor. Hashioka (1951ab) was the first researcher who reported that resistance to sheath blight was controlled by one or two single dominant genes. The research of Masajo (1976) and Goita (1985) suggested that there were two pairs of complementary genes with a high level of dominance controlling resistance. Jentong (1985) reported that the resistance in the source rice was controlled by the three pairs of dominant genes.

Out of 200 plants, the F_3 populations showed 77 resistant, 57 moderately resistant, and 66 susceptible plants in the ratio of 3 : 2 : 3. Similarly, Wang *et al.* (2012) studied mode of inheritance of resistance to *Rhizoctoniasolani Kuhn* wild type in the cross Teqing × Lemont and reported that F_3 populations were classified into three distinct classes in the ratio of 3:2:3. Further, the F_3 populations were classified in only two groups as resistant and susceptible then their ratio was 5R/MR:3S. These findings are in agreement with earlier report by Liu *et al.* (2009), they classified the F_3 populations in the ration of 5:3. The chi square value for F_3 populations were 2.11 which was non-significant at 5% level of significance indicating that observed data are in accordance with expected ratio and follow Mendelian pattern of inheritance to sheath blight resistance. Results of present study support by the earlier findings of Wang *et al.* (2012) that chi-square values for F_3 populations were 1.24 in the cross Teqing × Lemont which was non-significant at 5% level of significance. Interestingly, when we compared the level of sheath blight resistance of segregating population (resistant plants) with that Tetep, it was observed that resistant plants showed almost similar level of resistance as Tetep.

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