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Short Communication

Phenotyping of improved rice lines and landraces for blast and sheath blight resistance

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Abstract

Globally, two major fungal diseases of rice, *viz.*, blast caused by *Magnaporthe oryzae* and sheath blight incited by *Rhizoctonia solani* Kuhn. occur in all agro-ecosystems resulting in significant yield losses. In the present study, a set of 100 rice lines were evaluated for blast and sheath blight resistance. Twenty seven genotypes were identified to be resistant against *M. oryzae* isolate (Mo-ni-0066). However, evaluation of these genotypes with highly virulent *M. oryzae* Karnataka isolate (Mo-si-mnd) revealed that only two genotypes *viz.,* Bhusan San and P1490-03 were resistant. Same set of genotypes were screened for sheath blight resistance. Four entries, *viz.*, BPL7-12, BML27-1, BML 21-1 and Kajarahwa possess high degree of tolerance to sheath blight but none of the rice entries was completely resistant.

Key words : Rice, *Magnaporthe oryzae*, *Rhizoctonia solani*, relative lesion height, virulence, resistance

Rice is one of the most important food crops in the world. Ninety per cent rice is being produced in Asian countries with China and India being the major producers. Rice cultivation is often subjected to several biotic stresses. Rice blast (*Magnaporthe oryzae*) and sheath blight (*Rhizoctonia solani*) are two major fungal diseases of rice which cause significant losses in rice production.

Blast is common in irrigated, rainfed uplands and lowlands in which rice is grown resulting 11 to 30% crop losses annually. Sheath blight is another important disease of rice resulting in losses up to 54.3% in Indian conditions [1]. Though resistant varieties use is most economical and environmentally safe to develop resistant cultivars but, it could not be easy due to lack of suitable donors. No rice germplasm in the world has been found to be completely resistant to sheath blight fungus because of the polyphagous nature of the pathogen [2].

In the present study, a set of 100 rice genotypes including a susceptible check (Pusa Basmati-1) and a resistant check (Tetep) were used for phenotyping against blast and sheath blight diseases. Two isolates of *M. oryzae* (Mo-ni-0066 from Uttar Pradesh and Mo-si-mnd from Karnataka) available in the Division of Plant Pathology, IARI, New Delhi were used for phenotyping of rice genotypes under controlled conditions. Virulence pattern of these isolates on major blast resistance genes are mentioned in Table 1. Inoculum was prepared following the standard procedures established by Bonman *et al.* [3]. Inoculated plants were kept in a humid chamber (>95 per cent relative humidity) maintained at 25 ± 1^{o}C temperature in dark for 24 h and then with proper illumination for rest of the period. After seven days of inoculation, disease reaction of the inoculated plants was scored using 0-5 scale [4].

A total of twenty seven genotypes were

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considered as resistant against, whereas, rest of the genotypes were categorized as susceptible against *M. oryzae* Meerut isolate (Mo-ni-0066) (Data not shown). These 27 rice genotypes were further evaluated for blast resistance with highly virulent *M. oryzae* Karnataka isolate (Mo-si-mnd). The results showed that only two entries, *viz.,* P1490-3 and Bhusan San exhibited high degree of blast resistance and rest of the genotypes were susceptible including the resistant check Tetep which is known to contain major *R*-genes like *Pi1, Pita* and *Pi54*.

With regards to sheath blight phenotyping, twenty-five-days-old seedlings of 100 rice genotypes were transplanted with a spacing of 20×15 cm in a randomized complete block design (RCBD) with three replications during *kharif* 2012-2013 at the research farm of the Division of Genetics, IARI, New Delhi.

Highly virulent isolate of *R. solani* from Kapurthala (ITCC No-7479) available in the Division of Plant Pathology, IARI, New Delhi was used for phenotyping. The isolate was mass multiplied on water sedge (*Typha angustata*) by the procedure described by Bhaktavatsalam *et al.* [5]. The plants were inoculated at maximum tillering stage (45 days after transplanting) with the Kapurthala isolate by placing the mass multiplied typha stem pieces with the fungal mycelia in between tillers of each rice hills, just above the water level and tied for better contact with the sheath region. The water level (5-10cm) was maintained constantly for ensuring enough humidity to promote disease development. The lesion length and plant height were recorded ten days and twenty five days after inoculation (DAI). The relative lesion height (RLH) was calculated using the formula given by Sharma *et al.* [6] *i.e.,* RLH (%) = Lesion length (cm)/plant height (cm) x 100. The lesion length of inoculated entries was subjected to analysis of variance (ANOVA) using OPSTAT software. Since the calculated critical difference value for lesion length was found to be 3.203 for 10 DAI and 5.362 for 25 DAI was less than the mean value for lesion length of 100 rice genotypes, 15 for 10 DAI and 28.61 for 25 DAI, hence it could be concluded that there was a significant difference among the treatments. Based on the 0-9 scale of Ahn *et al.* [7], the genotypes were categorized into different grades from highly resistant to highly susceptible. RLH was recorded as 6.5 per cent in Tetep as compared to 51.1 per cent in PB-1. Out of one hundred rice genotypes, 27 lines were sheath blight resistant under field conditions. The genotypes showing resistant reactions were further evaluated under controlled conditions by providing the optimum growth conditions for the sheath blight pathogen (more than 90 per cent

Table 1. Virulence pattern of Meerut *M. oryzae* isolate (Mo-ni- 0066) and Karnataka *M. oryzae* isolate (Mo-si-mnd)

Monogenic lines	*R*-gene	*M. oryzae* isolates	
		Mo-ni-0066	Mo-si-mnd
IRBL1-CL	*Pi 1*	*vir*	*vir*
IRBLB-B	*Pi b*	*vir*	*vir*
IRBL9-W	*Pi 9*	*avr*	*vir*
IRBLZ5-CA	*Pi z5*	*vir*	*vir*
IRBLta-K1	*Pita*	*vir*	*vir*
-	*Pi 54*	*avr*	*vir*
CO39	-	*vir*	*vir*
TETEP	*Pi 1, Pikh, Pita*	*avr*	*vir*

vir- virulent, *avr*- avirulent

Table 2. Comparative study of phenotypic observation of resistant lines under field and artificial conditions

S.No.	Resistant lines	Field conditions			Artificial conditions		
		RLH (%) on 25 DAI	Disease reaction	Horizontal spread (%)	RLH (%) on 25 DAI	Disease reaction	Horizontal spread (%)
1	BPL7-12	10.2	R	39.5	16.9	R	44.4
2	BML27-1	9.6	R	46.8	18.1	R	61.1
3	BML 21-1	4.5	R	40.0	16.4	R	48.3
4	Kajarahwa	4.9	R	34.8	15.7	R	40.2
5	PB-1	46.2	S	100.0	51.1	S	100
6	Tetep	6.4	R	21.1	6.5	R	25.0

RLH-Relative Lesion Height; DAI-Days After Inoculation; R- Resistant; S-Susceptible

relative humidity and 28±2^{o}C temperature) and the observations were subjected to statistical analysis. Since the calculated critical difference value for lesion length was found to be 1.812 for 10 DAI and 3.576 for 25 DAI was less than the mean value for lesion length of 100 rice genotypes, 13.89 for 10 DAI and 30.89 for 25 DAI, hence it could be concluded that there was a significant difference among the treatments. Out of 27 rice genotypes only four *viz.,* BPL7-12, BML27-1, BML 21-1 and Kajarahwa were observed to be highly tolerant to sheath blight (Table 2). Further, molecular validation of these four resistant lines with the flanking simple sequence repeats (SSR) markers revealed the presence of major sheath blight QTL, *qSBR11-1* (Data not shown).

Since rice lines *viz.*, BPL7-12 and BML27-1 have shown resistance to both major fungal diseases, these can be used in breeding programme for developing improved rice cultivars with combined resistance to blast and sheath blight. Horizontal spread is calculated by using following formula, Horizontal spread = Total number of infected tillers/Total number of tillers x 100. The horizontal spread was recorded as 25 per cent in the resistant genotype Tetep as compared to 100 per cent in susceptible rice variety PB-1. Significant difference in resistance level to sheath blight was observed in various genotypes (data not shown).

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References

1. **Chahal S. S.** 2005. Disease scenario in rice during post revolution era in Punjab. Plant Dis. Res., **20**: 1-11.
2. **Sha X. Y. and Zhu L. H.** 1989. Resistance of some rice varieties to sheath blight (ShB). Intern. Rice Res. Newsletter, **15**: 7-8.
3. **Bonman J. M., Vergel de Dios T. I. and Khin M. M.** 1986. Physiologic specialization of *Pyricularia oryzae* in the Philippines. Plant Dis., **70**: 767-769.
4. **Mackill D. J., and Bonmman J. M.** 1992. Inheritance of blast resistance in near isogenic lines of rice. Phytopathol., **82:** 746-749.
5. **Bhaktavatsalam G., Satyanarayana K., Reddy A. P. K. and John V. T.** 1978. Evaluation of sheath blight resistance in rice. Intern. Rice Res. Newsletter, **3**: 9-10.
6. **Sharma N. R., Teng P. S. and Olivares P. M.** 1990a. Comparison of assessment methods for rice sheath blight disease. Philippines Phytopathol., **26**: 20-24.
7. **Ahn S. W., Denadela R. C., Candole B. L. and Mew T. W.** 1986. A new scale for rice sheath blight disease assessment. Intern. Rice Res. Newsletter, **11**: 17.